Supplementary Table 1. Differentially methylated CpG sites between normal ovaries and PCOS ovaries

Index	TargetID	ProbeID_A	ProbeID_B	Control.AV	Control.Dif	Control.Del	PCOS.AV	PCOS.Diff
98	cg0000407	38766357	38766357	0.4877385	0	1	0.6701809	54.39702
159	cg0000681	18804378	18804378	0.3903461	0	1	0.2755172	-25.25451
224	cg0000930	74728390	74728390	0.3015871	0	1	0.4091758	21.95797
231	cg0000952	42761437	42761437	0.5701457	0	1	0.0714224	-371.3336
329	cg0001365	44675355	31736405	0.2812709	0	1	0.4013246	26.90836
415	cg0001715	53626407	53626407	0.6147654	0	1	0.469742	-34.69786
560	cg0002299	43668467	31767442	0.3937696	0	1	0.2653006	-30.7724
562	cg0002302	37787505	37787505	0.232677	0	1	0.4068173	54.01976
599	cg0002451	15677432	15677432	0.2896788	0	1	0.4033222	24.34162
668	cg0002715	36681337	36681337	0.8852143	0	1	0.7519315	-59.68505
695	cg0002829	38749489	38749489	0.3398032	0	1	0.4454381	20.50223
696	cg0002830	58620505	58620505	0.2323112	0	1	0.1259464	-33.1063
824	cg0003320	35667425	35667425	0.654247	0	1	0.4958171	-41.77448
825	cg0003321	73611364	73611364	0.0963077	0	1	0.2558973	69.0565
831	cg0003349	67770302	67770302	0.5435941	0	1	0.7134237	50.91593
882	cg0003544	51625403	51625403	0.6984555	0	1	0.5373095	-45.47
903	cg0003613	62807489	62807489	0.6000488	0	1	0.700279	21.05247
946	cg0003802	71732358	71732358	0.5287921	0	1	0.6662758	33.27204
976	cg0003948	26722425	26722425	0.1949387	0	1	0.3052893	27.94724
993	cg0004010	63772389	63772389	0.8424819	0	1	0.7041904	-51.85731
1008	cg0004053	34668426	34668426	0.6787458	0	1	0.9038784	138.4738
1113	cg0004507	61760432	61760432	0.6724313	0	1	0.7748435	25.88484
1166	cg0004769	54689478	54689478	0.2974049	0	1	0.4016206	20.98347
1235	cg0005115	70761365	70761365	0.7306336	0	1	0.3669483	-220.0996
1344	cg0005643	13810448	13810448	0.5771261	0	1	0.4552421	-25.3231
1380	cg0005800	47670413	34681339	0.6615468	0	1	0.5506545	-23.26248
1460	cg00061551	72748427	72748427	0.6708563	0	1	0.8283972	60.10462
1517	cg0006398	53716300	53716300	0.6853769	0	1	0.8041213	35.63484
1556	cg0006623	46751326	46751326	0.2044397	0	1	0.3116123	26.06163
1642	cg00069771	30764342	30764342	0.9147561	0	1	0.6208712	-213.0645
1933	cg0008379	46801467	13659322	0.2334792	0	1	0.3459002	26.30115
1944	cg00084271	36640339	36640339	0.6616695	0	1	0.7781184	31.87796
2173	cg0009347	16757450	14611473	0.5856227	0	1	0.466532	-24.44925
2228	cg0009525	60656333	60656333	0.3817442	0	1	0.517468	30.37065
2312	cg0009818	47651469	50685321	0.4850096	0	1	0.8497164	374.3439
2371	cg0010115	30746351	30746351	0.2640281	0	1	0.3892573	29.57645
2372	cg0010122	59747444	59747444	0.5819107	0	1	0.6917845	23.97051
2380	cg0010160	33735361	33735361	0.2292879	0	1	0.3313853	22.81434
2470	cg0010656	74721382	74721382	0.6489338	0	1	0.7792793	38.17567
2530	cg0010894	24657395	24657395	0.2200168	0	1	0.1174222	-32.48067
2741	cg0011878	71730440	30680362	0.1737434	0	1	0.2995465	36.38452

2767	cg00119778	65649460	65649460	0.1914038	0	1	0.3250918	38.1762
2807	cg00121626	19779393	19779393	0.0492732	0	1	0.1891522	71.8237
2811	cg00121876	11641490	11641490	0.5379918	0	1	0.6982139	45.01088
2825	cg00122779	50730351	50730351	0.6064615	0	1	0.8073435	82.9363
2842	cg00123214	16683390	16683390	0.6684531	0	1	0.7865573	33.41087
2870	cg00124902	66794348	66794348	0.5088089	0	1	0.3622006	-34.95581
2873	cg00124993	26637438	24755330	0.5281388	0	1	0.4094916	-24.03202
2889	cg00125893	31787444	31787444	0.7427309	0	1	0.6356573	-25.48688
2948	cg00128718	64701377	64701377	0.8697295	0	1	0.6599032	-108.8322
3090	cg00136547	12733385	12733385	0.1711139	0	1	0.3477179	63.16172
3277	cg00146240	44697466	44697466	0.7899763	0	1	0.4230724	-237.9115
3348	cg00149537	28618375	52810459	0.6130087	0	1	0.7180613	23.43864
3466	cg00154902	59771461	71747396	0.6442125	0	1	0.7989946	53.121
3510	cg00156497	74780459	74780459	0.9142308	0	1	0.7955391	-59.92753
3525	cg00157016	54695379	54695379	0.3825853	0	1	0.5304716	35.2604
3530	cg00157199	67794389	67704375	0.4445814	0	1	0.6982733	102.7366
3682	cg00163702	59703408	59703408	0.2837618	0	1	0.4388668	41.08584
3739	cg00166722	55760432	14676335	0.767555	0	1	0.6264921	-41.94953
3748	cg00167248	69734324	69734324	0.7318605	0	1	0.5775554	-44.79804
3756	cg00167670	47678333	47678333	0.5687125	0	1	0.6990626	31.95439
3764	cg00167913	34621465	34621465	0.6590453	0	1	0.800259	46.11084
3835	cg00171092	47771303	47771303	0.2128353	0	1	0.3149059	23.67109
3871	cg00172603	50632452	73639386	0.3547425	0	1	0.2439154	-25.1876
4081	cg00182893	64744407	64744407	0.7273014	0	1	0.8796801	70.548
4160	cg00187244	54743510	54743510	0.3251532	0	1	0.0850805	-134.3289
4251	cg00192882	58670408	58670408	0.1446309	0	1	0.2477272	29.41486
4434	cg00204802	64623441	47756405	0.4341714	0	1	0.6211633	54.7084
4467	cg00206507	70732476	70732476	0.5442189	0	1	0.6689163	28.40732
4516	cg00209612	27678431	27678431	0.6774021	0	1	0.8240893	52.9756
4543	cg00210856	12772328	12772328	0.5153254	0	1	0.6204551	20.42368
4550	cg00211215	12790319	39622342	0.6676571	0	1	0.3398855	-169.9291
4566	cg00212031	29674443	38703326	0.1133291	0	1	0.3524014	121.9356
4601	cg00213805	71737411	71737411	0.4638245	0	1	0.3373573	-27.57928
4693	cg00218628	60625336	60625336	0.4282582	0	1	0.6003063	46.57256
4753	cg00221185	54678344	24788422	0.2144859	0	1	0.337492	31.61109
4776	cg00222015	17719383	17719383	0.6054494	0	1	0.4968444	-21.26645
4797	cg00223245	50693357	50693357	0.4734471	0	1	0.6036795	28.67913
4919	cg00230120	14662484	19720437	0.7819089	0	1	0.8837823	40.13985
4957	cg00231519	19627374	19627374	0.4116288	0	1	0.7533038	374.3439
4980	cg00232388	35709315	35709315	0.6401244	0	1	0.9173192	374.3439
5022	cg00234370	48684425	48684425	0.1582235	0	1	0.2792385	35.90932
5050	cg00235754	28719502	28719502	0.724811	0	1	0.8266135	30.59868
5141	cg00239742	51742392	51742392	0.6707383	0	1	0.7900235	34.29369

5168	cg0024100	54771452	57737407	0.2905654	0	1	0.4230091	31.22339
5186	cg0024190	43619318	10732399	0.4018812	0	1	0.2754538	-29.51978
5252	cg0024492	47710335	47710335	0.6551744	0	1	0.4654171	-57.52374
5296	cg0024709	22631327	22631327	0.4299978	0	1	0.6470946	73.29041
5332	cg0024886	64710346	64710346	0.357409	0	1	0.6233817	108.2252
5435	cg0025373	60729344	60729344	0.4596887	0	1	0.2940491	-45.48247
5443	cg0025409	69780487	69780487	0.5708256	0	1	0.7835477	85.92299
5446	cg0025430	54748461	17645336	0.4332845	0	1	0.3230464	-22.29561
5482	cg0025588	63789443	63789443	0.3060787	0	1	0.1953582	-28.06241
5486	cg0025604	73700305	73700305	0.6378322	0	1	0.7757366	41.34131
5497	cg0025632	34663423	34663423	0.6128048	0	1	0.7193904	24.04136
5572	cg0025984	15806472	15806472	0.6960363	0	1	0.9377137	374.3439
5770	cg0026972	67766493	67766493	0.6012082	0	1	0.840215	121.0875
5771	cg0026980	61752345	61752345	0.3269524	0	1	0.2234852	-23.58945
5802	cg0027187	11808416	11808416	0.0068376	0	1	0.2126269	153.5253
5810	cg0027279	74632377	74632377	0.5579413	0	1	0.6697971	23.85066
5811	cg0027290	41724510	41724510	0.5025862	0	1	0.6065403	19.83427
5840	cg0027464	47758438	47758438	0.6215541	0	1	0.4705952	-37.36186
5858	cg0027582	19804392	19804392	0.7183216	0	1	0.8323202	37.13152
5914	cg0027975	13644355	13644355		0	1		-4.34E-09
5952	cg0028183	56772418	56772418	0.6166537	0	1	0.4934157	-26.38166
6017	cg0028610	10622467	10622467	0.7655643	0	1	0.8761911	43.42421
6059	cg0028784	34718404	34718404	0.7733057	0	1	0.5908943	-64.77754
6070	cg0028859	34722501	44649372	0.3508348	0	1	0.5102373	40.70222
6110	cg0029060	64718396	62628499	0.5104077	0	1	0.245746	-112.7841
6157	cg0029266	13644450	13644450		0	1	0.1353777	4.34E-09
6201	cg0029455	52807349	52807349	0.3588103	0	1	0.4835544	26.57167
6225	cg0029541	41681387	41681387	0.5740335	0	1	0.7436702	53.73215
6260	cg0029690	27749328	27749328	0.6293271	0	1	0.7333634	23.84962
6278	cg0029787	24757500	24757500	0.4720151	0	1	0.2497136	-80.97279
6381	cg0030276	60641446	60641446	0.4486659	0	1	0.5543896	19.87812
6418	cg0030452	27747375	37645353	0.0170795	0	1	0.1268006	64.10091
6572	cg0031188	43616362	62666317	0.1853134	0	1	0.3118581	35.55143
6605	cg0031400	54769436	54769436	0.6604575	0	1	0.7701944	28.41892
6684	cg0031816	30729329	30729329	0.8876944	0	1	0.775729	-47.02844
6699	cg0031863	64702450	64702450	0.6962287	0	1	0.5672875	-31.24535
6757	cg0032100	34743356	34743356	0.2244426	0	1	0.3250996	22.55418
6777	cg0032170	29758495	29758495	0.3482544	0	1	0.5029081	38.6384
6844	cg0032497	11750373	59799481	0.7907788	0	1	0.6015454	-71.90366
6846	cg0032512	73798400	39785417	0.3920734	0	1	0.2261386	-50.36866
6847	cg0032513	31648385	31648385	0.6550539	0	1	0.7630957	27.20718
6860	cg0032591	14694367	14694367	0.6974657	0	1	0.8516454	63.48054
6911	cg0032821	72703382	72703382	0.4842268	0	1	0.6437661	41.86397

6919	cg0032859	38675330	38675330	0.8108135	0	1	0.9215826	57.23984
6931	cg0032891	72644443	72644443	0.931043	0	1	0.7796789	-92.78088
7171	cg0033948	50602324	21801407	0.3874254	0	1	0.2324567	-44.38596
7207	cg0034106	18773370	41686495	0.3376615	0	1	0.2062459	-35.81312
7317	cg0034662	47697349	29663318	0.6527706	0	1	0.5289307	-27.53068
7340	cg0034762	51782356	65801309	0.6607138	0	1	0.7848387	35.92228
7359	cg0034803	20645464	20645464	0.8101259	0	1	0.6225847	-74.73534
7468	cg0035257	46794399	46794399	0.517943	0	1	0.640379	26.65797
7481	cg0035340	29767306	29767306	0.9285453	0	1	0.8022724	-71.74111
7497	cg0035438	53661303	53661303	0.2916796	0	1	0.4594197	46.61121
7685	cg0036375	73802349	73802349		0	1	0.3235186	4.34E-09
7745	cg0036660	71632347	71632347	0.3948264	0	1	0.5678179	46.72945
7795	cg0036905	22723346	22723346	0.4061009	0	1	0.5156639	21.05602
7837	cg0037041	68769470	68769470	0.2537548	0	1	0.3615871	23.68404
7845	cg0037106	70750478	70750478	0.3083043	0	1	0.4087651	19.53635
7897	cg0037343	35689309	35689309	0.5450431	0	1	0.7143257	50.71206
7911	cg0037401	34614467	34614467	0.4690894	0	1	0.3394035	-28.71997
8081	cg0038175	35726399	51656485	0.2326673	0	1	0.1054444	-47.22473
8126	cg0038470	45767476	45767476	0.497659	0	1	0.3572219	-32.52185
8235	cg0039019	12611477	12611477	0.8008755	0	1	0.6807278	-35.89886
8332	cg0039471	24737432	24737432		0	1		-4.34E-09
8413	cg0039804	15783450	15783450	0.2432983	0	1	0.3720044	32.04579
8449	cg0039995	24614302	24614302	0.3313107	0	1	0.4366068	20.54902
8486	cg0040110	36612418	59687450	0.5505452	0	1	0.4457809	-19.56911
8535	cg0040347	62610321	62610321	0.4293275	0	1	0.3234897	-20.87441
8548	cg0040418	59806369	59806369	0.5678366	0	1	0.4353766	-29.0793
8588	cg0040601	60735327	60735327	0.5489819	0	1	0.6625613	24.20676
8633	cg0040823	57607304	33655303	0.6827136	0	1	0.5681886	-25.24189
8692	cg0041089	41650376	41650376	0.2531839	0	1	0.1177812	-49.32533
8738	cg0041335	40637333	40637333	0.5117602	0	1	0.6875343	52.00707
8774	cg0041538	36702431	36702431	0.7964512	0	1	0.456613	-205.6306
9085	cg0042845	36769351	65619420	0.6925805	0	1	0.5923864	-20.75856
9233	cg0043696	51693491	51693491	0.6664475	0	1	0.50984	-41.49477
9293	cg0044079	46608309	46608309	0.1441054	0	1	0.2595815	35.0344
9483	cg0045002	70611456	70611456	0.5669092	0	1	0.7607941	69.78075
9619	cg0045634	16712478	16712478	0.8580703	0	1	0.541483	-203.6598
9682	cg0045893	69765306	69765306	0.1242167	0	1	0.244417	40.11396
9703	cg0045962	19772395	27705498	0.1675778	0	1	0.0292722	-79.92907
9817	cg0046374	55797393	55797393	0.3337444	0	1	0.4375008	20.02645
9866	cg0046611	36716493	36716493	0.1775915	0	1	0.4147727	102.4503
9894	cg0046727	57640486	71694449	0.7709463	0	1	0.9259002	92.6925
10020	cg0047284	20810380	20810380	0.4264116	0	1	0.5842133	39.66524
10059	cg0047409	13684467	13684467	0.6616473	0	1	0.4905437	-48.13664

10065	cg0047437	72662453	72662453	0.381675	0	1	0.685994	146.1217
10159	cg0047847	38625510	38625510	0.5106996	0	1	0.4068238	-19.2938
10177	cg0047982	45616421	45616421	0	0	1	0.1308355	91.91531
10295	cg0048625	67693416	67693416	0.444092	0	1	0.5632187	24.26474
10344	cg0048882	41699391	28727411	0.1401444	0	1	0.0328822	-55.27039
10448	cg0049330	45680342	44609483	0.9227313	0	1	0.766117	-92.24722
10554	cg0049790	62600457	62600457	0.1753982	0	1	0.2959976	33.88949
10583	cg0049913	38801390	38801390	0.565307	0	1	0.6920523	30.17727
10613	cg0050002	48607448	48607448	0.4419087	0	1	0.5569382	22.85472
10753	cg00505001	47660336	47660336	0.4624488	0	1	0.5719085	21.1501
10796	cg0050705	33615313	33615313	0.8909215	0	1	0.5396249	-264.5838
10872	cg0051032	60780470	60780470	0.2356981	0	1	0.3564608	29.3422
10887	cg0051071	38763374	38763374	0.4743826	0	1	0.5809178	20.31512
10898	cg0051133	20665459	20665459	0.3095471	0	1	0.427974	25.3995
11134	cg0052360	70747313	70747313	0.1748342	0	1	0.2767201	26.14756
11135	cg0052362	39768400	39768400	0.5779462	0	1	0.7304254	43.79782
11150	cg0052437	56689304	56689304	0.2831903	0	1	0.401425	26.18002
11185	cg0052582	73696304	22732478	0.9839413	0	1	0.714254	-253.0507
11252	cg0052974	39696318	39696318	0.2902426	0	1	0.4325881	35.23641
11303	cg0053212	61800426	61800426	0.0524256	0	1	0.503257	374.3439
11354	cg0053421	61781303	50644369	0.9852603	0	1	0.5683572	-371.3336
11453	cg0053936	59744470	59744470	0.3836901	0	1	0.4886221	19.74508
11470	cg0054029	37809366	37809366	0.6904176	0	1	0.4131027	-121.3784
11552	cg0054403	23632499	23632499	0.3385054	0	1	0.4891903	37.13638
11597	cg0054675	74625369	74625369	0.4546407	0	1	0.8299717	374.3439
11795	cg0055508	42616447	42616447	0.2194534	0	1	0.3229758	23.82449
11803	cg0055543	12606324	12606324	0.0938143	0	1	0.2525676	69.23317
11940	cg0056226	13644472	13644472		0	1	0.7723164	4.34E-09
11941	cg0056226	74692473	62764304	0.1954326	0	1	0.0912162	-37.49272
11970	cg0056335	54631509	54631509	0.5267427	0	1	0.6363078	22.15691
11979	cg0056382	42786475	62697453	0.1597987	0	1	0.0488238	-52.07261
12030	cg0056618	64810375	64810375	0.6199332	0	1	0.9046483	374.3439
12050	cg0056698	54768470	54768470	0.4335096	0	1	0.5363402	18.94921
12089	cg00569101	11653362	11653362	0.7706046	0	1	0.9408507	114.9219
12123	cg0057063	17775315	17775315	0.2787165	0	1	0.3878819	23.18136
12145	cg0057151	45708350	45708350	0.5151454	0	1	0.413296	-18.66733
12165	cg0057258	55740317	55740317	0.2644066	0	1	0.0938616	-77.10144
12185	cg0057341	69654380	69654380	0.5319522	0	1	0.6499016	25.33753
12240	cg0057564	16668481	16668481	0.5604975	0	1	0.7242595	48.77661
12257	cg0057613	22668323	22668323	0.5659805	0	1	0.6673153	20.31834
12519	cg0058652	54681481	17654386	0.6761359	0	1	0.5498232	-29.30053
12535	cg00587301	23781313	23781313	0.6486195	0	1	0.7500512	23.85412
12537	cg0058734	39716491	39716491	0.4286765	0	1	0.5290638	18.21761

12550	cg00587941	55710466	28715476	0.6664951	0	1	0.9265002	374.3439
12577	cg00588920	70627410	70627410	0.1391872	0	1	0.2802477	48.55938
12732	cg00595051	15623412	15623412	0.4701355	0	1	0.3527191	-24.11751
12788	cg00598204	37644350	37644350	0.3284011	0	1	0.4475105	25.16149
12858	cg00601450	48675301	10730370	0.1295909	0	1	0.2765968	53.54831
13060	cg00612751	14741434	14741434	0.6286693	0	1	0.7398571	26.85531
13137	cg00616572	49789428	49789428	0.7180879	0	1	0.5802696	-36.20538
13229	cg00621559	41739321	41739321	0.3986572	0	1	0.504959	20.06866
13233	cg00621666	67737500	67737500	0.2662944	0	1	0.1503767	-34.4824
13356	cg00628211	55631375	55631375	0.7837675	0	1	0.8869645	41.6381
13423	cg00631329	61711456	61711456	0.2644017	0	1	0.0953791	-75.59556
13428	cg00631759	42626386	42626386	0.6123421	0	1	0.8420122	114.1186
13430	cg00631877	61665304	61665304	0.9072573	0	1	0.637906	-182.2036
13476	cg00634652	52795423	41801408	0.1474447	0	1	0.2733383	39.56255
13485	cg00635343	45612424	45612424	0.5873916	0	1	0.7038772	26.86475
13504	cg00636194	62744391	62744391	0.3024641	0	1	0.4207427	25.55326
13547	cg00638021	71783431	71783431	0.2866273	0	1	0.4059949	26.46232
13578	cg00639615	64697321	64697321	0.5713869	0	1	0.4034761	-44.2562
13874	cg00655552	27604337	27604337	0.3895652	0	1	0.4944894	19.69985
14054	cg00664454	16703404	16703404	0.1884971	0	1	0.3289084	41.60725
14127	cg00667789	36621334	42661429	0.2047575	0	1	0.086431	-46.28261
14134	cg00667948	51734472	51734472	0.8212805	0	1	0.9345529	64.79012
14141	cg00668212	47690491	47690491	0.5186922	0	1	0.6734148	40.98476
14276	cg00675336	68697397	68697397	0.2694949	0	1	0.3834738	25.18804
14355	cg00679624	47712346	47712346	0.3294179	0	1	0.1914336	-40.15641
14606	cg00691948	53710382	53710382	0.4040763	0	1	0.5112553	20.31585
14655	cg00694040	56600501	56600501	0.7070803	0	1	0.8492287	55.57246
14662	cg00694353	61688483	61688483	0.7468158	0	1	0.932932	123.0061
14701	cg00696044	51669430	51669430	0.574074	0	1	0.7415552	52.36635
14767	cg00698771	31681444	63692413	0.4114547	0	1	0.2395079	-52.24946
14819	cg00700969	15679389	15679389	0.3057416	0	1	0.1840003	-33.56726
14859	cg00702561	19740489	19740489	0.6008085	0	1	0.2466059	-204.8976
15202	cg00718261	53605491	53605491	0.4853301	0	1	0.6194556	30.46602
15263	cg00720581	60679475	73642307	0.5321772	0	1	0.4103576	-25.12515
15336	cg00724315	60657423	60657423	0.5194259	0	1	0.6650076	36.57686
15344	cg00725145	49647457	13676315	0.6071774	0	1	0.7252793	28.61739
15384	cg00727777	72788303	72788303	0.7628074	0	1	0.9101859	78.89736
15423	cg00729708	15681478	15681478	0.3841349	0	1	0.5006087	23.42867
15522	cg00733978	58790502	58790502	0.6241071	0	1	0.778683	50.05071
15567	cg00735883	19649370	23759389	0.4380135	0	1	0.3367122	-19.22618
15620	cg00738849	73775371	38801335	0.638712	0	1	0.5344118	-20.52921
15654	cg00740510	31607333	31607333	0.6839408	0	1	0.4819172	-66.28573
15772	cg00745855	28753437	28753437	0.8517084	0	1	0.9545701	67.32502

15803	cg0074747	73744465	73744465	0.5113566	0	1	0.6145996	19.74185
15807	cg0074765	11786475	19759505	0.9510524	0	1	0.7137111	-184.815
15862	cg0075048	35758454	35758454	0.2242119	0	1	0.3601344	36.34761
15921	cg0075354	23677356	23677356	0.1365604	0	1	0.2630899	41.41857
15933	cg0075392	13628431	13628431	0.3443798	0	1	0.4725431	28.05628
15955	cg0075498	16601458	16601458	0.6120485	0	1	0.7285987	28.21721
16036	cg0075905	52808361	52808361	0.65514	0	1	0.805392	51.67983
16121	cg0076283	66714317	68648306	0.6449261	0	1	0.5125805	-30.47187
16162	cg0076498	12689492	12689492	0.73082	0	1	0.8457513	39.74984
16230	cg0076817	17658469	17658469	0.6121849	0	1	0.7156454	22.7749
16431	cg0077756	58611311	58611311	0.6606444	0	1	0.8075203	50.19828
16459	cg0077905	11738337	36742405	0.6415886	0	1	0.7601179	31.20117
16550	cg0078313	19738414	19738414	0.4193072	0	1	0.316181	-20.18185
16577	cg0078458	47661355	23706371	0.5830381	0	1	0.4750648	-20.78384
16602	cg0078594	52804397	52804397	0.1426994	0	1	0.2737515	42.7915
16641	cg0078799	72773359	72773359	0.3611874	0	1	0.4618725	18.69161
16649	cg0078817	10758443	27641454	0.3711234	0	1	0.2314366	-37.45719
16776	cg0079393	36619332	72628509	0.1528303	0	1	0.30523	52.45032
16782	cg0079399	29629398	29629398	0.8292232	0	1	0.6447983	-77.18924
16803	cg0079491	25661471	25661471	0.3818859	0	1	0.5499886	44.36048
16809	cg0079520	56635320	56635320	0.146375	0	1	0.2582214	33.09596
16975	cg0080424	54773334	45725488	0.5166212	0	1	0.6194642	19.70126
17196	cg0081421	64602355	64602355	0.4157308	0	1	0.6547706	88.50002
17251	cg0081651	14806404	14806404	0.5409213	0	1	0.6637129	27.51303
17335	cg0082118	70683476	70683476	0.7822867	0	1	0.584215	-75.94869
17351	cg0082203	18798349	10688394	0.7912116	0	1	0.6584904	-40.6733
17487	cg0082964	61646498	38687433	0.6045564	0	1	0.7089638	22.80337
17547	cg0083213	62629352	62629352	0.2065738	0	1	0.3081315	23.84835
17630	cg0083610	33668367	33668367	0.3909716	0	1	0.5580688	43.8467
17664	cg0083789	55725467	55725467	0.5070915	0	1	0.6213215	23.37319
17674	cg0083842	16654482	16654482	0.1840394	0	1	0.2916504	27.68867
17763	cg0084363	68647386	68647386	0.7016295	0	1	0.5976094	-22.36484
17860	cg0084837	19743484	19743484	0.597561	0	1	0.699817	21.70268
17934	cg0085151	47624412	47624412	0.1765089	0	1	0.2927083	31.87593
17956	cg0085260	47669404	30621348	0.2964385	0	1	0.3992281	20.55665
17984	cg0085394	60716487	60716487	0.2127016	0	1	0.345275	35.78688
18101	cg0085987	32640506	32640506	0.6921458	0	1	0.9145197	142.5562
18125	cg0086121	49625401	49625401	0.3880026	0	1	0.5745876	53.79526
18193	cg0086417	52799325	52799325	0.4539747	0	1	0.3164589	-32.31712
18309	cg0086930	71621326	71621326	0.9080755	0	1	0.6845008	-139.5938
18401	cg0087360	18668468	60679306	0.4840441	0	1	0.3253206	-41.03856
18483	cg0087675	43778390	41784387	0.490046	0	1	0.3892749	-18.4576
18507	cg0087816	39764486	58726385	0.6287758	0	1	0.4911793	-32.04788

18523	cg0087921	19790496	19790496	0.7853533	0	1	0.6714219	-31.4803
18527	cg0087949	49788354	13644469		0	1	0.6680779	4.34E-09
18528	cg00879541	47671476	47671476	0.4011107	0	1	0.604714	63.69984
18574	cg0088189	68677465	68677465	0.4249568	0	1	0.9164275	374.3439
18646	cg00886571	15612500	15612500	0.3214796	0	1	0.4399989	25.1193
18688	cg0088875	24721332	24721332	0.6842133	0	1	0.7940284	30.55881
18712	cg0089007	63730395	63730395	0.3654357	0	1	0.4662722	18.68779
18756	cg0089236	48731416	51671432	0.507829	0	1	0.4020602	-19.88889
18894	cg0090073	29702359	14789326	0.8092887	0	1	0.9216885	58.44061
18998	cg0090531	64770334	64770334	0.2555588	0	1	0.3640394	23.8325
19003	cg0090552	33623413	24656365	0.4397592	0	1	0.3105673	-29.27958
19006	cg0090574	62698386	62698386	0.4424376	0	1	0.3359763	-20.82791
19087	cg00908601	70794326	70794326	0.5711282	0	1	0.4688715	-18.93096
19222	cg0091395	72679382	72679382	0.6058694	0	1	0.7599317	47.48814
19300	cg00918181	70622484	70622484	0.6018964	0	1	0.2456335	-207.6492
19315	cg0091912	14642320	14642320	0.4832474	0	1	0.5976112	23.01564
19353	cg0092066	36693338	23620361	0.5525063	0	1	0.6759126	28.19801
19447	cg0092508	70796393	70796393	0.1868355	0	1	0.3216949	39.17377
19474	cg0092642	61804339	73696387	0.2358557	0	1	0.3895555	43.50841
19757	cg0093968	23660333	23660333	0.3908856	0	1	0.5946859	63.68467
19852	cg00944631	33644501	33644501	0.5413433	0	1	0.8024355	127.6763
19916	cg0094778	22655509	11725434	0.0255214	0	1	0.1703407	87.0724
19963	cg0094998	23653380	50799380	0.4252528	0	1	0.312909	-23.23013
20014	cg0095278	20734465	20734465	0.3781765	0	1	0.4996309	25.17802
20082	cg0095578	48794300	48794300	0.6264518	0	1	0.4875776	-32.49273
20100	cg0095649	30773316	30773316	0.7737476	0	1	0.6698388	-26.38488
20123	cg0095769	27697394	27697394	0.3202077	0	1	0.4729107	38.5239
20347	cg0096816	41790387	41790387	0.262027	0	1	0.3717615	24.00037
20363	cg00968771	64794380	16624467	0.6011539	0	1	0.500222	-18.84724
20395	cg0097027	38750401	43783437	0.3350363	0	1	0.1992646	-38.37355
20478	cg0097452	12731470	12731470	0.4506799	0	1	0.5616955	21.57428
20480	cg0097457	37653347	37653347	0.6202055	0	1	0.5128465	-21.11871
20506	cg0097574	57691312	57691312	0.1209652	0	1	0.2862327	66.24072
20569	cg0097884	52680431	52680431	0.3957377	0	1	0.5690189	46.87591
20586	cg0097928	64652323	10616422	0.443745	0	1	0.3079751	-31.89791
20651	cg0098187	15731476	28704329	0.5849195	0	1	0.4045814	-50.54544
20680	cg0098298	48702333	48702333	0.61374	0	1	0.4788722	-30.62597
20689	cg0098369	51787353	51787353	0.6497052	0	1	0.7716147	33.62696
20690	cg0098370	22623502	22623502	0.8175781	0	1	0.9276887	59.29258
20721	cg0098538	36700401	36700401	0.1408757	0	1	0.2413798	28.69344
20774	cg0098805	37707449	31720502	0.7761006	0	1	0.573949	-77.47209
20836	cg0099076	68787438	68787438	0.3733887	0	1	0.4814401	20.80149
20907	cg0099383	67633457	67633457	0.6469377	0	1	0.7486776	23.88445

20909	cg00993903	26725474	26725474	0.7580072	0	1	0.6445808	-28.96066
20953	cg00995368	49810395	49810395	0.7723302	0	1	0.614825	-50.75345
20995	cg00997251	40617310	40617310	0.259348	0	1	0.3639905	22.36749
21042	cg00999163	34802473	57752377	0.2487538	0	1	0.4115882	46.90366
21049	cg00999638	58704438	58704438	0.7710326	0	1	0.6629233	-27.83346
21074	cg01000657	67673486	35768392	0.147542	0	1	0.0173908	-80.01437
21086	cg01001314	49793311	49793311	0.7203438	0	1	0.8417692	42.45524
21093	cg01001959	57762422	57762422	0.4722784	0	1	0.3706741	-18.86017
21158	cg01005180	72747446	72747446	0.4078679	0	1	0.5138558	19.93423
21166	cg01005425	13730504	13730504	0.639474	0	1	0.7681657	36.28926
21169	cg01005486	49765459	49765459	0.2629581	0	1	0.1562112	-29.79357
21191	cg01006802	39651497	64691402	0.3083982	0	1	0.2007137	-26.50354
21317	cg01013031	35631361	35690419	0.5807728	0	1	0.795859	90.15868
21376	cg01015662	21666465	26648376	0.6919252	0	1	0.5058638	-57.78933
21384	cg01016092	21694469	21694469	0.5326455	0	1	0.36054	-46.5186
21528	cg01022117	17782395	42638353	0.4536819	0	1	0.5545027	18.40499
21531	cg01022189	25786466	25786466	0.9164178	0	1	0.800821	-58.60995
21544	cg01022670	15660474	15660474	0.5954645	0	1	0.7630956	54.96465
21559	cg01023242	67743501	67743501	0.7373105	0	1	0.6250218	-27.11636
21569	cg01023703	33783394	33783394	0.2909643	0	1	0.3981129	22.11601
21604	cg01025095	68672467	64763345	0.5315912	0	1	0.3736983	-39.68333
21693	cg01029331	73787312	14657451	0.9667825	0	1	0.7639384	-166.9801
21707	cg01029685	63766436	63766436	0.3929411	0	1	0.2905731	-20.58465
21741	cg01031312	11690361	11690361	0.3223857	0	1	0.4388436	24.38768
21803	cg01034813	28693312	28693312	0.5059395	0	1	0.6539437	37.15122
21945	cg01042202	43649477	21654418	0.8294322	0	1	0.6535847	-71.64841
22088	cg01048272	66719465	66719465	0.6311114	0	1	0.5056903	-27.49313
22249	cg01055691	63796358	63796358	0.7108428	0	1	0.8203871	33.37178
22251	cg01055696	51629480	25614359	0.7707782	0	1	0.6627012	-27.80069
22272	cg01056467	10629329	16649394	0.3430042	0	1	0.2116207	-35.35745
22327	cg01059116	69731430	69731430	0.5559142	0	1	0.3966959	-40.15797
22332	cg01059385	61780487	61780487	0.3570359	0	1	0.2142153	-40.24322
22334	cg01059432	37645427	38781310	0.3565813	0	1	0.2547905	-21.59309
22368	cg01061164	34769367	25702481	0.7413358	0	1	0.8923135	74.08971
22373	cg01061520	61760464	61760464	0.3114851	0	1	0.1932178	-31.28918
22400	cg01062539	57764394	21718483	0.6619301	0	1	0.7643456	25.13253
22410	cg01062942	52752434	52752434	0.1040089	0	1	0.2456348	55.84582
22413	cg01063088	53684349	53684349	0.1687982	0	1	0.3097011	44.14992
22435	cg01064265	58621422	51611437	0.4557274	0	1	0.3073374	-37.10577
22616	cg01072388	62787373	62787373	0.4063252	0	1	0.5261592	24.44593
22650	cg01074083	17770500	17770500	0.655261	0	1	0.8867612	134.6604
22824	cg01081584	63773393	63773393	0.7438583	0	1	0.2739802	-371.3336
22920	cg01085399	34667319	34667319	0.5902252	0	1	0.7186599	32.31227

23150	cg0109744	13617312	37610325		0	1	0.017107	4.34E-09
23253	cg0110166	57773374	57773374	0.454101	0	1	0.3256346	-28.58717
23254	cg0110167	35652338	35652338	0.5880892	0	1	0.7054773	27.27685
23339	cg0110540	58625305	58625305	0.7139421	0	1	0.3134831	-271.9647
23403	cg0110863	52758389	52758389	0.4574442	0	1	0.5730567	23.15359
23523	cg0111413	71625399	71625399	0.5532788	0	1	0.702067	39.96653
23579	cg0111727	24632368	24632368	0.7418416	0	1	0.5774972	-50.7658
23602	cg0111864	72739319	72739319	0.5072579	0	1	0.2260535	-129.6227
23703	cg0112413	53638343	53638343	0.7368794	0	1	0.6176736	-29.77578
23756	cg0112760	24715331	24715331	0.233899	0	1	0.0879151	-62.68643
23762	cg0112804	18724455	18724455	0.5443834	0	1	0.6651385	26.82159
23998	cg0113969	45607388	45607388	0.6763784	0	1	0.916365	374.3439
23999	cg0113969	16700378	16700378	0.2481685	0	1	0.3549436	23.55949
24270	cg0115262	32644411	32644411	0.3067365	0	1	0.4399427	30.93636
24288	cg0115337	45738320	50626330	0.3677785	0	1	0.584482	71.64358
24311	cg0115433	44652369	44652369	0.6299962	0	1	0.7445893	28.47252
24448	cg0116105	62747307	62747307	0.3750246	0	1	0.5085895	29.60917
24543	cg0116590	35653429	35653429	0.6443579	0	1	0.7607034	30.34842
24734	cg0117514	47769365	47769365	0.4946208	0	1	0.2574361	-90.45715
24872	cg0118207	37774380	37774380	0.6685133	0	1	0.7855726	32.85421
24947	cg0118564	22706469	22706469	0.3806311	0	1	0.4980236	23.76656
25051	cg0119091	14707477	27750351	0.7839438	0	1	0.9178117	72.35423
25059	cg0119115	50612384	50612384	0.2017615	0	1	0.317154	29.45092
25106	cg0119336	21647360	26755371	0.6902781	0	1	0.5579758	-32.28323
25117	cg0119407	72697401	32694336	0.2663782	0	1	0.3758532	23.7383
25129	cg0119476	24770508	24770508	0.1637495	0	1	0.2820756	34.07571
25164	cg0119633	64764433	64764433	0.2586228	0	1	0.3599216	21.28437
25275	cg0120251	59676304	47600463	0.4357339	0	1	0.3027748	-30.97444
25303	cg0120376	74635411	74635411	0.3315597	0	1	0.4493576	24.6396
25544	cg01215761	23623339	62672339	0.3909582	0	1	0.271363	-27.13545
25657	cg0122158	24784320	24784320	0.8916348	0	1	0.686173	-115.1591
25792	cg01228941	55600356	35613357	0.7909966	0	1	0.4978701	-153.6902
25817	cg0123032	18649346	18649346	0.6445942	0	1	0.9360674	374.3439
25824	cg0123063	72809365	72809365	0.3362632	0	1	0.4726653	31.34789
25848	cg01231921	35765480	35765480	0.4886275	0	1	0.37521	-22.49986
25856	cg01232331	11624391	11624391	0.5923041	0	1	0.7602555	54.77787
25860	cg01232511	34701365	35621479	0.6021866	0	1	0.491347	-21.9318
25943	cg0123656	38743488	38743488	0.5860829	0	1	0.7413703	46.1566
26102	cg0124522	70663375	70663375	0.2962722	0	1	0.458753	43.88079
26170	cg0124874	44690486	44690486	0.4397899	0	1	0.3009491	-33.37103
26272	cg0125430	32766403	50639305	0.1246399	0	1	0.4224883	374.3439
26338	cg0125778	25672372	25672372	0.3976262	0	1	0.5113661	22.43646
26468	cg0126491	73763380	73763380	0.5032518	0	1	0.6944514	60.83808

26535	cg0126921	37698464	37698464	0.7409231	0	1	0.8651326	48.72203
26553	cg0127000	52631391	43650379	0.1506638	0	1	0.0342277	-61.2644
26642	cg0127490	52722315	52722315	0.6468804	0	1	0.4794667	-45.67482
26800	cg0128333	61774489	61774489	0.7005204	0	1	0.5785991	-28.73744
26819	cg0128428	64720495	64720495	0.4253918	0	1	0.6394984	71.07223
26841	cg0128550	50703500	50703500	0.446228	0	1	0.3398747	-20.72545
26849	cg0128592	28747346	62630489	0.3706437	0	1	0.2571912	-25.51675
26859	cg0128668	67740487	61726375	0.1059447	0	1	0.2243159	42.28858
26864	cg0128700	71733390	38620464	0.4503463	0	1	0.3500149	-18.73097
26927	cg0128954	36615507	36615507	0.3754013	0	1	0.2710961	-21.82288
26935	cg0128987	24806427	24806427	0.6559485	0	1	0.7761502	33.30973
27002	cg0129253	68748466	68748466	0.6726671	0	1	0.7840507	30.2772
27008	cg0129281	50683422	50683422	0.1971644	0	1	0.3188645	32.40123
27041	cg0129428	63706392	63706392	0.2101784	0	1	0.3241834	28.30911
27067	cg0129564	63606406	63606406	0.2833413	0	1	0.1649635	-33.97006
27129	cg0129810	35734489	35734489	0.2307952	0	1	0.3773761	40.5964
27136	cg0129867	12736491	12736491	0.4538442	0	1	0.5619927	20.66872
27143	cg0129891	35809352	35809352	0.9004936	0	1	0.636203	-172.8215
27192	cg0130128	10771424	10771424	0.4275876	0	1	0.3089637	-25.48488
27517	cg0131647	67705342	67705342	0.6811837	0	1	0.5685879	-24.50689
27539	cg0131818	35704452	62802401	0.5825996	0	1	0.467898	-22.94254
27570	cg0132057	46731406	41796418	0.6581322	0	1	0.5253892	-31.07323
27595	cg0132196	47774394	47774394	0.3568466	0	1	0.5055475	35.91703
27634	cg0132426	30671344	30671344	0.5188496	0	1	0.6570737	33.20673
27658	cg0132546	40647340	40647340	0.7453305	0	1	0.8589378	41.45735
27671	cg0132642	32630496	32630496	0.6288849	0	1	0.4421675	-54.79694
27723	cg0132969	30690303	30690303	0.3227202	0	1	0.5065502	53.40446
27948	cg0134180	23754361	23754361	0.0427401	0	1	0.2150719	99.45876
28061	cg0134858	55740334	17663399	0.2795927	0	1	0.407914	30.06989
28109	cg0135080	47628373	47628373	0.4235545	0	1	0.7001749	121.7572
28189	cg0135478	34742332	34742332	0.2821983	0	1	0.3963863	24.78479
28281	cg0135982	28651441	46697474	0.6968617	0	1	0.7982233	27.4092
28460	cg0136922	20742450	20742450	0.6364825	0	1	0.4778726	-41.18238
28478	cg0136989	55620332	55620332	0.2381542	0	1	0.3403322	22.42401
28509	cg0137142	44612418	44612418	0.2542953	0	1	0.3553513	21.3693
28617	cg0137726	55689445	71681318	0.4093705	0	1	0.5167109	20.34803
28712	cg0138182	15732482	15732482	0.1770395	0	1	0.310531	39.58197
28736	cg0138286	19729390	55803378	0.616247	0	1	0.4668537	-36.56134
28803	cg0138595	28748320	28748320	0.3093176	0	1	0.470599	42.76727
28837	cg0138790	36640437	36640437	0.7403839	0	1	0.8496817	37.51372
28854	cg0138869	49677502	49677502	0.3887718	0	1	0.2019348	-64.576
28957	cg0139416	12717498	12717498	0.3958937	0	1	0.6255424	80.75972
28992	cg0139554	62685325	62685325	0.6447748	0	1	0.8885707	146.5356

29041	cg0139749	73746324	73746324	0.4617675	0	1	0.8173266	374.3439
29076	cg0139931	13760327	70639478	0.7726565	0	1	0.5890194	-65.40347
29086	cg0140004	49616453	49616453	0.525993	0	1	0.6411438	24.13321
29249	cg0140744	43638467	43638467	0.6552965	0	1	0.7771925	34.14968
29286	cg0140934	55651304	55651304	0.1947286	0	1	0.3027769	27.06044
29299	cg0140970	70799373	70799373	0.1931905	0	1	0.3296989	39.29461
29334	cg0141092	56726407	56726407	0.4708053	0	1	0.6465733	49.77295
29362	cg0141240	49660476	49660476	0.6731756	0	1	0.775337	25.82468
29363	cg0141241	72610302	69694413	0.8008996	0	1	0.6783165	-37.03577
29379	cg0141297	57688456	12650324	0.3761131	0	1	0.2465737	-32.19078
29401	cg0141358	32689494	32689494	0.2904899	0	1	0.3970934	21.95148
29407	cg0141384	38718438	40801417	0.8961551	0	1	0.7858641	-48.32117
29411	cg0141418	57719415	39804430	0.9472281	0	1	0.8357391	-70.09364
29460	cg0141656	12766393	31702477	0.7356013	0	1	0.5811127	-45.2233
29707	cg0142837	39602445	61800414	0.2808608	0	1	0.1138398	-69.09982
29731	cg0142944	48610458	38713324	0.2427424	0	1	0.1288747	-36.28166
29960	cg0144048	67620425	67620425	0.4301635	0	1	0.5462449	23.16638
30020	cg0144284	62673347	62673347	0.168951	0	1	0.2704632	26.47497
30091	cg0144568	17793335	37710470	0.7977538	0	1	0.8994616	43.92517
30092	cg0144579	46745432	29695498	0.6976989	0	1	0.5223101	-52.53246
30171	cg0144856	10771502	27630358	0.9260696	0	1	0.7985137	-71.50535
30229	cg01451101	39754340	39754340	0.2109727	0	1	0.3116128	23.26398
30293	cg0145459	48725359	48725359	0.3372683	0	1	0.1617614	-64.105
30398	cg0146043	61777484	61777484	0.3223408	0	1	0.4362579	23.52855
30443	cg0146272	58768363	58768363	0.5330851	0	1	0.6502417	25.0708
30451	cg0146311	10715421	10715421	0.4047323	0	1	0.2829981	-27.45662
30463	cg0146406	49746427	49746427	0.5167318	0	1	0.6792452	44.9157
30575	cg0146986	10809390	10809390	0.3772071	0	1	0.2446948	-33.51675
30671	cg0147468	10701448	10701448	0.3222894	0	1	0.0294513	-220.7617
30685	cg0147538	20620412	53605402	0.4068924	0	1	0.2992853	-22.02687
30738	cg0147817	69693345	69693345	0.5144091	0	1	0.3686331	-34.5224
30808	cg0148365	70649496	70649496	0.6018847	0	1	0.4124464	-55.59628
30825	cg0148484	23790396	23790396	0.3134336	0	1	0.5064957	58.75988
30925	cg0149009	53695420	53695420	0.2047913	0	1	0.3967248	67.21056
30948	cg0149142	15709507	15709507	0.2500164	0	1	0.3984726	40.05838
30971	cg0149300	12753507	12753507	0.5676609	0	1	0.711545	38.40781
31096	cg0149981	57646393	43678317	0.2369099	0	1	0.0647248	-88.92109
31148	cg0150246	54808314	54808314	0.55853	0	1	0.6979724	35.63928
31448	cg0151822	50676477	19679386	0.8884813	0	1	0.768931	-51.91384
31476	cg0151922	64745443	64745443	0.3862339	0	1	0.1421627	-116.6658
31485	cg0151950	36802474	67694477	0.6294492	0	1	0.5235194	-20.84557
31566	cg0152302	18756452	18756452	0.3925437	0	1	0.5773168	52.82951
31756	cg0153425	27658321	27658321	0.6013397	0	1	0.7087295	23.82435

31925	cg0154358	33710356	33710356	0.6960163	0	1	0.4716074	-81.40386
31976	cg0154681	53787464	53787464	0.9259464	0	1	0.6532279	-199.1004
32005	cg0154846	66707495	66707495	0.2023638	0	1	0.3099241	26.34541
32015	cg0154922	16643509	16643509	0.5673799	0	1	0.6767282	23.23245
32037	cg0155034	57800438	57800438	0.2690748	0	1	0.3884188	27.13938
32061	cg0155138	59663305	59663305	0.3168015	0	1	0.7259785	374.3439
32139	cg0155477	29748349	29748349	0.3332668	0	1	0.5089561	48.88505
32251	cg0155930	21687389	21687389	0.1138182	0	1	0.2182894	33.89233
32291	cg0156087	16674376	16674376	0.5873391	0	1	0.4714103	-23.40243
32311	cg0156175	53619391	53619391	0.3964749	0	1	0.7989693	374.3439
32318	cg0156186	48704344	48704344	0.523517	0	1	0.4202498	-19.0795
32332	cg0156281	21632448	21632448	0.4540577	0	1	0.5580661	19.37351
32509	cg0156998	42778479	42778479	0.8464193	0	1	0.7091262	-52.11637
32722	cg0157960	67692433	67692433	0.171493	0	1	0.2721469	25.92834
32736	cg0158022	26693475	26693475	0.6258196	0	1	0.7502161	32.86076
32750	cg0158103	35778319	35778319	0.2386489	0	1	0.3459068	24.16847
32759	cg0158134	45618385	45618385	0.8144183	0	1	0.6728895	-48.45395
32770	cg0158206	61600338	61600338	0.4121338	0	1	0.5273644	22.87776
32834	cg0158572	34695470	34695470	0.5517092	0	1	0.3730979	-49.63688
32937	cg0159134	35649365	35649365	0.8515914	0	1	0.542827	-191.9235
32960	cg0159235	74631308	74631308	0.7318841	0	1	0.8375754	33.85196
33130	cg0160171	22645432	22645432	0.4790837	0	1	0.7011731	80.34711
33180	cg0160400	56664402	56664402	0.5230348	0	1	0.6547742	30.56437
33341	cg0161229	38678327	60736393	0.9101471	0	1	0.746197	-91.42204
33352	cg0161265	33661463	14650472	0.3493249	0	1	0.4532256	19.81639
33383	cg0161410	66709389	51669418	0.6232883	0	1	0.5091808	-23.37203
33529	cg01620701	45739403	45739403	0.4203559	0	1	0.5403606	24.48945
33548	cg0162139	23710488	23710488	0.3970261	0	1	0.533228	30.46095
33677	cg0162900	29673359	29673359	0.2772619	0	1	0.3821853	21.81691
33717	cg0163133	58620420	58620420	0.5066646	0	1	0.6109964	20.01785
33803	cg0163657	66756369	66756369	0.1752286	0	1	0.2830292	28.48321
33812	cg0163687	50613508	13770417	0.5485265	0	1	0.7561784	77.75213
33823	cg0163724	14719443	14719443	0.4210663	0	1	0.5347021	22.34325
33826	cg0163748	31720477	31720477	0.2364439	0	1	0.337005	21.95085
33833	cg0163778	63665456	63665456	0.325869	0	1	0.5071182	51.94813
33844	cg0163822	51719450	43603388	0.2493636	0	1	0.3613093	25.33134
34017	cg0164794	29767500	29767500	0.5367252	0	1	0.6916203	42.08566
34043	cg01649611	69642419	69642419	0.5658734	0	1	0.7725711	79.82115
34067	cg0165116	18772368	18772368	0.2762174	0	1	0.4394817	45.29072
34089	cg0165224	20802475	26638420	0.9778587	0	1	0.8739803	-85.46902
34143	cg0165565	14611329	14611329	0.4332351	0	1	0.060365	-296.9087
34146	cg01655721	42695500	61791376	0.7862659	0	1	0.8878734	40.9292
34369	cg0166865	34664417	57628330	0.862324	0	1	0.6873432	-80.28867

34511	cg01678701	12684333	14738326	0.5033584	0	1	0.3553087	-35.66949
34567	cg01681863	38675349	38675349	0.2029171	0	1	0.3117504	26.79529
34628	cg01685883	49689328	49689328	0.3970692	0	1	0.2583829	-35.28607
34763	cg01693328	52662346	52662346	0.638665	0	1	0.764219	34.53627
34803	cg01695994	26726427	26726427	0.2463662	0	1	0.376129	32.29324
34864	cg01699880	10749443	10749443	0.9119216	0	1	0.8099425	-47.78122
34908	cg01702501	66667497	66667497	0.6160984	0	1	0.9224252	374.3439
35024	cg01708377	50717377	50717377	0.3627818	0	1	0.4719499	21.2728
35083	cg01710670	14745317	42785427	0.6524809	0	1	0.4813695	-47.70937
35131	cg01713505	66622481	66622481	0.272829	0	1	0.0788423	-99.47445
35232	cg01717482	71740418	71740418	0.5164223	0	1	0.6351503	25.21323
35593	cg01737026	66789447	66618329	0.6184667	0	1	0.5158275	-19.62201
35645	cg01740135	69676427	69676427	0.4575159	0	1	0.2198209	-95.37771
35659	cg01741056	70642504	16632414	0.4499165	0	1	0.3113638	-32.8918
35661	cg01741372	49677332	49677332	0.3166417	0	1	0.4932537	49.90146
35708	cg01744396	37747425	37747425	0.1747992	0	1	0.0576023	-53.31369
35780	cg01748757	24802426	24802426	0.3459311	0	1	0.4500897	19.94644
35819	cg01750375	37724327	13644489	0.1569815	0	1		-4.34E-09
35898	cg01754423	68737322	68737322	0.4911289	0	1	0.6406024	37.29332
35899	cg01754525	18686381	21736365	0.5850595	0	1	0.3793183	-64.78815
36014	cg01759674	23650393	23650393	0.4733613	0	1	0.3498896	-26.2625
36024	cg01760090	33662376	33662376	0.5796831	0	1	0.4096609	-45.32622
36091	cg01763947	32688424	32688424	0.6103902	0	1	0.9243134	374.3439
36119	cg01765322	16704479	16704479	0.8682088	0	1	0.9692668	75.71433
36577	cg01786704	56664461	32808388	0.4102499	0	1	0.5947229	52.81959
36700	cg01792601	34798432	34798432	0.5211605	0	1	0.4195439	-18.58651
36775	cg01796223	65731500	65731500	0.6864066	0	1	0.8100846	38.72423
36801	cg01797371	52795419	10640304	0.0538221	0	1	0.2056299	78.54268
36810	cg01797652	23670458	23670458	0.8964718	0	1	0.7871281	-47.82
36887	cg01801090	59654474	59654474	0.6823622	0	1	0.8875042	112.9095
36992	cg01804934	30652499	30652499	0.7751557	0	1	0.6719716	-26.20895
37176	cg01812434	42648449	42648449	0.6373375	0	1	0.4878725	-37.18172
37207	cg01813738	70692408	70692408		0	1	0.9210706	4.34E-09
37249	cg01815567	38792328	71641451	0.7186694	0	1	0.5482057	-51.69393
37313	cg01818369	48799312	48799312	0.9381061	0	1	0.7434837	-134.1726
37356	cg01820273	37709389	66738353	0.5475357	0	1	0.3801396	-44.03192
37440	cg01823585	54804382	54804382	0.8096027	0	1	0.5270173	-149.1471
37449	cg01824063	43696400	43696400	0.2195804	0	1	0.327788	25.52014
37560	cg01829632	74607370	74607370	0.6504281	0	1	0.7630561	29.02316
37701	cg01835922	21638313	21638313	0.0930566	0	1	0.2074354	42.62806
37709	cg01836455	27725379	27725379	0.683126	0	1	0.804101	36.67192
37748	cg01838004	62755506	62755506	0.3849495	0	1	0.2380734	-40.18
37791	cg01840183	13742471	19667410	0.6269426	0	1	0.4610209	-44.26107

37828	cg0184277	44678464	17673382	0.6269081	0	1	0.9391788	374.3439
37841	cg0184326	27791413	27791413	0.2916803	0	1	0.4491116	41.75764
37893	cg0184706	74642468	74642468	0.6129752	0	1	0.8972105	374.3439
38025	cg0185501	51601347	51601347	0.2304163	0	1	0.3335453	23.11826
38067	cg0185715	24772402	24772402	0.6219208	0	1	0.7733738	47.75494
38082	cg0185783	36653390	36653390	0.217901	0	1	0.3324095	28.00059
38096	cg0185871	38792447	38792447	0.2269235	0	1	0.3498659	30.7396
38160	cg0186155	52778438	52778438	0.6604158	0	1	0.9507636	374.3439
38182	cg0186268	36734461	45740407	0.5691721	0	1	0.4661144	-19.15614
38210	cg0186440	28711435	49785475	0.6954322	0	1	0.5756943	-27.6723
38211	cg0186446	10669341	10669341	0.1525481	0	1	0.0069841	-99.49196
38348	cg0187091	16718504	16718504	0.1912917	0	1	0.3344822	42.63706
38352	cg0187102	49793376	49793376	0.7730291	0	1	0.6613412	-29.44091
38389	cg0187298	51730335	51730335	0.4207536	0	1	0.6732321	99.62267
38419	cg0187486	43663398	43663398	0.5696757	0	1	0.4545685	-22.95914
38420	cg0187486	31606304	31606304	0.5887598	0	1	0.4591583	-28.22039
38433	cg0187546	26673508	26673508	0.1878343	0	1	0.3310125	43.00665
38444	cg0187633	43725462	43725462	0.2286536	0	1	0.3451487	28.10733
38542	cg0188056	54806507	54806507	0.4783973	0	1	0.5801036	18.84234
38553	cg0188106	58767390	58767390	0.3446805	0	1	0.4657449	25.50859
38559	cg0188128	35697305	35697305	0.7434219	0	1	0.6203596	-31.79001
38587	cg0188205	57666334	44643344	0.6664376	0	1	0.8008917	42.77571
38588	cg0188208	44622465	44622465	0.4418976	0	1	0.5420421	18.16308
38604	cg0188277	21623380	21623380	0.6489518	0	1	0.5323298	-24.84839
38634	cg0188377	19693345	19693345	0.5887425	0	1	0.4688626	-24.75678
38741	cg0188989	13602332	13602332	0.2632144	0	1	0.3799356	26.43277
38744	cg0188995	41802369	41802369	0.3937032	0	1	0.502818	20.97256
38767	cg0189158	60666352	60666352	0.4757539	0	1	0.2033439	-125.7698
38769	cg0189173	43638342	59657395	0.3329616	0	1	0.4348417	19.46641
38821	cg0189487	64760482	64760482	0.4770377	0	1	0.227017	-103.5937
38950	cg0190170	48643410	48643410	0.4219288	0	1	0.528578	20.11219
39019	cg0190547	34688463	34688463	0.6403254	0	1	0.7455028	24.9523
39190	cg0191319	66697436	54617510	0.5183525	0	1	0.416204	-18.75014
39246	cg0191640	20640482	20640482	0.6273031	0	1	0.7773836	47.55752
39253	cg0191669	35690442	35690442	0.5760315	0	1	0.8777246	374.3439
39287	cg0191860	26687384	26687384	0.5279275	0	1	0.7364756	75.55006
39316	cg0191994	33759365	33759365	0.4437957	0	1	0.6027378	40.45235
39349	cg0192148	24711510	24711510	0.5489081	0	1	0.8239898	146.9932
39452	cg0192573	27652432	36748389	0.4854667	0	1	0.2885086	-62.21781
39472	cg0192681	48794458	48794458	0.8362092	0	1	0.7132779	-42.28316
39487	cg0192782	17753408	26749428	0.3719826	0	1	0.2302443	-38.45297
39545	cg0193074	24720508	24720508	0.5870671	0	1	0.8417969	135.0434
39553	cg0193122	23666344	23666344	0.4848226	0	1	0.588046	19.3765

39790	cg0194158	61651486	61651486	0.3159329	0	1	0.4262615	22.48854
39816	cg0194255	57796400	57796400	0.1948463	0	1	0.30069	26.20066
39895	cg0194609	31608438	31608438	0.571136	0	1	0.8819889	374.3439
39945	cg0194821	66810339	66810339	0.7198527	0	1	0.8335621	37.17409
39947	cg0194822	71746375	71746375	0.5248659	0	1	0.7070929	56.91673
39969	cg0194983	55734495	55734495	0.9139854	0	1	0.5000361	-371.3336
40076	cg0195458	21647351	21647351	0.5880929	0	1	0.7193787	33.52977
40133	cg0195818	26702322	26702322	0.4764547	0	1	0.6482149	47.84415
40193	cg0196074	32809432	32809432	0.8742878	0	1	0.7290584	-64.08896
40277	cg0196363	16698453	16698453	0.6820107	0	1	0.5319122	-39.36488
40338	cg0196627	46681479	46681479	0.5604058	0	1	0.7117552	41.79499
40362	cg0196692	27633458	27633458	0.4186853	0	1	0.5864527	44.30391
40424	cg0197033	73637467	73637467	0.2847533	0	1	0.4048403	26.79015
40541	cg0197454	33705326	33705326	0.4534852	0	1	0.642799	56.71609
40560	cg01975591	69648422	69648422	0.3960138	0	1	0.2820518	-24.71116
40566	cg0197585	59694310	59694310	0.6067417	0	1	0.7727221	55.34533
40605	cg0197823	29660412	29660412	0.1611298	0	1	0.266229	28.62439
40613	cg0197870	27711305	69625371	0.5235168	0	1	0.6255644	19.56752
40810	cg0198920	11611407	11611407	0.4157505	0	1	0.5202097	19.44686
40852	cg0199174	60789496	60789496	0.388667	0	1	0.6813217	134.4673
40884	cg0199355	15679463	15679463	0.2603859	0	1	0.4165175	42.89376
40962	cg0199741	48680440	22726367	0.2005657	0	1	0.0884544	-42.32327
40967	cg0199759	59640444	59640444	0.6871272	0	1	0.5737658	-25.00423
40974	cg0199788	22666461	22666461	0.554424	0	1	0.7027309	39.7934
41034	cg0200106	66717351	66717351	0.1852845	0	1	0.290633	26.70031
41095	cg02004401	14658436	25690377	0.3855273	0	1	0.2216446	-49.75232
41253	cg0201139	63759488	63759488	0.6265416	0	1	0.5098924	-24.29762
41266	cg0201172	73613315	54669365	0.1649072	0	1	0.0584884	-46.2268
41277	cg0201237	30653507	30653507	0.4111057	0	1	0.6300857	73.81918
41289	cg02012821	54691403	54691403	0.5114045	0	1	0.3633514	-35.54225
41320	cg0201439	72718380	72718380	0.5673051	0	1	0.7441345	57.6771
41401	cg02018291	31768427	31768427	0.2569881	0	1	0.378258	28.40474
41443	cg0202038	41641503	41641503	0.5226818	0	1	0.6424748	25.77604
41473	cg0202191	66773311	66773311	0.6239618	0	1	0.7591847	38.37726
41655	cg02031121	43772385	43772385	0.8539966	0	1	0.9641249	79.99045
41924	cg02045971	36753465	49639309	0.5639834	0	1	0.4005626	-42.1046
41949	cg02047051	69657408	69657408	0.3843833	0	1	0.5108482	26.8959
42086	cg0205313	40754486	40754486	0.5472087	0	1	0.7034014	43.4586
42101	cg0205389	62761334	62761334	0.3413335	0	1	0.2274373	-27.18982
42200	cg0205840	20630471	73725428	0.2960832	0	1	0.1243581	-69.49243
42475	cg0206959	11701350	11701350	0.5300692	0	1	0.6411781	22.7783
42576	cg0207346	18787317	18787317	0.5778268	0	1	0.7059793	31.45205
42624	cg02075791	35650440	35650440	0.3288946	0	1	0.4388082	22.06589

42893	cg0208798	44624356	44624356	0.4812312	0	1	0.581548	18.44476
42896	cg0208819	26700405	26700405	0.6848962	0	1	0.5804092	-21.89103
43007	cg0209428	73653485	73653485	0.2612579	0	1	0.4192665	43.71553
43028	cg02095601	71613376	71613376	0.5911394	0	1	0.7123171	29.06641
43042	cg0209622	38701337	38701337	0.7570575	0	1	0.8881804	59.20897
43169	cg0210207	42690304	42690304	0.2101439	0	1	0.3153349	24.96397
43251	cg0210607	67692407	67692407	0.6038589	0	1	0.8887458	374.3439
43378	cg0211305	22668459	22668459	0.6874413	0	1	0.408947	-122.1351
43486	cg02118671	58650332	35735454	0.742529	0	1	0.5306357	-78.51492
43502	cg0211969	12715504	12715504	0.1195057	0	1	0.2473439	44.88185
43505	cg0211979	41653398	69806312	0.159513	0	1	0.036569	-64.97071
43510	cg0211993	57761451	43808480	0.2875295	0	1	0.4275816	34.40289
43635	cg0212689	21603365	21603365	0.6415803	0	1	0.3576401	-124.2992
43648	cg0212741	19740340	19740340	0.9197813	0	1	0.8179865	-50.31499
43741	cg0213205	46729363	46729363	0.3469575	0	1	0.7727129	374.3439
43788	cg0213402	49760428	49760428	0.4915508	0	1	0.6163087	26.9177
43809	cg0213512	57807302	57807302	0.4456778	0	1	0.5479659	18.81386
43898	cg0214057	26657344	26657344	0.3547099	0	1	0.4700493	23.38919
43902	cg0214120	69664372	69664372	0.7346956	0	1	0.6116027	-31.18751
43934	cg0214393	34696308	34696308	0.623396	0	1	0.421169	-63.31657
44118	cg0215223	55703450	34610416	0.9339578	0	1	0.8064886	-75.44418
44212	cg0215672	14803389	14803389	0.1589014	0	1	0.2672166	30.19634
44235	cg0215762	53781451	53781451	0.7141777	0	1	0.8259446	35.14265
44265	cg0215948	29807491	20791359	0.3257598	0	1	0.0428483	-200.0124
44318	cg0216191	64650410	31701429	0.5345104	0	1	0.4319921	-18.85352
44322	cg0216228	12807354	56601450	0.3938442	0	1	0.2891739	-21.36191
44433	cg0216858	26797508	26797508	0.2238123	0	1	0.3270618	23.4952
44457	cg0216971	72641379	72641379	0.4453712	0	1	0.3146632	-29.72948
44466	cg0217010	39697472	39697472	0.2058756	0	1	0.3112944	25.31107
44517	cg0217288	49699431	49699431	0.8077406	0	1	0.9147736	52.1055
44523	cg0217306	36681393	26757342	0.4177277	0	1	0.2596273	-43.86496
44545	cg0217409	15664467	72608378	0.2312004	0	1	0.1164894	-38.56046
44709	cg0218422	37622508	37622508	0.6567134	0	1	0.7688935	29.30266
44716	cg0218454	42771474	42771474	0.9303995	0	1	0.63525	-226.6221
44724	cg0218500	72694378	72694378	0.2252795	0	1	0.3383596	27.00717
44774	cg0218814	44745437	44745437	0.778127	0	1	0.4451059	-192.3109
44784	cg0218866	10787450	10787450	0.5484048	0	1	0.7275042	57.11839
44853	cg0219252	64801367	64801367	0.3616371	0	1	0.470724	21.26149
44878	cg0219380	59631353	59631353	0.5323994	0	1	0.6696471	33.31846
44899	cg0219490	38687336	48773344	0.6049986	0	1	0.4328817	-46.69324
44914	cg0219625	37619333	37619333	0.3850197	0	1	0.5035523	24.1151
44948	cg0219762	19743370	41784469	0.5948592	0	1	0.479586	-23.27904
44999	cg0220175	46662451	46662451	0.5063073	0	1	0.894922	374.3439

45042	cg02203761	43722355	43722355	0.3999472	0	1	0.5070291	20.30355
45078	cg02205962	38789501	38789501	0.5978894	0	1	0.4889227	-21.27277
45217	cg02214597	46607504	63775303	0.3974456	0	1	0.2587899	-35.25015
45270	cg02217247	28616345	28616345	0.3870442	0	1	0.2795718	-22.58373
45296	cg02218932	13644467	13644467		0	1	0.799684	4.34E-09
45325	cg02220418	18675470	51631381	0.7385683	0	1	0.8389265	31.50704
45364	cg02222362	34644438	34644438	0.4830998	0	1	0.369072	-22.76566
45373	cg02222844	63665449	46801339	0.7396	0	1	0.5555776	-61.17403
45397	cg02224314	54760479	33722311	0.7577752	0	1	0.6308674	-34.55595
45470	cg02227879	58654437	58654437	0.5390796	0	1	0.6406272	19.717
45578	cg02233197	26765412	26765412	0.606338	0	1	0.7091116	22.25379
45626	cg02235843	11800397	11800397	0.618974	0	1	0.7315788	26.89237
45768	cg02243386	16646325	16646325	0.4047467	0	1	0.5430256	31.25382
45774	cg02243630	59795312	59795312	0.5066769	0	1	0.4018738	-19.59454
45896	cg02249577	19661302	16740379	0.7094428	0	1	0.5855684	-29.9549
45950	cg02251771	14751370	14751370	0.5811924	0	1	0.763914	63.56574
45995	cg02254774	32607413	54600312	0.7700156	0	1	0.6451574	-34.76543
46151	cg02262167	45666375	70666403	0.7420775	0	1	0.475075	-119.3185
46156	cg02262553	12658476	12658476	0.3772548	0	1	0.6019183	76.95147
46247	cg02267270	60657497	60657497	0.6218292	0	1	0.4912821	-29.1626
46272	cg02268561	13671358	13671358	0.6329834	0	1	0.5293907	-20.18693
46411	cg02275226	65730497	65730497	0.8380045	0	1	0.6439107	-86.15196
46658	cg02286623	72747447	27628432	0.3665011	0	1	0.2533374	-25.58605
46659	cg02286642	26615326	26615326	0.2436031	0	1	0.1283641	-37.02055
46683	cg02287371	10605360	10605360	0.4238224	0	1	0.2523476	-50.95076
46701	cg02288345	19809433	19809433	0.493922	0	1	0.642342	36.90208
46779	cg02291561	15691331	15691331	0.1275901	0	1	0.2375913	34.60401
46813	cg02293501	28714496	28714496	0.8566543	0	1	0.7480882	-38.3448
46857	cg02295509	45796496	45796496	0.5035459	0	1	0.6122734	21.41411
46860	cg02295574	26612374	26612374	0.7854671	0	1	0.9128643	65.52663
46881	cg02296931	39721443	24783471	0.1828304	0	1	0.3332416	47.17025
46920	cg02299007	57603479	57603479	0.3663283	0	1	0.7338303	374.3439
46954	cg02300652	30661432	30661432	0.4268643	0	1	0.5287384	18.65824
46988	cg02301920	24763311	24763311	0.5437921	0	1	0.7810419	103.116
47009	cg02303209	34697354	34697354	0.6082451	0	1	0.7219917	26.77797
47036	cg02304092	47773302	48721351	0.4661187	0	1	0.179545	-143.6083
47052	cg02304584	30626500	30626500	0.4711645	0	1	0.311944	-41.72014
47082	cg02305687	48699436	48699436	0.6230667	0	1	0.5219465	-19.24103
47196	cg02311337	70681353	70681353		0	1	0.9501108	4.34E-09
47227	cg02312593	64807420	64807420	0.5030409	0	1	0.3806887	-25.46743
47239	cg02313379	22653369	51809345	0.1797345	0	1	0.2922796	30.04821
47288	cg02315732	23732351	23732351	0.3489465	0	1	0.4620878	22.75173
47310	cg02317299	64623415	58695329	0.4776257	0	1	0.5860178	20.94673

47368	cg02319829	46797387	46797387	0.8366599	0	1	0.6531951	-78.4893
47369	cg02319868	63707303	63707303	0.5814595	0	1	0.6848262	21.52022
47488	cg02326566	37675446	37675446	0.589416	0	1	0.4835986	-20.18297
47577	cg02330500	53770462	53770462	0.1873493	0	1	0.297888	28.60008
47682	cg02335251	67807477	67807477	0.4818901	0	1	0.6055936	26.33998
47762	cg02338840	58657370	58657370		0	1		-4.34E-09
47797	cg02340092	19620379	19620379	0.0766284	0	1	0.1977872	50.34867
47854	cg02342754	41775434	41775434	0.8106781	0	1	0.635265	-67.21432
47930	cg02345758	37710395	37710395	0.7449138	0	1	0.9520096	156.5356
47984	cg02348430	47783343	47783343	0.1907469	0	1	0.3368587	44.11095
48035	cg02351277	33786418	33786418	0.6326909	0	1	0.7494628	29.67407
48066	cg02352633	32803433	32803433	0.3103139	0	1	0.4208224	22.68652
48120	cg02355809	29764301	29764301	0.5323228	0	1	0.2934264	-88.82812
48169	cg02358382	54608494	54608494	0.6636671	0	1	0.775162	29.54073
48274	cg02363593	62732492	62732492	0.184226	0	1	0.3443543	52.03344
48486	cg02372404	33619327	33619327	0.3807668	0	1	0.0779546	-198.9454
48522	cg02374984	62778419	62778419	0.6188626	0	1	0.7585712	40.38428
48565	cg02376916	22802390	22802390	0.8317934	0	1	0.6986246	-46.94765
48607	cg02379549	52684309	52684309	0.4247615	0	1	0.1814153	-106.3663
48619	cg02380236	18773369	59737510	0.5609909	0	1	0.7623963	74.71088
48654	cg02381853	43676505	43676505	0.6086692	0	1	0.7329549	31.55353
48809	cg02389040	74604407	74604407	0.601229	0	1	0.4085817	-57.35221
48815	cg02389180	30634354	30634354	0.2719853	0	1	0.3984532	29.68691
48822	cg02389317	61663314	61663314	0.3166648	0	1	0.5338346	72.98967
48829	cg02389634	56808505	56808505	0.4901232	0	1	0.6094358	24.87179
48837	cg02389942	74642445	74642445	0.2988162	0	1	0.1048185	-90.02982
48860	cg02390813	72750329	66630365	0.9019092	0	1	0.7942221	-48.36368
48938	cg02394249	19662495	19662495	0.4142188	0	1	0.5705864	38.91103
49040	cg02398482	27722479	27722479	0.5237533	0	1	0.721069	66.82908
49101	cg02400773	67767450	67767450	0.7177667	0	1	0.827729	34.52588
49110	cg02401352	19620448	19620448	0.3288485	0	1	0.2003707	-35.03163
49113	cg02401524	63767396	63767396	0.9280311	0	1	0.8135502	-62.6526
49129	cg02402208	19740380	19740380	0.3153247	0	1	0.4243779	22.08628
49164	cg02403883	70783472	70783472	0.6470628	0	1	0.5167499	-29.76199
49217	cg02407415	66778398	61773490	0.2245016	0	1	0.0835365	-60.74213
49293	cg02413040	29678340	29678340	0.1116266	0	1	0.2150054	33.68401
49331	cg02415057	47715360	39807380	0.1716064	0	1	0.0644593	-45.06026
49497	cg02426178	36803354	36803354	0.5265145	0	1	0.6341314	21.47952
49519	cg02427576	56689398	56689398	0.4620129	0	1	0.5967543	30.26687
49635	cg02434554	73652409	73652409	0.4086443	0	1	0.306122	-20.22578
49675	cg02438026	65654422	65654422	0.3363521	0	1	0.4395677	19.81422
49848	cg02448295	21728441	21728441	0.1633467	0	1	0.2946992	40.16185
49851	cg02448481	36664410	10774420	0.9778093	0	1	0.7296582	-223.4693

49859	cg0244893	43770317	43770317	0.8241751	0	1	0.9462521	78.15036
49870	cg0244967	21667300	21667300	0.2943068	0	1	0.5916757	137.7275
49917	cg0245241	22803434	22803434	0.4287428	0	1	0.1901069	-101.0385
49931	cg0245296	32611456	19780360	0.2854286	0	1	0.0559143	-140.0173
49978	cg0245534	49740456	49740456	0.5770062	0	1	0.6801599	21.29377
50033	cg0245803	70648417	18723357	0.0512264	0	1		-4.34E-09
50041	cg0245818	32715306	32715306	0.6936828	0	1	0.8146709	38.03944
50129	cg0246219	34754444	34754444	0.479681	0	1	0.1034197	-276.0428
50140	cg0246266	52800491	52800491	0.1574624	0	1	0.2650353	30.0219
50174	cg0246445	35647474	35647474	0.5769475	0	1	0.8014255	98.23613
50175	cg0246448	41709400	41709400	0.3790692	0	1	0.5176941	31.5244
50183	cg0246480	26621487	26621487	0.8983376	0	1	0.7059019	-107.9352
50301	cg0247069	29660440	63650414	0.9242489	0	1	0.7970902	-70.34007
50461	cg0247836	62778410	62778410	0.5781619	0	1	0.7682375	68.58669
50479	cg0247902	28787373	28787373	0.5628821	0	1	0.6980047	33.83672
50486	cg0247930	73614314	73614314	0.4139893	0	1	0.5180516	19.32992
50505	cg0248032	55675493	55675493	0.5093203	0	1	0.615023	20.50763
50514	cg0248067	70810398	70810398	0.5421442	0	1	0.7142702	52.17098
50748	cg0249046	11677337	11677337	0.6483889	0	1	0.5049977	-35
50785	cg0249194	21602370	21602370	0.1808959	0	1	0.3582393	62.0506
50870	cg0249576	45745344	45745344	0.3075523	0	1	0.4544	36.44147
50932	cg0249930	62710352	62710352	0.7760295	0	1	0.8806436	40.99618
50940	cg0249964	72752352	72752352	0.6683778	0	1	0.7708466	25.6114
50996	cg0250214	13619464	13619464	0.2523493	0	1	0.4467317	63.40131
51072	cg0250595	60701359	60701359	0.500505	0	1	0.6473742	36.42036
51090	cg0250672	65732360	65732360	0.0614257	0	1	0.1755187	50.17897
51094	cg0250690	30785352	30785352	0.4194273	0	1	0.5494572	28.09144
51101	cg0250718	29708358	29708358	0.3484003	0	1	0.4953985	35.35902
51106	cg0250757	55603348	55603348	0.8030216	0	1	0.3299237	-371.3336
51209	cg0251355	50623440	50623440	0.5066915	0	1	0.6369669	29.44685
51238	cg0251521	57774402	57774402	0.1182887	0	1	0.2235625	33.63655
51253	cg0251589	45775478	45775478	0.5199417	0	1	0.6218052	19.44383
51270	cg0251669	55685455	55685455	0.8243901	0	1	0.6283048	-83.8158
51299	cg0251813	12627503	12627503	0.4826888	0	1	0.2752464	-69.28884
51317	cg0251926	24663407	24663407	0.4345119	0	1	0.5418841	20.34695
51384	cg0252293	29680371	29680371	0.3552572	0	1	0.118342	-118.389
51411	cg0252423	33677426	33677426	0.5761748	0	1	0.6806192	21.73048
51487	cg0252781	41782488	41782488	0.7218978	0	1	0.8264074	31.80667
51583	cg0253264	46751358	31767336	0.021427	0	1	0.1231208	55.98919
51610	cg0253372	37758449	37758449	0.6511697	0	1	0.5065007	-35.63333
51769	cg0254144	55644471	55644471	0.4434434	0	1	0.3085763	-31.52319
51785	cg0254281	47704302	47704302	0.3929986	0	1	0.5053567	22.01267
51891	cg0254877	44637449	44637449	0.6484476	0	1	0.5400781	-22.06163

51923	cg02550308	18647437	18647437	0.1619093	0	1	0.2687373	29.27465
51934	cg02550738	31707440	31707440	0.7256363	0	1	0.8648773	57.65231
52178	cg02564175	13637463	48691441	0.1369203	0	1	0.3516967	95.57898
52179	cg02564259	66654397	66654397	0.2689828	0	1	0.3726953	21.70159
52215	cg02566259	72648474	72648474	0.4606391	0	1	0.356926	-19.65383
52242	cg02567750	59810364	59810364	0.7460223	0	1	0.6251642	-31.07703
52245	cg02567769	56600477	34766486	0.6399065	0	1	0.5309547	-22.04087
52248	cg02567879	44632442	44632442	0.4737625	0	1	0.598668	26.65534
52409	cg02574844	38756423	17704375	0.8559373	0	1	0.702683	-64.02131
52467	cg02577387	31618469	37668450	0.4725696	0	1	0.320291	-38.33617
52505	cg02578709	62603494	62603494	0.5493556	0	1	0.6628218	24.17611
52529	cg02579959	55778355	55778355	0.2499334	0	1	0.3617383	25.25437
52554	cg02580986	23730425	66742361	0.3804917	0	1	0.2789723	-20.65911
52644	cg02584498	29652303	29652303	0.3702662	0	1	0.5181566	35.38246
52664	cg02585440	56782510	56782510	0.5429543	0	1	0.6739902	31.03119
52756	cg02590088	44686465	44686465	0.2012578	0	1	0.305061	25.00144
52835	cg02594532	73663496	73663496	0.4606605	0	1	0.5918122	28.83652
52903	cg02598335	10689459	10689459	0.4264881	0	1	0.5309663	19.44368
52918	cg02598807	51673307	71733392	0.6014717	0	1	0.7023478	21.34434
52934	cg02599498	27809452	55635418	0.2950025	0	1	0.4297433	31.95529
53007	cg02603022	64671423	64671423	0.5746658	0	1	0.4694651	-19.84821
53040	cg02604730	51751449	51751449	0.5199868	0	1	0.6733103	40.34913
53064	cg02605760	24668498	31717474	0.5508568	0	1	0.4389275	-21.81676
53080	cg02606566	17781341	17781341	0.0944493	0	1	0.2476444	65.45028
53172	cg02611240	22734449	22734449	0.250102	0	1	0.0575675	-107.9412
53217	cg02613370	17799351	17634499	0.5362187	0	1	0.3912513	-33.99244
53244	cg02614549	32703318	32703318	0.7219862	0	1	0.8526608	49.66444
53364	cg02620335	31791443	31791443	0.5648934	0	1	0.6748021	23.35627
53407	cg02622251	38804348	38804348	0.5770063	0	1	0.6812023	21.66859
53433	cg02623604	61753476	17783396	0.2676648	0	1	0.1438546	-39.03301
53495	cg02626269	50637301	50637301	0.7385549	0	1	0.9320853	128.8492
53530	cg02628016	59615327	59615327	0.5589347	0	1	0.6695458	23.41905
53648	cg02632314	27615380	27615380	0.4673632	0	1	0.6357874	45.74184
53662	cg02633036	25763469	25763469	0.3221044	0	1	0.447286	27.47062
53851	cg02640147	44716428	44716428	0.3016914	0	1	0.470838	46.81897
53890	cg02642117	40687465	40687465	0.5915287	0	1	0.7172577	31.13506
53921	cg02643580	26774414	26774414	0.2934281	0	1	0.4678902	49.84671
54036	cg02649063	16701425	16701425	0.585595	0	1	0.6894001	21.82572
54102	cg02653117	71715378	60658342	0.304143	0	1	0.4224251	25.50432
54222	cg02659217	18801476	18801476	0.3201953	0	1	0.4238216	20.25095
54248	cg02660643	59607315	59607315	0.519718	0	1	0.6243448	20.33861
54368	cg02667103	35784414	35784414	0.5102207	0	1	0.6203215	21.99783
54586	cg02678768	14641394	39634389	0.4445547	0	1	0.3361188	-21.45051

54655	cg0268357	16704484	16704484	0.5849316	0	1	0.6909274	22.6129
54691	cg0268666	44685306	44685306	0.8650162	0	1	0.7592995	-38.38007
54785	cg0269211	29670508	29670508	0.664956	0	1	0.7707963	26.91746
54813	cg0269322	27785423	27785423	0.4505386	0	1	0.6626707	70.9939
54928	cg0269858	47740452	35810392	0.6554446	0	1	0.5453252	-22.82586
54968	cg0270010	66802462	66802462	0.4594787	0	1	0.5634323	19.38744
54997	cg0270102	56803304	56803304	0.672082	0	1	0.7782823	27.64913
55014	cg0270244	66611456	66611456	0.3185478	0	1	0.0404804	-196.6535
55030	cg0270324	47632385	47632385	0.8600272	0	1	0.6638431	-94.6985
55053	cg0270448	17772323	17772323	0.6691594	0	1	0.7897791	34.86643
55184	cg0271029	65777339	10733343	0.5494024	0	1	0.3525682	-59.74054
55222	cg0271166	19654361	19654361	0.8525824	0	1	0.7348357	-42.47304
55252	cg0271258	67736389	67736389	0.7030313	0	1	0.6000983	-22.05582
55330	cg0271630	64765382	64765382	0.6139092	0	1	0.4973323	-24.01914
55335	cg0271649	66661469	66661469	0.295307	0	1	0.4199241	28.07097
55387	cg02719221	61739485	61739485	0.7320845	0	1	0.8802692	67.92042
55393	cg0271963	57633449	57633449	0.8591261	0	1	0.746266	-41.08969
55444	cg0272259	57608460	57602461	0.3794911	0	1	0.2740677	-22.08952
55463	cg0272339	12798321	69766403		0	1	0.0267209	4.34E-09
55565	cg0272748	10611473	10611473	0.1959111	0	1	0.31571	31.70716
55615	cg0273030	18609364	18609364	0.2242887	0	1	0.0423244	-107.4237
55623	cg0273086	35730376	35730376	0.1709745	0	1	0.2760911	27.75393
55702	cg0273505	64732455	72650504	0.8350692	0	1	0.7015931	-47.71207
55708	cg0273542	24708417	24708417	0.8485552	0	1	0.5395985	-190.7297
55797	cg0273928	22683502	22683502	0.5479608	0	1	0.6706976	27.74738
55835	cg0274132	66636431	66636431	0.8404231	0	1	0.373017	-371.3336
55891	cg0274363	30668416	30668416	0.5050168	0	1	0.6461591	33.99766
55933	cg0274578	40672311	40672311	0.6324273	0	1	0.4253642	-66.48005
56067	cg0275293	28722350	28722350	0.1829682	0	1	0.4388489	115.9998
56102	cg0275494	28662413	28662413	0.512208	0	1	0.4062653	-19.92576
56140	cg0275668	49771487	49771487	0.655277	0	1	0.7950402	44.64226
56163	cg0275757	74665399	74665399	0.6577504	0	1	0.4992469	-41.95947
56371	cg0276763	35693455	11653451	0.2374446	0	1	0.364238	31.626
56394	cg02768671	37621403	37621403	0.5332478	0	1	0.6925833	44.21772
56527	cg0277358	48657414	17667350	0.7459394	0	1	0.64452	-23.60898
56608	cg0277665	25789310	25789310	0.1281171	0	1	0.2297321	30.63873
56748	cg0278607	25802510	25802510	0.2724483	0	1	0.373575	20.74245
56777	cg0278798	38673342	59767330	0.5514458	0	1	0.4349332	-23.32553
56828	cg02790691	44660376	44660376	0.2986192	0	1	0.3989334	19.72582
56874	cg0279332	74753409	74753409	0.1785468	0	1	0.3584966	63.93426
56900	cg0279492	41734374	41734374	0.8118175	0	1	0.6564318	-55.62379
56932	cg0279647	47728452	47728452	0.2428308	0	1	0.3680468	30.67732
57041	cg0280250	54621330	54621330	0.0787037	0	1	0.2875847	111.1756

57200	cg0281143	29749452	29749452	0.8954307	0	1	0.6356049	-165.4051
57224	cg02812891	35743415	15771381	0.13205	0	1	0.2960579	62.98347
57241	cg0281413	45768426	45768426	0.5493886	0	1	0.8223261	144.4944
57328	cg0281965	57804497	57804497	0.5564154	0	1	0.7799467	92.77396
57341	cg0282041	55667427	55667427	0.5092604	0	1	0.6399505	29.68904
57440	cg0282623	10684376	10684376	0.5339791	0	1	0.6372038	20.16105
57453	cg02827061	39741477	39741477	0.2928917	0	1	0.4087482	25.00449
57557	cg0283251	17780384	17780384	0.4905379	0	1	0.6895947	64.96909
57631	cg0283623	29694415	29632381	0.7359896	0	1	0.9148808	105.7346
57666	cg0283753	23802370	41627337	0.5851619	0	1	0.4675988	-23.92549
57715	cg0283982	54743405	54743405	0.459275	0	1	0.3512388	-21.07258
57781	cg0284334	16645310	16645310	0.2078092	0	1	0.3399639	36.00541
57838	cg0284722	32642474	32642474	0.1689623	0	1	0.3018381	40.21508
57873	cg0284883	71766444	71766444	0.8438092	0	1	0.9628161	86.86865
57881	cg0284950	51739320	51739320	0.2104454	0	1	0.3117939	23.54754
58022	cg0285490	33789400	33789400	0.4292993	0	1	0.5434766	22.52939
58130	cg0285955	61635426	65725476	0.4112353	0	1	0.2321517	-56.72171
58164	cg0286117	67749342	67749342	0.2561886	0	1	0.3590929	21.90876
58231	cg0286463	17648329	17648329	0.3073495	0	1	0.4756558	46.16729
58354	cg0287131	14607466	14607466	0.7854568	0	1	0.6845468	-26.12533
58379	cg0287276	38641425	28689384	0.8261415	0	1	0.6611586	-64.09856
58404	cg0287378	31665328	31665328	0.3718165	0	1	0.104539	-150.1653
58468	cg02877261	15650309	15650309	0.4886603	0	1	0.221096	-118.5856
58534	cg0288016	62794434	62794434	0.2818074	0	1	0.4175724	32.90649
58624	cg02884661	36660387	36660387	0.7295953	0	1	0.6135654	-28.07707
58746	cg0289023	64667483	64667483	0.76537	0	1	0.2863828	-371.3336
58749	cg0289025	67607477	67607477	0.0615517	0	1	0.2677569	117.0495
58752	cg0289036	70618332	23673423	0.3534715	0	1	0.2443443	-24.55974
58915	cg0289766	28808457	28808457	0.3885963	0	1	0.256864	-32.50154
58927	cg0289815	31806316	31806316	0.2357237	0	1	0.3490851	26.52897
58999	cg0290152	50743364	50743364	0.6539343	0	1	0.4862311	-46.11378
59175	cg0290957	57637340	57637340	0.6400204	0	1	0.8692443	124.4137
59200	cg0291049	48751465	48751465	0.8499777	0	1	0.665711	-82.84892
59271	cg0291409	19613479	19613479	0.5850543	0	1	0.7024533	27.13399
59368	cg0291825	74716395	71640376	0.2696206	0	1	0.1581115	-31.65674
59381	cg0291908	13612435	13612435	0.3791015	0	1	0.5076897	27.71315
59390	cg0291956	60730314	13641509	0.02886	0	1	0.1600752	74.68999
59410	cg0292019	33797315	33797315	0.5436841	0	1	0.7121131	50.09339
59468	cg0292273	50807418	50807418	0.6544135	0	1	0.7998989	48.27808
59620	cg02929371	27744394	65657383	0.3529751	0	1	0.1421148	-91.39391
59679	cg0293160	27668432	27668432	0.8049569	0	1	0.6565455	-50.61364
59743	cg0293471	64691421	64691421	0.3869179	0	1	0.4892555	18.93824
59782	cg0293659	33623322	33623322	0.63216	0	1	0.8296803	86.21307

59804	cg02937671	38742373	38742373	0.4712198	0	1	0.3618225	-21.35755
59815	cg02938066	50657379	15635405	0.760397	0	1	0.8990289	68.00166
59931	cg02944007	46759419	47701300	0.7068905	0	1	0.5869141	-28.31994
60072	cg02951719	61754442	61754442	0.838622	0	1	0.6513644	-81.59679
60156	cg02954704	44606340	44606340	0.5782227	0	1	0.6831238	21.9662
60322	cg02961798	42782402	42782402	0.2889422	0	1	0.4013418	23.93868
60334	cg02962597	17628444	17628444	0.4551424	0	1	0.5558054	18.36466
60384	cg02964385	23729497	23729497	0.7888586	0	1	0.9083361	58.26189
60405	cg02965295	40706498	40706498	0.1579178	0	1	0.2667973	30.53663
60426	cg02966475	62807390	62807390	0.4451267	0	1	0.6000808	38.62899
60450	cg02968094	57674469	57674469	0.3047724	0	1	0.4176747	23.63343
60462	cg02968537	10625360	10625360	0.7519359	0	1	0.8661215	43.23056
60677	cg02978201	39717400	39717400	0.5343648	0	1	0.7551358	86.34249
60706	cg02979711	62796426	62796426	0.2156268	0	1	0.3340989	29.70193
60717	cg02980047	65768429	65768429	0.3820184	0	1	0.5402244	39.75377
60777	cg02983090	36689346	36689346	0.2075979	0	1	0.3246459	29.69143
60788	cg02983911	73756507	73756507	0.6133736	0	1	0.7159575	22.48844
60952	cg02992067	64607371	64607371	0.6590289	0	1	0.7664607	27.21629
61052	cg02996355	19683374	42635509	0.4543187	0	1	0.3230792	-29.69384
61121	cg02999390	74772397	25804416	0.675084	0	1	0.5432359	-31.39637
61200	cg03003335	29612384	53756368	0.3400439	0	1	0.503265	42.68961
61281	cg03007623	25767405	62797494	0.1376031	0	1	0.283172	51.27799
61396	cg03014326	21794330	42801352	0.2380085	0	1	0.1180171	-41.01349
61406	cg03014829	51660482	51660482	0.647522	0	1	0.4515947	-60.59442
61475	cg03018931	19795429	62677307	0.3912751	0	1	0.5118592	24.77256
61486	cg03019812	47769345	47769345	0.3505855	0	1	0.6277224	117.8952
61491	cg03020006	44797510	16750437	0.8325795	0	1	0.7255087	-33.81332
61495	cg03020379	14783428	14783428	0.9143205	0	1	0.7325081	-107.7949
61504	cg03020684	71641342	71641342	0.5031481	0	1	0.7826048	138.6117
61544	cg03022891	74698328	19758354	0.7586831	0	1	0.58969	-55.14503
61571	cg03024489	39704422	39704422	0.7987553	0	1	0.6574794	-45.92762
61611	cg03025825	49712375	49712375	0.1771186	0	1	0.2774437	25.36258
61612	cg03025830	28705352	36682333	0.6333725	0	1	0.5288313	-20.49029
61618	cg03026119	66747309	66747309	0.4221438	0	1	0.5230502	18.37323
61663	cg03028786	16691439	16691439	0.373799	0	1	0.2363728	-36.12506
61684	cg03030267	43711485	43711485	0.3492257	0	1	0.5446337	58.99117
61788	cg03035213	57606356	46785348	0.6431295	0	1	0.3995139	-91.2673
61896	cg03040423	74732478	74732478	0.9552442	0	1	0.8361211	-81.489
61955	cg03043127	74784429	74784429	0.7870818	0	1	0.6402945	-47.13943
61989	cg03044281	45628426	45628426	0.3504729	0	1	0.4573827	20.73009
62089	cg03048372	36677492	47662333	0.7607927	0	1	0.6502753	-28.01112
62092	cg03048488	26676361	26676361	0.1964829	0	1	0.3590012	51.76283
62097	cg03048921	34718455	34718455	0.5938275	0	1	0.8496003	139.0537

62107	cg03049445	69758346	69758346	0.6321641	0	1	0.7572389	33.72087
62156	cg03052004	67625419	67625419	0.7984551	0	1	0.9109881	54.49392
62171	cg03052502	31713501	40601382	0.4678152	0	1	0.351877	-23.63286
62188	cg03053358	71775473	31601472	0.4834427	0	1	0.7462232	116.5109
62207	cg03053980	64799492	64799492	0.3481477	0	1	0.4530445	20.13968
62303	cg03058412	44779447	44779447	0.4363786	0	1	0.5380269	18.5986
62331	cg03059876	19659320	64653445	0.2522212	0	1	0.3770965	30.02832
62388	cg03062944	33708469	57620507	0.4493307	0	1	0.6401196	57.41329
62433	cg03065090	31620397	31620397	0.2101744	0	1	0.3103386	23.13916
62532	cg03069731	58731498	58731498	0.2793725	0	1	0.4456541	46.56261
62575	cg03072082	22794385	22794385	0.0687551	0	1	0.2643136	105.0335
62651	cg03075889	20639350	20639350	0.502463	0	1	0.2472484	-105.0351
62686	cg03078006	29670350	51658304	0.5354564	0	1	0.6576177	27.07607
62694	cg03078363	37712341	24651301	0.793761	0	1	0.6781958	-33.03359
62734	cg03080336	16655374	16655374	0.3773166	0	1	0.4976463	24.79751
62793	cg03084184	52659317	67714456	0.1520565	0	1	0.3549166	83.45274
62837	cg03086707	23709502	23709502	0.2925703	0	1	0.3944398	20.3714
62872	cg03088958	65682469	65682469	0.1946908	0	1	0.3478983	47.18609
62879	cg03089717	54644378	54644378		0	1		-4.34E-09
63009	cg03097134	20764406	20764406	0.5412318	0	1	0.692463	40.46712
63092	cg03102494	54735359	29622494	0.6314608	0	1	0.5257484	-20.81814
63148	cg03105556	36725473	36725473	0.5478951	0	1	0.4374672	-21.32525
63188	cg03108070	69757501	42616429	0.5522762	0	1	0.4364722	-23.09198
63227	cg03109913	21688303	21688303	0.1526918	0	1	0.3278771	65.57548
63272	cg03112518	69725325	69725325	0.6874291	0	1	0.5836226	-21.75567
63328	cg03115532	54616458	54616458	0.3781948	0	1	0.515346	30.95581
63338	cg03116016	27631430	27631430	0.2937029	0	1	0.4047323	23.3241
63375	cg03117611	46765327	46765327	0.2800465	0	1	0.4092774	30.40187
63420	cg03120147	10786355	33658325	0.8938226	0	1	0.7751781	-52.91061
63425	cg03120461	43717452	72646479	0.5870118	0	1	0.440071	-35.00428
63463	cg03122926	52703317	52703317	0.536204	0	1	0.2982558	-87.86978
63478	cg03123709	27808379	27808379	0.0748012	0	1	0.266215	99.18104
63532	cg03126739	72746442	72746442	0.2671841	0	1	0.4702105	67.23669
63552	cg03127584	51677413	51677413	0.2437076	0	1	0.3936278	41.15914
63576	cg03128499	50803403	50803403	0.2806188	0	1	0.3922864	23.96792
63624	cg03130910	18723328	71768350	0.3438088	0	1	0.5464743	63.28363
63676	cg03133408	67624445	67624445	0.8930849	0	1	0.7894709	-43.39633
63717	cg03135948	16702378	16702378	0.8221748	0	1	0.9367501	66.87945
63721	cg03136151	72796315	72796315	0.7418388	0	1	0.9251688	115.5027
63724	cg03136493	25795438	25795438	0.5089836	0	1	0.6142426	20.35665
63840	cg03142741	53804372	53804372	0.3658462	0	1	0.4850114	24.52642
63861	cg03143591	72635510	72635510	0.7743165	0	1	0.9014348	60.98091
63965	cg03147852	61755437	61755437	0.6597325	0	1	0.7625607	25.16676

64063	cg0315250	20603307	30748437	0.7410886	0	1	0.6278043	-27.73442
64125	cg0315654	54620402	54620402	0.5448032	0	1	0.6809006	33.35898
64295	cg0316501	37801383	26609473	0.2045365	0	1	0.0950136	-39.60526
64296	cg0316517	25652440	25652440	0.5039909	0	1	0.3883477	-23.12007
64343	cg0316788	40793322	40793322	0.2860181	0	1	0.4453466	42.90721
64649	cg0318370	27689358	27689358	0.6664761	0	1	0.9088972	156.5356
64674	cg0318477	64615357	64615357	0.4747957	0	1	0.5946598	24.82888
64686	cg0318570	46675353	46675353	0.4930738	0	1	0.3865386	-20.21539
64726	cg0318766	65795451	65795451	0.7075221	0	1	0.5468251	-45.90239
64742	cg0318839	40618341	40618341	0.583124	0	1	0.4623162	-25.01106
64751	cg0318902	58780320	40648391	0.4646834	0	1	0.3631201	-18.93001
64967	cg0320133	64645445	64645445	0.184081	0	1	0.3137348	37.06762
64976	cg0320206	22773327	65733324	0.3816589	0	1	0.211026	-54.38079
65185	cg0321320	71778483	19757345	0.4109575	0	1	0.2441514	-49.23264
65371	cg0322139	23660495	23660495	0.8114033	0	1	0.232072	-371.3336
65373	cg0322148	32772437	32772437	0.5687267	0	1	0.6832715	25.27058
65442	cg0322462	65721411	65721411	0.3710231	0	1	0.496402	26.63685
65456	cg0322544	36697398	38670430	0.6120681	0	1	0.4830543	-28.38307
65540	cg0322903	61601301	12768448	0.3547814	0	1		-4.34E-09
65740	cg03240981	23786387	23786387	0.6117014	0	1	0.738581	33.0176
65838	cg0324647	74694436	74694436	0.3396165	0	1	0.4433999	19.93281
65969	cg0325433	14684453	14684453	0.2377247	0	1	0.3420901	23.1979
66000	cg0325609	35665324	46752368	0.2252183	0	1	0.1233847	-31.33154
66006	cg0325668	48703475	55689305	0.4025598	0	1	0.2958796	-21.8199
66024	cg0325742	11697450	11697450	0.2451067	0	1	0.3540328	24.45273
66038	cg0325813	25724501	25724501	0.3102023	0	1	0.4347669	27.57458
66083	cg03260621	32632363	32632363	0.3836093	0	1	0.5372689	37.72635
66126	cg0326269	30772379	30772379	0.5910429	0	1	0.7170851	31.24999
66140	cg0326319	36697485	36697485	0.1705744	0	1	0.2796466	29.4134
66159	cg0326413	34617348	15745431	0.5621538	0	1	0.243724	-163.462
66166	cg0326455	20767486	68790453	0.3244422	0	1	0.2017491	-32.44657
66180	cg0326526	38785503	38785503	0.6515241	0	1	0.758857	26.63012
66252	cg0326936	74623352	74623352		0	1	0.7857058	4.34E-09
66284	cg0327148	29659310	29659310	0.4762709	0	1	0.6719469	61.77413
66294	cg0327190	49612398	49612398	0.3479614	0	1	0.4535728	20.36345
66311	cg0327249	45687351	45687351	0.777857	0	1	0.892138	49.66611
66313	cg0327293	26785499	26785499	0.7212726	0	1	0.8412647	41.61351
66380	cg0327688	24762468	24762468	0.5490087	0	1	0.6506964	19.99161
66381	cg0327692	38610449	38610449	0.6321263	0	1	0.8723428	135.2323
66393	cg0327755	15760501	55775356	0.9302716	0	1	0.7876168	-85.37446
66558	cg0328704	24810478	24810478	0.3038893	0	1	0.4117783	21.99423
66661	cg0329222	48643368	40807439	0.9422039	0	1	0.7550021	-130.7037
66675	cg0329320	71631447	10656419	0.8926784	0	1	0.7721364	-53.77606

66679	cg03293507	65794484	67747316	0.2711247	0	1	0.378318	22.78388
66733	cg03296304	43767507	53655437	0.2533529	0	1	0.5323856	124.1077
66855	cg03302281	17625478	17625478	0.5036703	0	1	0.6111256	20.9922
66940	cg03307177	36784509	36784509	0.8281302	0	1	0.7080747	-39.51239
66947	cg03307659	29779377	21661421	0.6392015	0	1	0.507629	-30.00267
67054	cg03312406	35720308	35720308	0.4400452	0	1	0.5966074	39.28075
67060	cg03312587	12722321	12722321	0.3727398	0	1	0.5413052	44.65098
67098	cg03314029	36773421	19738374	0.7263099	0	1	0.5288669	-67.47447
67131	cg03315469	32760433	15738422	0.5140034	0	1	0.8827224	374.3439
67371	cg03327325	56714412	56714412	0.3734586	0	1	0.2478622	-30.54495
67395	cg03328299	72790425	72790425	0.3284386	0	1	0.4980368	46.03003
67425	cg03329597	30766334	30766334	0.3039433	0	1	0.4860495	53.26237
67427	cg03329714	17746301	17746301	0.7474611	0	1	0.8790839	56.79912
67504	cg03333149	61768320	73756355		0	1		-4.34E-09
67545	cg03335262	61766455	67632339	0.462972	0	1	0.3063478	-40.75814
67571	cg03337057	69804327	64785367	0.5065246	0	1	0.3394868	-44.49525
67660	cg03340754	38784345	38784345	0.5279606	0	1	0.4034443	-26.09268
67675	cg03341641	41716440	41716440	0.5579544	0	1	0.7338946	56.061
67684	cg03342032	24770426	24770426	0.248874	0	1	0.3570396	24.01302
67713	cg03343571	20631385	65602498	0.0266368	0	1	0.253008	156.5356
67846	cg03349091	47708439	47708439	0.7369801	0	1	0.6224329	-27.96018
67869	cg03350138	23625367	23625367	0.6495028	0	1	0.5433753	-21.36354
67961	cg03354554	44712471	44712471	0.7122416	0	1	0.8171164	30.85732
67963	cg03354616	52704320	52704320	0.4880176	0	1	0.709479	80.77098
67999	cg03356172	47793323	47793323	0.5318978	0	1	0.6608149	29.69736
68033	cg03357999	64655397	63787408	0.5298198	0	1	0.3155503	-71.20322
68254	cg03370193	35655452	43662303	0.5967351	0	1	0.4931015	-19.6027
68330	cg03373960	61720304	61720304	0.6559454	0	1	0.7561769	23.78902
68331	cg03374148	66647422	66647422	0.6689925	0	1	0.7747427	27.18649
68387	cg03378197	63667510	24806498	0.4451108	0	1	0.3279701	-24.49286
68532	cg03386715	21618356	21618356	0.6223033	0	1	0.8494228	114.7229
68600	cg03389890	73783404	27792304	0.4379037	0	1	0.3176101	-25.83728
68641	cg03392100	62733384	62733384	0.9012131	0	1	0.7905684	-50.04179
68757	cg03398919	41748327	41748327	0.7091421	0	1	0.5648351	-38.43362
68759	cg03398989	26691355	26691355	0.8445033	0	1	0.412993	-361.1803
68834	cg03401875	47738484	47738484	0.66998	0	1	0.5564182	-24.44328
68966	cg03408135	10759351	10759351	0.3702856	0	1	0.1741872	-74.55656
68971	cg03408497	40659498	40659498	0.5095244	0	1	0.6368232	28.33098
69043	cg03412618	19668486	19668486	0.2725483	0	1	0.4319811	43.68996
69130	cg03418136	42620358	47803332	0.9728447	0	1	0.860968	-88.56892
69172	cg03420970	59754449	59754449	0.8613195	0	1	0.5683349	-179.9176
69206	cg03422552	17711503	17711503	0.5108354	0	1	0.6552935	35.70187
69207	cg03422583	33804439	33804439	0.5250508	0	1	0.825414	374.3439

69209	cg0342274	46741444	46741444	0.7036464	0	1	0.8177525	35.16476
69319	cg0342861	66699313	66699313	0.6646553	0	1	0.5327565	-30.98973
69356	cg0343102	17719341	17719341	0.7105713	0	1	0.8107383	28.1186
69380	cg0343217	40652429	40652429	0.4328155	0	1	0.5639415	28.55441
69383	cg03432241	60770382	60770382	0.1994723	0	1	0.3114417	28.25581
69387	cg0343258	39795458	39795458	0.4317319	0	1	0.210166	-85.40671
69405	cg0343331	52731440	52731440	0.5839351	0	1	0.6986109	25.95921
69443	cg0343490	68617390	68617390	0.4593382	0	1	0.587404	27.63964
69523	cg0343855	74622436	14758435	0.3399796	0	1	0.4456719	20.51713
69590	cg0344149	23789460	23789460	0.0794624	0	1	0.2238951	64.18126
69596	cg0344184	29779397	29779397	0.3580693	0	1	0.22555	-34.78594
69632	cg0344314	44675453	11721413	0.3008666	0	1	0.195337	-26.04642
69865	cg0345510	28621319	28621319	0.4518984	0	1	0.552866	18.44105
69870	cg0345531	49799466	27783425	0.826606	0	1	0.7200844	-32.76095
70053	cg0346441	62602353	62602353	0.5167838	0	1	0.4048104	-21.83135
70112	cg0346658	37758489	37758489	0.5727733	0	1	0.683242	23.84743
70118	cg0346678	29736451	29736451	0.6080379	0	1	0.253856	-204.123
70132	cg0346723	14657490	14657490	0.3749022	0	1	0.4823554	20.59957
70188	cg0346968	72709302	72709302	0.1586619	0	1	0.261	27.70803
70191	cg0346976	40613300	40613300	0.7481936	0	1	0.9313701	119.415
70472	cg0348566	52759305	52759305	0.3103098	0	1	0.4289208	25.44264
70488	cg0348637	65799476	65799476	0.1259738	0	1	0.2388229	36.19925
70502	cg0348702	61625442	24710412	0.5768982	0	1	0.719795	38.54693
70521	cg0348798	13617335	13617335	0.6540635	0	1	0.7565265	24.63263
70579	cg0349189	62794477	62794477	0.1074061	0	1	0.2107418	34.30007
70623	cg0349461	42732495	42732495	0.6382176	0	1	0.9209131	374.3439
70634	cg0349508	65757507	65757507	0.4808925	0	1	0.6713472	58.80442
70699	cg0349888	42799501	42799501	0.3675101	0	1	0.2658285	-21.14772
70853	cg0350759	51754433	13666340	0.229197	0	1	0.3562538	32.25643
70889	cg0350946	58778459	58778459	0.4559609	0	1	0.7072551	101.8517
70997	cg0351408	28743489	28743489	0.4113219	0	1	0.3101971	-19.69691
71065	cg0351728	20641477	53717306	0.5527264	0	1	0.3258087	-79.03867
71093	cg0351872	66687328	66687328	0.6125053	0	1	0.7946221	68.20657
71338	cg0352990	51795445	51795445	0.7352316	0	1	0.8429879	35.66042
71386	cg0353201	34623394	57743396	0.2875279	0	1	0.4387253	39.15532
71450	cg0353445	41700477	41700477	0.6786669	0	1	0.5062319	-49.73705
71510	cg0353688	51663335	51663335	0.2478392	0	1	0.3569957	24.40819
71660	cg03543861	52790378	64740380	0.5872692	0	1	0.4762505	-21.79502
71964	cg0355772	50699401	50699401	0.4776279	0	1	0.349286	-28.03008
72053	cg0356235	17636481	55688419	0.559204	0	1	0.377744	-51.0819
72088	cg0356384	54607508	20655340	0.7320652	0	1	0.8451912	38.72309
72213	cg0357026	38765376	38765376	0.7734368	0	1	0.6548809	-32.34997
72357	cg0357715	69605321	69605321	0.5705237	0	1	0.7021099	32.61829

72455	cg0358228	21687304	21687304	0.4389023	0	1	0.2735006	-46.47985
72533	cg0358588	60646402	60646402	0.6548398	0	1	0.3511242	-143.6871
72549	cg0358682	72795423	72795423	0.6454001	0	1	0.5121335	-30.84225
72655	cg0359282	40639392	40639392	0.2859149	0	1	0.388122	20.66794
72686	cg0359450	20602395	20602395	0.4608296	0	1	0.5679458	20.38603
72695	cg0359490	59742309	59742309	0.9275497	0	1	0.8187574	-58.27331
72708	cg0359534	65622382	65622382	0.6559044	0	1	0.4193611	-86.78516
72771	cg0359815	10604387	10604387	0.2803742	0	1	0.1443025	-45.11832
72795	cg0359919	19632507	19632507	0.3177539	0	1	0.4210176	20.19037
72830	cg0360105	38759429	38759429	0.3711364	0	1	0.5648552	57.7693
72936	cg0360511	69666366	69666366	0.6558692	0	1	0.5496073	-21.57333
73347	cg0362657	46612344	46612344	0.6852565	0	1	0.5738766	-24.23801
73447	cg0363145	14740468	68777388	0.4422379	0	1	0.2052878	-97.08677
73514	cg0363544	42783481	43778393	0.1225399	0	1	0.2271272	32.72548
73553	cg0363776	31719455	24706345	0.5486533	0	1	0.6715567	27.84144
73703	cg0364552	17765492	31614469	0.1288839	0	1	0.311371	75.32765
73764	cg0364867	13644314	13644314		0	1	0.0886288	4.34E-09
73784	cg0364929	24798428	24798428	0.670414	0	1	0.4679156	-65.63519
73867	cg0365357	42760314	42760314	0.6120999	0	1	0.7136736	22.04394
73870	cg0365372	31769394	27709421	0.8545868	0	1	0.705676	-60.95823
73887	cg0365429	14661378	68652322	0.343896	0	1	0.2274539	-28.15807
73979	cg0365855	30737368	30737368	0.5004591	0	1	0.6449187	35.32215
74023	cg03660901	38787488	38787488	0.4170183	0	1	0.5253922	20.65511
74034	cg0366138	20751449	20751449	0.7226513	0	1	0.8283706	32.61577
74089	cg0366444	24714510	24714510	0.3432446	0	1	0.4908634	35.72712
74178	cg0366876	17638311	17638311	0.1655544	0	1	0.2675365	26.9499
74269	cg0367299	21735405	21735405	0.2128672	0	1	0.3687781	46.61259
74364	cg0367926	10777355	18679416	0.4994668	0	1	0.3739174	-26.66544
74412	cg0368211	69640406	46602385	0.7642501	0	1	0.6628082	-24.75926
74420	cg03682581	10616328	10616328	0.1354536	0	1	0.2676596	44.49441
74424	cg0368271	49754473	58606305	0.515417	0	1	0.3560024	-40.61189
74441	cg0368389	30785408	48621402	0.1608287	0	1	0.0556844	-46.22451
74489	cg0368696	49768495	49768495	0.6101272	0	1	0.4901566	-25.11125
74711	cg0369907	23641470	23641470	0.7620561	0	1	0.6508655	-28.37199
74727	cg0369976	35785392	35785392	0.6372208	0	1	0.8403605	93.30875
74854	cg0370578	39696395	39696395	0.6709207	0	1	0.7973119	38.39444
74921	cg0370942	55726380	55726380	0.4914461	0	1	0.3751039	-23.46711
75068	cg0371698	47778337	37801394	0.5666075	0	1	0.4630089	-19.30089
75136	cg0371942	50610459	50610459	0.3404592	0	1	0.2387213	-22.24828
75193	cg0372188	65787500	65787500	0.9243839	0	1	0.6712942	-178.1602
75230	cg03723481	74699400	74699400	0.7497771	0	1	0.8768048	53.31104
75271	cg0372511	63676473	69618420	0.1213002	0	1	0.2593617	50.12405
75508	cg0373623	36778506	36778506	0.3034489	0	1	0.4102725	21.66004

75529	cg03737424	31720431	31720431	0.5371137	0	1	0.6469983	22.52061
75581	cg03739955	62631370	62631370	0.4542488	0	1	0.30343	-38.30273
75657	cg03743861	47696316	18739419	0.4253424	0	1	0.5884994	42.15722
75666	cg03744383	39625318	39625318	0.2910418	0	1	0.3944592	20.90527
75689	cg03745491	21769466	21769466	0.2181913	0	1	0.339134	30.51537
75739	cg03748376	23756382	36759456	0.0827994	0	1	0.2941691	111.4038
75753	cg03749207	32766445	20798314	0.2221185	0	1	0.0914314	-52.33752
75769	cg03750315	42668374	62616418	0.5028204	0	1	0.3870043	-23.18723
75798	cg03751967	21636307	26676348	0.5258483	0	1	0.4019244	-25.88726
75867	cg03754882	45731391	45731391	0.355326	0	1	0.5979172	89.60994
75985	cg03761216	26675439	26675439	0.3576562	0	1	0.4767795	24.6237
76113	cg03767353	65697342	43604403	0.1321144	0	1	0.4052435	145.0743
76250	cg03773862	16713429	16713429	0.4997854	0	1	0.6151202	23.62337
76269	cg03774803	58629324	58727362	0.3143368	0	1	0.2028637	-27.82084
76328	cg03777875	59709412	27678374	0.4240888	0	1	0.5435477	24.30483
76334	cg03778207	59698354	59698354	0.1496094	0	1	0.2738301	38.46903
76400	cg03781748	23616336	23616336	0.5237368	0	1	0.6853552	44.84992
76445	cg03784363	63810344	11686466	0.5317448	0	1	0.6826223	39.74437
76455	cg03784886	72630371	72630371	0.691379	0	1	0.7920093	26.56031
76555	cg03790740	38691422	38691422	0.7853925	0	1	0.6612133	-36.00604
76660	cg03796943	60733357	60733357	0.4973647	0	1	0.6277229	29.23317
76686	cg03798915	12611322	65706440	0.3947006	0	1	0.2942289	-19.88879
76816	cg03805357	48606424	48606424	0.8862692	0	1	0.7700229	-49.25449
76866	cg03808001	51627426	51627426	0.1751868	0	1	0.3344626	52.8019
76895	cg03810198	33712327	33712327	0.9243516	0	1	0.7548982	-103.4992
76896	cg03810282	69694309	69694309	0.6433545	0	1	0.8817958	138.2105
76941	cg03813151	38671404	63737358	0.689262	0	1	0.498844	-60.00003
76969	cg03814957	14746308	14746308	0.1792828	0	1	0.2826737	26.3911
76991	cg03816625	61605441	68702328	0.9135029	0	1	0.8132669	-47.14553
77108	cg03823901	18676319	18676319	0.4052261	0	1	0.5100851	19.59791
77163	cg03826976	60791386	60791386	0.321767	0	1	0.1978168	-33.2997
77164	cg03827118	71608382	71608382	0.8369331	0	1	0.7274372	-35.60378
77210	cg03830006	22735337	22735337	0.6199766	0	1	0.4275178	-57.65442
77297	cg03834116	73629419	73629419	0.5887989	0	1	0.6973295	23.73013
77341	cg03836586	25758330	25758330	0.4228269	0	1	0.5285418	19.82308
77351	cg03837313	29653407	29653407	0.2506523	0	1	0.4300662	55.23475
77361	cg03837909	52677414	52677414	0.3735937	0	1	0.2422116	-33.20248
77392	cg03839782	33725393	33725393	0.5738992	0	1	0.6840203	23.75688
77476	cg03844894	46743301	42629423	0.4190891	0	1	0.317561	-19.65882
77484	cg03845409	21660398	21660398	0.3945526	0	1	0.2790519	-25.35944
77535	cg03847896	47666370	47666370	0.2890778	0	1	0.436025	37.23429
77671	cg03854098	52617426	52617426	0.7697346	0	1	0.6596402	-28.52622
77749	cg03858673	15689482	27753327	0.4819301	0	1	0.3266482	-39.45785

77803	cg03861065	37747316	37747316	0.3245088	0	1	0.4834375	41.15671
77906	cg03867465	20600339	24667343	0.2422971	0	1	0.3851921	38.10147
77921	cg03868770	45755499	45755499	0.4309246	0	1	0.5403146	20.97798
77972	cg03871140	62706422	36772431	0.0792667	0	1	0.3767724	374.3439
78008	cg03873153	20701450	20701450	0.582825	0	1	0.403232	-50.14304
78054	cg03875819	24674469	24674469	0.7076665	0	1	0.8409057	48.6945
78067	cg03876548	54735462	54735462	0.3748675	0	1	0.5053021	28.43615
78136	cg03880506	37672364	17649329	0.2827784	0	1	0.4224078	34.43868
78230	cg03885343	20804380	20804380	0.3957615	0	1	0.5630865	43.9541
78249	cg03886436	44773505	44773505	0.6552508	0	1	0.7609237	26.13599
78265	cg03887438	32679333	32679333	0.4886374	0	1	0.5946276	20.29846
78275	cg03887721	38655438	38655438	0.549849	0	1	0.7231951	53.611
78278	cg03887906	46708323	46708323	0.6050515	0	1	0.7307452	31.97812
78289	cg03888553	17680413	17680413	0.4409047	0	1	0.5489768	20.58437
78456	cg03896685	28760490	28760490	0.388794	0	1	0.5710621	51.48518
78472	cg03897406	14727422	14727422	0.8512599	0	1	0.6212722	-117.7298
78509	cg03899215	45683355	45683355	0.3351305	0	1	0.4681907	30.0853
78532	cg03900028	73681507	73681507	0.3996596	0	1	0.7201023	374.3439
78647	cg03905819	35676433	35676433	0.4746813	0	1	0.248843	-83.43768
78733	cg03910557	41728473	41728473	0.2330527	0	1	0.3429125	25.38408
78762	cg03913278	55660410	55660410	0.4035897	0	1	0.6436369	88.69113
78805	cg03915932	55706303	55706303	0.6428354	0	1	0.50463	-32.70231
78821	cg03916630	13715369	13715369	0.3435929	0	1	0.5184953	48.22385
78920	cg03922251	50715360	50715360	0.6153749	0	1	0.5129048	-19.51903
78924	cg03922381	15647405	15647405	0.6964605	0	1	0.8048183	31.03384
78978	cg03925642	46631507	60719487	0.4652608	0	1	0.6342214	45.94609
79004	cg03927302	21607475	55799503	0.4700404	0	1	0.3362457	-30.34041
79055	cg03930097	64626443	64626443	0.6807285	0	1	0.8773652	101.6938
79180	cg03936031	19732471	19732471	0.8030005	0	1	0.6859914	-34.70386
79274	cg03940883	47771340	47771340	0.5142586	0	1	0.2531964	-109.0094
79330	cg03944375	55626364	55626364	0.4269406	0	1	0.5376198	21.38539
79339	cg03945122	34680310	34680310	0.9219007	0	1	0.8183455	-52.30064
79380	cg03947384	41640303	41640303	0.5754514	0	1	0.6943769	27.32248
79457	cg03951394	27605463	27605463	0.7994831	0	1	0.6889589	-31.41779
79463	cg03951833	60764350	55616472	0.5677499	0	1	0.4406013	-27.11578
79472	cg03952520	30712464	30712464	0.4342769	0	1	0.5768722	33.11036
79493	cg03953626	73703331	52738498	0.1599204	0	1	0.2640299	28.32517
79587	cg03957898	65681454	65681454	0.576456	0	1	0.7203988	39.05753
79599	cg03958308	52675474	52675474	0.3445699	0	1	0.46909	26.7319
79643	cg03960382	55717341	46725335	0.9770927	0	1	0.8632431	-94.24936
79663	cg03961283	35678323	54648301	0.4700567	0	1	0.336354	-30.30275
79665	cg03961401	34642452	34642452	0.7888157	0	1	0.6794767	-29.85758
79673	cg03961824	10714496	72799304	0.4085963	0	1	0.2970542	-23.39611

79732	cg03964373	12623394	12623394	0.867262	0	1	0.4919419	-282.762
79780	cg03966955	46709395	20713394	0.2114293	0	1	0.3325586	31.06457
79791	cg03967448	17763502	17763502	0.4904777	0	1	0.5952593	19.93436
79844	cg03970567	30702313	30702313	0.1564359	0	1	0.3564586	80.58689
79852	cg03970900	29755467	29755467	0.256814	0	1	0.3882062	32.36697
79967	cg03977174	60708333	60708333	0.4106514	0	1	0.5606018	36.06932
79982	cg03977831	65797345	71688451	0.2344157	0	1	0.4245715	62.67719
79985	cg03978067	49650305	49650305	0.9380382	0	1	0.8058623	-81.44724
80037	cg03980550	36689398	36689398	0.4760651	0	1	0.5779344	18.87129
80073	cg03982831	47650436	40804378	0.3760654	0	1	0.4815	19.96445
80186	cg03987818	51643436	51643436	0.7416827	0	1	0.8580146	42.75845
80193	cg03988092	13710427	13710427	0.1417867	0	1	0.3644946	100.1277
80226	cg03989520	49681350	49681350	0.816204	0	1	0.9172961	48.97188
80233	cg03989711	33807483	71810430	0.5481194	0	1	0.8139292	135.2002
80348	cg03995300	41704350	11604489	0.755233	0	1	0.5625631	-68.23992
80386	cg03997145	28610445	28610445	0.3728726	0	1	0.4892297	23.4954
80415	cg03998338	15708503	15708503	0.5767573	0	1	0.7375431	48.51908
80442	cg03999583	28696355	30670361	0.7772583	0	1	0.9754465	374.3439
80461	cg04001071	19737355	19737355	0.5606012	0	1	0.6809327	27.26326
80531	cg04004561	11720499	11720499	0.446358	0	1	0.5935723	35.20842
80643	cg04010296	12795452	12795452	0.3166391	0	1	0.42383	21.45437
80991	cg04026937	41732346	41732346	0.5296656	0	1	0.7607715	94.58603
81027	cg04028570	24670475	10773329	0.0652271	0	1	0.1925806	57.49886
81034	cg04028695	31763342	31763342	0.2790486	0	1	0.439036	43.58172
81051	cg04029664	66718398	31689385	0.534752	0	1	0.423287	-21.63642
81295	cg04045544	41600309	41600309	0.4742397	0	1	0.6711654	62.43921
81355	cg04049719	47707333	47707333	0.1681762	0	1	0.6758328	374.3439
81370	cg04050824	65726481	42808445	0.3862748	0	1	0.2442024	-37.61185
81395	cg04052466	15726311	30744315	0.1707228	0	1	0.0401221	-68.99545
81424	cg04054303	50614476	50614476	0.5398355	0	1	0.7105599	51.13646
81462	cg04056384	65659471	65659471	0.5238913	0	1	0.3953442	-27.5815
81484	cg04057378	61607418	61607418	0.4015113	0	1	0.6704062	112.5771
81516	cg04058752	74773314	53740335	0.5436546	0	1	0.3858602	-39.54559
81568	cg04061372	42790393	42790393	0.1461052	0	1	0.3671507	97.75995
81646	cg04064998	44739322	44739322	0.5576388	0	1	0.7011841	37.59137
81773	cg04071689	13644319	44696344	0.9829204	0	1		-4.34E-09
81788	cg04072301	34790439	17704395	0.6214567	0	1	0.3038459	-158.117
81831	cg04074536	22685497	26702345	0.8480115	0	1	0.6987988	-59.52073
81859	cg04076044	25793345	25793345	0.3834851	0	1	0.4856257	18.90513
81899	cg04077979	22760414	22760414	0.3320453	0	1	0.4448713	22.95504
81944	cg04080091	53682455	53682455	0.9349995	0	1	0.5992186	-278.2814
81948	cg04080282	47697447	16806436	0.3532918	0	1	0.2216025	-34.72027
82011	cg04084173	33785396	33785396	0.737121	0	1	0.6092664	-33.31854

82016	cg04084354	19803510	19803510	0.3796192	0	1	0.5092841	28.10407
82087	cg04088474	55790411	55790411	0.1178288	0	1	0.2183608	31.4546
82113	cg04089743	63791383	63791383	0.8554007	0	1	0.7222791	-51.67941
82132	cg04090794	14706411	14706411	0.4358236	0	1	0.5527944	23.48401
82188	cg04093633	50690440	50690440	0.3411904	0	1	0.4597333	24.70109
82286	cg04098176	40694344	40694344	0.9239377	0	1	0.8215073	-52.28312
82399	cg04102894	65796411	51770392	0.2661571	0	1	0.3861063	27.4883
82408	cg04103251	70694425	70694425	0.5586307	0	1	0.661999	20.81325
82454	cg04105416	62734499	36735379	0.3138981	0	1	0.4328499	25.46405
82687	cg04116469	16629405	16629405	0.6133292	0	1	0.7156096	22.36921
82745	cg04118610	24633384	24633384	0.0690853	0	1	0.4741311	374.3439
82978	cg04130557	60630321	60630321	0.1999053	0	1	0.331923	36.6286
83011	cg04131969	65713421	65713421	0.934383	0	1	0.2236527	-371.3336
83026	cg04132418	10725414	10725414	0.4229158	0	1	0.273153	-39.2482
83138	cg04137323	38671432	38671432	0.2223368	0	1	0.3313859	25.67274
83149	cg04138046	28701482	28701482	0.701883	0	1	0.8174673	35.82554
83220	cg04141080	48617498	10741347	0.4186882	0	1	0.6191063	62.14251
83273	cg04143348	20794319	20794319	0.1690652	0	1	0.2968345	37.79781
83277	cg04143592	62748360	62748360	0.3272408	0	1	0.4336496	20.97789
83319	cg04145539	29613448	29613448	0.563121	0	1	0.3266778	-85.59254
83325	cg04145681	64786405	64786405	0.5232766	0	1	0.0513057	-371.3336
83367	cg04148163	72691505	72691505	0.479932	0	1	0.5940154	22.87421
83456	cg04152793	69793334	69793334	0.8131344	0	1	0.6765642	-45.63487
83498	cg04154653	26748302	31658404	0.4680455	0	1	0.6946056	82.72103
83513	cg04155289	66691464	66691464	0.8559113	0	1	0.7510618	-36.2879
83563	cg04157272	37726509	40626453	0.4902683	0	1	0.6996026	72.0122
83657	cg04163391	32771384	44700368	0.417028	0	1	0.548413	28.59596
83767	cg04168479	67712315	67712315	0.1527279	0	1	0.404072	119.639
83790	cg04169747	29742458	29742458	0.503036	0	1	0.6907691	58.62139
83843	cg04172345	19607404	19607404	0.721167	0	1	0.910812	112.2411
83928	cg04176452	28673491	69744457	0.590883	0	1	0.903857	374.3439
83959	cg04178011	73754376	73754376	0.8743023	0	1	0.6366229	-133.9316
83992	cg04180046	54600475	54600475	0.1647565	0	1	0.2659159	26.6868
84005	cg04180623	55606429	55606429		0	1		-4.34E-09
84118	cg04187039	20735354	20735354	0.3723914	0	1	0.4845239	22.11115
84144	cg04188920	22781319	14717364	0.3292363	0	1	0.4505731	25.92136
84148	cg04189187	55635408	34753355	0.5255608	0	1	0.739248	79.23567
84201	cg04192412	49720372	49720372	0.2495103	0	1	0.3551477	23.10798
84227	cg04193779	29756474	29756474	0.4582918	0	1	0.6089945	36.95764
84284	cg04195941	33747415	33747415	0.6904966	0	1	0.7948305	28.32497
84359	cg04200010	11606507	11606507	0.6667445	0	1	0.7758063	28.60055
84457	cg04205653	23688303	23688303	0.7025515	0	1	0.824071	39.63373
84474	cg04206342	10679419	52733447	0.3157426	0	1	0.2068781	-26.54517

84550	cg0420991	14635360	48705467	0.635618	0	1	0.4787018	-40.39012
84656	cg0421493	58754429	17690433	0.5833479	0	1	0.8209072	113.585
84666	cg0421528	29723399	29723399	0.4275618	0	1	0.5342715	20.13122
84709	cg0421717	48747345	48747345	0.589594	0	1	0.7066301	27.20291
84893	cg0422578	63641301	36627303	0.5074603	0	1	0.3766415	-28.56049
84901	cg0422611	21633351	21633351	0.5515469	0	1	0.669337	25.90502
85013	cg0423104	42740411	42740411	0.2365657	0	1	0.3403609	23.05436
85027	cg0423167	26740419	26740419	0.2006339	0	1	0.3334993	36.94058
85062	cg0423362	54649330	54649330	0.7065014	0	1	0.8091908	29.03661
85150	cg0423791	54624473	54624473	0.2108624	0	1	0.3290062	29.89914
85244	cg0424265	43759422	43759422	0.4289553	0	1	0.5297029	18.32401
85296	cg0424554	41682325	41682325	0.1953014	0	1	0.3019128	26.46383
85306	cg0424587	55739300	55739300	0.8598088	0	1	0.6673245	-91.90171
85325	cg0424670	15809316	15809316	0.6233433	0	1	0.7266642	23.25092
85410	cg0425120	12723403	12723403	0.371675	0	1	0.5361431	42.71761
85514	cg0425686	49672435	57665313	0.7328553	0	1	0.6038628	-33.48778
85550	cg0425813	29610361	29610361	0.2044167	0	1	0.3054936	23.80237
85561	cg0425867	64664362	64664362	0.3345172	0	1	0.439041	20.24968
85673	cg0426443	55714325	55714325	0.8257955	0	1	0.7040751	-39.99305
85745	cg0426777	19708438	19708438	0.6734753	0	1	0.5311313	-35.59092
85896	cg0427569	25630462	25630462	0.3052494	0	1	0.4393807	31.34645
85926	cg0427662	65695394	65695394	0.1885428	0	1	0.3217938	38.25949
85938	cg0427705	63702454	63702454	0.4166876	0	1	0.3117034	-20.86631
85961	cg0427816	65795333	65795333	0.6146146	0	1	0.5121018	-19.51968
85976	cg0427941	10740331	10740331	0.4854253	0	1	0.6096587	26.60093
86061	cg0428414	66658300	66658300	0.3845228	0	1	0.2806058	-21.37996
86097	cg0428547	63703394	54606510		0	1		-4.34E-09
86126	cg0428673	54677371	57724403	0.4903956	0	1	0.626947	31.58899
86215	cg0429140	54610397	54610397	0.3299553	0	1	0.4356389	20.69618
86239	cg0429297	57794473	57794473	0.5706849	0	1	0.6729354	20.77428
86331	cg0429740	22686369	22686369	0.6601667	0	1	0.7650251	26.11159
86337	cg0429766	53709380	53709380	0.749018	0	1	0.590394	-48.59758
86345	cg0429799	36722316	36722316	0.61777	0	1	0.7223579	23.4826
86391	cg0430134	31784487	18629332	0.4144304	0	1	0.2829354	-31.16166
86511	cg0430648	20604407	20604407	0.3954047	0	1	0.5204814	26.32563
86544	cg0430808	23717416	23717416	0.1426346	0	1	0.2448223	29.23385
86666	cg0431436	48680374	48680374	0.25214	0	1	0.3951428	37.50583
86701	cg0431653	27713329	27713329	0.9164054	0	1	0.7345114	-109.0422
86743	cg0431832	48628377	48628377	0.4212812	0	1	0.5367271	22.94229
86932	cg0432938	59712409	59712409	0.1068195	0	1	0.2314664	45.52414
86974	cg0433156	34804418	34804418	0.3650765	0	1	0.7273562	374.3439
87001	cg0433292	31677454	31677454	0.6356366	0	1	0.7653466	36.47517
87196	cg0434248	51793470	51793470	0.4276364	0	1	0.3083388	-25.73938

87237	cg0434419	24707481	24707481	0.2854054	0	1	0.4129149	29.52238
87258	cg0434533	62676500	62676500	0.6416653	0	1	0.7882924	47.22067
87275	cg0434628	57650456	57650456	0.4458468	0	1	0.6216109	48.89748
87363	cg0434998	14680348	14680348	0.2361821	0	1	0.3873725	42.30546
87369	cg0435021	20649484	20649484	0.6081352	0	1	0.7181373	25.20078
87469	cg0435467	50762343	12708313	0.4925851	0	1	0.3376226	-39.01622
87661	cg0436607	64714487	64714487	0.2613747	0	1	0.368571	23.15295
87960	cg0438264	63775343	41620489	0.2937678	0	1	0.1790932	-30.99425
87997	cg0438468	58699305	58699305	0.7091278	0	1	0.809664	28.16639
88033	cg0438675	30780483	12632309	0.4880698	0	1	0.6080368	25.07308
88043	cg0438739	74728348	74728348	0.1828835	0	1	0.2950455	29.6224
88146	cg0439229	29727438	31669319	0.7320919	0	1	0.8781807	65.85463
88278	cg0439845	31692348	53722489	0.7833999	0	1	0.6737272	-29.50334
88436	cg0440678	23738383	23738383	0.6243641	0	1	0.8088194	72.4782
88649	cg0441611	47656320	47656320	0.2018476	0	1	0.3277087	33.77929
88718	cg0442086	39624466	39624466	0.2734469	0	1	0.3877408	25.14479
89016	cg0443699	50606366	10676470	0.3386595	0	1	0.4604085	25.86429
89200	cg0444736	37705438	37705438	0.6325727	0	1	0.756167	33.00124
89288	cg0445312	70784496	64778315	0.6088598	0	1	0.4890315	-25.03955
89356	cg0445649	42668379	42668379	0.8928843	0	1	0.4037198	-371.3336
89403	cg0445892	46692322	31679409	0.8265943	0	1	0.9320531	57.77433
89452	cg0446114	74779469	74779469	0.6207346	0	1	0.7268503	24.24968
89515	cg0446452	17674305	17674305	0.5535296	0	1	0.8001494	115.0121
89565	cg0446763	63703470	63703470	0.540747	0	1	0.4091279	-28.682
89586	cg0446874	24733338	24733338	0.3462595	0	1	0.4696049	26.28212
89608	cg0447005	46713489	71707481	0.7299043	0	1	0.8469911	41.09357
89664	cg0447340	37756496	37756496	0.5121402	0	1	0.6411626	29.09546
89669	cg0447365	34713510	34713510	0.1140271	0	1	0.2391589	44.42192
89692	cg0447498	21737403	67710393	0.5184531	0	1	0.41803	-18.23606
89755	cg0447818	67706389	67706389	0.5697587	0	1	0.4512109	-24.11266
89805	cg0448107	24728365	73620326	0.4286607	0	1	0.2560326	-51.26035
89823	cg0448192	52700462	52700462	0.5679423	0	1	0.4071978	-40.87634
89870	cg0448398	51717475	51717475	0.2125449	0	1	0.3146936	23.71558
89922	cg0448683	61780346	61780346	0.5338998	0	1	0.8762054	374.3439
90135	cg0449761	64633508	64633508	0.6220059	0	1	0.8345391	98.43392
90140	cg0449782	17807329	17807329	0.2809226	0	1	0.0578472	-133.2784
90187	cg0449970	50767325	50767325	0.6500983	0	1	0.7505444	23.52645
90205	cg0450090	59763439	59763439	0.5584885	0	1	0.6600826	20.20086
90294	cg0450611	60742376	60742376	0.2334549	0	1	0.3364277	22.91662
90336	cg0450846	12601343	12601343	0.4793909	0	1	0.3339598	-35.03519
90341	cg0450860	60779380	60779380	0.8388102	0	1	0.5962427	-123.5478
90349	cg0450887	13685312	13685312	0.4667192	0	1	0.6148336	35.98759
90363	cg0450954	20802351	20802351	0.1857829	0	1	0.2911039	26.65218

90522	cg0451818	24810402	24810402	0.8088288	0	1	0.7077608	-28.30766
90560	cg04520251	25723405	25723405	0.7378203	0	1	0.8468866	36.93364
90703	cg0452701	59694500	61646402	0.5554521	0	1	0.4468546	-20.77489
90946	cg0454088	55660423	55660423	0.2639273	0	1	0.3733285	23.80887
91043	cg0454641	27692361	48797310	0.5710542	0	1	0.4360095	-30.08548
91070	cg0454767	56639317	60731417	0.4390171	0	1	0.557623	24.05703
91146	cg0455150	35639474	35639474	0.433055	0	1	0.5443085	21.58016
91256	cg0455655	30700461	30700461	0.2022389	0	1	0.380586	59.66002
91316	cg0455950	67748477	67748477	0.3409329	0	1	0.5417819	62.28558
91432	cg04565201	26796328	26796328	0.4570683	0	1	0.5737395	23.51233
91438	cg0456533	16658336	16658336	0.5364695	0	1	0.3822196	-37.99432
91457	cg0456647	27702400	27702400	0.5180882	0	1	0.7980468	143.3134
91539	cg0457020	20621488	20621488	0.8944752	0	1	0.7818292	-49.31246
91581	cg0457184	47714450	67730454	0.156132	0	1	0.0277391	-73.09524
91605	cg0457331	43739323	43739323	0.2651044	0	1	0.3999968	33.3503
91686	cg0457660	51641403	51641403	0.6475827	0	1	0.7837798	41.45161
91706	cg04577451	72658302	72658302	0.3980019	0	1	0.5303466	28.98168
91750	cg0457939	69669504	19709324	0.2448193	0	1	0.1360604	-32.92365
91767	cg0458034	25651423	25651423	0.7747241	0	1	0.5982918	-61.5034
91776	cg0458101	13632488	13632488	0.4084252	0	1	0.278865	-30.57981
91890	cg0458722	28773426	49617473	0.2037384	0	1	0.3121404	26.57521
92139	cg0460079	12768416	12768416		0	1	0.9071345	4.34E-09
92326	cg04609971	51746418	51746418	0.6252135	0	1	0.8340586	95.56445
92345	cg0461074	73737474	73737474	0.4540644	0	1	0.6305962	49.5588
92346	cg0461089	33741308	33741308	0.6524378	0	1	0.7645305	28.92187
92397	cg0461345	46669321	46669321	0.6190464	0	1	0.8133456	79.89603
92399	cg0461373	53697417	53697417	0.3543251	0	1	0.8290947	374.3439
92412	cg0461433	58717451	58717451	0.6335045	0	1	0.7487967	29.03694
92509	cg0461988	26668420	26668420	0.1740536	0	1	0.2985101	35.74258
92645	cg04628741	36639383	36639383	0.848596	0	1	0.6403324	-99.75523
92646	cg0462874	62642490	62642490	0.6731626	0	1	0.7990417	38.36358
92718	cg0463367	32794308	32794308	0.3615389	0	1	0.5337963	46.57854
92787	cg0463772	26709488	26709488	0.1640144	0	1	0.3252766	55.54493
92803	cg0463871	51654333	51654333	0.3945563	0	1	0.512054	23.70065
92901	cg0464507	31737440	31737440	0.3229088	0	1	0.5149415	57.82364
92903	cg0464515	66707449	64668343	0.7070335	0	1	0.5002807	-71.11276
92919	cg0464591	26762316	26762316	0.3080914	0	1	0.2018455	-25.88061
92931	cg0464667	17674322	17674322	0.292868	0	1	0.4228835	30.19388
92938	cg0464698	38752364	20800510	0.7331859	0	1	0.8927659	80.39609
92953	cg0464791	34703440	34703440	0.67722	0	1	0.5599416	-26.0109
92978	cg0464958	28701345	28701345	0.4253874	0	1	0.570974	34.28618
92995	cg0465067	19801302	12656422	0.1992815	0	1	0.3145924	29.60254
93062	cg0465429	26694475	26694475	0.4653251	0	1	0.638586	48.20424

93090	cg04656015	48755337	48755337	0.3484223	0	1	0.459751	22.16882
93122	cg04657470	40674393	71674460	0.0696852	0	1	0.2621754	102.2177
93433	cg04674421	29671443	29671443	0.5753838	0	1	0.6847888	23.54
93551	cg04680738	32758383	32758383	0.4343387	0	1	0.5651982	28.46251
93600	cg04683035	38634378	38634378	0.8793342	0	1	0.7661745	-45.63044
93611	cg04683516	51686418	51686418	0.4477043	0	1	0.635264	55.47098
93664	cg04686117	58738369	58738369	0.8022925	0	1	0.9189939	60.41079
93680	cg04687040	70733410	70733410	0.6461043	0	1	0.4627043	-53.68753
93722	cg04689178	65787344	65787344	0.7454386	0	1	0.8529456	37.14716
93729	cg04689606	53746496	74787350	0.4185177	0	1	0.5965209	49.48533
93731	cg04689676	52679475	38638386	0.1649455	0	1	0.0548964	-49.55379
93739	cg04690342	22674468	22674468	0.5552648	0	1	0.6722671	25.72938
93788	cg04693014	37737489	25700413	0.227966	0	1	0.0575231	-90.75703
93841	cg04696840	22623365	22623365	0.1740395	0	1	0.309071	40.65081
94018	cg04706655	49736325	23731389	0.4156328	0	1	0.3143144	-19.66442
94167	cg04716530	32649445	27671323	0.3973107	0	1	0.2959179	-20.13141
94188	cg04717802	70612470	43628375	0.2326547	0	1	0.0729862	-76.64477
94261	cg04721775	71733492	40773328	0.8424913	0	1	0.9523476	71.79822
94285	cg04722610	69631444	69631444	0.4922163	0	1	0.6045848	22.46358
94303	cg04723343	56759391	73789489	0.5048302	0	1	0.6188418	23.25188
94335	cg04724556	51798439	51798439	0.4446238	0	1	0.6607531	73.38917
94395	cg04727458	15647330	15647330	0.720044	0	1	0.5730056	-40.42879
94590	cg04738028	50687365	50687365	0.8588581	0	1	0.960593	70.16787
94659	cg04741094	34664418	34664418	0.5717647	0	1	0.719034	40.45842
94673	cg04741728	29673307	55646402	0.6775353	0	1	0.8159602	47.05571
94694	cg04742556	38787419	38787419	0.6320981	0	1	0.5198475	-22.94335
94806	cg04748098	67770356	59728417	0.9066746	0	1	0.6913075	-131.567
94851	cg04750517	12704357	12704357	0.8077068	0	1	0.9477659	94.10933
94933	cg04755386	67777468	67777468	0.9003145	0	1	0.7961362	-45.69021
95033	cg04762129	59633472	59633472	0.3854823	0	1	0.5119354	26.883
95038	cg04762351	33726399	33726399	0.6361988	0	1	0.7805021	45.03209
95067	cg04764476	23729413	48630353	0.4162549	0	1	0.2757723	-35.1219
95140	cg04768488	11726510	11726510	0.6951048	0	1	0.8104118	34.80332
95294	cg04775631	63713495	63713495	0.5146707	0	1	0.6246902	22.05631
95333	cg04777551	51795368	51795368	0.5281041	0	1	0.7544398	90.09959
95502	cg04785902	13637343	13637343	0.1369698	0	1	0.2434538	31.77579
95509	cg04786142	21802497	69752328	0.685837	0	1	0.7944445	30.0842
95542	cg04787784	17610381	17610381	0.3385318	0	1	0.7144521	374.3439
95580	cg04789475	59774428	65809342	0.5767478	0	1	0.4752295	-18.75664
95643	cg04791718	43680426	43680426	0.7869757	0	1	0.6370361	-48.75393
95768	cg04798314	22669441	22669441	0.8849808	0	1	0.7080871	-89.90721
95787	cg04799210	33704489	58709466	0.8347	0	1	0.7168572	-39.41828
95837	cg04801779	70767489	28790376	0.5058546	0	1	0.7215377	78.30984

95988	cg04810745	71757363	71757363	0.5775908	0	1	0.7212179	38.97638
96053	cg04814784	23715415	23715415	0.4383512	0	1	0.0785488	-267.1822
96076	cg04816171	52656395	52656395	0.4023894	0	1	0.2931713	-22.73388
96107	cg04818594	10772349	10772349	0.5747904	0	1	0.6790394	21.6139
96126	cg04819497	65742498	50659359	0.4027613	0	1	0.7205006	374.3439
96195	cg04823299	27605338	27605338	0.4611258	0	1	0.5923807	28.883
96214	cg04824469	60670408	60670408	0.6865287	0	1	0.8064528	36.46878
96218	cg04824555	35717372	35717372	0.327229	0	1	0.4356849	21.62998
96330	cg04830958	62753323	62753323	0.8403749	0	1	0.6235906	-103.4817
96358	cg04832245	74756468	74756468	0.5064057	0	1	0.7081137	68.14713
96433	cg04835652	11793330	11793330	0.3976585	0	1	0.5151639	23.68686
96460	cg04836851	42810329	42810329	0.6470757	0	1	0.4346657	-70.34494
96534	cg04840163	21717353	40702418	0.1753526	0	1	0.3135152	42.00229
96593	cg04843066	14661409	53617378	0.5043691	0	1	0.3815333	-25.6293
96604	cg04843555	11792390	11792390	0.2825597	0	1	0.4347444	39.83435
96605	cg04843568	20664453	20664453	0.3646265	0	1	0.5230826	40.04493
96614	cg04843821	65737502	65737502	0.9379416	0	1	0.7652332	-114.9746
96621	cg04844038	71684466	71684466	0.5399772	0	1	0.6449615	20.8878
96767	cg04850148	49780437	49780437	0.6041432	0	1	0.8571135	139.6336
96771	cg04850286	40677367	40677367	0.2525081	0	1	0.3815579	31.66004
96816	cg04852399	66716355	66716355	0.8355354	0	1	0.7149929	-40.93212
96972	cg04860432	47788359	47788359	0.429716	0	1	0.328675	-19.28987
97042	cg04864199	64737453	64737453	0.5454916	0	1	0.3360404	-67.53727
97278	cg04875706	64738345	64738345	0.0715336	0	1	0.4227591	374.3439
97326	cg04878159	11640487	11640487	0.4989346	0	1	0.6241145	27.23838
97370	cg04880091	72782399	30807398	0.6660654	0	1	0.4799034	-56.14834
97483	cg04885068	37672455	19804385	0.67229	0	1	0.5310305	-35.08301
97489	cg04885343	33675510	33675510	0.3053872	0	1	0.419879	24.15598
97606	cg04890607	31650394	33631300	0.4653584	0	1	0.6387139	48.25584
97621	cg04891577	71749414	71749414	0.2205915	0	1	0.4492476	88.80526
97650	cg04892643	44686303	44686303	0.4879772	0	1	0.6434843	40.033
97656	cg04892766	32609356	32609356	0.4339045	0	1	0.5928693	40.29867
97796	cg04900186	51623431	51623431	0.8322492	0	1	0.6210119	-96.78413
97893	cg04904561	46702384	28655481	0.4063672	0	1	0.2736108	-32.07234
97957	cg04907849	38628462	38628462	0.7271008	0	1	0.8474522	42.91127
97960	cg04908077	59694326	59694326	0.4723703	0	1	0.5862384	22.70812
97974	cg04908625	39653503	65636462	0.3693899	0	1	0.2628225	-22.88251
98086	cg04914221	39603336	39603336	0.6072674	0	1	0.71249	23.24003
98338	cg04926385	55636431	55636431	0.2859139	0	1	0.4363066	38.87749
98414	cg04930693	57798484	57798484	0.2847239	0	1	0.4145908	30.45413
98488	cg04935109	52753423	52753423	0.0930709	0	1	0.2219644	50.88702
98681	cg04944853	11722332	11722332	0.3309492	0	1	0.4531299	26.18073
98744	cg04947555	58797382	58797382	0.4225937	0	1	0.5483419	26.52357

98747	cg0494768	52674493	40797436	0.5825382	0	1	0.4345706	-35.38099
98869	cg0495511	55807479	32768451		0	1		-4.34E-09
98918	cg0495790	23701353	23701353	0.5212257	0	1	0.6325655	22.65326
98990	cg0496166	43701398	43701398	0.5345632	0	1	0.6691079	32.21039
99027	cg0496369	39699304	39699304	0.2143389	0	1	0.324733	26.65146
99123	cg0496980	31745472	31745472	0.0540754	0	1	0.2224621	90.77164
99133	cg0497028	42628435	42628435	0.7971191	0	1	0.9026398	47.20562
99446	cg0498632	10608343	10608343	0.3441105	0	1	0.4657015	25.7033
99536	cg0499037	57701483	57701483	0.678371	0	1	0.512132	-46.65612
99593	cg0499327	49795447	49795447	0.365009	0	1	0.4822766	23.89286
99601	cg0499360	40755441	40755441	0.0803998	0	1	0.2372933	72.16726
99627	cg0499531	61765307	60715439	0.8425586	0	1	0.7337939	-36.09475
99678	cg0499832	66624499	66624499	0.6603729	0	1	0.8098125	51.96743
99754	cg0500193	58718381	58718381	0.4277182	0	1	0.3043726	-27.30698
99816	cg0500507	68653306	68653306	0.5838602	0	1	0.7603753	59.51945
99828	cg0500538	43602318	35604442	0.569892	0	1	0.7044037	33.94742
99848	cg0500623	29722314	32626329	0.6730338	0	1	0.5204675	-39.99636
99900	cg0500882	29686412	29686412	0.5485117	0	1	0.6734822	28.68631
99937	cg0501064	62808422	62808422	0.465718	0	1	0.5896247	26.17262
100010	cg0501472	35803400	11650317	0.6523047	0	1	0.4930613	-42.06523
100161	cg0502319	73670346	73670346	0.4112937	0	1	0.694602	127.0809
100330	cg0503284	40772427	40772427	0.6947245	0	1	0.815995	38.35678
100339	cg0503323	56793502	56793502	0.365779	0	1	0.478935	22.51898
100346	cg0503336	13689323	13689323	0.550189	0	1	0.6507845	19.656
100380	cg0503506	31708457	31708457	0.5082215	0	1	0.6381546	29.35127
100497	cg0504034	17788344	17788344	0.2593885	0	1	0.4196127	44.88744
100503	cg0504050	56744475	56744475	0.3861738	0	1	0.2827186	-21.16441
100562	cg0504371	44750351	44750351	0.5057768	0	1	0.6094333	19.78666
100630	cg0504658	10713425	10713425	0.5780141	0	1	0.7077041	32.16635
100634	cg0504672	73735407	73735407	0.4162827	0	1	0.540558	25.98778
100709	cg0505005	57704510	69704315	0.3796997	0	1	0.5110887	28.74347
100730	cg0505126	27733467	27733467	0.3017143	0	1	0.1775656	-35.24593
100793	cg0505468	47799466	29804509	0.9498188	0	1	0.8389568	-71.09911
100800	cg0505500	53600355	53600355	0.6000075	0	1	0.7422553	40.04251
100841	cg0505735	48676426	48676426	0.2220129	0	1	0.3247259	23.3996
100955	cg0506248	55672506	55672506	0.3688583	0	1	0.5140426	34.27551
101041	cg0506584	36760325	36760325	0.4938982	0	1	0.5953907	18.9415
101115	cg0507027	74735361	74735361	0.3201436	0	1	0.4232598	20.09376
101196	cg0507530	53659444	53659444	0.5777795	0	1	0.6984356	28.15722
101243	cg0507904	37750481	20718489	0.6168587	0	1	0.4759458	-33.07233
101375	cg0508644	40631330	40631330	0.7189029	0	1	0.607112	-25.89069
101395	cg0508762	65796378	65796378	0.8263854	0	1	0.668494	-59.89026
101407	cg0508815	70699479	11603418	0.7153841	0	1	0.5894368	-31.11082

101481	cg0509237	44765425	44765425	0.7974231	0	1	0.6836408	-32.6322
101541	cg0509641	16639308	16639308	0.9349862	0	1	0.7359739	-135.7564
101549	cg0509663	23740403	23740403	0.1424627	0	1	0.2438296	28.89732
101623	cg0510006	74770356	74770356	0.6280153	0	1	0.525404	-19.78588
101763	cg0510846	49607442	49607442	0.1242305	0	1	0.2280646	32.14932
101769	cg0510956	63659395	63659395	0.3570979	0	1	0.4842598	27.46822
101800	cg0511164	35658390	35658390	0.4613468	0	1	0.6400992	51.02819
101804	cg0511189	60744436	60744436	0.3427811	0	1	0.4856773	33.78705
102042	cg0512651	31756325	31756325	0.6392564	0	1	0.8564253	109.404
102145	cg0513148	22610307	22610307	0.2122725	0	1	0.3359213	32.0364
102152	cg0513169	26788413	26788413	0.5864746	0	1	0.4794215	-20.53293
102209	cg0513473	21667314	21667314	0.3690366	0	1	0.1684136	-78.5538
102301	cg0513889	23627462	23627462	0.6175989	0	1	0.7404417	31.48499
102306	cg0513902	44804476	44804476	0.7966906	0	1	0.6715418	-37.73316
102430	cg0514481	43802320	43802320	0.1662558	0	1	0.26674	26.28941
102619	cg0515504	74711312	74711312	0.2793415	0	1	0.4009028	27.5347
102680	cg0515762	67795434	67795434	0.1798367	0	1	0.2816136	25.71954
102740	cg0516056	37643374	37643374	0.3185539	0	1	0.4231217	20.5801
102758	cg0516177	17630455	17630455	0.737543	0	1	0.4721424	-117.2348
102823	cg0516454	27745334	27745334	0.5469084	0	1	0.6786997	31.53243
102832	cg0516493	60782338	35771437	0.5457045	0	1	0.4388943	-20.1815
102840	cg0516525	11635354	11635354	0.7130585	0	1	0.5972485	-27.07211
103011	cg0517388	46787473	46787473	0.638967	0	1	0.9167242	374.3439
103041	cg0517580	48646417	48646417	0.6517056	0	1	0.7920858	44.55603
103050	cg0517655	36699356	36699356	0.4477629	0	1	0.5995412	37.2386
103098	cg0517949	30707435	30707435	0.7317395	0	1	0.8649902	54.03433
103155	cg0518194	23806365	74751351	0.7050812	0	1	0.5955749	-24.4035
103157	cg0518221	61755450	61755450	0.3394938	0	1	0.4892493	36.71579
103239	cg0518715	30652418	30652418	0.3233918	0	1	0.4551593	29.88584
103357	cg0519442	29773460	29773460	0.3473811	0	1	0.5109004	42.65977
103365	cg0519463	50704485	50704485	0.6921065	0	1	0.8309203	49.87082
103379	cg0519531	64698331	64698331	0.4474664	0	1	0.5675395	24.61722
103410	cg0519706	15746499	57747438	0.0348209	0	1	0.2016795	99.42105
103421	cg0519766	30610409	30610409	0.3220524	0	1	0.4270897	20.65262
103615	cg0520860	35706389	35706389	0.0596871	0	1	0.1968997	65.93365
103663	cg0521068	50646447	50646447	0.2655058	0	1	0.3676265	21.30244
103708	cg0521289	20718326	20718326	0.5288414	0	1	0.7460648	82.53926
103889	cg0522344	19777426	19777426	0.4694902	0	1	0.5736855	19.53399
103952	cg0522606	13644381	49734466		0	1		-4.34E-09
104113	cg0523294	55732352	55732352	0.4398991	0	1	0.9194194	374.3439
104151	cg0523456	22664389	63716334	0.8161591	0	1	0.6756575	-48.19193
104200	cg0523726	38699421	38699421	0.3128603	0	1	0.462261	37.34072
104308	cg0524182	69780466	22600367	0.1855408	0	1	0.3234845	40.75354

104350	cg0524401	60716387	60716387	0.1485159	0	1	0.2583863	31.96555
104354	cg0524423	63742314	55731365	0.0129557	0	1	0.1196668	63.85846
104358	cg0524468	61615347	61615347	0.3466013	0	1	0.4968332	36.76001
104376	cg0524551	46695455	46695455	0.2437699	0	1	0.3877216	38.46774
104421	cg0524823	35685425	33667479	0.214865	0	1	0.0292448	-118.295
104462	cg0525093	16606320	24728332	0.506601	0	1	0.607647	18.97099
104600	cg0525800	22771355	74616339	0.8053862	0	1	0.9483696	97.00725
104774	cg0526588	44763466	18750386	0.7296329	0	1	0.6217679	-25.02807
104798	cg0526678	17733366	17733366	0.2153139	0	1	0.3290685	27.8744
104806	cg0526739	24754470	74622419	0.3819155	0	1	0.0578278	-235.4707
104839	cg0526932	56681340	56681340	0.4289831	0	1	0.552107	25.59879
104876	cg0527075	60810486	60810486	0.2393531	0	1	0.1250832	-37.02207
104922	cg0527431	30668497	30668497	0.7696814	0	1	0.8813788	45.26786
104955	cg0527615	55614329	55614329	0.299427	0	1	0.4163534	25.17174
104965	cg0527646	56713435	56713435	0.451605	0	1	0.3138366	-32.499
104968	cg0527697	48800415	48800415	0.0993151	0	1	0.3808953	374.3439
104981	cg0527750	14769334	22620442	0.3028125	0	1	0.4883712	55.14283
105011	cg0527933	65802421	65802421	0.49545	0	1	0.6895855	62.12418
105020	cg0527973	10734455	10734455	0.5888029	0	1	0.7373613	42.54586
105034	cg0528033	46730385	46730385	0.5129238	0	1	0.6206507	21.24352
105071	cg0528226	54763316	74643422	0.681569	0	1	0.7829333	26.10168
105107	cg0528472	26726429	26726429	0.2407449	0	1	0.3755079	34.7016
105150	cg0528737	26636348	26636348	0.3771577	0	1	0.4958939	24.25367
105165	cg0528817	43740492	43740492	0.4227976	0	1	0.5622219	31.73971
105421	cg0530147	34644326	16671467	0.2497139	0	1	0.1457358	-29.67962
105438	cg0530210	63795474	63795474	0.2798277	0	1	0.398788	26.56691
105532	cg0530602	57645327	57645327	0.1541428	0	1	0.2574526	28.54026
105580	cg0530824	24788496	24788496	0.6226157	0	1	0.8230758	86.49803
105620	cg0530998	43799373	43799373	0.2310008	0	1	0.3730786	38.54743
105639	cg0531099	61756328	12600421	0.3294418	0	1	0.2154231	-27.96945
105686	cg0531391	66616450	66616450	0.4534197	0	1	0.5747131	25.09563
105749	cg0531720	55733446	55733446	0.5500979	0	1	0.42184	-27.43879
105768	cg0531827	29749314	29749314	0.3092286	0	1	0.4388572	29.48579
105805	cg0532122	18708411	26771434	0.4344945	0	1	0.31341	-26.22954
105920	cg0532805	12687466	40657444	0.8779778	0	1	0.6877397	-97.05561
105984	cg0533176	73723426	73723426	0.2281518	0	1	0.7962071	374.3439
106054	cg0533605	61607478	61607478	0.7761353	0	1	0.6680248	-28.24254
106096	cg05337761	29669478	52623471	0.5235026	0	1	0.1377316	-274.2978
106121	cg05338731	63790402	63790402	0.2548933	0	1	0.0844595	-80.12089
106205	cg0534246	33611312	33611312	0.5039571	0	1	0.6277536	26.82456
106238	cg05343811	37807421	22788356	0.160053	0	1	0.2792693	34.87949
106247	cg0534449	41766314	59774305	0.4873297	0	1	0.2773363	-70.70065
106257	cg0534515	71714446	74795345	0.236239	0	1	0.0254148	-142.9293

106348	cg0534885	47681322	47681322	0.4323739	0	1	0.5909655	40.1036
106357	cg0534901	48603467	48603467	0.1039658	0	1	0.2120162	37.23025
106462	cg0535419	43785387	43785387	0.9077501	0	1	0.802061	-48.87491
106515	cg0535703	73681375	73681375	0.3295087	0	1	0.4705399	33.3513
106584	cg0536017	13644444	57798408		0	1	0.0051239	4.34E-09
106632	cg0536231	51624441	51624441	0.6272603	0	1	0.5003451	-27.94407
106665	cg0536395	48629338	48629338	0.3973395	0	1	0.5201062	25.49823
106683	cg0536456	35650419	35650419	0.4223966	0	1	0.3155487	-21.3696
106697	cg0536503	50628338	50656399	0.8347162	0	1	0.6577964	-73.65076
106722	cg0536605	36747348	36747348	0.7376692	0	1	0.8421532	33.92982
106728	cg0536616	46809478	46809478	0.6934081	0	1	0.8608121	74.63701
106815	cg0537063	62802309	14641348	0.5313552	0	1	0.4137804	-23.66078
106860	cg0537244	68766487	12685351	0.1002916	0	1	0.2567034	65.89664
106919	cg0537480	18625342	18625342	0.2476643	0	1	0.3639035	26.97975
106983	cg0537712	43729306	43729306	0.5915694	0	1	0.6917572	20.72746
107014	cg0537869	58773343	58773343	0.2368732	0	1	0.0574713	-97.63934
107112	cg0538361	34752490	34752490	0.5457646	0	1	0.6900917	37.28179
107172	cg0538571	24681459	20709500	0.8345914	0	1	0.684692	-56.90888
107203	cg0538739	55706492	67765452		0	1	0.0671452	4.34E-09
107306	cg0539244	18694399	53806343	0.7982588	0	1	0.5781485	-94.29161
107320	cg0539298	48634406	48634406	0.4571436	0	1	0.3499008	-20.84296
107325	cg0539308	60695447	60695447	0.5405786	0	1	0.6554396	24.42895
107479	cg0540073	22781377	22781377	0.2039884	0	1	0.3044145	23.59196
107490	cg0540157	16750363	16750363	0.4683267	0	1	0.7465642	129.7962
107580	cg0540720	36709476	36709476	0.1984926	0	1	0.5726491	374.3439
107605	cg0540867	25687314	25687314	0.1127184	0	1	0.2748564	66.28784
107649	cg0541159	29600456	29600456	0.2300908	0	1	0.3376186	24.69485
107660	cg0541213	27777372	27777372	0.4157422	0	1	0.2676185	-38.82939
107680	cg0541295	70659300	70659300	0.584977	0	1	0.4276479	-39.46237
107683	cg05413061	47649504	47649504	0.3041865	0	1	0.4214372	25.14221
107744	cg0541633	23758313	23758313	0.6182364	0	1	0.4512805	-44.50652
107803	cg0541962	15679354	15679354	0.0262978	0	1	0.1381617	61.35777
107889	cg0542436	62680335	62680335	0.3266785	0	1	0.1747545	-48.97697
107937	cg0542845	45790381	45790381	0.7479971	0	1	0.8818128	58.99155
107984	cg0543203	65788499	65788499	0.7528928	0	1	0.8570474	36.12513
108033	cg0543539	54763400	54763400	0.7979914	0	1	0.9016854	45.77775
108088	cg0544082	31727406	31727406	0.391471	0	1	0.6518676	104.5473
108220	cg0545033	18797427	18797427	0.646566	0	1	0.7818211	40.76951
108267	cg05453001	28709352	48752321	0.5029329	0	1	0.7247487	82.74958
108274	cg0545335	26780499	39755368	0.7639693	0	1	0.6635687	-24.35099
108307	cg0545537	25618490	25618490	0.6829837	0	1	0.8232775	49.29497
108344	cg0545773	20682433	46804394	0.3725333	0	1	0.185414	-67.12616
108436	cg0546358	74757478	42741510	0.5362997	0	1	0.3064851	-81.77359

108535	cg0546981	27641340	27641340	0.4128228	0	1	0.5738739	41.04808
108563	cg0547116	66715450	58792400	0.3406461	0	1	0.487611	35.51186
108573	cg0547149	35724480	35724480	0.4849016	0	1	0.656144	47.94038
108593	cg0547246	38742324	51726304	0.1155135	0	1	0.2700105	60.89796
108647	cg0547552	11770420	54677365	0.2371243	0	1	0.1023666	-52.179
108689	cg0547758	72609395	29778323	0.5741422	0	1	0.7746835	76.18436
108727	cg0547962	41672359	41672359	0.3436664	0	1	0.4601519	23.9552
108759	cg05481961	20808492	20808492	0.2042373	0	1	0.3212866	29.9351
108789	cg0548338	64758315	64758315	0.6620594	0	1	0.5619633	-19.78614
108800	cg05483731	33804472	66666305	0.2176494	0	1	0.3201548	23.55951
108823	cg0548494	74646447	32655314	0.2473982	0	1	0.41054	47.15711
108849	cg05486191	13749432	13749432	0.1580932	0	1	0.2709526	32.25068
109165	cg0550236	29714300	29714300	0.682013	0	1	0.233032	-361.9467
109305	cg0550922	16658506	16658506	0.6629541	0	1	0.901006	148.0846
109384	cg0551315	59733359	59733359	0.8375681	0	1	0.957857	84.31824
109406	cg0551429	19661387	19661387	0.5952669	0	1	0.7192737	30.57014
109425	cg0551524	48649474	48649474	0.6117806	0	1	0.8121421	83.70258
109584	cg0552403	13743318	13743318	0.537143	0	1	0.6729763	32.89118
109616	cg0552636	47799399	47799399	0.5740361	0	1	0.6785442	21.6823
109625	cg0552680	44650361	44650361	0.6346212	0	1	0.7932999	54.36098
109667	cg0552889	54661458	54661458	0.7876841	0	1	0.9273376	81.42205
109728	cg0553140	13799421	13799421	0.4407108	0	1	0.8297278	374.3439
109982	cg0554839	70714466	70714466	0.7583455	0	1	0.6493049	-27.25546
109984	cg0554842	50692329	50692329	0.4133222	0	1	0.5542628	32.31908
110212	cg0556351	33659451	37700348	0.1196907	0	1	0.27063	57.83602
110423	cg0557427	67759423	31698311	0.4300393	0	1	0.2673617	-45.54379
110446	cg0557550	44635308	44635308	0.378571	0	1	0.6520595	115.4287
110448	cg0557561	64745329	21727313	0.4930258	0	1	0.385443	-20.54852
110518	cg0557959	25738399	25738399	0.4232076	0	1	0.6919174	114.1846
110540	cg0558080	64802438	64802438	0.7060372	0	1	0.5145601	-61.96921
110554	cg0558187	30628482	30628482	0.5865272	0	1	0.7555486	54.77495
110582	cg0558363	46659302	46659302	0.5396081	0	1	0.6600834	26.54872
110691	cg0558978	11736345	69604436	0.3565287	0	1	0.2513405	-22.87624
110701	cg0559025	30699439	69690416	0.1991113	0	1	0.0752229	-52.38939
110846	cg05597181	32754347	62789334	0.3236563	0	1	0.4240088	19.1771
110929	cg0560162	24741423	24741423	0.1730212	0	1	0.0617676	-48.30635
111009	cg0560611	19715310	19715310	0.8491317	0	1	0.6631688	-83.77103
111015	cg0560645	19706326	12671388	0.6222477	0	1	0.7661796	43.17974
111122	cg0561274	18642335	18642335	0.2240393	0	1	0.1095159	-39.62247
111293	cg0562134	31682310	67795408	0.0299439	0	1	0.3342476	374.3439
111313	cg0562257	27694449	27694449	0.5266725	0	1	0.6405618	23.69116
111431	cg0562850	41697390	41697390	0.552953	0	1	0.6718998	26.4113
111460	cg05630111	44650460	45650392	0.7058975	0	1	0.5722696	-33.66928

111464	cg05630272	63604429	63604429	0.5248813	0	1	0.4198509	-19.61521
111523	cg05634637	71771403	71771403	0.3858883	0	1	0.4937499	20.6321
111551	cg05636175	29763331	29763331	0.5205776	0	1	0.4108285	-21.1011
111601	cg05638648	29643404	46795366	0.711623	0	1	0.8979532	102.8937
111638	cg05640533	28683489	22722453	0.6182386	0	1	0.7199274	22.36289
111791	cg05649077	57772441	57772441	0.287241	0	1	0.5025141	73.32173
111875	cg05653481	59616435	59616435	0.7306267	0	1	0.8545583	46.25751
111945	cg05656210	17758490	64650421	0.5079496	0	1	0.1105668	-303.9002
111982	cg05657656	20687501	20687501	0.326219	0	1	0.480153	38.87645
112146	cg05666820	51636353	49620410	0.4421226	0	1	0.3026008	-33.58598
112413	cg05682128	54772377	54772377	0.1185407	0	1	0.2443547	43.97498
112434	cg05683630	11611477	63673338	0.4878224	0	1	0.3073408	-52.26245
112523	cg05689413	43736462	43736462	0.3576692	0	1	0.47909	25.41705
112536	cg05690644	61628317	41624466	0.1715239	0	1	0.2832747	30.44867
112619	cg05695699	55753504	70682427	0.5021583	0	1	0.6164778	23.30945
112621	cg05695876	51767359	51767359	0.4154906	0	1	0.5167193	18.47832
112718	cg05701478	15736509	15736509	0.6568927	0	1	0.7743914	31.98551
112767	cg05704942	54720467	54720467	0.185864	0	1	0.0465912	-72.51063
112779	cg05705335	57763359	24659427	0.2366095	0	1	0.3456203	24.89438
112866	cg05710060	58692328	58692328	0.8788147	0	1	0.7635155	-46.7636
112941	cg05713856	24654401	24654401	0.4663995	0	1	0.566416	18.23565
112944	cg05713954	15619486	15619486	0.3501269	0	1	0.2186673	-34.84143
113101	cg05722035	37645504	37645504	0.2198813	0	1	0.3394968	29.87207
113119	cg05723179	19643461	19643461	0.1873858	0	1	0.2971903	28.30267
113139	cg05724777	42650320	17720392	0.5101254	0	1	0.3816257	-27.65788
113200	cg05728166	38761400	38761400	0.413994	0	1	0.7161129	147.5047
113250	cg05730975	57661493	57661493	0.3761342	0	1	0.5984299	75.34387
113293	cg05733463	12626393	12626393	0.2699385	0	1	0.3723854	21.25401
113365	cg05738749	26798357	26798357	0.1012268	0	1	0.2061623	36.09843
113393	cg05740465	26607306	68601390	0.7750757	0	1	0.658468	-31.66861
113445	cg05743713	10754333	21656445	0.3890468	0	1	0.2722188	-26.09555
113549	cg05751055	71632416	71632416	0.3391707	0	1	0.8595735	374.3439
113554	cg05751189	62667342	62667342	0.0522794	0	1	0.1760638	59.44805
113685	cg05758978	15708458	48696497	0.6040829	0	1	0.4884092	-23.5475
113803	cg05766605	57620314	40810434	0.55098	0	1	0.4318137	-24.22164
113822	cg05767411	31782365	34773427	0.226885	0	1	0.3340213	24.72296
113912	cg05772155	60764301	51746329	0.3746723	0	1	0.2421841	-33.66081
113975	cg05775862	21695381	21695381	0.271219	0	1	0.4008043	30.93006
114053	cg05779595	65709488	65709488	0.2603545	0	1	0.3706553	24.26596
114083	cg05781417	29648301	64671432	0.4775724	0	1	0.3490518	-28.09994
114170	cg05785424	14634377	37653502	0.172236	0	1	0.2848649	30.75374
114194	cg05786140	34710350	34710350	0.1947445	0	1	0.3234012	35.60611
114286	cg05790828	57639389	57639389	0.7951227	0	1	0.5415973	-119.3387

114421	cg0579785	34754487	34754487	0.6701692	0	1	0.7781195	28.34156
114456	cg0579916	45648303	49757422	0.5499204	0	1	0.6576573	22.10228
114585	cg0580664	42653354	42653354	0.4551519	0	1	0.3500666	-20.16928
114625	cg0580958	47748455	47748455	0.8472602	0	1	0.9501417	64.76236
114783	cg05819221	19633331	19633331	0.4334054	0	1	0.5357398	18.79981
114810	cg05820861	61761478	42702498	0.9091506	0	1	0.804485	-48.65236
114940	cg0582860	17657409	17657409	0.6546339	0	1	0.7610032	26.40891
114977	cg0583108	60732331	60732331	0.8847328	0	1	0.7813577	-41.21788
115008	cg05833351	43687316	60660364	0.9182571	0	1	0.8153679	-50.52065
115089	cg0583799	67797503	63734392	0.8164073	0	1	0.6399422	-69.06747
115117	cg05839741	31774410	27712404	0.7779002	0	1	0.6355197	-43.76244
115119	cg0583976	60790473	42737448	0.002694	0	1	0.1565977	109.9111
115226	cg0584559	15645506	58733352	0.017141	0	1	0.184776	111.1189
115257	cg0584707	71762411	71762411	0.6589811	0	1	0.7792485	33.63522
115342	cg0585227	24780491	33620417	0.5760545	0	1	0.3090031	-109.7586
115440	cg0585799	35725469	53770372	0.4836798	0	1	0.2960043	-56.62321
115494	cg0586095	46756506	46756506	0.4186194	0	1	0.1258054	-166.1658
115566	cg0586524	60680491	45667398	0.2679316	0	1	0.4022016	32.95407
115607	cg0586724	72691431	72691431	0.8995842	0	1	0.7837218	-52.8988
115619	cg0586788	70766497	70766497	0.4280412	0	1	0.3081467	-25.95575
115639	cg05868531	23655430	16636475	0.6835118	0	1	0.5595915	-28.70655
115813	cg0587688	62609471	62609471	0.3043869	0	1	0.4868974	53.45394
115863	cg0587907	19630488	19630488	0.7896008	0	1	0.9159509	66.05614
116056	cg0588889	36646450	36646450	0.3219005	0	1	0.4264139	20.49172
116088	cg0589045	73789453	73789453	0.4677153	0	1	0.6503761	53.48736
116103	cg0589095	28736421	28736421	0.5037169	0	1	0.6080366	19.96859
116159	cg0589384	47708472	47708472	0.7131306	0	1	0.9195104	131.622
116213	cg0589668	43787408	43787408	0.2639716	0	1	0.1393367	-40.06682
116300	cg0590056	64696429	64696429	0.9414544	0	1	0.7301759	-151.813
116314	cg0590146	61780480	59786389	0.4647294	0	1	0.7522579	139.2928
116362	cg0590372	15673451	15673451	0.5583972	0	1	0.6619192	20.85998
116556	cg0591489	34617449	34617449	0.6734615	0	1	0.7897923	32.95995
116629	cg0591871	47716437	47716437	0.3022402	0	1	0.4667998	44.59313
116686	cg0592176	68642362	68642362	0.862406	0	1	0.6792791	-86.04171
116695	cg0592221	55756442	55756442	0.6976388	0	1	0.5800409	-26.98141
116696	cg0592225	29795415	18626373	0.453424	0	1	0.3276671	-27.54101
116782	cg0592592	19725472	19725472	0.91217	0	1	0.6906285	-140.3073
116861	cg0592927	68636326	68636326	0.1608778	0	1	0.2885714	38.71649
116874	cg0592986	57686485	57686485	0.3920987	0	1	0.5038061	21.80825
116903	cg0593136	61691305	61691305	0.8311029	0	1	0.5685768	-138.0171
116997	cg0593590	19706355	19706355	0.4490286	0	1	0.5492091	18.19528
117004	cg0593621	73743360	65633311	0.5474922	0	1	0.4408823	-20.12477
117046	cg0593820	13669487	13669487	0.4249734	0	1	0.2702187	-41.65883

117095	cg05940452	42729309	54606483	0.3931223	0	1		-4.34E-09
117146	cg05942349	66605322	66605322	0.7857263	0	1	0.9398773	100.6067
117148	cg05942459	33666445	24706418	0.6407966	0	1	0.4336956	-66.82456
117219	cg05945782	11806482	41603461	0.632854	0	1	0.497714	-31.19626
117271	cg05948955	69613476	69613476	0.8054051	0	1	0.7045493	-27.87844
117272	cg05948962	65710411	65710411	0.2952443	0	1	0.4087438	24.11551
117307	cg05950572	57658365	57658365	0.5014794	0	1	0.6376676	31.74394
117372	cg05953243	19760425	19760425	0.5216274	0	1	0.643625	26.59083
117435	cg05956518	14636450	14636450	0.5319307	0	1	0.7870957	118.683
117456	cg05957544	21789302	21635341	0.7442222	0	1	0.8576552	41.11595
117497	cg05959430	73612424	73612424	0.3774399	0	1	0.5440338	43.66822
117639	cg05966431	59724427	59724427	0.8072281	0	1	0.6923323	-34.23193
117729	cg05971102	74626404	74626404	0.8016809	0	1	0.3146167	-371.3336
117747	cg05971911	22669432	35631500	0.0149929	0	1	0.1379134	75.5998
117863	cg05977333	32673456	32673456	0.9372555	0	1	0.8305113	-61.12087
117930	cg05981038	66692405	66692405	0.2678284	0	1	0.3868437	27.07181
118211	cg05994819	30625300	30682303	0.4865621	0	1	0.3506869	-30.84411
118213	cg05994974	24671300	24671300	0.3042638	0	1	0.4320042	28.93303
118309	cg05999364	65737401	65737401	0.1882883	0	1	0.3238976	39.3723
118313	cg05999628	74634432	74634432	0.4736419	0	1	0.5755129	18.851
118335	cg06000878	57671398	57671398	0.3473116	0	1	0.4667682	24.90405
118360	cg06002203	56698398	56698398	0.8446839	0	1	0.6670154	-76.80507
118375	cg06002687	24632477	52784353	0.4168306	0	1	0.2839114	-31.68063
118554	cg06013395	47646471	47646471	0.2565102	0	1	0.3857324	31.5138
118559	cg06013769	64700324	57768426	0.5406662	0	1	0.4124859	-27.40166
118612	cg06016684	35736339	35736339	0.5211477	0	1	0.3416399	-50.59887
118695	cg06021990	49639420	49639420	0.3411598	0	1	0.4593832	24.59217
118725	cg06023351	36691480	36691480	0.8984178	0	1	0.6149057	-190.8725
118731	cg06023791	53738457	53738457	0.2886775	0	1	0.398767	23.16377
118851	cg06032337	48708300	48708300	0.3408251	0	1	0.7485536	374.3439
119076	cg06044945	71687311	71687311	0.4199374	0	1	0.5224575	18.85547
119190	cg06051662	33803347	33803347	0.4040831	0	1	0.2977246	-21.66379
119195	cg06052090	21676383	21676383	0.4444728	0	1	0.5464591	18.71907
119199	cg06052372	47624464	47624464	0.3324273	0	1	0.4337794	19.31586
119343	cg06061081	71649437	71649437	0.720751	0	1	0.6126468	-24.6496
119424	cg06065495	26611336	26611336	0.1056077	0	1	0.2328872	47.22313
119600	cg06075393	49713492	49713492	0.3372018	0	1	0.0765563	-157.1448
119628	cg06077305	66671508	25699377	0.8670314	0	1	0.7581241	-40.50022
119783	cg06085726	47672424	47672424	0.1533693	0	1	0.2609603	30.44476
119880	cg06090818	58734382	66670400	0.7586129	0	1	0.8944813	64.45393
119935	cg06093861	67783467	67783467	0.4766338	0	1	0.344104	-29.6902
120193	cg06106763	29736310	29736310	0.1436122	0	1	0.0365102	-53.77113
120225	cg06108661	20803430	20803430	0.6754048	0	1	0.8211871	51.93651

120272	cg06112171	16684338	16684338	0.45849	0	1	0.6386257	51.68275
120273	cg06112204	64656387	64656387	0.7911128	0	1	0.9126001	61.2501
120365	cg06118302	40647492	40647492	0.4450401	0	1	0.5527503	20.48543
120406	cg06120313	47767466	47767466	0.8246896	0	1	0.6208112	-89.32552
120563	cg06129455	58661340	58661340	0.5678368	0	1	0.8211257	126.6145
120578	cg06130360	19774377	53699496	0.5416677	0	1	0.3789999	-41.81366
120613	cg06132727	67672504	63621429	0.4927728	0	1	0.3784019	-22.78144
120640	cg06134678	43631399	43631399	0.5737156	0	1	0.7361615	49.22223
120657	cg06135529	33738316	65637472	0.5041897	0	1	0.3912412	-22.21519
120677	cg06136702	48627478	48627478	0.2024512	0	1	0.3154695	28.45639
120706	cg06139006	24717442	41733314	0.4880476	0	1	0.6613349	49.20662
120772	cg06143315	73685375	56706412	0.8626935	0	1	0.7139863	-62.97623
120841	cg06147194	51660422	51660422	0.764342	0	1	0.8997394	66.0274
120866	cg06148736	73691439	49675416	0.2781022	0	1	0.1456643	-43.05858
120886	cg06150148	12697439	55755303	0.1283661	0	1	0.2558017	43.16036
120896	cg06150772	24683399	24683399	0.3869818	0	1	0.4944783	20.51018
120932	cg06152856	10766356	10766356	0.577328	0	1	0.4722094	-19.84612
121021	cg06157924	56734322	28736442	0.8204116	0	1	0.947542	83.12888
121051	cg06159404	30625391	28698390	0.3403523	0	1	0.0995841	-128.6469
121253	cg06173319	35726343	60720359	0.2796359	0	1	0.4236035	36.40211
121317	cg06176650	43701306	43701306	0.3009454	0	1	0.4352599	31.56797
121383	cg06179228	58688505	58688505	0.1824941	0	1	0.2980912	31.08175
121588	cg06190732	21644359	21644359	0.110196	0	1	0.2135248	33.87246
121647	cg06193597	54605425	40778416	0.5994748	0	1	0.3904907	-66.86836
121655	cg06193958	66632377	66632377	0.2278544	0	1	0.1260238	-30.99562
121797	cg06202470	56672358	50807436	0.7982261	0	1	0.5884879	-86.94759
121805	cg06202802	59743377	59743377	0.688089	0	1	0.8175909	42.682
121874	cg06206801	20679486	20679486	0.3083452	0	1	0.4379857	29.51802
121963	cg06211550	55734452	52660431	0.4164638	0	1	0.5215471	19.63589
122021	cg06213900	18623376	18623376	0.3652681	0	1	0.5086122	33.57015
122248	cg06225639	29665383	29665383	0.4517908	0	1	0.6579676	67.09174
122312	cg06230664	34757465	34757465	0.3651556	0	1	0.2470765	-27.69577
122326	cg06231362	54718487	54718487	0.4939315	0	1	0.3787579	-23.04298
122451	cg06238316	64747498	64747498	0.5699689	0	1	0.4442704	-26.60947
122503	cg06241208	32773363	32773363	0.282364	0	1	0.4426707	43.55225
122573	cg06245711	53646379	53646379	0.2406766	0	1	0.3458404	23.33801
122602	cg06247406	48713397	48713397	0.6366484	0	1	0.4851473	-38.03648
122614	cg06248701	39711332	39711332	0.3319832	0	1	0.4435087	22.52842
122623	cg06249604	59671348	41668405	0.010442	0	1	0.1854611	122.3675
122639	cg06250751	20661503	20661503	0.8036682	0	1	0.6947199	-31.16982
122666	cg06252276	71777325	74715399	0.4584931	0	1	0.3261132	-30.04717
122709	cg06255006	12730365	42684362	0.7658338	0	1	0.6551291	-28.46583
122862	cg06264882	13672375	13672375	0.6893077	0	1	0.3600159	-173.0218

122879	cg0626622	73642449	73642449	0.8594989	0	1	0.737659	-46.11888
122919	cg0626887	60793361	25655400	0.5810696	0	1	0.4752084	-20.10865
122961	cg0627104	52771317	52771317	0.0965081	0	1	0.2216742	47.95071
122969	cg0627138	16652309	16652309	0.2064118	0	1	0.3499793	41.29748
122974	cg0627169	55809408	32768487		0	1		-4.34E-09
123109	cg0628252	26626360	44734401	0.3018198	0	1	0.1789693	-34.53072
123152	cg0628557	52656335	52656335	0.3274021	0	1	0.4454299	24.81012
123188	cg0628754	10792391	10792391	0.6186359	0	1	0.719256	21.96826
123199	cg0628808	66766464	66766464	0.3877151	0	1	0.516829	27.83521
123302	cg0629378	28697451	28697451	0.3770683	0	1	0.1223469	-131.9776
123389	cg0629795	46733479	29713394	0.2159378	0	1	0.1086032	-36.10389
123398	cg0629848	56632370	56632370	0.3329375	0	1	0.4378775	20.40766
123440	cg0630088	17736396	17736396	0.6647685	0	1	0.868347	103.3985
123456	cg0630202	32682378	56655426	0.4846727	0	1	0.3836638	-18.56799
123506	cg0630575	33684488	33684488	0.781123	0	1	0.6045734	-62.56127
123514	cg0630656	34681342	34681342	0.7520805	0	1	0.3156782	-340.2837
123598	cg0631246	31807475	31807475	0.2857866	0	1	0.3989867	24.31805
123641	cg0631488	31801434	31801434	0.7995651	0	1	0.9222823	66.1516
123648	cg0631539	12656471	71690449	0.2836423	0	1	0.169473	-31.67188
123659	cg0631610	32645422	59657486	0.3421159	0	1	0.5772165	84.29151
123749	cg0632227	28786458	65607459	0.1836153	0	1	0.0748604	-43.43335
123887	cg0633059	45767371	34810417	0.8082952	0	1	0.659722	-51.24242
123933	cg0633323	68734430	68734430	0.3650567	0	1	0.5028927	31.37621
123944	cg0633423	63754370	37773495	0.7410017	0	1	0.8587899	43.71332
124072	cg0634207	39699315	39699315	0.3008035	0	1	0.4594947	41.924
124175	cg0634877	21770427	34717427	0.3283757	0	1	0.4435366	23.81157
124190	cg0634976	43635502	69640364	0.3255757	0	1	0.4452055	25.40755
124206	cg0635054	36770426	46765377	0.9445748	0	1	0.7701086	-121.3202
124248	cg0635261	58777301	47654342	0.1576189	0	1	0.0471314	-52.31247
124292	cg0635469	25729301	25729301	0.2653281	0	1	0.42721	45.29131
124338	cg06358191	63797319	63797319	0.5448875	0	1	0.6507796	21.32047
124369	cg0635988	38799348	38799348	0.3296655	0	1	0.4309811	19.35479
124384	cg0636082	31759367	31759367	0.8162514	0	1	0.6338391	-72.7927
124427	cg0636303	39683376	39683376	0.1885537	0	1	0.3251589	39.8082
124491	cg06366791	47605483	47605483	0.4081666	0	1	0.2736104	-32.79396
124661	cg0637443	53655465	53655465	0.6549168	0	1	0.8059267	52.18045
124788	cg06380401	16791420	16791420	0.6828575	0	1	0.7952408	31.79003
124953	cg0639036	12768371	71778401		0	1	0.9012603	4.34E-09
125033	cg0639482	64600507	64600507	0.083242	0	1	0.2110712	52.67126
125080	cg0639752	13644325	70688368		0	1		-4.34E-09
125089	cg0639824	62623438	62629443	0.1426565	0	1	0.0236616	-67.94889
125234	cg0640704	50810438	50810438	0.4265207	0	1	0.2445544	-57.13295
125378	cg0641668	29808391	29808391	0.3462587	0	1	0.2429499	-22.59585

125484	cg0642203	49645414	28720374	0.0881867	0	1	0.196751	40.42129
125504	cg0642275	16691453	16691453	0.3472868	0	1	0.5273753	50.76881
125592	cg0642919	10616505	10616505	0.5634673	0	1	0.6779373	25.04177
125613	cg0643068	65688320	65688320	0.6151443	0	1	0.487167	-28.06318
125627	cg0643168	14667388	14667388	0.3109756	0	1	0.4340647	27.01629
125658	cg0643380	15792435	15792435	0.2544277	0	1	0.3796901	30.06413
125720	cg0643720	60686369	60686369	0.9177117	0	1	0.800786	-60.05438
125736	cg0643793	70650364	70650364	0.3798566	0	1	0.2308581	-41.70465
125752	cg0643855	27606375	27606375	0.5648144	0	1	0.6789536	24.96334
125942	cg0645037	51739444	51739444	0.7918526	0	1	0.9129556	61.11934
126068	cg0645773	67621496	67621496	0.5318604	0	1	0.7332391	70.66274
126098	cg0645910	35778480	35778480	0.5279873	0	1	0.4213854	-20.09781
126119	cg0646018	51774338	51774338	0.4991718	0	1	0.6230404	26.74227
126123	cg0646047	36624324	55735341	0.6827845	0	1	0.5585932	-28.77746
126141	cg0646158	71687503	71687503	0.5223001	0	1	0.8940502	374.3439
126191	cg0646407	49764417	49764417	0.3432816	0	1	0.7599837	374.3439
126263	cg0646838	70632375	70632375	0.7172235	0	1	0.617089	-21.71362
126285	cg0646944	73698361	73698361	0.4473203	0	1	0.5489936	18.63455
126307	cg0647085	57681456	66764464	0.7618363	0	1	0.5746795	-65.87816
126334	cg0647242	26623439	26623439	0.6958822	0	1	0.5747123	-28.22923
126406	cg0647669	48787484	48787484	0.6985025	0	1	0.8185366	38.10655
126432	cg0647850	67604416	42625372	0.6984588	0	1	0.5957973	-21.78481
126530	cg0648412	69796300	69796300	0.3718366	0	1	0.5188625	35.0026
126533	cg0648416	56663455	56663455	0.370115	0	1	0.6129801	89.9006
126673	cg0649159	35796438	35796438	0.6149403	0	1	0.3999029	-70.89273
126687	cg0649237	65606397	65606397	0.30199	0	1	0.4048279	20.42706
126714	cg0649380	35687442	35687442	0.6722213	0	1	0.8022178	40.75277
126884	cg0650325	39702400	23802427	0.8705717	0	1	0.6818839	-92.99949
126897	cg0650398	38736460	38736460	0.6934296	0	1	0.9078639	131.457
126965	cg0650763	70618405	70618405	0.2625931	0	1	0.1251798	-49.03654
127012	cg0651118	53644305	31626381	0.2607636	0	1	0.1431367	-36.16415
127016	cg0651133	14741422	14741422	0.2939254	0	1	0.4141659	26.5227
127055	cg0651386	73790437	56733367		0	1	0.0289087	4.34E-09
127191	cg0652147	29670416	38737311	0.5048316	0	1	0.394823	-21.2488
127233	cg0652315	20745504	20745504	0.5990594	0	1	0.7967461	78.502
127258	cg0652426	16628418	16628418	0.588086	0	1	0.4608111	-27.36042
127280	cg0652545	49601316	49601316	0.3004597	0	1	0.4393887	33.42489
127427	cg0653157	15760498	15760498	0.3286444	0	1	0.1779307	-47.93805
127532	cg0653615	72678327	72678327	0.5075263	0	1	0.1565896	-220.0791
127712	cg0654520	29750446	66809442	0.9046402	0	1	0.8003846	-46.99668
127790	cg0654923	10808332	37751507	0.4495991	0	1	0.347598	-19.26519
127803	cg0654987	32756434	32756434	0.2952527	0	1	0.4932916	62.45049
127806	cg0654992	51784479	16726332	0.1710357	0	1	0.0710223	-39.29499

127818	cg0655027	44615360	44615360	0.9256324	0	1	0.6456885	-206.3931
127978	cg0655957	11755457	11755457	0.4371162	0	1	0.5641296	27.04319
128030	cg0656271	51790496	51790496	0.942102	0	1	0.7944105	-96.68732
128090	cg0656603	36644315	30733327	0.721475	0	1	0.6158665	-23.79836
128123	cg0656834	44629445	44629445	0.7460089	0	1	0.854023	37.59364
128168	cg0657043	32654390	32654390	0.6551806	0	1	0.5438523	-23.22192
128203	cg0657309	26705468	26705468	0.5213007	0	1	0.4091724	-21.86781
128303	cg0657827	16637439	16637439	0.2207256	0	1	0.3344437	27.5214
128394	cg0658354	34632461	67678312	0.797662	0	1	0.6348735	-57.35844
128405	cg0658421	10757344	10757344	0.2517639	0	1	0.3899198	35.4486
128442	cg0658626	45613487	45613487	0.2316863	0	1	0.3865294	44.38956
128459	cg0658724	21769327	21685348	0.5518469	0	1	0.7146884	47.50702
128466	cg0658795	36701322	36701322	0.0833657	0	1	0.2098002	51.79736
128479	cg0658855	53606434	63683508	0.6544884	0	1	0.5246623	-29.82086
128493	cg0658919	27753383	13726352	0.6581166	0	1	0.7587938	24.11684
128494	cg0658919	35615321	35615321	0.2554225	0	1	0.3555531	21.02202
128559	cg0659375	36733361	36733361	0.4049804	0	1	0.2418023	-47.61417
128577	cg0659515	23641489	23641489	0.2093621	0	1	0.3334266	32.42647
128608	cg0659694	71618389	71618389	0.3451556	0	1	0.4718676	27.51118
128994	cg0661749	32784332	32784332	0.915158	0	1	0.6760054	-158.2923
129009	cg0661813	49798311	49798311	0.6653062	0	1	0.5591956	-21.7916
129041	cg0661962	23669487	68801420	0.3867481	0	1	0.2660491	-27.77125
129046	cg0661993	66703337	55610394	0.2058238	0	1	0.101464	-35.76552
129051	cg0662011	10731450	10731450	0.4938672	0	1	0.5961281	19.18052
129076	cg0662102	43726361	43726361	0.1615877	0	1	0.278955	33.87855
129172	cg0662452	25798433	10630451	0.554207	0	1	0.4482887	-19.93701
129249	cg0662879	19665466	19665466	0.1748868	0	1	0.033033	-80.73279
129283	cg0663083	52715317	32741367	0.3299969	0	1	0.2251095	-24.00941
129299	cg0663177	24644310	56680385	0.3608665	0	1	0.5692111	66.42929
129353	cg0663436	16610505	11714504	0.4162266	0	1	0.9232849	374.3439
129361	cg0663457	33763414	35721391	0.8135511	0	1	0.4916213	-190.7719
129365	cg0663471	14804417	35630510	0.3209844	0	1	0.4459929	27.43675
129393	cg0663576	50764414	53675436	0.6963878	0	1	0.8253763	43.63864
129624	cg0664592	61626420	38633476	0.2366855	0	1	0.1262347	-35.00513
129675	cg0664793	43653440	43653440	0.3509032	0	1	0.5030199	37.48166
129694	cg0664903	54780312	22711458	0.2024755	0	1	0.099191	-35.59822
129723	cg0665024	51790402	33744484	0.4867047	0	1	0.662387	50.46664
129739	cg0665078	41798378	41798378	0.1303292	0	1	0.2949326	63.71275
129885	cg0665791	49756328	30766450	0.8804027	0	1	0.7687411	-45.01006
130008	cg0666533	11641398	43666501	0.6074587	0	1	0.498263	-21.48519
130013	cg0666562	27804429	27804429	0.2073497	0	1	0.3379641	35.3719
130146	cg0667411	25647452	25647452	0.6909047	0	1	0.8330295	52.12275
130167	cg0667541	36780493	36780493	0.4300424	0	1	0.5949184	43.04725

130376	cg06686422	43760371	43760371	0.8664057	0	1	0.6384469	-122.1321
130416	cg06688803	54745316	54745316	0.5453171	0	1	0.3675949	-49.2342
130431	cg06689619	67729462	67729462	0.8189496	0	1	0.9210645	50.99629
130439	cg06690085	36632421	36632421	0.3385201	0	1	0.4908964	37.86454
130465	cg06691616	52766478	52766478	0.5474404	0	1	0.6881224	35.61942
130573	cg06698332	67659489	67659489	0.3016113	0	1	0.4309106	29.60889
130601	cg06699489	29618468	29618468	0.8517437	0	1	0.6522403	-94.29826
130608	cg06699669	53673361	48603472	0.904757	0	1	0.7035603	-118.4479
130736	cg06706443	74749383	74749383	0.9265606	0	1	0.6679045	-185.3064
130748	cg06707236	59657317	55660419	0.7441181	0	1	0.6069927	-37.88247
130795	cg06709297	23667375	23667375	0.4919438	0	1	0.6265461	30.82058
130846	cg06711418	59719305	59719305	0.3758124	0	1	0.4965731	24.96113
130881	cg06713116	15697445	15697445	0.0665271	0	1	0.2281911	80.49416
130977	cg06718159	36768332	36768332	0.2187036	0	1	0.4458254	87.99928
130984	cg06718920	19726359	19726359	0.3485556	0	1	0.4654372	24.00422
131042	cg06721546	71751418	71751418	0.3380242	0	1	0.1609095	-65.21651
131127	cg06726231	11759300	11759300	0.4313909	0	1	0.5420669	21.39039
131150	cg06727338	52647447	52647447	0.1358528	0	1	0.2429689	32.1971
131167	cg06728252	17687483	53744414	0.3267144	0	1	0.1964936	-36.13859
131312	cg06736229	35758367	35758367	0.4060301	0	1	0.5936494	54.48923
131325	cg06737308	27715457	27715457	0.8146468	0	1	0.6778713	-45.97857
131340	cg06738063	27652434	27652434	0.3435914	0	1	0.4956057	37.5897
131412	cg06741336	37611325	50676357	0.7008451	0	1	0.8015528	27.44827
131450	cg06743454	20769409	20769409	0.6211321	0	1	0.8663349	136.8508
131530	cg06747330	50797362	50797362	0.3777644	0	1	0.2281913	-42.18738
131695	cg06755258	12697311	12697311	0.8066372	0	1	0.9172908	55.49945
131770	cg06758191	30630472	30630472	0.1615884	0	1	0.3270701	58.30573
131850	cg06760904	36602415	16749429	0.6528393	0	1	0.7705718	31.74533
131869	cg06761912	63615329	63615329	0.2530061	0	1	0.5318499	123.9805
131900	cg06763776	49682499	49682499	0.2918882	0	1	0.4328868	34.60833
131903	cg06763829	31694485	27758434	0.1239852	0	1	0.0201577	-58.14479
132028	cg06769820	11806416	11806416	0.2950535	0	1	0.4528845	41.78418
132201	cg06778662	26715408	26609404	0.5532014	0	1	0.6702121	25.65905
132265	cg06781948	26739477	26739477	0.6155054	0	1	0.7960716	67.52711
132424	cg06789824	73669314	73669314	0.8387184	0	1	0.6886593	-57.89428
132481	cg06792262	54757347	18617354	0.494887	0	1	0.3510306	-34.01086
132488	cg06792428	17787407	17787407	0.6392149	0	1	0.2384541	-272.7782
132525	cg06794141	30800394	30800394	0.114762	0	1	0.2363345	42.39663
132572	cg06796435	60704500	63750357	0.2803451	0	1	0.1293125	-55.89855
132579	cg06796713	55650417	55650417	0.1537052	0	1	0.2553406	27.88104
132617	cg06798115	30656349	30656349	0.357432	0	1	0.5039128	34.97811
132630	cg06798887	43788459	43788459	0.6283844	0	1	0.7717711	43.53958
132648	cg06799747	61602392	61602392	0.5042233	0	1	0.6514327	36.71506

132653	cg0680022	69728463	69728463	0.3527836	0	1	0.4824601	28.46075
132733	cg06804411	43684436	43684436	0.219976	0	1	0.3462436	32.56204
132778	cg0680686	35635464	35635464	0.1865344	0	1	0.2971103	28.67954
132838	cg0680928	44783365	44783365	0.8520042	0	1	0.739407	-39.62689
132884	cg0681206	47611437	50686435	0.764048	0	1	0.6591793	-26.04634
132902	cg0681279	49703384	49703384	0.4517816	0	1	0.6570248	66.48178
132904	cg0681283	70635328	70635328	0.3045815	0	1	0.4180554	23.8322
132991	cg0681655	29782437	29782437	0.8036452	0	1	0.9171333	57.41179
133024	cg0681815	51757488	51757488	0.4160916	0	1	0.537834	25.0929
133046	cg0681886	24810505	24810505	0.5125247	0	1	0.6321293	25.44501
133104	cg0682107	72731423	72731423	0.6669881	0	1	0.775818	28.50751
133118	cg0682182	17685494	17685494	0.6946895	0	1	0.5673252	-30.54743
133130	cg0682219	59677439	59677439	0.3734156	0	1	0.49317	24.63983
133146	cg0682303	74683424	66622482	0.1935842	0	1	0.0666021	-56.83191
133210	cg0682612	41603422	42687466	0.9199639	0	1	0.778935	-78.72994
133254	cg0682814	52714396	52714396	0.5484653	0	1	0.6543366	21.40639
133324	cg0683106	47715326	23803388	0.7074202	0	1	0.603037	-22.72867
133389	cg06833981	30630339	30630339	0.7577312	0	1	0.4877199	-124.7242
133437	cg0683581	54768320	54768320	0.6534176	0	1		-4.34E-09
133495	cg0683821	18744339	18744339	0.6513389	0	1	0.8338683	77.12499
133512	cg06839111	24758505	24758505	0.2709469	0	1	0.3722482	20.84856
133623	cg0684471	72651489	72651489	0.8080668	0	1	0.698742	-31.81477
133625	cg0684484	19796492	19796492	0.8792211	0	1	0.610693	-164.6727
133696	cg0684848	21716407	21716407	0.2853105	0	1	0.3998363	24.79395
133902	cg0685808	53796358	53796358	0.5734274	0	1	0.6852916	24.40771
134034	cg0686564	73713481	73713481	0.6684377	0	1	0.4951816	-49.5619
134080	cg0686748	27650399	24604317	0.7028953	0	1	0.8052731	28.50645
134146	cg0687011	38774451	38774451	0.8210083	0	1	0.7034237	-37.26043
134171	cg0687134	41643338	41643338	0.1935619	0	1	0.3938987	74.00336
134297	cg0687607	28674327	28674327	0.3715269	0	1	0.2626098	-23.69421
134461	cg0688449	46682499	46682499	0.6436164	0	1	0.539021	-20.7332
134495	cg0688673	61790357	42731362	0.3367413	0	1	0.4593748	26.21573
134532	cg0688846	43681321	32771453	0.7356281	0	1	0.6009943	-36.09797
134709	cg0689576	37722354	37722354	0.6809694	0	1	0.5297065	-39.82669
134737	cg0689744	31666360	31666360	0.4789838	0	1	0.3616538	-23.95775
134809	cg06900571	11749329	11749329	0.5668501	0	1	0.6769024	23.47729
134905	cg0690576	30674312	29675455		0	1		-4.34E-09
134982	cg0690925	19690510	19690510	0.3922799	0	1	0.5007782	20.78735
135075	cg0691351	62658445	69802376	0.8512978	0	1	0.7235714	-47.70833
135269	cg0692490	13759383	13759383	0.8817637	0	1	0.5708129	-210.1768
135276	cg0692530	19801472	19801472	0.4646529	0	1	0.5744858	21.28961
135403	cg0693253	31652477	31652477	0.327464	0	1	0.4361291	21.69233
135468	cg0693543	28700404	28700404	0.4878466	0	1	0.6396315	38.25864

135485	cg0693629	23804420	23804420	0.4264482	0	1	0.6044539	49.62234
135531	cg0693792	36675346	36675346	0.3186301	0	1	0.4551023	31.8396
135541	cg0693826	35664356	40687337	0.3179055	0	1	0.1683432	-48.61809
135594	cg0694115	46659489	46659489	0.6185852	0	1	0.7408825	31.29373
135614	cg0694211	15602396	15602396	0.578531	0	1	0.7519274	56.71382
135757	cg0694898	20774355	58714333	0.4988409	0	1	0.3865838	-22.02349
135793	cg0695112	14612478	44784383	0.7610736	0	1	0.6362478	-33.94233
135893	cg0695595	16625306	16625306	0.8969814	0	1	0.6048881	-198.9609
135948	cg0695876	24600374	60790506	0.4480273	0	1	0.611859	42.88183
135964	cg0695944	23708426	23708426	0.7731875	0	1	0.8951507	55.45601
135988	cg0696071	65763472	65763472	0.7549906	0	1	0.5652317	-66.46093
136015	cg0696142	69617424	69617424	0.5661094	0	1	0.6838949	26.45539
136156	cg0696871	14737440	14737440	0.7003436	0	1	0.5880243	-25.19012
136215	cg0697122	39602432	39602432	0.4141939	0	1	0.6116691	60.26929
136307	cg0697597	22680370	58647446	0.4715982	0	1	0.3713763	-18.44416
136314	cg0697622	32734337	32734337	0.84817	0	1	0.7459216	-33.73677
136362	cg0697902	11702434	11702434	0.5212708	0	1	0.6378168	24.52594
136370	cg0697938	27693451	27693451	0.3080958	0	1	0.1685015	-43.53809
136417	cg0698216	50801467	50801467	0.7218206	0	1	0.6074159	-27.01455
136429	cg0698282	50657301	50657301	0.8054988	0	1	0.9137506	52.57099
136451	cg0698420	15792440	15792440	0.657383	0	1	0.5551925	-20.31675
136613	cg0699550	72669423	72669423	0.3631596	0	1	0.581502	72.71685
136856	cg0700712	48715323	48715323	0.6249961	0	1	0.7258225	22.34372
136959	cg0701153	24806349	24806349	0.4523519	0	1	0.5998566	35.43084
137048	cg0701574	14780443	28697376	0.7940425	0	1	0.618704	-64.01305
137124	cg0701843	69725465	69725465	0.7009133	0	1	0.5962396	-22.55669
137191	cg0702153	23767478	23767478	0.0850509	0	1	0.2563781	80.54282
137227	cg0702349	16735430	16735430	0.2723078	0	1	0.4233221	39.8508
137273	cg0702598	61761330	60706463	0.1918252	0	1	0.2962985	25.88662
137328	cg0702895	16757359	16757359	0.2902935	0	1	0.4132683	27.64246
137343	cg0702977	36775473	36775473	0.2374855	0	1	0.3400856	22.59919
137370	cg0703140	19606305	30614363	0.7151587	0	1	0.5885044	-31.38016
137404	cg0703329	55606483	55606483	0.2383559	0	1	0.3420588	22.93891
137466	cg0703596	32670378	50677405	0.2187151	0	1	0.1139958	-33.98669
137505	cg0703796	34643500	34643500	0.9134346	0	1	0.8121894	-47.78734
137555	cg0704148	57693376	57693376	0.8802577	0	1	0.7788242	-39.11638
137674	cg0704821	11754467	11754467	0.3219377	0	1	0.4279205	20.95289
137732	cg0705116	37752468	24601384	0.2367418	0	1	0.0978054	-55.71799
137773	cg0705311	69632377	18728350	0.6780066	0	1	0.7817257	26.93745
137811	cg0705468	27678345	12778447	0.2752807	0	1	0.425844	39.48902
137951	cg0706178	17644464	65610316	0.5887991	0	1	0.4223737	-43.69286
137991	cg0706355	13760348	30774479	0.6358883	0	1	0.7397204	24.12474
138013	cg0706449	58683483	13674339	0.2015432	0	1	0.0537086	-75.71036

138084	cg0706818	28608460	28608460	0.9316788	0	1	0.8179788	-63.7425
138233	cg0707534	59760319	26780402	0.359107	0	1	0.2499979	-24.29396
138234	cg0707538	49604440	42704427	0.7488379	0	1	0.6266093	-31.85004
138296	cg0707895	64671370	64671370	0.6148985	0	1	0.8017944	72.5717
138366	cg0708245	47687428	35795412	0.7467541	0	1	0.6361019	-27.08945
138384	cg0708381	16708468	16708468	0.2826065	0	1	0.4042865	27.45168
138562	cg0709288	17741334	17741334	0.7211084	0	1	0.8532647	50.645
138567	cg0709306	24677315	24677315	0.4900171	0	1	0.3718168	-24.12735
138738	cg0710120	16671320	16671320	0.2685241	0	1	0.3741143	22.34052
138746	cg0710184	23606375	67630445	0.1434442	0	1	0.2471044	29.78679
138786	cg0710384	31649399	60701397	0.2849885	0	1	0.4654329	53.37933
138830	cg0710594	28654322	29639424	0.1692813	0	1	0.0570069	-50.33597
138850	cg0710692	30800449	30800449	0.8911998	0	1	0.7859344	-43.90322
138964	cg0711319	56696398	18634480	0.2401372	0	1	0.1344815	-31.69878
138979	cg0711431	16646394	16646394	0.388598	0	1	0.2461652	-37.6397
138990	cg0711481	63676506	63676506	0.279444	0	1	0.3915718	24.16762
139031	cg0711663	69808469	36794428	0.5429079	0	1	0.4402729	-18.90276
139033	cg0711671	20799343	72652348	0.148087	0	1	0.2702562	37.68419
139086	cg0711915	37708397	37708397	0.416292	0	1	0.5593679	33.19637
139188	cg0712418	18742431	18742431	0.6300343	0	1	0.8739329	139.2117
139289	cg0712850	47802391	47802391	0.7753536	0	1	0.9057165	64.78946
139412	cg0713436	31604480	31604480	0.4202435	0	1	0.5454443	26.32223
139456	cg0713625	18664440	18664440	0.4060949	0	1	0.5112257	19.67759
139471	cg0713692	11658305	10709499	0.457676	0	1	0.6292428	47.04786
139479	cg0713733	25632370	25632370	0.4763469	0	1	0.340482	-31.0442
139542	cg0713952	17733357	17733357	0.7070895	0	1	0.822872	36.64743
139620	cg0714315	32685420	35752322	0.280761	0	1	0.4185829	33.788
140064	cg0716199	15623461	15623461	0.4218968	0	1	0.3133266	-21.97714
140187	cg0716793	69741325	69741325	0.4997515	0	1	0.6100785	21.88975
140294	cg0717354	13618386	13618386	0.1964482	0	1	0.0852096	-42.52386
140419	cg0717903	38633370	38633370	0.1891595	0	1	0.3257124	39.72149
140489	cg0718170	61745374	61745374	0.1845014	0	1	0.3042365	32.6574
140500	cg0718261	60691506	60691506	0.4773466	0	1	0.2501387	-84.23383
140591	cg0718720	60725377	60725377	0.4787579	0	1	0.6473965	46.28606
140616	cg0718859	73779374	32785438	0.1516852	0	1	0.0444619	-51.03911
140842	cg0720087	62797430	40779370	0.7989091	0	1	0.6938999	-28.9935
140845	cg0720093	66618309	66618309	0.3414045	0	1	0.5186955	49.47559
140855	cg0720147	51673397	51673397	0.501365	0	1	0.6527978	38.58912
140917	cg0720466	35802327	63636368	0.2452544	0	1	0.3665987	29.0322
140943	cg0720579	40763390	29665340	0.2668081	0	1	0.3672222	20.70293
141121	cg0721318	31748390	31748390	0.2399205	0	1	0.3668068	31.51364
141137	cg0721378	13608319	13608319	0.3197476	0	1	0.4420325	26.48801
141160	cg0721550	63601400	69745364	0.5731859	0	1	0.3688527	-63.94715

141165	cg0721569	25803509	69798377	0.7194481	0	1	0.6001083	-28.75616
141185	cg0721652	44631403	44631403	0.2645345	0	1	0.3748462	24.10006
141187	cg0721661	16609425	16609425	0.7221271	0	1	0.269128	-370.3835
141262	cg0722065	24778345	24778345	0.2595974	0	1	0.3610176	21.2879
141275	cg0722125	20797361	20797361	0.1955063	0	1	0.3049413	27.54582
141319	cg0722320	65740494	49653476	0.8266762	0	1	0.6557544	-67.88306
141398	cg0722718	68679473	13794443	0.6455215	0	1	0.7763352	38.07747
141409	cg07228241	56749353	60751355	0.5021158	0	1	0.604713	19.39539
141427	cg0722976	26611405	26611405	0.585779	0	1	0.695962	24.248
141434	cg0723035	72645482	46695468	0.4300697	0	1	0.541086	21.4978
141465	cg0723200	46717453	46717453	0.3386892	0	1	0.5169298	50.02559
141632	cg0724084	35619467	35619467	0.2216574	0	1	0.3675859	41.03727
141636	cg0724108	48806509	37709383	0.3174666	0	1	0.421354	20.39084
141784	cg0724948	24611488	24611488	0.6580282	0	1	0.9006954	151.7644
141865	cg07254421	19650479	19650479	0.6246968	0	1	0.8131824	76.02532
141910	cg0725782	28751331	39657373	0.2644255	0	1	0.3835478	27.25898
141915	cg0725840	41739423	37800497	0.8692248	0	1	0.3585295	-371.3336
141934	cg0725898	61749335	61749335	0.830179	0	1	0.5365865	-167.0316
141964	cg0726059	60648498	60648498	0.4523048	0	1	0.3417867	-22.01738
142067	cg0726580	13716447	13716447	0.6858023	0	1	0.7885029	27.09414
142094	cg0726760	14746373	14746373	0.120221	0	1	0.2405058	40.79978
142107	cg0726824	30758428	30758428	0.4695117	0	1	0.6046403	30.54819
142116	cg0726872	12744392	12744392	0.8593485	0	1	0.6499932	-104.4061
142181	cg0727322	35708382	35708382	0.5394451	0	1	0.6811516	35.6927
142384	cg07284261	13671359	13671359	0.3720583	0	1	0.5455776	47.0773
142406	cg0728523	64612381	64612381	0.4613942	0	1	0.6523701	58.056
142413	cg0728567	27652378	27652378	0.6598333	0	1	0.7836698	35.6682
142538	cg0729411	58629344	58629344	0.7118466	0	1	0.6066574	-23.19952
142551	cg0729478	68716445	27622334	0.5279478	0	1	0.6564484	29.38494
142558	cg0729524	57635507	57635507	0.5044901	0	1	0.3931727	-21.67634
142677	cg0730150	71714478	67810399		0	1		-4.34E-09
142826	cg0731050	58778310	58778310	0.2371814	0	1	0.3375164	21.84122
142840	cg0731102	59645339	59645339	0.2548713	0	1	0.1366871	-37.28358
142973	cg0731673	53683400	53683400	0.5727301	0	1	0.7013881	31.4031
143081	cg0732214	48755323	48755323	0.3532428	0	1	0.2449856	-24.22197
143320	cg0733712	41648304	41648304	0.7777936	0	1	0.6701486	-28.19092
143585	cg0735116	15625403	13644383		0	1	0.0279873	4.34E-09
143673	cg0735568	39768474	39768474	0.2848807	0	1	0.38616	20.40382
143681	cg0735592	25621344	61624473	0.4016612	0	1	0.2796725	-27.67919
143725	cg0735771	33649493	33649493	0.2839445	0	1	0.4378465	40.53376
143842	cg0736512	45618394	45618394	0.2970636	0	1	0.1569792	-45.32166
143850	cg07365741	61780399	61780399	0.63161	0	1	0.4603078	-46.99538
143950	cg0737141	51725339	51725339	0.4850506	0	1	0.6209527	31.18734

143960	cg0737174	40673411	40673411	0.3927568	0	1	0.4992716	20.16716
144031	cg07376381	10710408	19680443	0.3173959	0	1	0.2136259	-24.23935
144116	cg0738020	11717415	11717415	0.4266227	0	1	0.5819161	38.52582
144143	cg0738150	33659300	30603504	0.4040647	0	1	0.2616905	-36.66499
144166	cg0738234	18809480	52801344	0.0349598	0	1	0.3161171	374.3439
144203	cg0738452	35693419	35693419	0.7101743	0	1	0.8666489	69.13546
144525	cg0740293	29764440	29764440	0.5186281	0	1	0.6444268	27.99355
144550	cg0740448	14653354	14653354	0.6194373	0	1	0.514022	-20.49441
144593	cg0740773	64794458	64794458	0.1128337	0	1	0.2586352	56.30824
144599	cg0740823	10764503	10764503	0.5970359	0	1	0.7279721	33.95928
144669	cg0741395	24651408	24651408	0.4806562	0	1	0.6459058	44.60377
144677	cg0741442	17763405	17763405	0.5807054	0	1	0.7617205	62.26743
144763	cg0741970	13644507	12806455		0	1	0.1759494	4.34E-09
144765	cg0741979	53683423	53683423	0.2056965	0	1	0.3123724	25.79322
144802	cg0742132	14643465	14643465	0.440189	0	1	0.5574115	23.58827
145093	cg0743792	41664365	41664365	0.4376923	0	1	0.6144984	49.23421
145099	cg0743824	58738403	58738403	0.473044	0	1	0.5846203	21.945
145153	cg0744127	32783348	32783348	0.1882135	0	1	0.2971657	27.89864
145321	cg0745180	29693347	29693347	0.3032554	0	1	0.428712	28.11593
145352	cg0745344	22631335	22631335	0.709561	0	1	0.3696769	-187.3133
145360	cg0745385	63781398	63781398	0.3688247	0	1	0.480698	22.06648
145391	cg0745579	47702338	44613324	0.6457832	0	1	0.4058378	-88.71102
145411	cg0745658	68672490	68672490	0.2191868	0	1	0.4594216	97.33704
145487	cg0746084	25602402	25602402	0.4155318	0	1	0.2455744	-50.71325
145544	cg0746344	18688340	18688340	0.1661307	0	1	0.2715715	28.30924
145598	cg0746616	66752401	36759444	0.5186785	0	1	0.3638076	-38.4631
145713	cg0747096	52763427	52763427	0.6918033	0	1	0.7944984	27.6183
145798	cg0747467	68614381	68614381	0.4909409	0	1	0.3646953	-27.02688
145816	cg0747539	18794413	28623314	0.6510935	0	1	0.5505644	-19.64292
145833	cg0747623	16794477	16794477	0.580516	0	1	0.7490373	53.74023
145910	cg0747961	71612425	25622453	0.8906528	0	1	0.7823595	-45.58389
146073	cg07488141	69607345	69607345	0.2500978	0	1	0.3555929	23.03399
146108	cg0749007	35716390	47692406	0.3122988	0	1	0.1506862	-57.96284
146142	cg0749204	65743337	57795458	0.5559128	0	1	0.4016248	-37.94548
146161	cg0749304	39621398	32729495	0.4017543	0	1	0.5093382	20.45139
146163	cg0749319	52717438	52717438	0.4282987	0	1	0.6029607	47.91171
146206	cg0749540	53603450	53603450	0.3935118	0	1	0.5989568	64.71526
146247	cg0749808	32632486	32632486	0.5018086	0	1	0.6635982	43.75057
146270	cg0749918	19642415	19642415	0.1802037	0	1	0.3129531	38.89052
146302	cg0750102	48646448	48646448	0.3986031	0	1	0.2365616	-47.48291
146404	cg0750615	30804471	30804471	0.9517365	0	1	0.8371479	-75.35973
146476	cg0750993	35669497	40808423	0.2396571	0	1	0.0477566	-112.5421
146619	cg0751773	41655378	41655378	0.5170674	0	1	0.6215166	20.23154

146644	cg0751942	40786373	54737359	0.7256919	0	1	0.8402264	38.62522
146655	cg0751990	68617489	40707471	0.3804106	0	1	0.2571374	-29.15942
146704	cg0752297	19647471	19647471	0.2631283	0	1	0.3930335	31.44499
146718	cg0752371	15798465	15798465	0.8391458	0	1	0.5343207	-182.1912
146750	cg0752547	59768415	45696375	0.5292978	0	1	0.6363153	21.3358
146812	cg0752912	51782346	55734325	0.2499731	0	1	0.3611517	25.02852
146875	cg0753208	66676374	52766421	0.8445504	0	1	0.7172697	-46.11628
146926	cg0753484	40738358	28717345	0.2234419	0	1	0.0873077	-56.68053
146983	cg0753756	34743307	34743307	0.4432833	0	1	0.2754633	-47.54159
146993	cg0753782	60767362	60767362	0.3091408	0	1	0.4274648	25.37487
147474	cg0756361	57705400	69681379	0.1420827	0	1	0.2749263	43.79524
147508	cg0756497	69750510	69750510	0.7914305	0	1	0.6383789	-51.0286
147711	cg0757468	65680381	65680381	0.3028323	0	1	0.4132535	22.85593
147899	cg0758409	20662320	20662320	0.2750582	0	1	0.3779875	21.23864
147908	cg0758462	33708372	33708372	0.6273305	0	1	0.9041181	374.3439
147918	cg0758485	18629366	26751504	0.4411911	0	1	0.5871307	34.59011
147927	cg0758542	50730344	50730344	0.4875546	0	1	0.6035434	23.64451
147960	cg0758698	38602306	38602306	0.5568754	0	1	0.6630372	21.74172
148094	cg0759272	36761355	36761355	0.4377516	0	1	0.3241956	-23.36541
148096	cg0759277	12673368	12673368	0.8074283	0	1	0.5829436	-99.73914
148200	cg0759797	32649400	32649400	0.5968012	0	1	0.7169671	28.93409
148226	cg0759895	44802330	54623508	0.4295614	0	1	0.3179693	-22.85641
148228	cg0759913	30633361	30633361	0.5643181	0	1	0.8069795	113.6625
148253	cg0760062	71672475	12755445	0.4158979	0	1	0.6529431	86.98335
148378	cg0760752	39677319	39677319	0.441299	0	1	0.3175653	-27.06555
148435	cg0761112	29737489	29737489	0.8381348	0	1	0.7117807	-44.42548
148529	cg0761580	60627488	60627488	0.772718	0	1	0.6276082	-44.4942
148596	cg0761968	27762364	39611482	0.49187	0	1	0.6025833	21.897
148615	cg0762085	70743481	70743481	0.6211501	0	1	0.8547722	122.0733
148635	cg0762169	53769468	53769468	0.2294347	0	1	0.3933275	49.02733
148711	cg0762577	59768425	70628390	0.3056701	0	1	0.4249829	25.82224
148780	cg0762962	50723326	15760401	0.4922109	0	1	0.8226824	374.3439
148844	cg0763366	37800461	37800461	0.7096494	0	1	0.6026205	-23.73973
148946	cg0763919	19621471	19621471	0.8902836	0	1	0.5484398	-252.0738
148993	cg0764157	58611359	58611359	0.9465476	0	1	0.832108	-72.09411
149013	cg0764276	12687381	12687381	0.7341797	0	1	0.9146224	106.8496
149119	cg0764961	45763323	73790462		0	1	0.0453841	4.34E-09
149152	cg0765218	49739311	49739311	0.5897704	0	1	0.7174112	31.91293
149204	cg0765526	68715408	68715408	0.9113884	0	1	0.7174591	-116.1058
149292	cg0766083	70620322	70620322	0.3736822	0	1	0.2640119	-23.89854
149320	cg0766212	33664390	12712374	0.0481372	0	1	0.1653274	56.45424
149363	cg0766457	35709459	35709459	0.7326398	0	1	0.5905578	-39.16093
149379	cg0766522	40601507	40601507	0.2889297	0	1	0.4005153	23.66162

149464	cg0767051	47794342	47794342	0.6589616	0	1	0.5447557	-24.31004
149504	cg0767281	11618327	11618327	0.8333495	0	1	0.727267	-33.4495
149507	cg0767302	10645390	10645390	0.3947096	0	1	0.2811269	-24.61185
149532	cg0767413	66667457	22611489	0.3722043	0	1	0.2593864	-25.19431
149576	cg0767636	48778458	46705324	0.8349367	0	1	0.6906264	-53.74508
149585	cg0767715	18621333	18621333	0.7424531	0	1	0.8619332	45.30906
149737	cg0768694	62687300	70644435	0.4856949	0	1	0.3392237	-35.33887
149789	cg0768973	47623328	47623328	0.1398371	0	1	0.2435396	30.20187
149901	cg0769627	11720369	11720369	0.8021473	0	1	0.9160036	57.23637
149925	cg0769722	26785447	13644463		0	1		-4.34E-09
149950	cg0769819	22657484	22657484	0.3776085	0	1	0.4908533	22.42012
149997	cg0770039	59645308	59645308	0.7015389	0	1	0.8247829	40.60561
150021	cg0770130	54789502	54789502	0.2416711	0	1	0.3459703	22.99311
150031	cg0770175	57744315	13608390	0.7448199	0	1	0.6360977	-26.23208
150037	cg0770223	20646417	20646417	0.3579215	0	1	0.5012036	33.65566
150229	cg0771108	22672493	66748471	0.5496975	0	1	0.6669875	25.64569
150241	cg0771216	36762442	63613473	0.4591823	0	1	0.6672152	68.75102
150474	cg0772462	62627470	62627470	0.6344336	0	1	0.5210387	-23.37727
150759	cg0774030	60667476	32658314	0.3985036	0	1	0.5263575	27.31366
150857	cg0774570	28677340	68655410	0.9461694	0	1	0.8062468	-92.90601
150888	cg0774725	64713395	39679370	0.7444395	0	1	0.6055681	-38.69505
150907	cg0774796	30725447	24621454	0.1438762	0	1	0.3257674	71.50509
150939	cg0774959	52632437	52632437	0.5591731	0	1	0.6956364	34.26067
151000	cg0775240	42685376	42685376	0.7418952	0	1	0.6199451	-31.22429
151012	cg0775336	65787348	65787348	0.4507769	0	1	0.5899691	31.89937
151179	cg0776405	27785330	27785330	0.7084142	0	1	0.8094648	28.36471
151210	cg0776598	58716480	58716480	0.0827275	0	1	0.2199086	58.58063
151325	cg0777442	26672398	26672398	0.3930528	0	1	0.2617883	-32.05433
151332	cg0777488	43685418	43685418	0.281127	0	1	0.1055695	-76.95684
151367	cg0777704	71750361	71750361	0.4093586	0	1	0.6279089	73.47298
151422	cg0778034	20804304	20804304	0.627684	0	1	0.5148189	-23.05055
151462	cg0778170	42706506	66726492	0.52256	0	1	0.6630753	34.3764
151554	cg0778754	21627306	21627306	0.4630288	0	1	0.5795686	23.52227
151657	cg0779287	37774469	37774469	0.6909856	0	1	0.2737306	-299.3461
151697	cg0779516	41604509	41702418	0.3263245	0	1	0.5603312	83.8867
151872	cg0780447	29663367	29663367	0.2061276	0	1	0.3172422	27.45816
151890	cg0780506	48751392	48751392	0.7659854	0	1	0.8782819	44.87391
151901	cg0780554	11719474	33743421	0.2626745	0	1	0.4374904	51.89871
151936	cg0780711	28755369	28755369	0.3964482	0	1	0.5787122	51.50676
151942	cg0780737	56788301	56788301	0.347375	0	1	0.6320238	124.743
152217	cg0782078	37641313	69718340	0.5160674	0	1	0.4094844	-20.11283
152228	cg0782137	36780352	36780352	0.7291528	0	1	0.6006014	-33.04596
152412	cg0783131	61647402	61647402	0.3919386	0	1	0.5858384	57.87875

152422	cg0783200	45781488	70708348	0.7717862	0	1	0.6137207	-50.97744
152575	cg0783992	62620439	52777432	0.5478258	0	1	0.4249084	-25.51474
152666	cg0784513	13644465	13644465		0	1	0.9444641	4.34E-09
152689	cg0784687	12763311	12763311	0.7222976	0	1	0.8652934	60.09278
152711	cg0784848	28767464	28767464	0.7276893	0	1	0.4796936	-101.8943
152740	cg0785032	53702395	53702395	0.4613978	0	1	0.6532553	58.58609
152766	cg0785126	56711481	56711481	0.8012025	0	1	0.6267867	-64.76083
152803	cg0785411	10734336	10734336	0.503373	0	1	0.6219854	24.87281
152833	cg0785557	14780479	14780479	0.4912502	0	1	0.6744604	55.06049
152927	cg0786246	34704447	34704447	0.2897675	0	1	0.4369828	37.3185
152940	cg0786302	57771331	68707371	0.3701217	0	1	0.4705316	18.51207
152992	cg0786672	28615375	28615375	0.4330168	0	1	0.1401722	-161.0091
152995	cg0786690	41604333	41604333	0.3898901	0	1	0.5391595	35.79926
153057	cg0787054	55751327	55751327	0.6947929	0	1	0.594503	-20.86874
153065	cg0787092	17666406	17666406	0.8899102	0	1	0.6736146	-123.2732
153123	cg0787401	16673473	16673473	0.816714	0	1	0.7121019	-30.69435
153142	cg0787506	46632507	46632507	0.3679916	0	1	0.4867688	24.36756
153170	cg0787632	17621427	17621427	0.8266126	0	1	0.9452972	74.80877
153179	cg0787683	50661376	50661376	0.874776	0	1	0.7612961	-44.74007
153205	cg0787862	18757475	18757475	0.6351039	0	1	0.3375252	-137.0987
153282	cg0788283	55609344	55609344	0.5246048	0	1	0.3561826	-44.80286
153315	cg0788486	20720372	20720372	0.6120472	0	1	0.7654341	47.78
153373	cg0788900	49677481	55756510	0.6296168	0	1	0.5278493	-19.55855
153506	cg0789600	35729356	35729356	0.1889738	0	1	0.2941399	26.35678
153617	cg0790151	28689449	28689449	0.2454481	0	1	0.3988475	42.64138
153657	cg0790429	58651475	39795354	0.7295662	0	1	0.8382076	35.37425
153698	cg0790626	13766454	53717395	0.5712174	0	1	0.440017	-28.63169
153763	cg0790917	30800340	30800340	0.2971048	0	1	0.3983184	20.04422
153900	cg0791597	42781406	42781406	0.6297705	0	1	0.747811	30.06479
153933	cg0791760	69634403	69634403	0.4968379	0	1	0.3670061	-28.30536
154087	cg0792506	41794502	24744335	0.2754197	0	1	0.3905331	25.35882
154195	cg0792976	27741510	27741510	0.4752218	0	1	0.3443685	-29.05379
154210	cg0793058	63750350	63750350	0.7974007	0	1	0.6167723	-67.8131
154241	cg0793289	25694489	25694489	0.8068022	0	1	0.6989552	-31.02296
154245	cg0793307	54680309	28641391	0.7289073	0	1	0.6061733	-30.66089
154323	cg0793695	73760356	74623336	0.3401639	0	1	0.2395954	-21.81328
154422	cg0794383	28624394	28624394	0.5279411	0	1	0.6705053	35.5472
154542	cg0795097	33721323	33721323	0.2440025	0	1	0.1295917	-36.44369
154571	cg0795242	11676351	11676351	0.4276774	0	1	0.3140261	-23.64042
154620	cg0795510	72695488	72695488	0.4488847	0	1	0.901095	374.3439
154718	cg0796062	62713349	62713349	0.4471646	0	1	0.5929185	34.59227
154768	cg0796293	60709444	30743500	0.8963992	0	1	0.7175492	-96.33426
154803	cg0796421	48640371	48640371	0.2468919	0	1	0.36418	27.40888

154809	cg0796475	67661509	23759375	0.7169023	0	1	0.8681728	66.18538
154918	cg0797079	46613418	31718497	0.1577416	0	1	0.284904	38.84739
154931	cg0797159	30638432	30638432	0.6104464	0	1	0.7116907	21.84765
154972	cg0797316	72765306	72765306	0.3208818	0	1	0.1227038	-87.60863
154975	cg0797330	71741400	71741400	0.7934957	0	1	0.9205216	68.53181
155030	cg0797678	44746439	44746439	0.5229662	0	1	0.6387951	24.305
155066	cg0797934	53691440	53691440	0.4801704	0	1	0.5959164	23.45093
155108	cg0798126	67766331	67766331	0.1002127	0	1	0.2325623	51.26328
155162	cg0798438	69795483	69795483	0.0752829	0	1	0.2139658	61.72425
155361	cg0799683	28746438	28746438	0.2410423	0	1	0.3412217	21.61955
155436	cg08000731	52628380	52628380	0.3274027	0	1	0.4411957	23.37373
155473	cg0800340	55749387	55749387	0.7048661	0	1	0.8276444	40.81111
155555	cg0800823	50707487	50707487	0.9014547	0	1	0.6812903	-132.7291
155587	cg08010331	64762362	64762362	0.6856555	0	1	0.8670691	86.42607
155703	cg0801763	39801427	39801427	0.530213	0	1	0.6502585	26.08677
155717	cg0801814	71767433	71767433	0.455568	0	1	0.5583754	19.01374
155814	cg0802426	66713451	66713451	0.1974193	0	1	0.5259973	374.3439
155890	cg0802929	48617371	48617371	0.3394081	0	1	0.4712277	29.5193
155897	cg0802996	61672364	73645392	0.3790468	0	1	0.490403	21.79552
155911	cg0803092	36730347	36730347	0.3049318	0	1	0.4492903	35.49082
155996	cg08035351	43606408	43606408	0.3495753	0	1	0.4599204	21.83322
156056	cg0803803	10739488	10739488	0.2135275	0	1	0.3314539	29.62771
156095	cg0803958	10696356	10696356	0.6972103	0	1	0.8372053	51.74782
156131	cg0804144	36801357	14739409	0.4733297	0	1	0.5986517	26.80418
156247	cg0804826	49647508	41755442	0.6195458	0	1	0.2848347	-178.0858
156318	cg0805313	35684432	35684432	0.7361644	0	1	0.4817337	-108.1265
156468	cg0806220	39733387	35620477	0.4161235	0	1	0.5999547	52.55811
156507	cg0806429	58725450	58725450	0.0961571	0	1	0.2202621	47.42279
156522	cg0806522	56800391	56800391	0.4436899	0	1	0.5581894	22.68607
156743	cg0807643	38678341	17774500	0.5436103	0	1	0.3693095	-47.49291
156844	cg0808178	53621420	53621420	0.6680812	0	1	0.7692778	25.01332
156889	cg0808415	46694365	21755423	0.8735717	0	1	0.761645	-43.57604
157032	cg0809166	65671470	65671470	0.2623669	0	1	0.4244458	45.57776
157137	cg0809781	37758335	37758335	0.4709447	0	1	0.6047426	30.04036
157208	cg0810130	20654307	28717434	0.253865	0	1	0.1380037	-35.9946
157230	cg0810256	29676374	29676374	0.5832511	0	1	0.3507328	-82.36449
157244	cg0810347	27698360	27698360	0.1667331	0	1	0.2829968	32.85236
157308	cg0810637	57799424	57799424	0.6337157	0	1	0.7547454	31.81048
157375	cg0810980	54645374	54645374	0.5033714	0	1	0.4018361	-18.61339
157539	cg0811828	33687506	63705377	0.8360828	0	1	0.6873968	-56.51527
157569	cg0811952	29757498	29757498	0.6662713	0	1	0.8876209	126.3862
157613	cg0812140	50683352	50683352	0.5769901	0	1	0.8242858	122.5841
157614	cg0812145	29648478	69782310	0.7171095	0	1	0.5906408	-31.42239

157620	cg0812168	67779397	67779397	0.454441	0	1	0.5579813	19.23178
157668	cg0812341	47778399	47778399	0.1259625	0	1	0.3111877	77.86628
157723	cg0812582	74679390	74679390	0.1864904	0	1	0.3009533	30.26879
157764	cg0812826	12676359	12676359	0.6652054	0	1	0.8869808	126.4284
157885	cg0813366	65716403	65716403	0.3750424	0	1	0.5036352	27.75538
157886	cg0813369	66746321	66746321	0.4513209	0	1	0.6415713	57.17692
158020	cg0814011	17754498	17754498	0.3166531	0	1	0.4288426	23.08608
158088	cg0814304	39734330	39734330	0.7583328	0	1	0.9124593	85.02718
158152	cg0814670	24809380	58767470	0.9241979	0	1	0.718407	-134.1786
158156	cg0814686	26716431	26716431	0.9021776	0	1	0.5705329	-247.4586
158231	cg0815162	67731429	47650332	0.3359508	0	1	0.224	-26.65697
158334	cg0815731	34648300	34648300	0.1161208	0	1	0.242952	44.95237
158350	cg0815810	26747343	26747343	0.4805285	0	1	0.7655529	139.7232
158417	cg0816094	31700426	31700426	0.0182292	0	1	0.1566081	86.1452
158539	cg0816663	15660481	15660481	0.5829183	0	1	0.4063224	-48.61238
158606	cg0817029	38600397	32703303	0.3642831	0	1	0.2614951	-21.66774
158646	cg0817210	29651467	29651467	0.2093445	0	1	0.3373784	34.10011
158651	cg0817247	43682494	43682494	0.5675597	0	1	0.3872365	-50.46397
158694	cg0817478	29778377	66723452	0.648998	0	1	0.5201566	-29.26649
158721	cg0817641	41780301	41780301	0.6786843	0	1	0.4763577	-66.08575
158727	cg0817701	10682320	10682320	0.2697694	0	1	0.3765563	22.69628
158981	cg0819178	53774317	53774317	0.6812408	0	1	0.7856931	27.56233
159021	cg0819432	26713357	26713357	0.4867583	0	1	0.374073	-22.2729
159060	cg0819598	24722422	33772334	0.5868458	0	1	0.4751966	-21.99311
159156	cg0820054	49726317	49726317	0.4670585	0	1	0.1758283	-148.9279
159160	cg0820062	13714477	49744305	0.3154812	0	1	0.4304278	24.04178
159214	cg0820346	15742320	15742320	0.3843769	0	1	0.6329061	94.564
159265	cg0820609	64636505	64636505	0.4730451	0	1	0.6039075	28.91784
159389	cg0821286	13607487	13607487	0.8903419	0	1	0.7756007	-49.44648
159479	cg0821735	21657325	21657325	0.6552961	0	1	0.9512551	374.3439
159511	cg0821917	23631406	23631406	0.0401664	0	1	0.1729856	70.59248
159514	cg0821921	10722412	37623347	0.8468269	0	1	0.951526	67.04122
159575	cg0822251	65721447	29784479	0.4412928	0	1	0.2688529	-50.26077
159580	cg0822261	38686484	44694343	0.406462	0	1	0.252176	-42.58023
159747	cg0823169	38645482	71666438	0.7846342	0	1	0.5011969	-142.7912
159765	cg0823314	35780324	35780324	0.7590563	0	1	0.593694	-53.24065
159856	cg0823756	55635419	55635419	0.4804826	0	1	0.6158429	30.86109
159867	cg0823831	35661439	35661439	0.824931	0	1	0.6315804	-82.08709
159868	cg0823837	47615483	47615483	0.5420833	0	1	0.0520686	-371.3336
159886	cg0823969	56785368	50644420	0.5768607	0	1	0.4634635	-22.45782
159947	cg0824223	61655384	16797406	0.5860413	0	1	0.7531648	53.4739
159957	cg0824285	16673423	16673423	0.5289068	0	1	0.6344367	20.82306
159967	cg0824372	43786494	33657422	0.4485365	0	1	0.3227541	-27.67276

160103	cg08250118	44675342	44675342	0.6271629	0	1	0.214448	-295.6992
160175	cg08253809	62661502	62661502	0.216493	0	1	0.6379082	374.3439
160244	cg08258654	11782430	11782430	0.0506667	0	1	0.2055061	82.14428
160336	cg08263140	54700302	54700302	0.2986088	0	1	0.413599	24.52474
160385	cg08265392	51662354	51662354	0.2872509	0	1	0.4215587	32.09138
160464	cg08268692	68794349	68794349	0.6697163	0	1	0.7699409	24.69174
160489	cg08269974	27605303	16682363	0.4110267	0	1	0.1879704	-90.10209
160546	cg08272429	24608456	24608456	0.6190628	0	1	0.8863562	374.3439
160550	cg08272591	70605446	70605446	0.8438547	0	1	0.9573036	78.03999
160591	cg08274589	28666467	37803421	0.3764062	0	1	0.2345916	-38.16601
160756	cg08282819	42753354	42753354	0.2027964	0	1	0.3186589	29.56342
160821	cg08285768	34793433	34793433	0.3212919	0	1	0.4872897	44.53801
160891	cg08289272	23652432	23652432	0.3721999	0	1	0.7491265	374.3439
160970	cg08292959	70754447	36781418	0.3511442	0	1	0.5264274	48.25304
160972	cg08293002	20705346	20705346	0.2747902	0	1	0.4124361	33.99496
160978	cg08293242	47695457	43706315	0.8831775	0	1	0.7344519	-69.25495
160982	cg08293392	58736354	58736354	0.5661416	0	1	0.8093105	114.7149
161041	cg08296868	37627429	27764490	0.8515797	0	1	0.9558761	69.32859
161089	cg08299859	52694424	52694424	0.7268049	0	1	0.9682131	374.3439
161100	cg08300475	10660302	10660302	0.9510549	0	1	0.7223728	-176.4181
161196	cg08305942	20600451	20600451	0.5736362	0	1	0.7525421	59.851
161231	cg08308214	44803398	44803398	0.9392874	0	1	0.8361272	-59.35726
161254	cg08309687	50726380	50726380	0.3375191	0	1	0.4636754	27.46282
161311	cg08312765	63701438	63701438	0.4332794	0	1	0.568503	30.13568
161383	cg08316699	12625334	12625334	0.448076	0	1	0.5483056	18.20646
161404	cg08317694	40661481	58673376	0.3010083	0	1	0.2000512	-24.0254
161435	cg08319103	33739454	52676471	0.3676842	0	1	0.4763572	21.05796
161691	cg08333400	22642441	22642441	0.5209359	0	1	0.3895032	-28.68314
161720	cg08335008	54613424	69684370	0.8934143	0	1	0.7831979	-47.5032
161917	cg08348121	70650432	41667361	0.5761405	0	1	0.475657	-18.44573
162040	cg08355045	52778306	52778306	0.6957594	0	1	0.8401001	54.83845
162043	cg08355157	52777483	52777483	0.367596	0	1	0.2106378	-47.35567
162054	cg08355456	49704335	42675320	0.3305451	0	1	0.1792151	-48.0901
162090	cg08357436	14790391	62719414	0.678686	0	1	0.5460451	-31.86807
162141	cg08360511	36755457	30758505	0.1468022	0	1	0.2593333	33.35671
162257	cg08367801	35601365	35601365	0.574309	0	1	0.7494455	57.37041
162275	cg08368875	46750400	46750400	0.2040234	0	1	0.3056329	24.02006
162362	cg08373528	57676503	38676483	0.1674856	0	1	0.2683154	26.32463
162366	cg08373622	71729412	71729412	0.3250417	0	1	0.4982589	47.90746
162370	cg08373989	65751422	65751422	0.8173308	0	1	0.9448684	81.7797
162455	cg08378932	65704464	65704464	0.5507699	0	1	0.7055823	42.96406
162495	cg08381046	64661310	64661310	0.2662478	0	1	0.3720835	22.50609
162501	cg08381537	45777500	32712359	0.8349286	0	1	0.6668861	-68.01244

162636	cg08390209	16629508	16629508	0.6111504	0	1	0.4623588	-36.19107
162677	cg08392746	41786390	41786390	0.5076207	0	1	0.6702995	44.50493
162721	cg08395748	63799460	63799460	0.3388141	0	1	0.45129	22.70853
162722	cg08395784	42682355	42682355	0.6936617	0	1	0.8356495	52.56507
162723	cg08395793	70795332	34745451	0.3878398	0	1	0.2561163	-32.53844
162755	cg08397993	71613387	71613387	0.1529159	0	1	0.4060536	121.0726
162809	cg08401725	14735409	14735409	0.3958159	0	1	0.5273632	28.69123
162815	cg08401938	24802413	60775315	0.6869977	0	1	0.8147354	41.36852
162847	cg08404009	43785333	43785333	0.217813	0	1	0.1101681	-36.01071
162858	cg08404513	10750439	10750439	0.1679989	0	1	0.2957181	37.89486
162970	cg08412215	41660507	41660507	0.2352186	0	1	0.3373999	22.56009
163093	cg08419450	65690351	65690351	0.6555871	0	1	0.7618137	26.41089
163120	cg08421351	30674480	30674480	0.4819859	0	1	0.641538	41.78784
163134	cg08422420	47792331	14673478	0.3617313	0	1	0.1367715	-103.2045
163206	cg08426157	32668320	55698420	0.1326006	0	1	0.2391228	32.32499
163255	cg08429705	51699499	51699499	0.5505616	0	1	0.6591185	22.41317
163263	cg08430277	70781380	70781380	0.683938	0	1	0.8928223	118.5629
163297	cg08431931	62738320	38635408	0.3097551	0	1	0.1848079	-34.89292
163316	cg08433110	15624481	15624481	0.8470139	0	1	0.7088457	-52.74929
163413	cg08439880	23712406	17785323	0.7993295	0	1	0.6060874	-76.134
163460	cg08442052	52701303	52701303	0.4193655	0	1	0.5266932	20.32502
163481	cg08443563	54652399	54652399	0.6395811	0	1	0.7561741	30.09832
163533	cg08447044	55731332	55731332	0.5192577	0	1	0.6229188	20.01352
163586	cg08449138	33641400	33641400	0.9242579	0	1	0.818987	-54.4053
163593	cg08449558	39708435	39708435	0.8735501	0	1	0.7362522	-58.80029
163685	cg08454015	10677480	10677480	0.6826198	0	1	0.825673	51.24271
163805	cg08460078	54647413	54647413	0.3259273	0	1	0.5457079	74.32734
163850	cg08461772	65755313	65755313	0.5397853	0	1	0.3617912	-49.44389
163936	cg08465120	54709363	54709363	0.2111066	0	1	0.1109957	-32.19878
164036	cg08470157	41736488	59769377	0.3314852	0	1	0.1328017	-85.23451
164158	cg08476485	66810458	66810458	0.576548	0	1	0.8139461	111.4181
164168	cg08476984	12689487	12689487	0.4892699	0	1	0.5932684	19.67095
164258	cg08481002	13800314	13800314	0.0933234	0	1	0.2853926	92.51911
164326	cg08484992	56696315	56696315	0.5209221	0	1	0.6995172	54.35192
164431	cg08491487	35789426	50652323	0.0198527	0	1	0.1241001	58.59933
164498	cg08494843	49659388	49659388	0.6753677	0	1	0.8247396	54.61556
164509	cg08495239	12625354	24649304	0.7048984	0	1	0.5740604	-32.47111
164579	cg08498719	12646452	12646452	0.163922	0	1	0.2885159	36.90763
164597	cg08499861	71658448	71658448	0.0739824	0	1	0.1820693	43.25249
164603	cg08500138	22635426	22635426	0.3478611	0	1	0.4565468	21.3298
164665	cg08504662	47748432	47748432	0.52685	0	1	0.3126611	-71.2748
164700	cg08506606	25649385	25649385	0.796208	0	1	0.6531757	-46.46873
164702	cg08506672	22731330	22731330	0.2277635	0	1	0.336197	25.14624

164765	cg08510234	26625348	26625348	0.1882924	0	1	0.3055301	31.27019
164817	cg08514194	72705460	72705460	0.9338599	0	1	0.6652828	-201.1628
164827	cg08514594	26704441	26704441	0.6226327	0	1	0.724568	22.6659
164861	cg08516507	74769420	31620311	0.8391353	0	1	0.7273204	-37.08321
164895	cg08519385	40635303	40635303	0.4908264	0	1	0.6386597	36.52955
164958	cg08522473	53649408	53649408	0.5105103	0	1	0.6960643	57.82872
165066	cg08528516	50744305	50744305	0.3362347	0	1	0.0057803	-285.3784
165184	cg08534016	31770413	31770413	0.4213873	0	1	0.5302418	20.80279
165198	cg08534830	72715472	72715472	0.4423249	0	1	0.548735	20.06709
165372	cg08544331	36602436	36602436	0.2790386	0	1	0.3934163	24.96462
165382	cg08545129	49601481	35603438	0.4182189	0	1	0.2975518	-26.55601
165438	cg08548044	70708459	57646326	0.6202254	0	1	0.7392963	29.88383
165470	cg08549335	25671469	25671469	0.3035304	0	1	0.4856754	53.30183
165584	cg08554554	30790360	30790360	0.2919155	0	1	0.4245808	31.25752
165605	cg08555866	41732344	67769494	0.4589783	0	1	0.327523	-29.65977
165611	cg08556511	73691397	73691397	0.2230005	0	1	0.3344684	26.53417
165764	cg08568145	46628382	46628382	0.9020637	0	1	0.7792975	-58.2679
165798	cg08570077	41775416	41775416	0.8861473	0	1	0.766003	-51.62368
165801	cg08570243	44686396	44686396	0.3194541	0	1	0.4261431	21.23076
165867	cg08573687	50731446	73728429	0.3224545	0	1	0.4409716	25.09486
165896	cg08575621	17797489	42789326	0.1426659	0	1	0.0275519	-63.19968
165991	cg08579577	36793409	64755341	0.6328108	0	1	0.4994132	-30.52113
166008	cg08580224	21671300	73718316	0.6017116	0	1	0.7717276	57.43339
166023	cg08580942	46631351	46631351	0.3712543	0	1	0.259092	-24.97407
166164	cg08590939	22698447	22698447	0.2706348	0	1	0.1085425	-67.32371
166204	cg08593141	34654499	34654499	0.1388917	0	1	0.0260417	-62.2038
166220	cg08594246	23637373	23637373	0.65649	0	1	0.7891831	40.41285
166272	cg08597142	12766306	12766306	0.8779361	0	1	0.7181674	-75.00363
166322	cg08599792	56784382	10679329	0.345558	0	1	0.2451803	-21.51066
166330	cg08600378	27601382	27601382	0.7131137	0	1	0.8255851	35.43004
166342	cg08601628	40606444	64681421	0.6098142	0	1	0.4771032	-29.72241
166359	cg08602346	59802479	59802479	0.643197	0	1	0.5278468	-24.25435
166378	cg08603678	74712324	74712324	0.6481928	0	1	0.2764684	-226.2648
166414	cg08605899	73641389	73641389	0.5014809	0	1	0.0887933	-340.2166
166487	cg08610426	44703481	34722474	0.4788939	0	1	0.2846424	-60.91383
166521	cg08611810	14733362	65701446	0.2625514	0	1	0.3639502	21.17253
166553	cg08613577	38600454	38600454	0.3708372	0	1	0.2510585	-28.13394
166596	cg08616111	28786359	28786359	0.357944	0	1	0.4827718	26.61458
166615	cg08617160	16688382	27638409	0.5983524	0	1	0.4077921	-56.15481
166645	cg08619295	58688430	58688430	0.4822907	0	1	0.6049896	25.97444
166707	cg08621926	17740470	17740470	0.2049059	0	1	0.0918702	-42.12975
166708	cg08621957	31758403	31758403	0.4867662	0	1	0.5977464	21.914
166712	cg08622198	36738381	36738381	0.4954726	0	1	0.6182631	26.25579

166769	cg0862491	55739509	55739509	0.6061144	0	1	0.713865	24.18776
166808	cg0862664	26754487	20803365	0.5520323	0	1	0.4091966	-33.08308
166866	cg0862939	27702369	27702369	0.4187686	0	1	0.2366138	-57.96794
166905	cg0863216	30708378	47671432	0.2605713	0	1	0.1054625	-63.71534
166926	cg0863347	67714503	57641490	0.7343004	0	1	0.5563427	-57.20208
166942	cg0863422	56607509	74768387	0.6162201	0	1	0.423697	-57.59128
166968	cg0863540	52656319	52656319	0.6810945	0	1	0.7821164	25.90233
167021	cg0863863	56799350	56799350	0.453342	0	1	0.5812154	27.49803
167062	cg08640901	44605456	44605456	0.7115362	0	1	0.6048208	-23.71591
167133	cg0864399	15644504	38770333	0.1981669	0	1	0.0907821	-39.26753
167345	cg0865595	34747398	53704486	0.6621757	0	1	0.7736731	29.41656
167356	cg0865677	52684461	49781466	0.5964491	0	1	0.4911463	-20.10942
167363	cg0865722	67723380	67723380	0.579806	0	1	0.4788806	-18.60809
167433	cg08660971	45613376	45613376	0.4142652	0	1	0.5510772	30.67802
167449	cg0866167	73644489	73644489	0.7758573	0	1	0.9170396	77.44259
167564	cg0866916	33740361	33740361	0.9421169	0	1	0.7444332	-139.9831
167618	cg0867322	10730369	10730369	0.2977825	0	1	0.1111111	-82.92038
167640	cg0867511	65772402	65772402	0.5603033	0	1	0.4235799	-30.66994
167720	cg08679971	33602320	31609499	0.5919006	0	1	0.4789327	-22.48129
167753	cg0868147	36789373	36789373	0.2966128	0	1	0.4088916	23.65816
167782	cg08682981	35702373	35702373	0.3817978	0	1	0.2756213	-22.28601
167959	cg0869267	73808406	73808406	0.1964184	0	1	0.347211	45.78951
167967	cg0869314	63669365	63669365	0.5346779	0	1	0.6640779	30.00229
167968	cg0869317	40800304	40800304	0.4009558	0	1	0.2425653	-45.22002
168049	cg0869716	11621437	11621437	0.5541505	0	1	0.6860381	31.90986
168059	cg0869773	33712307	33712307	0.2627137	0	1	0.3761776	25.28263
168063	cg0869801	58624364	58624364		0	1	0.1316801	4.34E-09
168087	cg0869894	23600491	23600491	0.3541684	0	1	0.589639	84.42652
168088	cg0869899	28655508	44682395	0.6107435	0	1	0.7642152	47.68039
168178	cg0870352	69614440	66759488	0.2088311	0	1	0.3549026	42.24659
168192	cg0870415	41716415	41716415	0.6585505	0	1	0.8232947	63.34044
168202	cg0870456	26630392	14673368	0.3260767	0	1	0.219552	-24.90395
168264	cg08708231	26660462	26660462	0.7472957	0	1	0.8843607	61.88085
168370	cg0871443	62790489	69754401	0.7562539	0	1	0.5132127	-102.6377
168409	cg0871625	20732476	20732476	0.7091486	0	1	0.818189	32.86744
168478	cg0872002	69803482	44618480	0.1014576	0	1	0.3046428	97.89915
168529	cg08723131	54643455	54643455		0	1	0.0674847	4.34E-09
168544	cg0872397	72721356	72721356	0.7033581	0	1	0.8091391	30.37
168567	cg0872536	64717485	64717485	0.116929	0	1	0.2254507	35.40794
168590	cg08726801	26735476	62677324	0.3261904	0	1	0.2072065	-30.4996
168895	cg08743751	19709509	19709509	0.4588658	0	1	0.3552237	-19.65475
168925	cg0874596	36726498	36726498	0.5198793	0	1	0.3813346	-31.47268
169000	cg0875043	31749440	31749440	0.6403495	0	1	0.5184133	-26.47841

169024	cg0875184	37652351	37652351	0.6126353	0	1	0.853043	127.0809
169026	cg0875187	66702311	66702311	0.3615352	0	1	0.5697774	66.36089
169071	cg0875472	53774390	57711316	0.7052496	0	1	0.9035379	115.3788
169098	cg0875659	11755499	11755499	0.2634603	0	1	0.3675413	22.02339
169207	cg0876242	72782327	44675452	0.2661629	0	1	0.1136323	-60.14341
169212	cg0876260	64718325	57715309	0.6672922	0	1	0.5575141	-23.06589
169276	cg0876676	41769319	41769319	0.5774102	0	1	0.6794798	20.921
169290	cg0876768	26708436	54725351	0.9166197	0	1	0.7711518	-80.46941
169295	cg0876782	64622436	17761482	0.351326	0	1	0.1961667	-48.00384
169400	cg0877513	13644397	10761385		0	1		-4.34E-09
169447	cg0877859	20629338	18760384	0.4691324	0	1	0.1960893	-127.7329
169591	cg0878762	68644470	20784419	0.1151444	0	1	0.0072844	-67.86231
169600	cg0878798	69718393	69718393	0.1875841	0	1	0.2886009	24.86798
169616	cg08789101	60601499	47658449	0.5411084	0	1	0.6498514	22.21997
169794	cg0880003	55608402	55608402	0.6199999	0	1	0.4966289	-26.49846
169879	cg08805241	36619474	36619474	0.2516243	0	1	0.3580723	23.29644
169908	cg08806681	72794300	58644482	0.5033822	0	1	0.2899139	-72.01818
169921	cg0880804	57720364	19705326	0.5273578	0	1	0.3205138	-66.45077
169991	cg0881210	49736318	70704466	0.5585554	0	1	0.6808471	27.98397
170025	cg0881402	10723353	10723353	0.4898458	0	1	0.6334146	34.58541
170092	cg0881748	32807411	31629403	0.4268393	0	1	0.2824118	-36.46492
170123	cg0881882	12738459	62639458	0.3880298	0	1	0.5169967	27.77899
170128	cg0881902	64789365	34786465	0.8851324	0	1	0.7450277	-64.13069
170152	cg0882078	37658307	37658307	0.2750175	0	1	0.1185957	-61.35696
170215	cg0882335	50670510	63789405	0.3067807	0	1	0.0425617	-181.1113
170363	cg0883107	43701438	50623425	0.5166517	0	1	0.6762649	43.38257
170393	cg0883260	22730507	24800396	0.2940853	0	1	0.1780523	-31.6629
170490	cg08837481	46643471	46643471	0.5651588	0	1	0.6790565	24.88245
170533	cg0883980	50807329	42772412	0.6001059	0	1	0.8352727	116.2377
170542	cg08840441	53646483	46678500	0.6674201	0	1	0.5188331	-37.97564
170575	cg08842441	73622480	73622480	0.3330327	0	1	0.469516	31.45643
170726	cg0884962	21611369	21611369	0.7931623	0	1	0.6708576	-36.00357
170817	cg0885483	32621455	32621455	0.5130242	0	1	0.6288685	24.07535
170850	cg0885631	28731361	28731361	0.0903643	0	1	0.2770661	89.65047
170887	cg0885771	66670482	66670482	0.3695879	0	1	0.492997	25.9541
170907	cg0885829	54657471	54657471	0.4468091	0	1	0.5591272	21.97906
170916	cg0885854	11782329	40764344	0.6082141	0	1	0.5030541	-20.2301
170933	cg0885921	24711352	24711352	0.5328096	0	1	0.6336004	19.3394
170975	cg0886143	43725335	30676486	0.3036144	0	1	0.5191234	72.52983
171035	cg0886434	47644483	47644483	0.6505757	0	1	0.5079613	-34.75739
171073	cg0886666	29655384	52639411	0.4935813	0	1	0.6054059	22.29928
171074	cg0886669	30707379	30707379	0.2029244	0	1	0.3370951	37.31868
171081	cg08866991	25793447	61788475	0.317312	0	1	0.4437099	28.04331

171141	cg0887003	13778435	13778435	0.2113656	0	1	0.3836516	55.23022
171143	cg0887009	44761460	44761460	0.2556939	0	1	0.3852595	31.69403
171150	cg0887064	66725454	51730363	0.3422841	0	1	0.2368865	-23.59789
171165	cg0887123	15681417	15681417	0.4486316	0	1	0.5804207	28.93624
171233	cg0887394	33689432	70689423	0.743366	0	1	0.6378047	-24.96587
171361	cg0887984	19624427	19624427	0.877722	0	1	0.6380454	-137.3138
171534	cg0888820	16725414	55726318	0.7433766	0	1	0.6367199	-25.37114
171550	cg0888891	24794482	24794482	0.4604765	0	1	0.583588	25.81949
171556	cg0888911	12723366	12723366	0.6708527	0	1	0.7838081	30.91859
171632	cg0889289	44664353	44664353	0.3673443	0	1	0.2603493	-23.12484
171634	cg0889303	34672391	34672391	0.4618217	0	1	0.583865	25.44839
171648	cg0889381	32715460	32715460	0.4023581	0	1	0.5371838	29.91279
171744	cg0889886	31694463	31694463	0.5160125	0	1	0.6344743	25.10412
171899	cg0890630	45651328	45651328	0.4492163	0	1	0.5607098	21.72187
171972	cg0891185	23691310	23691310	0.2135559	0	1	0.3549752	39.65863
171993	cg0891352	23809314	23809314	0.2222248	0	1	0.3336511	26.56397
172038	cg0891683	34624375	13683355	0.441122	0	1	0.6951228	102.6607
172101	cg0892045	34635319	43616387	0.9522975	0	1	0.6424561	-262.9484
172149	cg0892359	37730375	37730375	0.5188257	0	1	0.674565	41.50566
172153	cg0892366	53698352	16617450	0.0948589	0	1	0.2206318	48.66361
172156	cg0892402	58652340	58652340	0.5850517	0	1	0.7996452	90.66657
172266	cg0893090	32738498	66800498	0.1891645	0	1	0.3621121	58.35657
172314	cg0893328	74759488	74759488	0.6223224	0	1	0.7311918	25.48088
172412	cg0893879	40803324	40803324	0.5977814	0	1	0.3419102	-99.88429
172484	cg0894252	72750374	72750374	0.6292511	0	1	0.7437918	28.39865
172518	cg0894417	61667441	61667441	0.2069995	0	1	0.3727133	52.22459
172551	cg0894580	30799426	30799426	0.7758877	0	1	0.8925386	51.26611
172761	cg0895918	49644505	49644505	0.4661785	0	1	0.5837877	23.92573
172778	cg0896054	30662428	30662428	0.6567084	0	1	0.7643871	27.15966
172826	cg0896301	43682431	43682431	0.7266797	0	1	0.3391154	-253.3111
172845	cg0896473	40751468	40751468	0.0482564	0	1	0.3008485	374.3439
172895	cg0896758	38708324	38708324	0.7187826	0	1	0.3899455	-175.7379
173001	cg0897321	53746316	53746316	0.7089574	0	1	0.8549773	59.27909
173042	cg0897583	58620476	58620476	0.9346009	0	1	0.6831127	-184.5269
173074	cg08977311	31717420	31717420	0.2496905	0	1	0.8059332	374.3439
173086	cg08977931	50694496	50694496	0.288382	0	1	0.4313738	35.5872
173205	cg0898557	29724312	29724312	0.6056124	0	1	0.4421931	-42.55631
173213	cg0898597	11618323	11618323	0.3147985	0	1	0.4244324	22.28819
173301	cg0899222	64715381	64715381	0.259542	0	1	0.3844528	29.67017
173338	cg0899408	62731396	62731396	0.5367939	0	1	0.6468371	22.56867
173347	cg08994891	60713466	19662452	0.3357445	0	1	0.2241249	-26.5256
173373	cg0899659	14613307	14613307	0.6233762	0	1	0.8583409	124.6239
173381	cg0899680	29671410	29671410	0.1756385	0	1	0.3150711	42.58471

173526	cg09006810	68781379	68781379	0.4453638	0	1	0.3435344	-19.2749
173636	cg09012411	47722454	47722454	0.2950757	0	1	0.1924082	-25.1597
173678	cg09014801	46749397	46749397	0.7411058	0	1	0.5524853	-63.99528
173682	cg09015232	65740305	65740305	0.7249683	0	1	0.6221981	-22.97489
173723	cg09017928	40738312	63803425	0.1977784	0	1	0.3252214	34.80586
173844	cg09025174	52707318	52707318	0.8633522	0	1	0.7240856	-57.27165
173919	cg09029902	43605483	43605483	0.4874037	0	1	0.5930554	20.17467
174081	cg09039561	31788448	31788448	0.462234	0	1	0.5628427	18.3867
174104	cg09040994	16652505	16652505	0.5867714	0	1	0.7722996	66.47557
174222	cg09047734	18789360	20681432	0.7239047	0	1	0.6209677	-22.9812
174270	cg09050832	39669307	39669307	0.6749867	0	1	0.5133877	-44.24471
174277	cg09051342	70723444	70723444	0.4285501	0	1	0.6349089	66.14703
174289	cg09052185	30675395	30675395	0.4473975	0	1	0.8181534	374.3439
174302	cg09053247	48664509	48664509	0.6949756	0	1	0.5925711	-21.56765
174305	cg09053536	13687487	13687487	0.8016937	0	1	0.9060659	47.50165
174497	cg09065629	56721316	48793480	0.2549883	0	1	0.3616419	23.22562
174564	cg09069446	23607486	61723462	0.4569018	0	1	0.6011899	34.12292
174576	cg09070191	69715359	69715359	0.3522551	0	1	0.4600466	20.98049
174631	cg09073348	62617399	62617399	0.4722117	0	1	0.2409397	-88.04536
174670	cg09075558	44691391	55726507	0.4426804	0	1	0.3258347	-24.44012
174675	cg09075844	15775384	15775384	0.607035	0	1	0.4895266	-24.21369
174735	cg09079882	29693349	29693349	0.3660031	0	1	0.4811855	23.18322
174750	cg09080788	25733472	25733472	0.6242965	0	1	0.9390052	374.3439
174775	cg09082518	65781502	65781502	0.7101709	0	1	0.9331223	156.5356
174800	cg09084244	53720344	53720344	0.1998204	0	1	0.3712314	56.11899
174805	cg09084391	26694311	30630454	0.6229621	0	1	0.5117054	-22.4244
174869	cg09088153	18651434	18651434	0.1087831	0	1	0.2373659	47.30885
174917	cg09091185	45778436	58766345	0.6825773	0	1	0.5301105	-40.45372
175061	cg09100271	65753302	65753302	0.6453886	0	1	0.5214995	-27.32369
175062	cg09100338	34641304	16627472	0.5310171	0	1	0.3525566	-49.83025
175071	cg09101062	50699371	50699371	0.7420939	0	1	0.9299841	122.5216
175085	cg09102030	50621483	50621483	0.7261704	0	1	0.8819749	73.67636
175119	cg09104029	44752306	44752306	0.6353878	0	1	0.5097847	-27.66943
175169	cg09107432	71729464	43641419	0.7061759	0	1	0.8131029	31.31369
175272	cg09115009	43694400	43694400	0.471864	0	1	0.6241601	38.00843
175305	cg09117448	10664468	25779417	0.3632743	0	1	0.2207401	-39.55891
175341	cg09119688	14679432	14679432	0.5545091	0	1	0.6562318	20.1405
175484	cg09126279	46810317	46810317	0.3417407	0	1	0.5332644	56.98519
175532	cg09129067	63697332	24746334	0.2794336	0	1	0.4096579	30.8138
175661	cg09135656	31614324	10734365	0.638662	0	1	0.3999766	-87.51292
175698	cg09138207	34645343	34645343	0.4114006	0	1	0.5832729	46.26031
175734	cg09140274	72623414	72623414	0.5999129	0	1	0.7056094	23.10089
175874	cg09147068	14689356	14689356	0.148135	0	1	0.267674	36.43332

175908	cg0914885	49790464	49790464	0.6922365	0	1	0.8819519	98.3005
176077	cg0915801	33693506	33693506	0.4978822	0	1	0.2064249	-142.3941
176164	cg0916300	61695508	61695508	0.3620392	0	1	0.2592994	-21.7343
176222	cg0916641	46645488	46645488	0.5843428	0	1	0.7268875	38.91755
176225	cg0916653	23692396	23692396	0.5822021	0	1	0.4758216	-20.2799
176259	cg0916872	39751484	39751484	0.4406474	0	1	0.6748803	86.36989
176384	cg0917481	34733453	34733453	0.5119133	0	1	0.612632	18.94766
176526	cg0918208	37645409	37645409	0.3602442	0	1	0.5514979	56.49776
176623	cg0918750	18689460	24679402	0.7604192	0	1	0.6464732	-29.35141
176911	cg0920874	38683434	42741493	0.1784315	0	1	0.3234154	44.98112
176974	cg0921417	21745343	21745343	0.6101031	0	1	0.3828999	-78.76447
177116	cg0922236	29764455	29764455	0.4727685	0	1	0.5810839	20.87144
177127	cg0922289	35723454	35723454	0.4863149	0	1	0.7231948	93.04712
177161	cg0922537	29799387	29799387	0.266534	0	1	0.4434576	52.71833
177214	cg0922766	14777384	14777384	0.8267264	0	1	0.678144	-54.55079
177276	cg09231171	55751311	55751311	0.2143734	0	1	0.1116858	-33.33986
177350	cg0923445	34761355	47705509	0.7376238	0	1	0.8417609	33.70439
177382	cg0923556	57682351	15675506	0.7877218	0	1	0.6625323	-36.72071
177458	cg0923970	50684442	50684442	0.5510408	0	1	0.6539586	20.45703
177551	cg0924500	53729338	53729338	0.9009416	0	1	0.7859304	-52.77589
177616	cg0924797	28668413	28668413	0.6338316	0	1	0.7756608	43.22834
177845	cg0925887	14635367	14635367	0.2165145	0	1	0.3278112	26.85868
177903	cg09261791	39749313	39749313	0.305135	0	1	0.5200583	72.08475
177987	cg0926614	54763332	54763332	0.5690172	0	1	0.7112554	37.66446
178033	cg0926871	66806458	13759348	0.2516864	0	1	0.3840139	33.03014
178077	cg0927086	67639301	67639301	0.067822	0	1		-4.34E-09
178219	cg0927869	52623414	52623414	0.3188208	0	1	0.4595697	33.54047
178242	cg0927973	20706454	15790347	0.0679777	0	1	0.3604961	374.3439
178302	cg0928420	49729377	49729377	0.8066376	0	1	0.6375997	-62.57341
178316	cg0928494	32618445	50615413	0.4797885	0	1	0.3380983	-33.40384
178347	cg0928688	73669337	73669337	0.512529	0	1	0.6139001	19.16317
178441	cg0929266	47722311	47722311	0.3098127	0	1	0.4133719	20.46196
178476	cg0929415	14668374	35739312	0.2686144	0	1	0.1634989	-28.41269
178477	cg0929424	21626310	21626310	0.4632969	0	1	0.5663173	19.12501
178507	cg0929645	49654360	35808326	0.0568209	0	1	0.20803	76.86203
178593	cg0930149	49688431	49688431	0.4554175	0	1	0.555796	18.28106
178693	cg0930719	26614375	26614375	0.5006491	0	1	0.3732935	-27.32334
178739	cg0930926	14719371	14719371	0.4380485	0	1	0.3355562	-19.60705
178789	cg0931289	52654394	52654394	0.534934	0	1	0.7813733	110.3068
178890	cg0931767	46637510	46637510	0.5071033	0	1	0.6625476	40.78531
178993	cg0932225	56681355	27673401	0.5242091	0	1	0.4177822	-20.04711
179016	cg0932340	54606301	54606301		0	1		-4.34E-09
179021	cg0932372	42679433	10738438	0.2653106	0	1	0.0913646	-80.24617

179035	cg0932411	55750413	55750413	0.1960625	0	1	0.0847399	-42.67231
179448	cg0934961	47637471	47637471	0.591204	0	1	0.693631	21.52525
179465	cg0935089	67715351	54602303	0.2932147	0	1	0.1685856	-36.40353
179494	cg0935233	36766335	36766335	0.3683144	0	1	0.5116568	33.52905
179496	cg0935251	49644447	49644447	0.7126532	0	1	0.512118	-67.88604
179539	cg0935455	24636339	62621337	0.7789991	0	1	0.9558817	132.6439
179596	cg0935776	61605474	61605474	0.6207642	0	1	0.7425843	31.22059
179623	cg0935911	46760494	24619494	0.4472842	0	1	0.3218369	-27.57427
179641	cg0936004	50648414	50648414	0.6656801	0	1	0.8018059	43.73949
179668	cg0936149	64613328	49665304	0.4486147	0	1	0.2560323	-62.05223
179678	cg0936196	16705402	23736493	0.8996255	0	1	0.7553259	-72.20609
179761	cg0936651	38653371	38653371	0.4100685	0	1	0.5832218	46.89156
179912	cg0937351	45691334	45691334	0.2548008	0	1	0.3595076	22.5697
179941	cg0937506	51652388	51652388	0.9331796	0	1	0.8195656	-64.38776
179985	cg0937828	47684491	47684491	0.5157493	0	1	0.7076378	62.34765
180016	cg0938006	55661463	55661463	0.7042555	0	1	0.8093061	30.06936
180127	cg0938748	42803315	72613508	0.4090157	0	1	0.2524303	-43.63806
180206	cg0939291	27725506	27725506	0.926664	0	1	0.8177193	-58.01007
180238	cg0939519	68777485	68777485	0.3519962	0	1	0.4778285	27.0701
180320	cg0939943	37793317	37793317	0.1677982	0	1	0.2791767	30.63932
180414	cg0940621	73790463	73790463		0	1		-4.34E-09
180457	cg0940819	20795464	20795464	0.093373	0	1	0.2055179	41.33955
180508	cg0941051	48782467	48782467	0.2945387	0	1	0.479352	55.15993
180538	cg0941191	53774381	53774381	0.6343389	0	1	0.8467322	102.2494
180565	cg0941325	20802377	20802377	0.6821866	0	1	0.8222267	48.97311
180576	cg0941394	35711450	35711450	0.9003445	0	1	0.7878276	-50.9768
180601	cg0941494	63742393	46678324	0.2220872	0	1	0.3357355	27.41197
180625	cg0941618	13620337	13620337	0.3172721	0	1	0.5528352	85.28867
180645	cg0941703	69626417	69626417	0.5152205	0	1	0.3341304	-51.6118
180693	cg0941925	61797307	61797307	0.4702044	0	1	0.575819	19.98478
180699	cg0941967	15624446	15624446	0.2089775	0	1	0.0861501	-48.96566
180782	cg0942516	70661382	70661382	0.6269778	0	1	0.5145121	-22.90345
180807	cg0942701	14785328	14785328	0.5812104	0	1	0.7301581	42.1095
180872	cg0943064	69676349	69676349	0.8371281	0	1	0.7059276	-46.85369
180942	cg0943460	38809442	38809442	0.3932112	0	1	0.5190409	26.60713
180953	cg0943517	59669343	59669343	0.478694	0	1	0.5892348	21.66461
181001	cg0943747	22650352	45648320	0.1402884	0	1	0.2482293	32.04155
181010	cg0943806	12618375	12618375	0.8205082	0	1	0.6535293	-64.10413
181095	cg0944245	27751347	69745434	0.1840146	0	1	0.5477698	374.3439
181104	cg0944279	22708472	22708472	0.6013082	0	1	0.7123479	25.2886
181265	cg0945121	17618421	17618421	0.3296444	0	1	0.4574502	28.24396
181343	cg0945588	50789347	50789347	0.573104	0	1	0.71881	39.73333
181461	cg0946228	35725439	46723333	0.6414244	0	1	0.9152712	374.3439

181553	cg09467607	22690379	22690379	0.157091	0	1	0.3252039	60.58217
181751	cg09478002	17627420	17627420	0.3268988	0	1	0.452129	27.36827
181891	cg09487575	43673449	43673449	0.4783346	0	1	0.6062667	27.87619
181954	cg09491897	52670370	62692490	0.8568454	0	1	0.7509024	-37.01231
182033	cg09496634	23706474	23706474	0.2126886	0	1	0.3182282	24.94025
182121	cg09501687	31735424	31735424	0.5093102	0	1	0.6948875	57.75003
182257	cg09508496	10692335	13645385	0.2728151	0	1	0.1295712	-51.44361
182308	cg09510698	21692351	21692351	0.7076231	0	1	0.8126894	30.44362
182403	cg09516200	19782308	19782308	0.6860366	0	1	0.792096	28.78951
182549	cg09524613	48745352	48745352	0.3180727	0	1	0.4355897	24.8568
182683	cg09532840	50750421	50750421	0.4571919	0	1	0.5924933	30.41825
182703	cg09533869	19733415	19733415	0.1642961	0	1	0.0318124	-74.19953
182706	cg09534232	66770392	66770392	0.672105	0	1	0.9091468	151.7644
182714	cg09535226	32765492	32765492	0.609586	0	1	0.7363603	32.81319
183178	cg09560078	22606468	13648395	0.2299967	0	1	0.0415629	-113.1558
183188	cg09560533	57647300	57647300	0.2790385	0	1	0.4334581	41.01914
183454	cg09576209	74797377	74797377	0.6755686	0	1	0.5684205	-22.45518
183581	cg09581911	74718307	74718307	0.508298	0	1	0.3877958	-24.76791
183601	cg09583302	46605357	46605357	0.6306406	0	1	0.7430556	27.52629
183627	cg09584711	41796336	41796336	0.4779373	0	1	0.5832113	19.94949
183724	cg09592244	53629317	53629317	0.0921259	0	1	0.2191183	49.99501
183801	cg09597022	10787338	42678415	0.5778665	0	1	0.7017497	29.55114
183808	cg09597400	23622386	31801457	0.5355945	0	1	0.4286543	-20.20368
183901	cg09603707	68689333	68689333	0.2211661	0	1	0.4553385	92.63416
183908	cg09603919	51701470	51701470	0.2225964	0	1	0.3910253	51.99865
184043	cg09611620	29737300	29737300	0.6208648	0	1	0.7711366	46.88228
184138	cg09616536	50800424	50800424	0.8921114	0	1	0.5918748	-204.6371
184191	cg09619488	13684495	48642443	0.7056608	0	1	0.9695261	374.3439
184193	cg09619624	68746346	37790478	0.4580032	0	1	0.2870935	-48.4037
184246	cg09623286	56608399	65619429	0.2078104	0	1	0.0653593	-67.48984
184347	cg09630417	40758440	40758440	0.3789285	0	1	0.5062954	27.2697
184351	cg09630706	20687478	18721434	0.3210278	0	1	0.4307062	22.15811
184371	cg09632136	35642329	35642329	0.2783172	0	1	0.4244795	37.40643
184452	cg09636756	53767385	53767385	0.6907277	0	1	0.3994482	-134.0059
184506	cg09639931	31687307	58640502	0.3289524	0	1	0.228089	-22.44559
184513	cg09640425	21705366	40779491	0.6808748	0	1	0.5687845	-24.31976
184598	cg09644806	51682447	51682447	0.5913343	0	1	0.9008769	374.3439
184662	cg09648454	12751316	12751316	0.621088	0	1	0.7691625	45.54799
184693	cg09650180	74722344	74722344	0.6234786	0	1	0.7616761	39.98866
184703	cg09650895	54737362	54737362	0.8505308	0	1	0.665442	-83.59003
184735	cg09653371	18653342	18653342	0.669421	0	1	0.7911394	35.51104
184943	cg09664314	31701446	31701446	0.2870664	0	1	0.1359193	-54.69399
184969	cg09665351	48780377	48780377	0.232896	0	1	0.3417048	25.01105

184978	cg09666011	60688471	74774454	0.437109	0	1	0.3289942	-21.48488
185098	cg09672255	62646475	62646475	0.4333909	0	1	0.8145311	374.3439
185218	cg09680007	59639463	59639463	0.3621626	0	1	0.5090215	35.06061
185762	cg09714852	52742438	52742438	0.7837039	0	1	0.8912041	45.24896
185764	cg09715009	49694411	49694411	0.2465337	0	1	0.3602335	26.10139
185770	cg09715545	66620425	66620425	0.1547001	0	1	0.2547874	27.14597
185797	cg09717927	48701360	48701360	0.2042592	0	1	0.3089979	25.15934
185820	cg09719342	56680359	56680359	0.7793909	0	1	0.6013561	-63.1543
185889	cg09723635	18749365	18749365	0.6810573	0	1	0.7858271	27.70242
185943	cg09727206	37740333	52756471	0.7242907	0	1	0.5251445	-68.27187
185944	cg09727210	65647467	35657353	0.7278513	0	1	0.5884029	-37.6139
185978	cg09729274	57748486	57748486	0.2046039	0	1	0.3048751	23.49935
185986	cg09729624	12741436	12741436	0.631385	0	1	0.7360851	24.23537
186031	cg09731946	64723470	64723470	0.677051	0	1	0.5738681	-21.20246
186173	cg09740450	64711383	64711383	0.1696904	0	1	0.293934	36.10781
186392	cg09755784	69641461	69641461	0.2715471	0	1	0.3758114	21.79374
186484	cg09760728	66609391	66609391	0.6606979	0	1	0.5360966	-28.07372
186548	cg09763439	64613357	64613357	0.5092474	0	1	0.6270097	24.6887
186636	cg09768983	34706422	34706422	0.4895225	0	1	0.7415864	107.1162
186691	cg09773458	29730503	29730503	0.2813194	0	1	0.383816	20.89918
186730	cg09775533	33713314	33713314	0.1693602	0	1	0.0641436	-43.98021
186763	cg09777775	26638501	52687504	0.70637	0	1	0.5761286	-32.31305
186764	cg09777776	22604405	22604405	0.2319665	0	1	0.1031309	-48.6116
186788	cg09779576	40607380	40607380	0.6864695	0	1	0.796056	30.66172
186829	cg09782560	32622429	32622429	0.6293653	0	1	0.7356244	24.77444
186879	cg09785377	41742374	41742374	0.7239154	0	1	0.9174019	119.2594
186893	cg09786098	67720469	32798444	0.8424972	0	1	0.7222394	-41.96803
186970	cg09790226	62741461	62741461	0.4380192	0	1	0.6237568	54.1135
187076	cg09795809	70611337	46645328	0.5095512	0	1	0.6395296	29.40769
187107	cg09797202	70668390	70668390	0.6136455	0	1	0.4960202	-24.37008
187197	cg09802066	33648424	33648424	0.2689523	0	1	0.3916993	28.40867
187246	cg09804649	21670387	21670387	0.1380257	0	1	0.2428499	30.90571
187306	cg09807817	21771379	21771379	0.5933853	0	1	0.738461	41.01535
187349	cg09810089	39664424	26752459	0.7315532	0	1	0.5763027	-45.22768
187367	cg09811510	18684453	18684453	0.6317528	0	1	0.7493091	29.97796
187404	cg09814029	45712411	45712411	0.5080515	0	1	0.623686	23.89269
187711	cg09829645	34701417	34701417	0.6022221	0	1	0.4646255	-31.46272
187719	cg09829904	70657476	70657476	0.1844671	0	1	0.3048092	32.92077
187724	cg09830083	20631334	20631334	0.4489259	0	1	0.5553185	20.08808
187748	cg09831875	38750445	57622344	0.1731637	0	1	0.2901517	32.53178
187758	cg09832276	21697348	21697348	0.2492222	0	1	0.3658915	27.06207
187789	cg09834172	61602344	61602344	0.1705607	0	1	0.2930169	35.20677
187795	cg09834465	31765305	31765305	0.3226633	0	1	0.1965032	-34.3604

187841	cg0983764	20708437	20708437	0.3117304	0	1	0.4229502	22.8859
187886	cg0984047	58662317	58662317	0.4152603	0	1	0.5188969	19.19853
188007	cg0984736	14607396	14607396	0.4806013	0	1	0.7504684	123.2213
188115	cg0985291	44761470	44761470	0.5490596	0	1	0.66919	26.73968
188145	cg0985462	39768378	39768378	0.8806001	0	1	0.6928937	-96.21102
188171	cg0985609	69773355	50633420	0.1560156	0	1	0.2830738	39.01263
188344	cg0986341	70614430	70614430	0.2174482	0	1	0.4615201	100.4617
188393	cg0986614	29794391	29794391	0.7115539	0	1	0.9539192	374.3439
188424	cg0986732	73678369	73678369	0.3090388	0	1	0.4158393	21.51006
188427	cg0986745	59609402	59609402	0.910131	0	1	0.7929403	-57.35209
188560	cg0987433	20609458	20609458	0.632669	0	1	0.7695681	40.1925
188682	cg0988328	41728417	13794301	0.6081927	0	1	0.5076206	-18.83745
188712	cg0988441	61781459	61781459	0.4899685	0	1	0.6219921	29.72293
188714	cg0988445	51639506	51639506	0.4115501	0	1	0.2979454	-24.06925
188727	cg0988550	37733313	33735343	0.3494864	0	1	0.5340031	53.03399
188769	cg0988790	57657397	57657397	0.5794308	0	1	0.6823773	21.29996
188913	cg0989532	38715470	39628431	0.1964277	0	1	0.3985101	74.66545
188952	cg0989737	56749413	70790434	0.359843	0	1	0.2380523	-29.60633
188975	cg0989898	20754477	20754477	0.8499075	0	1	0.9504977	63.0996
189050	cg0990345	12791479	12791479	0.3816852	0	1	0.5097098	27.48386
189108	cg0990692	40799410	40799410	0.7152289	0	1	0.8586565	58.61893
189134	cg0990804	51631444	51631444	0.542432	0	1	0.3465576	-59.30728
189283	cg0991665	63625400	63625400	0.3427527	0	1	0.4479896	20.32945
189289	cg0991684	25639320	25639320	0.8046491	0	1	0.3716293	-347.4175
189400	cg0992395	14773345	14773345	0.2943814	0	1	0.4964115	64.81797
189453	cg0992725	36675362	65676467	0.734139	0	1	0.8455633	37.91451
189456	cg0992731	58759457	58759457	0.6473473	0	1	0.815248	63.57607
189547	cg0993345	50635407	30770374	0.3272159	0	1	0.1969574	-36.11335
189919	cg0995786	64723399	46800423	0.2360386	0	1	0.3439856	24.54164
189988	cg0996308	64809446	64809446	0.8598362	0	1	0.6306602	-120.414
190140	cg0997260	36629427	36629427	0.7691446	0	1	0.8817136	45.86422
190297	cg0998143	25773436	25773436	0.3437622	0	1	0.4600218	23.87731
190306	cg0998192	29649484	74797315	0.7718962	0	1	0.6034445	-56.5895
190323	cg0998294	49748412	18605351	0.6893285	0	1	0.5887882	-20.75669
190363	cg0998526	32797451	32797451	0.5509197	0	1	0.4170865	-29.52718
190430	cg0998903	24657327	24657327	0.427	0	1	0.5350013	20.53456
190448	cg0999019	65605381	65605381	0.2246959	0	1	0.3430478	29.06562
190504	cg0999331	14642304	14642304	0.6540813	0	1	0.2595722	-261.1608
190575	cg0999754	45748362	57671390	0.500368	0	1	0.6049589	20.00641
190588	cg0999815	66795482	66795482	0.2414367	0	1	0.3828064	37.49044
190594	cg0999847	39694500	12708434	0.3817688	0	1	0.2567984	-29.82977
190934	cg1001762	46734487	46734487	0.1050228	0	1	0.2322955	47.33858
191017	cg1002187	53774376	63605419	0.2342991	0	1	0.0679807	-83.27925

191138	cg10028823	67770391	12704501	0.2522267	0	1	0.3627138	24.68074
191394	cg10044179	20628397	39648458	0.5833757	0	1	0.4365759	-34.90226
191486	cg10051493	50641429	50641429	0.7916456	0	1	0.6901632	-26.87244
191487	cg10051588	36644327	36644327	0.6120553	0	1	0.7451665	36.19341
191574	cg10056482	42642363	44755425	0.8489318	0	1	0.7447746	-34.79751
191608	cg10058204	46658359	46658359	0.4394643	0	1	0.2386764	-68.48821
191705	cg10063575	36606308	36606308	0.5360671	0	1	0.6593155	27.52862
191735	cg10064922	53768307	53768307	0.4813076	0	1	0.6974249	76.09773
191774	cg10067510	64604404	21764398	0.8786032	0	1	0.734111	-64.93639
191775	cg10067523	74698434	74698434	0.3821718	0	1	0.4848748	19.08353
191795	cg10068464	41718349	41718349	0.7076383	0	1	0.8240324	37.10529
191836	cg10070328	25698303	25698303	0.920518	0	1	0.7073883	-138.205
191875	cg10072319	74723489	74723489	0.1882872	0	1	0.2917003	25.73081
191937	cg10076068	10770329	10770329	0.0961358	0	1	0.2255839	50.50133
191943	cg10076560	19623402	67797490	0.1035021	0	1	0.2760525	75.53871
192027	cg10081994	39717404	39717404	0.5088095	0	1	0.6210374	22.70477
192041	cg10082647	42713510	12690452	0.5410049	0	1	0.4052341	-30.27216
192081	cg10085138	51671322	51671322	0.3509364	0	1	0.4968503	34.85882
192116	cg10087780	18679499	18679499	0.6311012	0	1	0.509632	-26.07555
192135	cg10088890	60701395	60701395	0.2098172	0	1	0.1046189	-35.67121
192182	cg10090591	26699355	26699355	0.7044186	0	1	0.8081965	29.40134
192204	cg10091686	65664331	65664331	0.1162655	0	1	0.2204243	33.38848
192210	cg10091792	46644403	46644403	0.3497359	0	1	0.5054184	39.06125
192350	cg10097313	35801339	35801339	0.4031441	0	1	0.5062025	19.06178
192367	cg10098373	26730410	26730410	0.6101993	0	1	0.7421328	35.43556
192383	cg10099275	36626469	36626469	0.9011351	0	1	0.6343961	-175.633
192415	cg10100585	10701414	10701414	0.7806164	0	1	0.3974653	-257.9031
192483	cg10104252	49750464	62603505	0.3441199	0	1	0.5939384	95.13174
192485	cg10104336	48667441	48667441	0.2126734	0	1	0.3152021	23.84504
192486	cg10104420	65770434	65770434	0.2901523	0	1	0.3980844	22.39861
192492	cg10104674	63686350	63686350	0.3629066	0	1	0.4658832	19.35643
192589	cg10109635	66763415	66763415	0.4060071	0	1	0.5379331	28.80147
192590	cg10109731	26610493	57771424	0.2875279	0	1	0.4160501	29.82548
192599	cg10110335	56642304	56642304	0.6318156	0	1	0.7685103	39.98561
192631	cg10111629	17632460	17632460	0.2096096	0	1	0.3236614	28.3658
192700	cg10115321	59657306	59657306	0.8512689	0	1	0.6925194	-66.26144
192734	cg10117077	38767335	38767335	0.6287603	0	1	0.4638844	-43.82382
192743	cg10117599	58659388	58659388	0.2393609	0	1	0.3595036	28.89316
192921	cg10127375	33693488	33693488	0.49366	0	1	0.59539	19.01244
192974	cg10130374	62620348	35738443	0.6686992	0	1	0.5238076	-36.44757
193163	cg10140536	63698418	26738315	0.9421256	0	1	0.8010952	-91.16594
193186	cg10141715	68626466	68626466	0.2718245	0	1	0.1368362	-45.72508
193242	cg10143883	20708490	20708490	0.7934275	0	1	0.9230481	71.617

193251	cg1014447	65705415	65705415	0.5950872	0	1	0.8296739	113.932
193262	cg1014486	23692465	23692465	0.3428894	0	1	0.4937552	37.1115
193299	cg1014633	74684498	33624416	0.3115919	0	1	0.6753516	374.3439
193386	cg1015090	71758432	71758432	0.5160663	0	1	0.3926893	-25.73768
193420	cg1015299	46736327	46736327	0.3377355	0	1	0.4830004	34.87336
193677	cg1016698	67703338	67703338	0.2089177	0	1	0.6021848	374.3439
193679	cg1016723	62695354	62695354	0.5884505	0	1	0.7111549	29.59332
193684	cg1016737	13650306	66699494	0.5178072	0	1	0.7072139	60.90091
193696	cg1016797	65742433	65742433	0.9356256	0	1	0.6982182	-171.6428
193895	cg1017798	71804313	71804313	0.6666328	0	1	0.8702114	104.1397
193937	cg1018009	18728379	18728379	0.5005173	0	1	0.6102572	21.70411
194006	cg1018432	37717325	37717325	0.6948512	0	1	0.5772682	-26.84933
194178	cg10193721	28779428	15772359	0.1756654	0	1	0.0649176	-47.12617
194261	cg1019733	24672333	24672333	0.2552858	0	1	0.1080415	-58.26193
194305	cg10200291	43600311	32739338	0.2273326	0	1	0.0885824	-57.95707
194308	cg1020037	33809357	33809357	0.5756686	0	1	0.4460659	-28.07678
194351	cg1020254	64646353	64646353	0.7167193	0	1	0.5717798	-39.23738
194363	cg1020283	41624389	21791419	0.0738164	0	1	0.2905851	119.7999
194418	cg10205431	14745467	57800340	0.8270274	0	1	0.6403946	-78.10133
194503	cg1020877	40616479	40616479	0.6083827	0	1	0.7087994	21.45019
194584	cg1021330	58784432	72762391	0.5275703	0	1	0.4143333	-22.21757
194593	cg1021365	68644458	68644458	0.2201541	0	1	0.3585359	37.74213
194599	cg1021387	36762446	71698444	0.8471951	0	1	0.709359	-52.59661
194652	cg1021705	62734347	62734347	0.1436247	0	1	0.5432426	374.3439
194715	cg1022054	68744315	68744315	0.7233846	0	1	0.8264785	31.16823
194724	cg1022101	48768314	48768314	0.2611159	0	1	0.3712521	24.17717
194779	cg1022453	48788306	48788306	0.6257455	0	1	0.8371242	98.37041
194802	cg10225951	63694309	63694309	0.5502698	0	1	0.7320655	59.08015
194940	cg1023447	34641380	34641380	0.3824147	0	1	0.4975428	22.9955
194959	cg1023545	72747457	72747457	0.565957	0	1	0.4339885	-28.88202
195048	cg1024035	61792426	61792426	0.4285659	0	1	0.5669634	31.35979
195063	cg1024118	58737492	58737492	0.5867655	0	1	0.6981156	24.74886
195118	cg1024334	44789485	58730396	0.773494	0	1	0.662371	-29.2484
195126	cg1024385	18793443	18793443	0.4121045	0	1	0.5361413	25.90452
195217	cg1024907	54753406	54753406	0.7426081	0	1	0.9263428	116.5898
195276	cg1025224	51767492	47795418	0.5358065	0	1	0.6924985	42.97214
195433	cg1026205	73673357	73673357	0.2865395	0	1	0.4026526	25.3073
195449	cg1026300	16672373	16672373	0.9502533	0	1	0.3737271	-371.3336
195473	cg1026538	20622426	14759462	0.3488677	0	1	0.2105158	-38.5299
195499	cg10266681	48690416	48690416	0.234715	0	1	0.3843098	41.67818
195845	cg1028852	36721481	36721481	0.4557852	0	1	0.5566803	18.43722
195862	cg1028974	39617333	39617333	0.3757955	0	1	0.5196625	33.65699
195894	cg1029199	69803510	47734337	0.4490813	0	1	0.3054608	-35.16396

195904	cg1029258	16687334	39646344	0.5834739	0	1	0.3561824	-78.70958
195919	cg1029382	58769488	58769488	0.7023255	0	1	0.8218706	38.33691
195948	cg1029595	55774489	55774489	0.7095852	0	1	0.5620083	-39.92223
195974	cg1029721	31682503	57660444	0.4108887	0	1	0.2969954	-24.19672
196106	cg1030619	19754448	19754448	0.1924088	0	1	0.4026679	80.59982
196148	cg1030862	37725360	37725360	0.470383	0	1	0.5877722	23.8972
196199	cg1031091	32759433	32759433	0.3690113	0	1	0.4924473	25.97047
196202	cg1031104	12710436	12710436	0.3841892	0	1	0.5495459	43.04004
196231	cg1031251	48627497	62620306	0.4461756	0	1	0.579567	29.53123
196334	cg1031731	11754397	46702490	0.2917202	0	1	0.0985281	-91.53165
196361	cg1031836	54669481	54669481	0.1383874	0	1	0.2424935	30.54426
196395	cg1031994	49746468	49746468	0.6193115	0	1	0.51891	-18.96021
196538	cg1032808	74799317	74799317	0.333906	0	1	0.4581059	26.83479
196551	cg1032854	42739345	42793430	0.9076254	0	1	0.6289781	-191.9018
196567	cg1032941	17781495	17781495	0.4231446	0	1	0.2601616	-46.1609
196642	cg1033314	72648369	72648369	0.8003443	0	1	0.9093319	51.55349
196675	cg1033474	62616428	41794445	0.5044827	0	1	0.397832	-20.18052
196702	cg1033602	59765370	59765370	0.8287678	0	1	0.9324754	56.66745
196707	cg1033619	66689473	66689473	0.3150435	0	1	0.4286817	23.61042
196745	cg1033853	32639331	32639331	0.1604938	0	1	0.2997841	44.43414
196779	cg1034090	67667448	68789383	0.6005599	0	1	0.3917626	-66.76717
196792	cg1034201	73764451	73764451	0.6021795	0	1	0.7082717	23.35287
196867	cg1034729	31743462	36775445	0.4947979	0	1	0.3861383	-20.88016
196923	cg1035049	28641376	28641376	0.4288897	0	1	0.3108577	-25.22528
196934	cg1035128	59704379	59704379	0.2989727	0	1	0.3993524	19.73711
196953	cg1035223	31715407	31715407	0.3216773	0	1	0.4526606	29.63467
197255	cg1037030	23744363	23744363	0.097594	0	1	0.2132536	42.42099
197299	cg1037277	17666483	17666483	0.736187	0	1	0.5773075	-47.4348
197354	cg1037559	16737369	16737369	0.7355627	0	1	0.5722157	-49.62096
197507	cg1038413	38628314	38628314	0.4891091	0	1	0.6374159	36.69022
197532	cg1038552	25755461	25755461	0.0310391	0	1	0.3656456	374.3439
197630	cg1039257	12774369	12774369	0.2809121	0	1	0.3943084	24.55468
197852	cg1040789	65651440	65651440	0.4506465	0	1	0.5640883	22.37311
197877	cg1040968	57807397	57807397	0.2482482	0	1	0.3939453	38.94124
197914	cg1041308	26784326	26784326	0.5706108	0	1	0.7135342	38.11898
197929	cg1041386	18762412	18762412	0.5218606	0	1	0.6264007	20.35061
197950	cg1041502	27769303	27769303	0.223686	0	1	0.4000007	56.07333
198088	cg1042360	11618340	11618340	0.2261839	0	1	0.3772828	43.07069
198093	cg1042384	61754407	61754407	0.5733827	0	1	0.7041187	32.38601
198106	cg1042468	43636484	56690452	0.4706398	0	1	0.3415228	-28.46481
198320	cg1043679	59662421	59662421	0.6268254	0	1	0.7395742	27.4325
198389	cg1044057	70725460	29631307	0.2378397	0	1	0.1062571	-49.5091
198546	cg1044932	28685469	28685469	0.8517932	0	1	0.7431114	-37.55486

198823	cg10466421	37620417	37620417	0.4036501	0	1	0.5124132	20.8126
198970	cg10475690	69766330	69766330	0.6993225	0	1	0.8059638	30.40638
199058	cg10481072	27771430	27771430	0.6930797	0	1	0.5742033	-27.24592
199084	cg10482512	72767486	72767486	0.3984154	0	1	0.6204134	75.5007
199102	cg10483660	52770325	52770325	0.4644748	0	1	0.6840159	77.16663
199118	cg10484673	70756443	70756443	0.678826	0	1	0.5744061	-21.66272
199143	cg10486069	26671487	74620448	0.764287	0	1	0.5797523	-64.68176
199177	cg10488050	73621324	73621324	0.4871798	0	1	0.680346	60.90435
199268	cg10493436	16743503	16743503	0.2858937	0	1	0.4100147	28.2285
199348	cg10497894	27600436	27600436	0.5744884	0	1	0.6947286	27.82707
199393	cg10500026	42755347	56698327	0.3886822	0	1	0.2157543	-55.08994
199416	cg10500702	52679452	52679452	0.7192851	0	1	0.8540182	52.30589
199429	cg10501093	58622410	29711507	0.2562732	0	1	0.3628876	23.15919
199432	cg10501210	43774458	66775341	0.1911157	0	1	0.321625	36.76616
199600	cg10507759	43648365	43648365	0.8576421	0	1	0.6936008	-71.4525
199603	cg10507965	33752434	33752434	0.2323495	0	1	0.1091288	-44.30248
199673	cg10511429	51782318	51782318	0.2923642	0	1	0.1893016	-25.52485
199716	cg10513323	69603337	69603337	0.535141	0	1	0.6582032	27.42328
199732	cg10513992	44786356	44786356	0.7243018	0	1	0.8742558	67.17198
199816	cg10518155	24682375	24682375	0.7390864	0	1	0.8392172	31.43956
200018	cg10528424	27765350	41611371	0.7818816	0	1	0.6005414	-65.51028
200255	cg10539898	35729325	38628452	0.6458896	0	1	0.5145916	-30.10046
200285	cg10541843	13613324	13613324	0.257839	0	1	0.3606395	21.8102
200329	cg10544018	16767305	42611322	0.9610099	0	1	0.8022776	-120.79
200360	cg10546210	74613345	74613345	0.5187827	0	1	0.6589482	34.06738
200416	cg10549071	59810379	59810379	0.7151939	0	1	0.8240839	33.53853
200489	cg10553103	33767380	33767380	0.4738955	0	1	0.3622203	-22.08229
200490	cg10553204	61671309	19659376	0.4352826	0	1	0.5357017	18.23189
200491	cg10553219	15624313	15624313	0.9605852	0	1	0.6355776	-289.2523
200558	cg10557683	47625505	47625505	0.7624828	0	1	0.6093349	-47.31697
200564	cg10557907	15629450	15629450	0.2271293	0	1	0.3317635	23.8139
200577	cg10559151	48602325	48602325	0.2615158	0	1	0.3920603	31.78065
200601	cg10560561	65732339	65732339	0.3428967	0	1	0.4851842	33.53755
200633	cg10564001	41624467	41624467	0.2090445	0	1	0.3113703	23.98133
200687	cg10568066	39730413	41722336	0.0403308	0	1	0.4199293	374.3439
200780	cg10574499	39690462	39690462	0.2261563	0	1	0.3268936	22.49675
200816	cg10576245	37667504	37667504	0.1093096	0	1	0.2677152	64.80154
200860	cg10578777	72761345	11607503	0.8885319	0	1	0.7759256	-47.64005
201035	cg10586672	73667307	73667307	0.2182739	0	1	0.3273773	25.92854
201045	cg10587183	16804357	16804357	0.7131625	0	1	0.8273014	36.47205
201181	cg10593416	19741306	19741306	0.4707285	0	1	0.3573278	-22.71008
201269	cg10599384	17680427	17680427	0.2261501	0	1	0.1018973	-46.29323
201316	cg10601171	16611329	16611329	0.644876	0	1	0.7474643	24.1209

201402	cg10606127	54774472	52617432	0.5934281	0	1	0.4139176	-50.21238
201467	cg10609868	20806344	20806344	0.4233478	0	1	0.5544385	28.49908
201540	cg10614809	44746361	45807398	0.4845547	0	1	0.2847721	-64.07866
201559	cg10616216	28810412	28810412	0.5772939	0	1	0.4635919	-22.56145
201629	cg10620881	53719509	39727434	0.472358	0	1	0.5810629	20.99366
201659	cg10622551	28629497	70809301	0.2987296	0	1	0.1980028	-24.06924
201733	cg10626169	26755468	26755468	0.5138428	0	1	0.723377	74.57735
201826	cg10631289	49739470	12756462	0.3781751	0	1	0.4923107	22.70624
201849	cg10632144	73771431	16606388	0.839309	0	1	0.9426655	61.16409
201863	cg10632656	45693300	45693300	0.2672202	0	1	0.1429529	-39.37914
201867	cg10632770	49764464	49764464	0.7117471	0	1	0.2673025	-352.0149
201871	cg10632894	49752455	45646503	0.4429239	0	1	0.3303583	-22.90353
201947	cg10635895	47783382	19651386	0.7556244	0	1	0.5695279	-64.38499
202116	cg10646968	21727497	21727497	0.4620561	0	1	0.5651382	19.13577
202190	cg10651657	67683365	67683365	0.7154658	0	1	0.8196237	30.82731
202251	cg10655551	74623332	35659384	0.507873	0	1	0.3895772	-24.00131
202280	cg10658203	19749453	19749453	0.3955228	0	1	0.2907744	-21.34026
202348	cg10662314	27686326	47643473	0.3134922	0	1	0.1228278	-82.36134
202383	cg10664305	60733432	60733432	0.6241343	0	1	0.7546375	35.85216
202422	cg10666341	71792334	71792334	0.4685312	0	1	0.6186957	36.94909
202492	cg10670396	42685325	42685325	0.4731885	0	1	0.3672798	-20.20056
202524	cg10672567	28763342	42751473	0.8611569	0	1	0.6611953	-97.92007
202565	cg10674805	20619509	60731404	0.6728159	0	1	0.7986975	38.32244
202638	cg10680224	18770414	41604395	0.6654974	0	1	0.5510105	-24.61408
202657	cg10681391	40676346	40676346	0.5699594	0	1	0.7548859	63.60258
202732	cg10687087	68731469	64679387	0.7982158	0	1	0.6366978	-56.73355
202734	cg10687131	55799382	55799382	0.2602974	0	1	0.3734396	25.27067
202760	cg10689404	62688381	20720486	0.1939053	0	1	0.3049618	28.30341
202772	cg10690152	37773346	49711327	0.0574568	0	1	0.2139518	80.42786
202803	cg10692140	24663433	24663433	0.2439508	0	1	0.3836262	36.58721
202839	cg10694727	10773446	10773446	0.3171908	0	1	0.4613881	35.00292
202853	cg10695549	33611395	33611395	0.8132875	0	1	0.7127901	-28.52244
202863	cg10696351	56781474	56781474	0.2721733	0	1	0.3728996	20.623
202904	cg10699171	26650456	26650456	0.6426752	0	1	0.7499738	26.02229
202940	cg10701033	65615318	65615318	0.5172709	0	1	0.6837956	47.1201
203131	cg10712476	43792404	43792404	0.5438232	0	1	0.6837046	35.05529
203155	cg10713589	33739367	33739367	0.5278577	0	1	0.6358107	21.62428
203180	cg10715272	51719344	51719344	0.5035151	0	1	0.3862242	-23.68622
203267	cg10719792	70612465	70612465	0.7515518	0	1	0.9322144	117.8374
203315	cg10722444	53683501	53683501	0.1782638	0	1	0.3043761	36.05555
203346	cg10724632	51626331	51626331	0.344129	0	1	0.220982	-31.21485
203361	cg10725344	26603501	26603501	0.2086065	0	1	0.3328277	32.54938
203369	cg10725843	54602367	54602367	0.8153774	0	1	0.9419471	79.22176

203396	cg1072766	21678464	21678464	0.795144	0	1	0.676253	-34.66993
203430	cg1072949	56800480	63799480	0.7864443	0	1	0.6563604	-38.8513
203508	cg1073547	54683477	54683477	0.3416869	0	1	0.2229668	-29.31868
203511	cg1073560	16760467	16760467	0.3560254	0	1	0.4896533	29.88937
203518	cg1073630	64642498	64642498	0.7839056	0	1	0.944113	108.6565
203552	cg1073864	44601351	44601351	0.7356861	0	1	0.6105205	-32.10106
203586	cg1074141	63646479	63646479	0.523804	0	1	0.7160012	63.31508
203615	cg1074407	37605414	37605414	0.2528036	0	1	0.3963363	37.69538
203651	cg1074748	53606504	65610464	0.7267292	0	1	0.9623065	374.3439
203681	cg1075026	57779501	57779501	0.7549734	0	1	0.5109869	-103.1303
203682	cg1075030	47659388	47659388	0.1500118	0	1	0.430079	145.7438
203724	cg1075361	19627345	19627345	0.3739349	0	1	0.5012141	27.28862
203736	cg1075439	26699375	46663315	0.6100686	0	1	0.7764744	56.10493
203825	cg1075981	14739477	14739477	0.5728632	0	1	0.4665663	-20.16994
203853	cg1076163	48664460	48664460	0.7517073	0	1	0.5726035	-59.85733
203882	cg1076323	64765384	33699316	0.2892794	0	1	0.1814269	-27.9923
204049	cg1077253	66671425	66671425	0.3987997	0	1	0.6883728	132.2059
204144	cg1077734	74689428	74689428	0.3787054	0	1	0.5132801	29.95687
204230	cg1078077	24632369	24632369	0.5064656	0	1	0.6273555	25.78312
204254	cg1078220	18809487	18809487	0.6197484	0	1	0.7542864	37.61365
204318	cg1078515	28625444	28625444	0.1680725	0	1	0.3606892	73.46073
204443	cg1079230	51612373	31716425	0.5345616	0	1	0.3145645	-74.88975
204453	cg1079291	14625395	14625395	0.307455	0	1	0.4730254	44.85247
204486	cg1079511	22779306	39773476	0.6104859	0	1	0.7121995	22.02747
204575	cg1080034	60620379	60620379	0.7173258	0	1	0.820271	30.36083
204636	cg1080357	57726430	57726430	0.8414994	0	1	0.7381079	-33.30662
204659	cg1080497	54606328	54606328		0	1		-4.34E-09
204737	cg1080919	30762401	38713319	0.8658586	0	1	0.716709	-64.14434
204738	cg1080928	17670482	17670482	0.2667298	0	1	0.3854108	26.99623
204774	cg1081142	47696321	47696321	0.1815158	0	1	0.2891982	27.91696
204796	cg1081263	67759420	70703360	0.3842651	0	1	0.1684404	-88.83799
204802	cg1081288	45734474	45734474	0.6824914	0	1	0.7890756	28.73178
204846	cg1081565	53795414	51795457	0.47833	0	1	0.1873725	-145.8998
204847	cg10815671	17802397	17802397	0.6156853	0	1	0.7404875	32.29366
204936	cg1082004	59617490	60758463	0.3113853	0	1	0.197335	-29.24178
204950	cg1082073	54723450	54723450	0.6204485	0	1	0.8333055	98.30006
204972	cg1082196	48742463	48742463	0.7807511	0	1	0.3807185	-283.5222
204999	cg10823511	39601303	39601303	0.8199483	0	1	0.9282041	58.16123
205079	cg1082765	41715408	41715408	0.6266115	0	1	0.733838	25.0271
205136	cg1083124	19744411	48735439	0.4236372	0	1	0.3005267	-27.34332
205151	cg1083209	50693368	52631312	0.6452745	0	1	0.4668614	-51.06237
205266	cg1083778	26715316	36715368	0.5779297	0	1	0.4238193	-37.96814
205305	cg1083972	28804403	28804403	0.2365492	0	1	0.1237875	-36.47261

205377	cg1084427	53653457	53653457	0.5560196	0	1	0.7267843	52.59577
205379	cg1084438	29765465	29765465	0.940088	0	1	0.8171902	-75.19838
205399	cg1084661	67669371	10643503		0	1	0.2168128	4.34E-09
205527	cg1085542	37707303	37707303	0.6412026	0	1	0.8141305	66.39854
205586	cg1085864	61677417	61677417	0.6208779	0	1	0.9139124	374.3439
205654	cg1086246	52672494	52672494	0.3045819	0	1	0.4222862	25.28893
205656	cg1086253	23757363	23757363	0.5242746	0	1	0.3966323	-27.24479
205667	cg1086296	59766311	59766311	0.6649225	0	1	0.862384	96.4939
205676	cg1086373	74759421	74759421	0.6147417	0	1	0.7950428	67.17581
205812	cg1087409	47607347	47607347	0.5161307	0	1	0.6351062	25.29829
205871	cg1087823	55679444	55679444	0.6579117	0	1	0.7811295	35.1274
205969	cg10883621	13644317	13644317		0	1	0.230087	4.34E-09
206050	cg10888811	56793416	56793416	0.2300164	0	1	0.3651753	35.59412
206070	cg1089064	66636357	66636357	0.3019593	0	1	0.1170732	-79.99968
206084	cg1089157	20679318	20679318	0.8547381	0	1	0.7192701	-52.89954
206112	cg1089327	41806353	41806353	0.4471269	0	1	0.3054949	-34.34173
206153	cg1089587	18781332	18781332	0.5977092	0	1	0.4640116	-29.88329
206226	cg1090031	20670427	20670427	0.2368239	0	1	0.3570893	29.08419
206280	cg1090285	42604354	42604354	0.1413821	0	1	0.3259104	73.73145
206376	cg1090918	69618411	69736444	0.5077274	0	1	0.6354414	28.44716
206413	cg1091128	63683505	63683505	0.641649	0	1	0.5290422	-23.28782
206442	cg1091297	12672439	53693413	0.5717084	0	1	0.4471695	-26.20936
206540	cg1092075	66645436	66645436	0.4632343	0	1	0.3420536	-25.59842
206628	cg10926851	59711416	59711416	0.7123902	0	1	0.8217647	33.46705
206687	cg1093030	73636451	49750505	0.0417148	0	1	0.2531583	132.5911
206779	cg1093740	40607452	37633345	0.3355566	0	1	0.4586455	26.40232
206830	cg1094020	51614481	58624406	0.4973477	0	1	0.6452363	36.77664
206934	cg1094626	21687351	21687351	0.8159381	0	1	0.9330034	66.92367
207073	cg1095315	22773335	22773335	0.4387712	0	1	0.5466077	20.50333
207092	cg1095433	25645386	25645386	0.7416039	0	1	0.8697947	52.19648
207137	cg10957001	62702473	62702473	0.1979232	0	1	0.5817538	374.3439
207310	cg1096702	13720352	28601475	0.3311312	0	1	0.1967048	-38.00304
207353	cg1096946	74632373	25717329	0.7696246	0	1	0.8873321	50.44429
207365	cg1097034	48671357	48671357	0.8324281	0	1	0.7261056	-33.43758
207413	cg1097362	17606321	17606321	0.6628187	0	1	0.5033469	-42.63545
207426	cg1097441	44729430	44729430	0.9378366	0	1	0.7316631	-144.3126
207438	cg1097535	39806406	39806406	0.3100429	0	1	0.1806353	-37.30603
207494	cg1097858	71789303	59608377	0.5895876	0	1	0.4853458	-19.70225
207518	cg1097984	62606363	62606363	0.5924067	0	1	0.7103962	27.75023
207568	cg1098204	10766315	10766315	0.6534234	0	1	0.5528562	-19.7112
207605	cg1098348	56735443	56735443	0.0929003	0	1	0.2224925	51.33793
207692	cg1098784	27796427	27796427	0.0925731	0	1	0.1995458	38.70404
207720	cg1098921	70728324	53740485	0.2113909	0	1	0.3298191	29.97598

207724	cg10989317	24719408	24719408	0.9805223	0	1	0.705961	-254.0816
207740	cg10989981	66708439	66708439	0.6650235	0	1	0.5456252	-26.32907
207744	cg10990188	18656427	18656427	0.9392588	0	1	0.8335811	-61.27249
207750	cg10990737	42615324	42615324	0.5388529	0	1	0.3127538	-78.97857
207770	cg10991855	69672418	69672418	0.8676916	0	1	0.9678956	73.91393
207830	cg10994944	64607349	66644423	0.4310613	0	1	0.3137291	-24.90491
207831	cg10995081	25735316	13767374	0.335272	0	1	0.1919212	-42.64685
207838	cg10995422	23622307	23622307	0.2163901	0	1	0.3930907	57.06613
207846	cg10995873	36602457	36602457	0.3070396	0	1	0.4202823	23.68605
207875	cg10997190	20780397	20780397	0.4712307	0	1	0.5774867	20.19679
207959	cg11002686	70796444	70796444	0.720292	0	1	0.6101689	-25.35443
207966	cg11002923	28620325	28620325	0.6738339	0	1	0.5640972	-23.26531
208000	cg11005628	70706315	47670353	0.4418814	0	1	0.300606	-34.37594
208005	cg11005845	30791422	39669490	0.431447	0	1	0.327748	-20.12075
208046	cg11008123	46645482	54708500	0.4166279	0	1	0.5370355	24.62822
208086	cg11010744	21757438	21757438	0.6297506	0	1	0.809072	69.30208
208090	cg11011512	10722313	43809366	0.525847	0	1	0.3645859	-41.31843
208103	cg11012153	72808343	33661308	0.3889416	0	1	0.6068175	72.55235
208164	cg11015768	73789466	73789466	0.7656347	0	1	0.8846037	50.47218
208168	cg11016151	72708381	72708381	0.3980041	0	1	0.4989367	18.45365
208228	cg11019791	68715414	68715414	0.5997161	0	1	0.4755575	-26.40534
208302	cg11024449	51660345	58651460	0.4999854	0	1	0.3433639	-39.61333
208339	cg11026604	17765356	17765356	0.3394212	0	1	0.4571091	24.44222
208424	cg11031567	21750367	21750367	0.3414563	0	1	0.4566872	23.57345
208492	cg11035303	11654432	11654432	0.1936242	0	1	0.0383847	-88.32603
208507	cg11036359	58702337	58702337	0.7560548	0	1	0.5053615	-108.5207
208539	cg11038231	68803380	68803380	0.470262	0	1	0.58449	22.80687
208616	cg11043993	40798374	40798374	0.6462311	0	1	0.7817932	40.91311
208620	cg11044162	68801378	68801378	0.866635	0	1	0.6581475	-106.5339
208655	cg11046772	29796509	29796509	0.4585247	0	1	0.60374	34.54988
208664	cg11047442	36635354	44677485	0.4905699	0	1	0.6272872	31.66284
208672	cg11048797	33699510	33699510	0.5951623	0	1	0.7556099	50.25614
208738	cg11053062	11802432	11802432		0	1		-4.34E-09
208749	cg11053632	38637330	38637330	0.5598042	0	1	0.3990816	-40.84737
208817	cg11059159	12606302	12606302	0.6824833	0	1	0.5491797	-32.30656
208844	cg11060532	27709499	27709499	0.3564525	0	1	0.2459902	-24.95792
208886	cg11063088	17792508	17792508	0.7278963	0	1	0.8471847	42.2944
208948	cg11066244	42649325	42649325	0.5200703	0	1	0.6602395	34.11985
208953	cg11066601	57787312	34636361	0.2128265	0	1	0.3569528	40.96913
208991	cg11068881	34643333	34643333	0.4642768	0	1	0.5713174	20.38772
209083	cg11073579	60741458	60741458	0.5157655	0	1	0.6410564	27.71017
209101	cg11074353	10705406	10705406	0.6356436	0	1	0.5218451	-23.54081
209107	cg11074783	49661459	42679464	0.343799	0	1	0.2191169	-31.9695

209237	cg1108127	66631343	66631343	0.1907746	0	1	0.3121785	32.81573
209265	cg1108263	27700403	27700403	0.9410316	0	1	0.8043659	-86.88321
209421	cg1109283	13748326	13748326	0.5451713	0	1	0.6479825	20.27625
209570	cg1110408	31681490	62791345	0.1078669	0	1	0.207959	32.64331
209634	cg1110847	10605372	42766351	0.3860861	0	1	0.2357326	-41.95108
209675	cg1111146	25733438	25733438	0.2709657	0	1	0.4046874	32.58414
209754	cg1111627	71647392	71647392	0.195675	0	1	0.3006259	25.80253
209830	cg1111976	11633490	11633490	0.2862088	0	1	0.4546289	47.22604
209881	cg1112361	44666354	44666354	0.6779099	0	1	0.9030443	137.9623
209893	cg1112413	70793333	67682493	0.720764	0	1	0.4688723	-103.9554
209948	cg11128021	56652322	56652322	0.6554573	0	1	0.7611081	26.14035
209950	cg1112821	30791331	30791331	0.4221212	0	1	0.5399126	23.73216
209960	cg1112895	52764301	52764301	0.2760793	0	1	0.378131	20.92164
210003	cg1113253	34739436	34739436	0.4604956	0	1	0.5618817	18.61023
210020	cg1113365	35656319	35656319	0.9061135	0	1	0.772486	-67.23
210110	cg1113924	65602468	65602468	0.4028031	0	1	0.5269845	25.97564
210200	cg1114410	33619359	33619359	0.1730007	0	1	0.4634277	148.7541
210266	cg1114786	21731367	21731367	0.1911095	0	1	0.2963606	26.23596
210412	cg1115543	23722457	23722457	0.1687002	0	1	0.2866773	33.4056
210438	cg1115687	24770432	34671340	0.4987013	0	1	0.6071665	21.24845
210600	cg1116645	71682363	20729361	0.6056774	0	1	0.4417006	-42.81678
210619	cg1116810	66770303	39654448	0.7473283	0	1	0.6275854	-30.71834
210635	cg1116984	48640443	48640443	0.5895336	0	1	0.7362809	41.60292
210694	cg1117360	30675437	30675437	0.1457856	0	1	0.2581055	33.37979
210697	cg1117382	12663331	12663331	0.3434559	0	1	0.4892893	34.97807
210819	cg1118169	17786435	54779449	0.7710768	0	1	0.6407216	-37.32569
210937	cg1118866	68683459	68683459	0.518903	0	1	0.6470894	28.96039
211112	cg11198851	26635475	26635475	0.3219083	0	1	0.4251541	20.09718
211130	cg1119963	35723384	44733367	0.3774671	0	1	0.2667739	-24.14397
211153	cg1120074	15605331	15605331	0.6974393	0	1	0.8011534	28.66555
211179	cg1120165	31712468	31712468	0.2430516	0	1	0.3495678	23.69996
211250	cg1120497	74804386	74804386	0.4602429	0	1	0.270528	-59.31372
211316	cg1120832	35677461	35677461	0.933093	0	1	0.8235528	-61.27816
211429	cg1121450	61632480	61632480	0.3885368	0	1	0.5215592	29.28752
211440	cg1121496	17728452	10767414	0.1827169	0	1	0.3018158	32.54634
211453	cg1121617	50717467	50717467	0.3022987	0	1	0.4259999	27.50185
211504	cg11219411	51645476	51645476	0.1869043	0	1	0.4474087	118.9654
211593	cg1122393	45608323	45608323	0.191155	0	1	0.30846	31.05895
211618	cg11225091	21723504	21723504	0.3193361	0	1	0.1357149	-74.43496
211702	cg1122927	37646416	37646416	0.5270033	0	1	0.6710918	36.21606
211766	cg1123173	29646482	29646482	0.5218753	0	1	0.665724	35.87502
211835	cg1123559	33659459	33659459	0.3715601	0	1	0.4954851	26.11337
211852	cg1123645	23667335	23667335	0.6533093	0	1	0.5356111	-25.35006

211897	cg1123895	10745507	55675345	0.4897759	0	1	0.3675637	-25.5584
211989	cg1124464	35662458	53636494	0.4082751	0	1	0.5132422	19.62024
212007	cg1124556	73703494	63631386	0.6325395	0	1	0.5282506	-20.3943
212200	cg1125676	74600393	27676391	0.6979563	0	1	0.8634738	74.18694
212208	cg1125730	34664436	34664436	0.4809797	0	1	0.6125954	29.36408
212262	cg1126141	56712505	56712505	0.3387745	0	1	0.4698528	29.25383
212462	cg1127365	61728324	61728324	0.5664344	0	1	0.4515389	-22.86572
212500	cg1127618	13703378	13703378	0.7823308	0	1	0.9083332	62.75547
212606	cg1128282	71675337	46766498	0.4160318	0	1	0.5817083	43.26226
212723	cg1129016	19810503	19810503	0.5614215	0	1	0.4567191	-19.60237
212791	cg1129462	15746406	27760466	0.9217269	0	1	0.7969202	-67.43902
212794	cg1129475	45729316	45729316	0.2972092	0	1	0.5123948	72.66722
212824	cg1129682	43725393	43725393	0.4874635	0	1	0.3838736	-19.33661
212974	cg1130594	47709386	47709386	0.6536415	0	1	0.7665765	29.42354
212998	cg1130771	46738432	46738432	0.4019943	0	1	0.650975	95.6173
213101	cg1131346	45809489	45809489	0.5337873	0	1	0.6467831	23.55077
213123	cg1131461	20789330	20789330	0.7256096	0	1	0.604864	-29.66638
213146	cg1131598	67658342	67658342	0.3666238	0	1	0.2442085	-29.5028
213250	cg1132240	43709503	64619450	0.3665135	0	1	0.2457971	-28.76226
213348	cg1132814	20625410	20625410	0.6863796	0	1	0.8164043	42.76876
213382	cg1133036	67757423	67757423	0.2388374	0	1	0.1072955	-49.26899
213402	cg1133183	11745317	11745317	0.6998564	0	1	0.8185186	37.43895
213425	cg1133323	43751304	43751304	0.2859545	0	1	0.153246	-42.12817
213438	cg1133409	66706319	66706319	0.8210284	0	1	0.9213623	49.88009
213584	cg1134219	69764364	65674451	0.3197677	0	1	0.1926309	-35.12944
213610	cg1134321	47637401	23764398	0.2337108	0	1	0.1051849	-48.00745
213641	cg1134461	14770336	14770336	0.56354	0	1	0.6976743	33.41254
213693	cg1134758	66606414	66679395	0.214705	0	1	0.051269	-88.31603
213716	cg1134858	70762458	29807455	0.8345629	0	1	0.9521316	78.10484
213841	cg1135676	10795372	11779447	0.3109052	0	1	0.1965046	-29.44564
213909	cg1136134	23608346	46604473	0.4057396	0	1	0.2631176	-36.6906
214001	cg1136735	65625460	38750478	0.4485747	0	1	0.3412755	-20.99878
214136	cg1137619	36695359	39793413	0.4037376	0	1	0.2920181	-23.60924
214223	cg1138165	40714400	40714400	0.6839551	0	1	0.8118886	41.05838
214229	cg1138208	33670461	33670461	0.5971221	0	1	0.4650625	-29.25456
214241	cg1138266	54618301	61739303	0.7073964	0	1	0.5425337	-47.93173
214252	cg1138313	12727427	48709346	0.7537018	0	1	0.875077	49.44318
214263	cg1138347	46689417	46689417	0.6230831	0	1	0.5018517	-25.80768
214338	cg1138798	10603474	10603474	0.6942661	0	1	0.8051134	32.16422
214398	cg1139173	49616463	49616463	0.3523542	0	1	0.5066684	38.40882
214447	cg1139506	59607487	59607487	0.8278616	0	1	0.6676263	-61.59982
214535	cg1139958	35765460	69623425	0.6993468	0	1	0.202855	-371.3336
214548	cg1140016	65791488	65791488	0.5720056	0	1	0.3551852	-71.79395

214569	cg1140129	74707387	18753308	0.5665837	0	1	0.6696383	20.93255
214579	cg1140182	57610366	57610366	0.7641246	0	1	0.8655544	36.20969
214607	cg1140373	71720352	71720352	0.1423688	0	1	0.2488738	31.15832
214658	cg1140697	23807351	23807351	0.2142932	0	1	0.3324831	29.68023
214728	cg1141064	41707436	41707436	0.3024811	0	1	0.4080416	21.2787
214900	cg1141860	28663477	28663477	0.5315717	0	1	0.842285	374.3439
214927	cg1142014	40618306	40618306	0.540506	0	1	0.4170044	-25.71263
214959	cg1142231	15807379	15807379	0.671384	0	1	0.7850139	31.31901
214999	cg1142437	15684506	15684506	0.4703139	0	1	0.5970374	27.28437
215008	cg1142477	12730499	12730499	0.3731512	0	1	0.5462905	46.8792
215145	cg1143470	48736392	60678355	0.5202268	0	1	0.3824514	-31.16157
215159	cg1143550	47788310	12673349	0.2322841	0	1	0.0994558	-51.71298
215190	cg1143746	63779342	40684324	0.3029003	0	1	0.8135076	374.3439
215200	cg1143828	53729382	53729382	0.6394736	0	1	0.8180851	70.78357
215293	cg1144510	30735412	38697402	0.2354865	0	1	0.3383436	22.78041
215347	cg1144907	31795338	10773428	0.3144431	0	1	0.1566519	-54.79686
215407	cg1145371	39675490	39675490	0.1164709	0	1	0.2290418	37.48499
215439	cg1145689	12760376	12760376	0.4565664	0	1	0.566057	21.11667
215467	cg1145964	61650494	61741509	0.5254964	0	1	0.3684612	-39.3587
215525	cg1146342	54630353	54630353	0.6402375	0	1	0.8407581	91.53431
215598	cg1146763	49685357	49685357	0.2402808	0	1	0.0678964	-87.74922
215606	cg1146814	52715444	31789306	0.5230007	0	1	0.6413345	25.23429
215655	cg11471401	36806374	36806374	0.410064	0	1	0.5459256	30.30399
215966	cg1149560	45775369	34713473	0.5165632	0	1	0.7187785	69.5304
216175	cg1151058	29790445	29707302	0.4148569	0	1	0.2580924	-43.33859
216261	cg1151746	17608352	57733485	0.3860582	0	1	0.23376	-43.0141
216299	cg1151970	66764502	66764502	0.6843808	0	1	0.880725	102.8845
216460	cg1152832	41789306	59802488	0.5213579	0	1	0.4062291	-22.8585
216477	cg1152923	58607316	58607316	0.5099645	0	1	0.6527044	34.88763
216492	cg1153040	29795504	29795504	0.4369635	0	1	0.6105291	47.52275
216541	cg1153371	60750330	60750330	0.2999468	0	1	0.4020431	20.24658
216548	cg1153429	70761405	70761405	0.0632959	0	1	0.1754161	48.41527
216625	cg1153967	24742430	24742430	0.5260989	0	1	0.4024965	-25.7715
216648	cg1154070	71744395	71744395	0.8369718	0	1	0.693469	-53.69868
216745	cg11547201	64696506	64696506	0.7392564	0	1	0.8518692	39.611
216822	cg1155207	42614480	65626337	0.2244246	0	1	0.3318569	24.9635
216884	cg1155506	18610442	18610442	0.8982424	0	1	0.7684466	-61.66685
216940	cg1155865	62620354	62620354	0.430835	0	1	0.3002748	-30.13559
216995	cg1156231	42736499	42736499	0.6870574	0	1	0.8025177	33.94339
217018	cg1156423	46721362	46721362	0.19426	0	1	0.2977983	25.36299
217047	cg11565911	24744444	24744444	0.385607	0	1	0.2830465	-20.86672
217088	cg1156831	11631401	11631401	0.8745821	0	1	0.7721705	-38.47167
217127	cg1157112	50647374	50647374	0.4834522	0	1	0.6172727	30.30003

217190	cg11574745	66802480	66802480	0.824422	0	1	0.7238856	-29.7697
217281	cg11580790	25751411	25751411	0.4870382	0	1	0.5980086	21.91442
217324	cg11583351	19794335	19794335	0.4414143	0	1	0.558842	23.66438
217329	cg11583762	34739476	34739476	0.409167	0	1	0.3064761	-20.26987
217374	cg11586189	55749302	55749302	0.3744833	0	1	0.2322563	-38.52031
217394	cg11587069	36628408	11720427	0.1038771	0	1	0.290589	85.1457
217642	cg11600734	47754482	47754482	0.566654	0	1	0.6670715	20.0232
217688	cg11604182	55609355	55609355	0.1581142	0	1	0.2697572	31.71498
217739	cg11608150	10777317	61659390	0.5148925	0	1	0.3889622	-26.66973
217800	cg11611580	64602334	64602334	0.0595495	0	1	0.1933854	63.68414
217841	cg11613741	59635467	59635467	0.3031674	0	1	0.5103564	67.41902
217860	cg11615029	59612379	60706338	0.2673221	0	1	0.4214762	41.55375
217912	cg11618093	39746495	39746495	0.2905219	0	1	0.3920862	20.33204
217935	cg11620135	63721382	63721382	0.6299401	0	1	0.8387764	96.99706
218016	cg11626496	39632421	39632421	0.2103747	0	1	0.3158791	25.06576
218028	cg11627968	65699398	65699398	0.824706	0	1	0.9416815	71.3711
218078	cg11630939	34709464	15666478	0.3809974	0	1	0.511948	28.56818
218157	cg11635197	58689347	58611358	0.8020265	0	1	0.6635191	-44.97785
218197	cg11637968	65748382	65748382	0.4161679	0	1	0.582495	43.57742
218225	cg11639615	56766398	56766398	0.4278066	0	1	0.5285497	18.32251
218349	cg11645453	70678460	70678460	0.4358856	0	1	0.5399305	19.32096
218352	cg11645539	36627324	36627324	0.4419008	0	1	0.563723	25.19695
218469	cg11651932	11709328	11709328	0.9093309	0	1	0.796193	-54.32259
218542	cg11655490	72635435	72635435	0.312673	0	1	0.4193631	21.38647
218571	cg11657323	45643453	45643453	0.5829905	0	1	0.6855543	21.28299
218630	cg11660815	22797392	22797392	0.2373671	0	1	0.0903477	-62.6596
218658	cg11662061	39723430	39723430	0.2125247	0	1	0.3138781	23.43159
218682	cg11663393	67761493	15688477	0.5470316	0	1	0.4415186	-19.78572
218688	cg11663691	17615336	17615336	0.8144469	0	1	0.9299193	64.25076
218734	cg11666534	18631405	18631405	0.8557835	0	1	0.6737002	-83.13294
218751	cg11667387	56612305	14770408	0.9655964	0	1	0.7557905	-172.3707
218768	cg11668419	74728327	74728327	0.3628491	0	1	0.4795811	23.74049
219053	cg11685843	13703448	22787371	0.8126988	0	1	0.5727512	-113.0893
219113	cg11689753	29610312	29610312	0.4466894	0	1	0.5728208	26.78771
219168	cg11692403	58733431	58733431	0.5887049	0	1	0.7091013	28.59458
219208	cg11695041	74647411	43604473	0.162902	0	1	0.264737	27.12078
219517	cg11712506	54694405	54694405	0.415379	0	1	0.5256584	21.26088
219645	cg11719509	52666370	10666383	0.5529512	0	1	0.6724634	26.63599
219669	cg11721100	36771440	15759409	0.4348116	0	1	0.3291032	-20.72048
219723	cg11723923	34635449	34635449	0.8606858	0	1	0.6591631	-98.92348
219728	cg11724147	50745468	50745468	0.7190585	0	1	0.6058688	-26.41352
219760	cg11725415	13727428	13727428	0.3726257	0	1	0.4763756	19.48453
219812	cg11728747	26802426	26802426	0.3818157	0	1	0.4952874	22.45625

219887	cg11733135	52698501	52698501	0.5252626	0	1	0.7438297	83.11549
219971	cg11737757	73704494	73704494	0.6038076	0	1	0.4487953	-38.72269
220030	cg11740348	44639397	37643418	0.056576	0	1	0.160147	44.99642
220205	cg11750736	59636326	59636326	0.3341493	0	1	0.4378639	20.00629
220238	cg11752699	65627450	65627450	0.2459998	0	1	0.4231149	54.40114
220356	cg11758283	23682302	23682302	0.3927826	0	1	0.5031104	21.36239
220444	cg11764747	39628357	39628357	0.6289418	0	1	0.4960905	-30.20888
220452	cg11765312	68621315	68621315	0.1659584	0	1	0.2784274	31.28239
220492	cg11769349	36795500	38669411	0.5337167	0	1	0.6932505	44.35443
220636	cg11778714	50746371	50746371	0.4175494	0	1	0.5859791	44.61594
220669	cg11781306	26694315	41715429	0.2800793	0	1	0.1776298	-26.15014
220711	cg11783520	71794496	71794496	0.8121118	0	1	0.7111664	-28.59194
220723	cg11784298	38799338	38799338	0.3288919	0	1	0.5686469	87.9016
220773	cg11786587	20739373	20739373	0.8006346	0	1	0.6851696	-33.73335
220867	cg11791078	19636496	19636496	0.4424365	0	1	0.834098	374.3439
220871	cg11791288	10745380	10745380	0.5543872	0	1	0.4335872	-24.79547
221018	cg11798406	64656334	64656334	0.4730869	0	1	0.603614	28.78766
221089	cg11801727	13714508	58789321	0.7021484	0	1	0.5965115	-22.93473
221098	cg11802299	35756476	35756476	0.7990912	0	1	0.6966066	-27.95412
221215	cg11807153	64719320	64719320	0.4425535	0	1	0.5706379	27.47736
221232	cg11808100	30622386	30622386	0.1024422	0	1	0.2030343	33.71416
221438	cg11818589	62638468	62638468	0.6125335	0	1	0.4746457	-31.77544
221472	cg11820650	25615372	25615372	0.792249	0	1	0.9222964	71.58326
221556	cg11824564	27806415	27806415	0.7127539	0	1	0.8652808	66.15262
221586	cg11825731	18661402	62632378	0.4406294	0	1	0.3220358	-25.13156
221609	cg11826726	52788439	16650359	0.5631977	0	1	0.3581339	-64.47083
221753	cg11834635	39775431	39775431	0.4102972	0	1	0.5171019	20.17915
221779	cg11835544	52804376	52804376	0.8373618	0	1	0.6186863	-103.9512
221861	cg11839566	17742472	17742472	0.7519878	0	1	0.8941473	68.63291
221864	cg11839681	69605379	59741403	0.8071133	0	1	0.7050806	-28.54428
221911	cg11841771	72702348	19639374	0.3655064	0	1	0.2549031	-24.60373
221912	cg11841863	29652450	29652450	0.8145001	0	1	0.5988466	-95.0665
222065	cg11849573	48660405	27635396	0.8840119	0	1	0.7680746	-48.46543
222248	cg11857805	30613358	30613358	0.7297926	0	1	0.4207316	-156.2247
222288	cg11859922	34662471	34662471	0.2735391	0	1	0.4006304	29.85748
222311	cg11861387	19803414	63613441	0.4194958	0	1	0.2325082	-61.06801
222328	cg11861905	67809443	30721352	0.2940986	0	1	0.1852809	-28.07273
222499	cg11871064	30688439	30688439	0.5853923	0	1	0.6903075	22.22757
222506	cg11871549	13644500	13644500		0	1	0.3703268	4.34E-09
222562	cg11874976	48786440	45700445	0.3138621	0	1	0.470516	40.4886
222612	cg11877812	26647449	26647449	0.6896395	0	1	0.8465458	63.89029
222633	cg11879096	30655510	30655510	0.3410534	0	1	0.4449941	19.95727
222658	cg11881038	24635354	24635354	0.8858743	0	1	0.7713125	-48.12226

222681	cg1188235	66678315	66678315	0.5495096	0	1	0.8864846	374.3439
222691	cg11883141	22757330	22757330		0	1		-4.34E-09
222721	cg1188483	35693488	35693488	0.211885	0	1	0.3821143	54.06985
222729	cg1188535	13736432	71638330	0.3797682	0	1	0.515689	30.4641
222826	cg1189139	51682484	51682484	0.4679013	0	1	0.3277285	-33.05333
222912	cg1189762	51606301	51606301	0.1639939	0	1	0.2903845	37.73452
222916	cg1189788	41757509	41757509	0.3296389	0	1	0.2132173	-29.05287
222921	cg1189834	24804430	24804430	0.0211864	0	1	0.1758714	97.62872
222943	cg1190032	63649415	63649415	0.3272738	0	1	0.1715188	-51.43425
222945	cg1190044	23645312	30728493	0.3245839	0	1	0.1044071	-109.8989
222998	cg1190320	37679389	37679389	0.2178999	0	1	0.4146295	68.40018
223060	cg1190732	56729493	56729493	0.4663833	0	1	0.6076525	33.01941
223098	cg1190957	70734487	69691433	0.6960154	0	1	0.5334089	-46.00715
223213	cg1191728	28715494	28715494	0.820695	0	1	0.7107793	-33.58269
223238	cg1191882	44775332	44775332	0.3877787	0	1	0.4929764	19.79562
223292	cg1192392	16652322	16652322	0.0711275	0	1	0.3051988	135.8168
223459	cg1193417	51707449	21754348	0.2222522	0	1	0.0895898	-53.97507
223584	cg1194106	59797491	41669341	0.8531722	0	1	0.7334856	-43.63805
223600	cg1194192	45725411	73626375	0.4013075	0	1	0.228428	-53.75978
223607	cg1194220	70765391	70765391	0.8871918	0	1	0.5994335	-188.3987
223618	cg1194259	32810500	32810500	0.2922952	0	1	0.3963276	21.06639
223703	cg1194671	14668488	73718429	0.2687017	0	1	0.0662853	-111.6415
223742	cg1194890	14775413	14775413	0.2777216	0	1	0.4305133	40.35461
223747	cg1194917	55763401	55763401	0.2852994	0	1	0.3991513	24.56009
223820	cg1195316	26752472	26752472	0.3147408	0	1	0.4644758	37.4196
223881	cg1195644	51600385	51600385	0.4637512	0	1	0.0772999	-305.6266
223902	cg1195740	13796331	13796331	0.4789735	0	1	0.3144516	-44.08382
224115	cg1196952	45736441	45736441	0.3930406	0	1	0.5922818	60.98225
224201	cg11973981	49644409	49644409	0.255354	0	1	0.4384666	56.84241
224222	cg1197539	61717500	61717500	0.3682247	0	1	0.2658222	-21.38336
224244	cg1197673	56765422	56765422	0.171478	0	1	0.2796977	28.97971
224291	cg1197987	28791379	28791379	0.7571641	0	1	0.6511134	-26.02304
224336	cg1198319	11806442	11806442	0.6049253	0	1	0.7097884	22.99569
224361	cg11984971	37634448	37634448	0.3044581	0	1	0.4442253	33.61829
224387	cg1198664	25709418	25709418	0.5839757	0	1	0.3883522	-58.84389
224388	cg1198674	44644324	44644324	0.4896352	0	1	0.6091478	24.93563
224407	cg11987751	11733380	65689343	0.7548022	0	1	0.9080826	82.3342
224508	cg1199335	62621397	50713487	0.1585534	0	1	0.5745974	374.3439
224634	cg1200245	55794335	55794335	0.2382256	0	1	0.3392455	22.02648
224670	cg1200541	47709311	47709311	0.5836288	0	1	0.6888992	22.29435
224728	cg1201047	35705472	35705472	0.1911765	0	1	0.2978867	26.79608
224750	cg1201242	66781467	66781467	0.3873818	0	1	0.7557994	374.3439
224777	cg12014181	17657505	15640378	0.7096951	0	1	0.8675346	70.30808

224931	cg1202482	38736307	72718469	0.4791617	0	1	0.3243047	-39.34095
224941	cg1202513	23680449	23680449	0.1955618	0	1	0.3084413	28.90596
225158	cg1203663	34610328	34610328	0.941532	0	1	0.6962793	-184.1435
225293	cg12044531	73684393	73684393	0.7877888	0	1	0.8986788	49.43438
225429	cg1205181	59730440	59730440	0.267755	0	1	0.3678576	20.57042
225542	cg1205826	30635302	56774418	0.5834765	0	1	0.433304	-36.32347
225774	cg1207002	48721390	27615377	0.6813709	0	1	0.5549706	-29.55545
225806	cg1207202	71732385	71732385	0.2946308	0	1	0.4327879	33.33619
225877	cg1207448	39644373	39644373	0.876909	0	1	0.6664634	-112.3659
225923	cg1207635	71604490	71604490	0.6519912	0	1	0.5149825	-32.53362
225979	cg1207877	51701343	39654350	0.6011941	0	1	0.3789909	-75.30598
226051	cg1208201	69749311	69749311	0.245325	0	1	0.3675958	29.38582
226166	cg1208907	39701347	39701347	0.170755	0	1	0.2710976	25.86488
226265	cg1209486	13752450	13752450		0	1	0.7826383	4.34E-09
226293	cg1209648	69672368	69672368	0.2532988	0	1	0.37734	29.64859
226312	cg1209755	74670410	74670410	0.1559067	0	1	0.2783825	36.85933
226313	cg12097671	42757396	42757396	0.5819258	0	1	0.7002902	27.38888
226407	cg1210297	59743375	59743375	0.7416903	0	1	0.6261526	-28.64882
226461	cg1210589	13790458	24602442	0.4284386	0	1	0.29476	-31.54582
226517	cg1210926	74638358	51763428	0.9371647	0	1	0.8266972	-63.92368
226553	cg1211114	36794431	36794431	0.7770219	0	1	0.9027598	60.51626
226701	cg1211998	38752400	38752400	0.1402686	0	1	0.245641	30.89285
226731	cg1212144	66659507	20782356	0.5406867	0	1	0.4046572	-30.37337
226736	cg1212166	45689375	52608417	0.4414684	0	1	0.3352932	-20.75045
226773	cg1212387	64640419	64640419	0.3698711	0	1	0.2130735	-47.03159
226840	cg12127811	51740387	51740387	0.5752826	0	1	0.7228913	40.90622
226852	cg1212844	15615502	15615502	0.7799673	0	1	0.9541526	128.7396
226880	cg1213001	11796352	72630412	0.3557671	0	1	0.2305993	-31.39827
227134	cg1214676	20676448	20676448	0.4711462	0	1	0.5978984	27.30783
227342	cg1215902	19779377	57795385	0.7516051	0	1	0.6042306	-43.31899
227374	cg1216042	74764369	61763322	0.6494986	0	1	0.5410362	-22.11905
227403	cg12161971	14739431	73762406	0.7807986	0	1	0.6599059	-34.06201
227500	cg1216700	63634497	57679423	0.6179948	0	1	0.9687865	374.3439
227527	cg1216850	25749369	25749369	0.7873477	0	1	0.9156411	67.32613
227591	cg1217315	14667323	12605439	0.3969585	0	1	0.2390581	-45.25869
227653	cg1217718	32796360	28663432	0.8181521	0	1	0.6902618	-41.94897
227708	cg1217965	10600406	10600406	0.5864068	0	1	0.7526056	52.91804
228006	cg1219814	17740335	17740335	0.2668806	0	1	0.3863184	27.26792
228168	cg1220863	27767440	27767440	0.7255276	0	1	0.475769	-102.9465
228188	cg12209881	44636452	44636452	0.9290205	0	1	0.7115759	-147.9599
228246	cg1221303	23751502	23751502	0.4657535	0	1	0.6909885	81.50523
228320	cg1221795	29749437	29749437	0.6091592	0	1	0.7856293	63.2453
228353	cg1221946	24798379	24798379	0.5553163	0	1	0.6834716	30.32408

228358	cg12219707	51713307	51713307	0.584762	0	1	0.472795	-22.07262
228466	cg12226028	21727322	44763391	0.4643249	0	1	0.3330836	-29.44329
228484	cg12226948	15672418	15672418	0.2051638	0	1	0.3549879	44.39921
228568	cg12232463	48788346	48788346	0.1942945	0	1	0.337907	42.52177
228570	cg12232731	71697384	42681335	0.2495721	0	1	0.3781721	31.64234
228685	cg12241333	32689477	32689477	0.5067064	0	1	0.6824954	51.68195
228713	cg12243267	65639315	48785495	0.8131636	0	1	0.6641158	-52.32315
228827	cg12250645	40669385	40669385	0.5870113	0	1	0.7027532	26.53782
228873	cg12253071	71659403	71659403	0.41829	0	1	0.6022834	52.68311
228928	cg12255897	74711503	74711503	0.2768776	0	1	0.1605894	-33.50395
228969	cg12258179	15655389	20620474	0.5928235	0	1	0.4618432	-28.78673
228992	cg12259892	53781503	53781503	0.518872	0	1	0.6353485	24.44138
229112	cg12269972	43644410	43644410	0.3815855	0	1	0.2302317	-42.85474
229134	cg12271317	10739502	10739502	0.5300159	0	1	0.6900672	44.39683
229254	cg12279734	32767338	32767338	0.3943494	0	1	0.7424559	374.3439
229492	cg12296550	28660318	28660318	0.5874946	0	1	0.6982366	24.53968
229515	cg12297590	50692476	66741323	0.6067707	0	1	0.4938032	-22.69405
229631	cg12303318	36649384	36649384	0.1319913	0	1	0.2882963	58.42113
229642	cg12303813	51607504	51607504	0.3352495	0	1	0.4517303	24.11384
229687	cg12307373	49606365	49606365	0.5745502	0	1	0.6944543	27.68917
229736	cg12310025	72708489	39781349	0.6523412	0	1	0.1856884	-371.3336
229777	cg12312457	30631400	39730423	0.3335862	0	1	0.2012448	-36.65305
229880	cg12321669	29698322	29698322	0.8634787	0	1	0.6432385	-114.5984
230113	cg12341429	16642311	16642311	0.6385858	0	1	0.8608939	115.2316
230121	cg12342501	18752444	18752444	0.6483566	0	1	0.8546035	100.3088
230361	cg12360046	70788465	42634485	0.2757527	0	1	0.3880798	24.36982
230389	cg12361987	14683391	14683391	0.4895566	0	1	0.6005669	21.96326
230493	cg12370174	58620371	58620371	0.4554617	0	1	0.6356357	51.59139
230601	cg12377816	55643407	55643407	0.1596576	0	1	0.3013085	45.74591
230680	cg12383699	64618426	60658391	0.3554719	0	1	0.243134	-25.77213
230727	cg12386614	42678409	42678409	0.2089041	0	1	0.6983482	374.3439
230753	cg12388523	15780459	15780459	0.4250042	0	1	0.2337547	-63.37432
230803	cg12391372	17745430	17745430	0.0444328	0	1	0.4683039	374.3439
230805	cg12391576	47783490	47783490	0.8604262	0	1	0.9612546	69.82124
230820	cg12392475	67717362	45613312	0.6544989	0	1	0.5539746	-19.72447
230876	cg12395823	42695344	11610410	0.679946	0	1	0.7893981	29.95971
230961	cg12400864	67609391	67609391	0.765239	0	1	0.6404853	-34.27985
230984	cg12401953	23721353	23721353	0.5322771	0	1	0.6386269	21.17458
231001	cg12403162	37764433	37764433	0.0980902	0	1	0.2093853	39.9729
231072	cg12406683	39642444	39642444	0.4649148	0	1	0.6212908	39.72307
231137	cg12410980	63628360	74804390	0.8181513	0	1	0.9327269	64.89903
231169	cg12412775	64764403	64764403	0.2373906	0	1	0.4105788	53.08447
231244	cg12417704	50725348	50627440	0.8173519	0	1	0.6658628	-54.42774

231254	cg12418043	15670433	15670433	0.2431093	0	1	0.3437491	21.68545
231277	cg12419383	38641411	13767478	0.4978532	0	1	0.3972379	-18.36427
231291	cg12420107	64652348	45732372	0.4109531	0	1	0.2727539	-34.32194
231303	cg12421087	74634484	74634484	0.7604606	0	1	0.9074767	77.42461
231326	cg12422539	12612468	29704333	0.5179629	0	1	0.6632922	36.39559
231390	cg12425861	52664318	52664318	0.0629725	0	1	0.1797269	51.40348
231416	cg12427162	57684372	27774501	0.3194048	0	1	0.4341889	23.88989
231465	cg12430776	11781506	11781506	0.2257702	0	1	0.0836729	-61.42344
231503	cg12432807	10741417	10741417	0.6342942	0	1	0.8339296	88.88631
231545	cg12434889	20673311	20673311	0.1861326	0	1	0.2979376	29.20927
231546	cg12434897	20616326	20616326	0.871666	0	1	0.6288278	-137.207
231681	cg12442246	17757417	65807459	0.3508424	0	1	0.095214	-143.543
231728	cg12444845	39719478	59656491		0	1		-4.34E-09
231825	cg12450016	26697303	26697303	0.5021087	0	1	0.6642054	43.92389
231887	cg12453623	64643493	64643493	0.4141798	0	1	0.5524747	31.2623
231896	cg12454169	55636429	55636429	0.8174929	0	1	0.497235	-190.3397
231995	cg12460133	47668470	56640492	0.5295671	0	1	0.4190632	-21.32851
232135	cg12468774	65744355	33762399	0.182422	0	1	0.0311707	-89.02635
232142	cg12469471	44602352	24782322	0.3438418	0	1	0.149825	-78.03783
232282	cg12478185	24720423	24720423	0.2547732	0	1	0.374206	27.82075
232290	cg12478440	51764498	72769417	0.8481046	0	1	0.6114407	-122.032
232362	cg12483005	53609398	53609398	0.4711101	0	1	0.5909411	24.76773
232413	cg12485185	37798323	33742393	0.5410249	0	1	0.4145313	-26.78573
232562	cg12493761	15634478	15634478	0.3206894	0	1	0.4260614	20.78679
232569	cg12494208	61705307	61705307	0.5691471	0	1	0.7225373	43.57268
232677	cg12500300	19792426	19792426	0.3302423	0	1	0.5285039	61.0834
232697	cg12501287	16765481	16765481	0.6525944	0	1	0.4227051	-81.99045
232701	cg12501761	15663356	10749417	0.7574485	0	1	0.6562065	-24.23962
232769	cg12505085	33715503	33715503	0.8734401	0	1	0.7489312	-50.9059
232868	cg12510999	50637410	50637410	0.5605531	0	1	0.6981315	34.86389
232939	cg12515659	21610491	21610491	0.458475	0	1	0.8401865	374.3439
233052	cg12523974	10612336	69641414	0.231195	0	1	0.1102482	-42.87266
233093	cg12526298	62624444	62624444		0	1		-4.34E-09
233192	cg12532095	51755472	51755472	0.377305	0	1	0.4950498	23.91628
233267	cg12537003	60713304	60713304	0.2052492	0	1	0.3113556	25.60782
233309	cg12539415	58609470	58609470	0.9002162	0	1	0.7997731	-43.35353
233388	cg12546355	61744370	67790412	0.5637949	0	1	0.4237195	-32.00613
233420	cg12548176	37622434	37622434	0.3010996	0	1	0.4311589	29.91558
233559	cg12556569	63705396	63705396	0.2354085	0	1	0.0740663	-77.42553
233645	cg12562822	25616402	66711311	0.6710239	0	1	0.4630792	-68.93953
233655	cg12563520	59700446	59700446	0.6180523	0	1	0.7206977	22.72734
233702	cg12565788	36716357	36716357	0.3064352	0	1	0.4096504	20.43506
233758	cg12569880	11794464	11794464	0.8452786	0	1	0.577348	-148.3084

233796	cg1257266	21613381	21613381	0.1554521	0	1	0.2671196	32.00587
233921	cg1258089	61808327	61808327	0.331181	0	1	0.1955642	-38.65339
233929	cg1258129	29693368	29693368	0.2487326	0	1	0.3505445	21.84284
234009	cg1258496	55799317	55799317	0.701965	0	1	0.5771188	-29.93514
234032	cg1258638	21646472	10807359	0.608285	0	1	0.5066509	-19.15657
234136	cg1259166	67703325	67703325	0.6352931	0	1	0.7802215	45.3097
234147	cg1259236	57675375	57675375	0.0795845	0	1	0.1933029	45.20319
234163	cg1259322	33788324	33788324	0.3788313	0	1	0.4916551	22.27168
234254	cg1259761	30728473	30728473	0.7808426	0	1	0.6633936	-32.56305
234321	cg1260053	13627485	13627485	0.3240187	0	1	0.4368273	23.12035
234419	cg1260669	62677356	62677356	0.1670757	0	1	0.3070486	43.90762
234531	cg1261240	42723447	42723447	0.6132676	0	1	0.7173205	23.05624
234644	cg1261827	44631474	44631474	0.1946709	0	1	0.298601	25.48338
234647	cg1261858	12792490	12792490	0.6524761	0	1	0.7715274	32.38957
234669	cg1261974	24654347	24654347	0.4721056	0	1	0.8392389	374.3439
234715	cg1262265	12675381	12675381	0.9437426	0	1	0.6319389	-257.1492
234729	cg1262314	27656419	73632474	0.4473141	0	1	0.3422014	-20.29995
234902	cg1263315	50649400	56766334	0.0738524	0	1	0.3824774	374.3439
234933	cg1263512	15798509	15798509	0.3843247	0	1	0.5250856	32.32751
234959	cg1263649	66659489	66659489	0.3902459	0	1	0.4915746	18.61574
234975	cg1263744	60623484	60623484	0.1565736	0	1	0.2615962	29.02588
235061	cg1264271	36748372	17689406	0.8883985	0	1	0.7500029	-64.07191
235295	cg1265576	18755483	18755483	0.6627605	0	1	0.7978751	42.69756
235305	cg12656291	44615392	44615392	0.3949992	0	1	0.5099523	22.84931
235333	cg1265741	36650391	36650391	0.2484756	0	1	0.4137904	48.14706
235352	cg1265892	68601326	68601326	0.6225815	0	1	0.7304665	25.08078
235519	cg1266852	10768401	37791311	0.175063	0	1	0.2804157	27.50661
235561	cg1267163	66621406	66621406	0.3890637	0	1	0.6626118	116.0225
235600	cg1267558	45738312	45738312	0.4670207	0	1	0.336539	-29.07903
235672	cg1268140	16744343	16744343	0.1858859	0	1	0.2892313	25.87789
235719	cg1268405	63666330	69645424	0.6252205	0	1	0.504581	-25.64703
235728	cg1268495	25719432	25719432	0.2632972	0	1	0.3928087	31.28075
235859	cg1269206	19807430	19807430	0.2921481	0	1	0.4181414	28.69495
235921	cg1269733	32605374	18611433	0.6735914	0	1	0.5009858	-49.52338
235934	cg1269862	45734417	45734417	0.4273204	0	1	0.543625	23.23575
236166	cg1271528	56624398	17604473	0.5683655	0	1	0.4555622	-22.19448
236206	cg1271858	59674465	59674465	0.1356094	0	1	0.2415288	31.68273
236220	cg1271984	69677404	69677404	0.1919239	0	1	0.3152707	33.5469
236221	cg1271990	20778318	20778318	0.6147985	0	1	0.7347751	29.94304
236321	cg1272736	60634435	60634435	0.9010549	0	1	0.5246919	-305.8616
236333	cg1272794	67795441	67795441	0.1491573	0	1	0.2598146	32.24471
236469	cg1273687	10770349	50650477	0.204291	0	1	0.3450457	40.18801
236587	cg1274341	66736391	66736391	0.6779101	0	1	0.4572176	-77.44901

236679	cg1274889	17670473	47654449	0.0883348	0	1	0.192641	38.08446
236988	cg1277042	38801326	38801326	0.7651343	0	1	0.5603232	-77.33035
237042	cg1277522	27621489	27621489	0.8378477	0	1	0.6912586	-55.66658
237371	cg1279815	24768440	62638473	0.3104047	0	1	0.1926187	-31.13832
237569	cg1280776	26801402	26801402	0.3740569	0	1	0.4878676	22.64019
237682	cg1281376	16676310	16676310	0.4448159	0	1	0.3321611	-22.89616
237692	cg1281411	53619503	69695446	0.3899815	0	1	0.6073291	72.22063
237764	cg1281953	19709454	19709454	0.2027446	0	1	0.5539941	374.3439
237877	cg1282904	29706324	29706324	0.1842989	0	1	0.3769988	70.70338
237950	cg1283368	69732368	69732368	0.8507268	0	1	0.5553244	-177.432
238100	cg1284432	17775456	17775456	0.4500162	0	1	0.5551679	19.70662
238137	cg1284665	31662374	31662374	0.3302405	0	1	0.4362056	20.77906
238198	cg1285037	41671327	30766302	0.4789055	0	1	0.3266447	-38.13328
238199	cg1285039	62624375	62624375	0.822189	0	1	0.7003076	-39.53596
238254	cg1285442	17691497	17691497	0.5011985	0	1	0.6288797	28.26541
238257	cg1285461	51755382	51755382	0.408858	0	1	0.5240834	22.88312
238286	cg1285652	38625322	38625322	0.2615845	0	1	0.4380583	52.83631
238317	cg1285816	24803314	24803314	0.2578575	0	1	0.67059	374.3439
238327	cg1285857	48618427	35705303	0.5790612	0	1	0.4334181	-34.37719
238412	cg1286502	19674471	19674471	0.424895	0	1	0.6315171	66.18296
238456	cg1286772	65606362	65606362	0.2740432	0	1	0.4263207	40.32127
238464	cg1286806	39648318	39735482	0.1729416	0	1	0.0458944	-64.07825
238465	cg1286817	42635367	30607507	0.2266878	0	1	0.0911066	-55.35735
238482	cg1286909	41744326	41744326	0.9328297	0	1	0.8327449	-54.16114
238502	cg1287021	72752369	72752369	0.9160991	0	1	0.6953551	-142.0941
238648	cg1288009	59650300	64739460	0.8581001	0	1	0.7286758	-50.14249
238800	cg1289075	49745331	28793481	0.4633369	0	1	0.3191287	-34.94659
238848	cg1289437	26658403	26658403	0.4291601	0	1	0.5354218	19.99329
239038	cg1290638	62636340	14765369	0.6773036	0	1	0.5474749	-30.70189
239202	cg1291658	58790404	62624315	0.1312605	0	1	0.2896021	59.76602
239354	cg1292764	68672507	24708479	0.9037697	0	1	0.7642641	-70.45378
239477	cg1293488	11642389	68758402	0.194939	0	1	0.0906306	-37.65064
239508	cg1293699	52695442	52695442	0.6925316	0	1	0.8353965	53.01299
239518	cg1293741	65750346	65750346	0.1827579	0	1	0.2892069	27.32714
239552	cg1293942	61804397	16640327	0.8230531	0	1	0.7099686	-35.37945
239677	cg1294713	68707481	68707481	0.2015841	0	1	0.3289842	34.46176
239799	cg1295530	69802385	69802385	0.8857693	0	1	0.7829531	-41.13615
239807	cg1295578	26792344	56703446	0.6833653	0	1	0.5333623	-39.39597
239910	cg1296442	62633339	62633339	0.3884577	0	1	0.5181441	28.04102
240032	cg1297270	51653422	51653422	0.3839129	0	1	0.5149442	28.57364
240161	cg1298054	66767338	66767338	0.6198227	0	1	0.7344789	27.84657
240178	cg1298157	28711442	28711442	0.3982684	0	1	0.5218071	25.76571
240379	cg1299500	21612374	21612374	0.3028207	0	1	0.4154733	23.60378

240425	cg12999084	57650306	57650306	0.3265461	0	1	0.4346171	21.52066
240430	cg12999267	39645503	39645503	0.4426917	0	1	0.5430561	18.23011
240485	cg13002506	34656427	34656427	0.6148694	0	1	0.7243883	25.34867
240510	cg13004509	43734355	12744437	0.077142	0	1	0.177571	38.21029
240562	cg13008339	67763423	67763423	0.1175546	0	1	0.298102	76.95275
240584	cg13009819	15796314	15796314	0.4901381	0	1	0.6058751	23.5974
240602	cg13010797	65732385	65732385	0.2023934	0	1	0.0673648	-61.83634
240605	cg13011003	65677367	65677367	0.7319189	0	1	0.841349	36.23831
240700	cg13017022	52689403	52689403	0.6346708	0	1	0.4963047	-32.51705
240710	cg13017929	74607403	74607403	0.5610073	0	1	0.7873926	96.40231
240733	cg13019553	20649506	58748301	0.0878536	0	1	0.2293449	59.863
240773	cg13022534	29702360	29702360	0.3207839	0	1	0.424296	20.2031
240779	cg13022905	74729492	42717468	0.8000829	0	1	0.692127	-30.36595
240807	cg13024511	48753301	14609420	0.9305454	0	1	0.7328062	-131.4557
240902	cg13031029	61688421	61688421	0.5402336	0	1	0.6475101	21.68321
240943	cg13033858	18605367	18605367	0.600883	0	1	0.7300901	33.38311
240994	cg13037245	43731416	43731416	0.1780646	0	1	0.3150239	41.11062
241101	cg13045351	23605470	23605470	0.5015422	0	1	0.381022	-24.82855
241118	cg13046608	18809380	18809380	0.2076392	0	1	0.4078858	71.88676
241126	cg13047157	42694384	42694384	0.3725342	0	1	0.2117337	-49.17806
241136	cg13047869	40640376	68808498	0.8200174	0	1	0.6077039	-94.10555
241224	cg13052638	49751453	49751453	0.6476868	0	1	0.761356	29.31162
241260	cg13054358	18653470	18653470	0.2913803	0	1	0.4068471	24.91786
241311	cg13058453	46747447	46747447	0.3834266	0	1	0.5101224	26.98696
241318	cg13058819	20716341	15736324	0.6132072	0	1	0.4779482	-30.76564
241357	cg13061469	31625467	31625467	0.3500343	0	1	0.4642403	23.08529
241440	cg13066461	74730398	74730398	0.5886862	0	1	0.7970328	85.72559
241466	cg13067635	73615343	73615343	0.4289751	0	1	0.5303132	18.49901
241472	cg13067974	72755340	72755340	0.6177325	0	1	0.9060673	374.3439
241520	cg13071508	74728372	74728372	0.7485004	0	1	0.953283	156.5356
241606	cg13076785	63802308	63802308	0.8379873	0	1	0.7371871	-31.58792
241639	cg13078381	67681305	10652505	0.4138924	0	1	0.2926397	-26.93168
241645	cg13078798	67702356	67702356	0.448294	0	1	0.2861601	-44.2113
241680	cg13080565	34620490	68688337	0.5383705	0	1	0.3717897	-43.71228
241697	cg13081498	62689375	62689375	0.4816394	0	1	0.3655651	-23.48548
241974	cg13099429	10639300	10639300	0.5025279	0	1	0.37742	-26.47146
241989	cg13100190	73796403	73796403	0.7368536	0	1	0.6069959	-34.1421
242154	cg13112404	69686420	49608353	0.824861	0	1	0.6909717	-46.12651
242348	cg13127920	14629366	14629366	0.820268	0	1	0.6605777	-59.70412
242437	cg13134448	35631470	35631470	0.0841207	0	1	0.3074593	120.5619
242497	cg13137809	60688366	70753505	0.5851917	0	1	0.3149155	-112.2526
242501	cg13138089	10675383	71751402	0.3046832	0	1	0.4264278	26.71846
242553	cg13142134	40624323	40624323	0.6875776	0	1	0.4936472	-61.85572

242742	cg13153708	41729481	41729481	0.1620166	0	1	0.2637346	27.15123
242844	cg13160852	56732304	56732304	0.1869043	0	1	0.5741636	374.3439
242947	cg13168042	44665366	48645411	0.3692113	0	1	0.2675754	-21.07175
242963	cg13168698	54790415	54790415	0.676715	0	1	0.7877169	30.45659
242973	cg13169132	28732384	17730383	0.6769601	0	1	0.5101209	-46.86648
242974	cg13169221	50629351	50629351	0.4567163	0	1	0.5801847	25.90859
243016	cg13171679	34693303	34693303	0.5349425	0	1	0.663837	29.79998
243045	cg13173392	72711319	72711319	0.6115093	0	1	0.712408	21.76206
243135	cg13178597	38711495	38711495	0.4566972	0	1	0.5637735	20.34567
243217	cg13183651	24757360	24757360	0.6595852	0	1	0.8720126	111.849
243229	cg13184448	30610477	30610477	0.6373649	0	1	0.771579	39.15033
243250	cg13185413	68665427	33656307	0.0418245	0	1	0.2591177	137.6707
243256	cg13185984	11653303	11653303	0.7248683	0	1	0.8369176	36.85909
243552	cg13205528	18746348	18746348	0.3223837	0	1	0.1977947	-33.57412
243586	cg13207326	65656400	58709472	0.4376158	0	1	0.3182116	-25.50939
243666	cg13211008	13615312	13615312	0.6626372	0	1	0.7652709	25.27894
243700	cg13213536	20774335	20774335	0.6601167	0	1	0.8046049	48.46562
243802	cg13219409	51703337	51703337	0.8864864	0	1	0.7298713	-75.86552
243805	cg13219552	30733342	30733342	0.4512776	0	1	0.5818401	28.49384
243848	cg13221924	60630370	60630370	0.5352118	0	1	0.659956	28.10087
243913	cg13225565	53699406	53630336	0.500696	0	1	0.6032282	19.35503
244002	cg13230208	39736499	39736499	0.5028976	0	1	0.3912541	-21.79306
244024	cg13232075	48807345	48807345	0.1999595	0	1	0.3888256	66.04156
244067	cg13235098	55804302	55804302	0.5837803	0	1	0.7163266	33.85787
244114	cg13238479	24692327	24692327	0.5156854	0	1	0.6503743	31.56018
244414	cg13257498	39804309	39804309	0.1733861	0	1	0.2748803	26.10817
244419	cg13257690	17725308	48652391	0.2158021	0	1	0.321913	24.96747
244500	cg13263323	60798335	60798335	0.7537975	0	1	0.8834415	56.81323
244533	cg13264811	66687414	66687414	0.5061541	0	1	0.7496372	101.8276
244597	cg13270055	61675434	61675434	0.4827353	0	1	0.3316756	-37.47223
244677	cg13275129	67743403	67743403	0.6405745	0	1	0.4957344	-35.33458
244777	cg13280524	13644367	13644367		0	1	0.6855243	4.34E-09
244827	cg13283952	28728410	21693303	0.2244088	0	1	0.1173206	-34.65089
244977	cg13293488	10679379	45674507	0.3751965	0	1	0.4837176	20.93094
245005	cg13295089	59763340	59763340	0.6275535	0	1	0.7278925	22.2757
245191	cg13305444	22750457	22750457	0.2002576	0	1	0.4274304	90.86579
245202	cg13306087	31664352	31664352	0.7794716	0	1	0.6725878	-28.02226
245209	cg13306815	19670468	19670468	0.692622	0	1	0.8432845	59.28519
245282	cg13312387	71734364	71734364	0.1451826	0	1	0.2808894	44.79698
245333	cg13315147	44686337	44686337	0.3344813	0	1	0.4546334	25.39142
245347	cg13316054	34636377	34636377	0.2041236	0	1	0.318793	28.99088
245373	cg13316813	32773489	32773489	0.2058591	0	1	0.0530169	-79.64192
245424	cg13319761	44669307	44669307	0.8777326	0	1	0.6065354	-166.4706

245459	cg1332110	71768423	71768423	0.3539111	0	1	0.4588709	20.07572
245507	cg1332387	43608313	10720370	0.8962931	0	1	0.7939833	-43.44407
245582	cg13327911	12684348	12684348	0.5919544	0	1	0.7789523	68.4354
245588	cg1332820	57655330	42684337	0.4706749	0	1	0.5897218	24.48362
245615	cg1333086	17795352	20737304		0	1	0.2473243	4.34E-09
245644	cg1333214	37674436	37674436	0.6508198	0	1	0.7590081	26.97124
245766	cg1333894	36617380	36617380	0.4346221	0	1	0.602437	44.56366
245791	cg1334089	15707495	15707495	0.8783576	0	1	0.7709628	-42.06691
245900	cg1334739	46672501	46672501	0.8306066	0	1	0.9389238	63.13958
245962	cg1335186	43675447	43675447	0.5000463	0	1	0.6067606	20.69108
245999	cg1335371	46781383	46781383	0.5884622	0	1	0.3811899	-65.731
246041	cg1335625	42751506	57649361	0.2877034	0	1	0.4071747	26.46122
246055	cg1335689	63763425	15707487	0.3943298	0	1	0.2667271	-30.36616
246100	cg1335999	29763477	29763477	0.4625971	0	1	0.7149005	103.5306
246101	cg1336000	73724421	73724421	0.4714031	0	1	0.5770193	19.99574
246206	cg1336540	61745505	61745505	0.528227	0	1	0.6413038	23.43654
246233	cg1336677	45710478	45710478	0.3664874	0	1	0.4858359	24.58109
246236	cg1336686	62607382	62607382	0.4858223	0	1	0.5976356	22.1815
246251	cg1336788	35644510	35644510	0.2835798	0	1	0.1620688	-35.69932
246398	cg1337546	62719409	62719409	0.2582768	0	1	0.3641994	22.8422
246434	cg1337696	31640450	30715301	0.7026455	0	1	0.3700519	-178.0362
246441	cg1337726	17690478	17690478	0.2983812	0	1	0.1882675	-28.35768
246505	cg1338089	56660355	56660355	0.7716054	0	1	0.5497401	-89.96902
246509	cg1338111	20648364	20648364	0.3611884	0	1	0.4857099	26.45777
246689	cg1339107	54702388	63745430	0.6398894	0	1	0.5395279	-19.33848
246896	cg1340024	41720443	41720443	0.4257692	0	1	0.5460528	24.59284
246935	cg1340189	47792379	39659478	0.0424393	0	1	0.3821086	374.3439
247049	cg1340802	50619367	50619367	0.4263614	0	1	0.539596	22.21444
247110	cg1341128	25692487	25692487	0.4181468	0	1	0.5414911	25.65726
247156	cg1341371	32644368	32644368	0.6982208	0	1	0.8153481	36.28014
247180	cg1341507	12740426	12740426	0.6437503	0	1	0.7600432	30.27494
247391	cg1342596	30702347	30702347	0.3943378	0	1	0.4980367	19.29848
247496	cg1343067	64741438	64741438	0.7082282	0	1	0.8224811	35.8595
247522	cg1343168	48649402	48649402	0.7551338	0	1	0.2579772	-371.3336
247610	cg1343513	39755502	39755502	0.9036121	0	1	0.6975042	-121.9278
247711	cg1343994	16700406	15807510	0.6716674	0	1	0.7728276	25.25323
247733	cg1344110	25778496	25778496	0.8066393	0	1	0.9144312	52.49877
247897	cg1344729	62628313	49742397	0.7935605	0	1	0.6898898	-27.93454
247915	cg1344819	43789481	12730440	0.1864866	0	1	0.0693413	-49.84581
248015	cg1345281	44787453	44787453	0.3520457	0	1	0.6197797	109.6641
248049	cg1345422	19696331	19696331	0.425963	0	1	0.5381626	21.87603
248112	cg1345752	24638403	24638403	0.584585	0	1	0.7059832	28.81442
248122	cg1345800	27735482	36709474	0.7316374	0	1	0.6297396	-23.00321

248228	cg1346255	37731366	37731366	0.8094186	0	1	0.5189734	-156.6134
248335	cg1346691	38778399	38778399	0.5680251	0	1	0.6785354	23.69089
248369	cg1346821	41673352	41673352	0.5238411	0	1	0.6451255	26.37841
248443	cg1347118	18756308	18756308	0.3466837	0	1	0.5041823	39.93119
248445	cg1347125	29732479	29732479	0.6509331	0	1	0.7594452	27.12782
248454	cg1347173	39803450	39803450	0.6435589	0	1	0.7467491	24.29784
248508	cg1347426	52638466	52638466	0.715217	0	1	0.9308317	147.5047
248718	cg1348460	20602304	57658429	0.3057357	0	1	0.4166789	22.95046
248853	cg1349023	64762462	64762462	0.3391007	0	1	0.4951569	39.46295
249012	cg1349675	61637457	61637457	0.928196	0	1	0.8202918	-57.90193
249048	cg1349875	39792356	49742459	0.4447905	0	1	0.2041763	-99.99402
249113	cg1350190	35694441	35694441	0.4199907	0	1	0.316563	-20.26728
249199	cg13506281	66615479	66615479	0.9358892	0	1	0.8158821	-70.64651
249230	cg1350789	13644391	13644391		0	1		-4.34E-09
249411	cg1351836	12695312	12695312	0.6191549	0	1	0.4642755	-39.00537
249462	cg1352053	38730337	33620350	0.8663632	0	1	0.7172652	-64.25539
249466	cg1352077	57808455	57808455	0.3721836	0	1	0.5444163	46.44032
249500	cg13521941	14787487	14787487	0.1161373	0	1	0.2356167	41.06459
249547	cg1352371	57794434	57794434	0.2185081	0	1	0.042248	-102.859
249548	cg13523731	66664363	66664363	0.473844	0	1	0.6172462	34.0895
249680	cg1353032	66646497	66646497	0.7936878	0	1	0.9116921	58.48505
249713	cg1353166	29803329	29803329	0.2482448	0	1	0.3873014	36.04713
249847	cg13538571	57745326	57745326	0.3767518	0	1	0.6253238	94.39517
249901	cg1354135	27690439	21763337	0.2660766	0	1	0.3975604	31.92614
249916	cg1354197	25616349	25616349	0.5995367	0	1	0.4978302	-19.05742
250042	cg1354855	46607455	46607455	0.4777049	0	1	0.5987106	25.28197
250092	cg1355107	73747308	73747308	0.5623506	0	1	0.7087646	39.34459
250409	cg1356445	21762471	21762471	0.4761512	0	1	0.5768102	18.50309
250412	cg1356452	11616419	11616419	0.6064156	0	1	0.3686834	-86.08218
250459	cg1356646	63681301	63681301	0.8767838	0	1	0.700201	-86.4728
250549	cg1357089	72672431	72672431	0.4269825	0	1	0.5724057	34.22899
250615	cg1357337	46721383	46721383	0.671468	0	1	0.4502768	-77.31814
250720	cg1357816	67712382	70778385	0.3905179	0	1	0.27957	-23.75786
250772	cg1358028	34644314	34644314	0.2583469	0	1	0.3586069	20.95476
250786	cg1358075	74636371	74636371	0.2432755	0	1	0.3920906	40.68531
250799	cg1358115	64768399	64768399	0.4070688	0	1	0.2912292	-25.05288
250832	cg1358245	41775406	41775406	0.2813849	0	1	0.60901	374.3439
250865	cg1358366	73671306	66714354	0.1112595	0	1	0.2146284	33.73349
250896	cg1358574	49600485	60740487	0.6913523	0	1	0.3598379	-175.723
250908	cg1358645	41752475	41752475	0.3624995	0	1	0.4647694	19.14859
251036	cg13593391	64652509	60798489	0.618108	0	1	0.5167363	-19.23168
251095	cg1359637	59628448	62637351	0.6758426	0	1	0.5693559	-22.24474
251222	cg1360199	39620393	36651379	0.4650169	0	1	0.5857798	25.02557

251249	cg13603318	73652478	73652478	0.2887954	0	1	0.08326	-106.5949
251260	cg13603879	13715484	18624335	0.2717901	0	1	0.1432734	-41.43358
251303	cg13606025	73649470	73649470	0.8551086	0	1	0.7423993	-40.25003
251387	cg13610138	21652347	21652347	0.2715658	0	1	0.3792762	22.94228
251394	cg13610455	51627488	51627488	0.2681685	0	1	0.4120885	36.9691
251515	cg13615998	23611369	70657374	0.5492647	0	1	0.3589099	-56.02069
251549	cg13617603	28731396	28731396	0.5009352	0	1	0.6141092	22.88663
251618	cg13620034	64629354	64629354	0.5550408	0	1	0.6651064	23.09389
251676	cg13622893	18704435	18704435	0.4055986	0	1	0.3001199	-21.3148
251831	cg13631318	47616465	47616465	0.420254	0	1	0.5717996	36.80696
252016	cg13641645	49614330	49614330	0.2836403	0	1	0.4585276	50.59103
252191	cg13649864	13798483	13798483	0.5426722	0	1	0.6427079	19.30005
252217	cg13651207	20695422	20695422	0.7046109	0	1	0.5271402	-54.16187
252233	cg13652008	73691307	73691307	0.2014134	0	1	0.312569	27.79814
252325	cg13655986	25619417	25619417	0.8312378	0	1	0.9450247	70.69141
252438	cg13661648	70649379	70649379	0.2743409	0	1	0.6024499	374.3439
252601	cg13670288	63774398	63803416	0.2389484	0	1	0.3459263	24.05504
252623	cg13671412	15647332	15647332	0.9114727	0	1	0.7889261	-61.55375
252643	cg13672200	45645324	45645324	0.750173	0	1	0.5334108	-82.84312
252657	cg13672736	20690433	10609506	0.9300014	0	1	0.6876105	-172.0215
252921	cg13683939	11708424	11708424	0.6996031	0	1	0.8100316	32.53079
252930	cg13684379	46808320	46808320	0.8080493	0	1	0.934418	74.82985
252950	cg13685349	31701488	31701488	0.9122123	0	1	0.696952	-134.7909
252952	cg13685506	45677454	45677454	0.595244	0	1	0.7241929	32.8773
252982	cg13686739	15614366	15614366	0.2548662	0	1	0.3616341	23.26995
253016	cg13688186	47755386	47755386	0.7375128	0	1	0.6157336	-30.84851
253077	cg13690543	20743482	20743482	0.1031361	0	1	0.2143222	38.99758
253166	cg13694680	73687362	73687362	0.3374357	0	1	0.4375544	18.85917
253239	cg13698168	64769494	64769494	0.1501924	0	1	0.2538731	29.08948
253264	cg13699152	55619346	65658365	0.2108116	0	1	0.1096026	-32.92911
253290	cg13700458	27626458	27626458	0.7954698	0	1	0.9084336	53.89686
253404	cg13706058	10640380	67719307	0.377728	0	1	0.2462045	-33.01966
253433	cg13707567	33610388	33610388	0.2540613	0	1	0.4117617	44.05107
253522	cg13711314	52794450	19687301	0.5782614	0	1	0.7286152	42.63945
253550	cg13713218	57666459	24714498	0.6558367	0	1	0.4809974	-49.71798
253627	cg13716760	12705336	65645460	0.239952	0	1	0.3579205	28.02932
253778	cg13724111	64661376	64661376	0.6528854	0	1	0.8216063	65.39885
253793	cg13724550	73734496	73734496	0.4570354	0	1	0.5777108	24.90958
253804	cg13725087	46769405	46769405	0.7650678	0	1	0.5717542	-70.07537
253867	cg13727946	62699392	62699392	0.2160749	0	1	0.3170114	23.08776
253869	cg13728003	70610397	70610397	0.4544662	0	1	0.5708027	23.37627
253908	cg13729816	60602308	17792313	0.4921111	0	1	0.3362585	-39.44399
254012	cg13735469	40754500	46743332	0.741776	0	1	0.5479232	-67.16181

254066	cg1373872	20662462	20662462	0.5639425	0	1	0.6822518	26.57882
254095	cg1374063	37775382	37775382	0.615212	0	1	0.1968072	-308.6905
254234	cg1374835	14625475	14625475	0.3334559	0	1	0.041722	-210.2102
254252	cg1374911	27651417	15717451	0.3757418	0	1	0.2345371	-37.90046
254265	cg1374954	70725351	59636392	0.2975473	0	1	0.7469212	374.3439
254326	cg1375272	14643338	14643338	0.7078744	0	1	0.4356256	-118.8686
254346	cg1375361	41669312	41669312	0.7122397	0	1	0.8177181	31.19681
254356	cg1375435	66771492	66771492	0.464051	0	1	0.5721828	20.73452
254382	cg1375551	13644358	50618434		0	1		-4.34E-09
254629	cg1376991	50803368	50803368	0.9405962	0	1		-4.34E-09
254666	cg1377179	67666468	63745415	0.0829029	0	1	0.1926989	42.21125
254673	cg1377221	48807457	25694326	0.255552	0	1	0.3693948	25.73024
254690	cg1377330	32769322	32769322	0.7446499	0	1	0.9284402	117.9938
254779	cg1377771	57708408	30628336	0.1977439	0	1	0.0961209	-35.2688
254799	cg1377856	69709303	69709303	0.7887281	0	1	0.6844592	-27.74966
254899	cg13783191	21682334	21682334	0.2519428	0	1	0.3855734	33.54962
255143	cg1379440	41639341	41639341	0.5105354	0	1	0.6444196	31.05069
255213	cg1379746	73751365	73751365	0.5331711	0	1	0.6660002	31.40625
255240	cg1379874	18768427	18768427	0.2027032	0	1	0.3236037	31.62445
255420	cg1380648	44707417	44707417	0.7964861	0	1	0.9436297	97.25165
255450	cg1380803	47649309	47649309	0.2798931	0	1	0.056	-135.0197
255625	cg1381703	67727454	67727454	0.5838038	0	1	0.6863701	21.31187
255699	cg13821051	40694387	40694387	0.6056516	0	1	0.3547856	-95.90824
255789	cg1382528	31738487	31738487	0.7945987	0	1	0.9024069	48.59037
255798	cg1382593	15798480	33600463	0.4250093	0	1	0.3113038	-23.72869
255874	cg1382910	60688420	60688420	0.5662876	0	1	0.7318295	50.37844
255880	cg1382962	59605469	59605469	0.7830966	0	1	0.5782682	-80.51099
255885	cg1382984	55793300	55793300	0.7555031	0	1	0.8736761	47.20859
255896	cg1383061	56803382	37715327	0.746716	0	1	0.9285896	116.4658
256092	cg1384263	66679384	27632433	0.8297709	0	1	0.7077386	-40.76558
256185	cg1384744	17788362	17788362	0.868524	0	1	0.7385201	-52.96652
256382	cg1385721	19772354	19772354	0.5923454	0	1	0.7396476	42.15827
256388	cg1385764	47803479	47803479	0.7780548	0	1	0.5640386	-85.74109
256437	cg13859771	57630509	57630509	0.6940321	0	1	0.8017692	30.44405
256447	cg13860281	15706467	15706467	0.1861625	0	1	0.2956474	28.27049
256562	cg1386626	69686405	30663316	0.5080699	0	1	0.6761523	47.42726
256635	cg1387053	25770477	25770477	0.3084787	0	1	0.4086667	19.44877
256704	cg1387442	52603344	64705354	0.3124393	0	1	0.4500385	32.47624
256712	cg1387475	73714364	10734352	0.9749987	0	1	0.6318512	-327.2581
256778	cg1387791	73751347	73751347	0.1486742	0	1	0.312943	59.85676
256794	cg1387864	29736459	29736459	0.4716889	0	1	0.3698715	-18.93187
256945	cg1388578	52680473	52680473	0.7845245	0	1	0.6159126	-58.53608
257098	cg1389485	52642474	62668499	0.4607156	0	1	0.5773474	23.53156

257112	cg1389565	22740391	22740391	0.2388765	0	1	0.3491512	25.23613
257149	cg1389734	53632377	53632377	0.0729315	0	1	0.2874463	118.3547
257151	cg1389738	15654377	15654377	0.3531185	0	1	0.5479693	58.60798
257223	cg1390077	15714346	48699432	0.2925563	0	1	0.1611993	-40.42974
257257	cg1390264	65734370	23712404	0.8316638	0	1	0.6592568	-69.98885
257311	cg1390529	20689494	20689494	0.6475716	0	1	0.5369359	-22.78345
257437	cg1391078	34779364	34779364	0.0591716	0	1	0.1993037	68.12987
257531	cg1391399	33706467	33706467	0.8667772	0	1	0.6385564	-122.5085
257565	cg1391572	52735355	52735355	0.6344593	0	1	0.4832704	-37.8314
257593	cg1391663	18655427	18655427	0.9367281	0	1	0.8304715	-60.49958
257658	cg1391875	21719430	20681309	0.0304538	0	1	0.1599074	72.56838
257761	cg1392337	59739471	61650427	0.3326574	0	1	0.1701902	-55.26378
257774	cg1392428	58759478	58759478	0.2156843	0	1	0.0822089	-56.40917
257782	cg1392463	48740453	71705427	0.9580324	0	1	0.8197492	-100.1331
257783	cg1392471	44757399	34704415	0.6397325	0	1	0.5160538	-27.08743
257810	cg1392580	54709451	54709451	0.2214627	0	1	0.3351819	27.47685
257843	cg1392750	24795399	24795399	0.1914593	0	1	0.2931058	24.83939
257866	cg1392847	73643338	73643338	0.4266686	0	1	0.3234923	-20.04338
257930	cg1393125	43640424	43640424	0.6613383	0	1	0.8122061	53.16344
258019	cg1393499	53634405	53634405	0.7301214	0	1	0.9317006	135.672
258082	cg1393762	67746374	52673303	0.4360551	0	1	0.3177271	-25.14648
258169	cg1394197	27797357	68657390	0.098831	0	1	0.2237847	47.32819
258195	cg1394333	68725365	68725365	0.347643	0	1	0.2292329	-28.81076
258219	cg1394450	44749313	44749313	0.5585244	0	1	0.6913856	32.56396
258239	cg1394557	18780428	18780428	0.2094133	0	1	0.321803	27.73194
258415	cg1395429	14722349	14722349	0.2860695	0	1	0.391879	21.82577
258610	cg1396561	73643485	73643485	0.3378117	0	1	0.4413115	19.87624
258672	cg1396932	70696502	70696502	0.4818303	0	1	0.5998353	24.26797
258677	cg1396966	59724471	67729467	0.7928274	0	1	0.6837459	-30.12912
258706	cg1397150	63642379	63642379	0.1975126	0	1	0.311347	29.14178
258724	cg1397242	15728324	15728324	0.4083484	0	1	0.5246246	23.23433
258728	cg1397266	29688442	29688442	0.5929356	0	1	0.470963	-25.53613
258774	cg1397456	71763399	56810505	0.4346081	0	1	0.2798745	-41.11744
258907	cg1397958	62695310	62695310	0.3189812	0	1	0.4606567	33.91163
258968	cg1398203	67788333	67788333	0.5042235	0	1	0.7285435	84.92231
259022	cg1398428	74759420	74759420	0.4263038	0	1	0.538715	21.9452
259137	cg1398929	58727359	58727359	0.4013708	0	1	0.2356953	-49.37134
259204	cg1399318	44692337	66773386	0.6638252	0	1	0.5230765	-34.50343
259237	cg1399473	32778500	32778500	0.1224696	0	1	0.4207934	374.3439
259252	cg1399542	31735405	17760352	0.3522932	0	1	0.4786488	27.25398
259289	cg1399692	58622429	58622429	0.2738946	0	1	0.1522579	-36.90876
259368	cg1400102	47714395	23603428	0.2911385	0	1	0.140661	-53.45439
259568	cg1400990	60778356	60778356	0.6359326	0	1	0.7395734	24.04751

259663	cg1401359	15685493	14745503	0.9839626	0	1	0.849817	-120.7767
259709	cg1401550	17614455	17614455	0.1220765	0	1	0.2368886	37.73879
259777	cg1401836	55785372	55785372	0.629591	0	1	0.7437955	28.26766
259845	cg1402117	63800497	63800497	0.106532	0	1	0.2110997	35.04827
259944	cg1402489	14639392	39722331	0.6093548	0	1	0.4829298	-27.38358
259968	cg1402610	56747341	56747341	0.2736718	0	1	0.4056893	31.7756
260111	cg14032261	16779407	16779407	0.3557106	0	1	0.5043125	35.89477
260165	cg1403524	61732499	61732499	0.9164067	0	1	0.8011369	-58.37681
260318	cg1404181	66763350	66763350	0.9510764	0	1	0.841617	-70.69642
260373	cg1404416	13767316	13767316	0.8155226	0	1	0.6688274	-51.43736
260387	cg1404466	49635493	49635493	0.9176259	0	1	0.3760553	-371.3336
260445	cg14047561	13705510	13705510	0.6630851	0	1	0.7931126	39.61281
260524	cg1405223	27659421	50627420	0.1521574	0	1	0.0276802	-70.14994
260558	cg1405427	48704449	48704449	0.6608447	0	1	0.7672736	26.88387
260574	cg1405500	23702406	23702406	0.5236322	0	1	0.6332124	22.09252
260600	cg1405684	70781354	70781354	0.6467785	0	1	0.8870775	142.5562
260670	cg1405983	34704426	34704426	0.280655	0	1	0.3874784	22.33198
260678	cg1406011	10718499	11806350	0.4312769	0	1	0.1768906	-116.1201
260779	cg1406552	69708390	69708390	0.3259925	0	1	0.2011556	-33.39984
260780	cg1406559	62675467	62675467	0.8109962	0	1	0.7104761	-28.29507
260813	cg1406752	50729438	50729438	0.3099527	0	1	0.4224599	23.36083
260826	cg1406818	49793437	49793437	0.6106209	0	1	0.2672452	-189.499
260834	cg1406878	35601496	35601496	0.1513634	0	1	0.2646067	33.15538
260991	cg1407545	74698433	10612313	0.1729188	0	1	0.0578438	-51.87217
261071	cg1407935	32652312	66804337	0.5306846	0	1	0.4244938	-19.96951
261073	cg1407946	47692328	47692328	0.810434	0	1	0.6040344	-87.45534
261121	cg1408166	28661448	28661448	0.1500588	0	1	0.266929	34.95728
261209	cg1408560	28693342	52792431	0.8027155	0	1	0.6699349	-42.19168
261249	cg1408741	64747435	64747435	0.3658754	0	1	0.4663019	18.56172
261281	cg1408904	16772482	16772482	0.7406406	0	1	0.8601296	44.93333
261283	cg1408910	36734471	36734471	0.355047	0	1	0.5326576	49.35351
261285	cg1408926	67756328	26777382	0.5688228	0	1	0.4470324	-25.22038
261368	cg1409299	42766372	42766372	0.5474284	0	1	0.4339606	-22.30572
261454	cg1409618	47710489	47710489	0.2614264	0	1	0.3913613	31.54252
261539	cg1410055	42714442	42714442	0.9048905	0	1	0.7214196	-104.0802
261621	cg1410470	24740407	24740407	0.8024318	0	1	0.4435572	-231.3076
261631	cg1410553	23766507	23766507	0.713701	0	1	0.8221337	33.07725
261636	cg14105781	54737451	54737451	0.2314495	0	1	0.0798923	-68.74492
261656	cg1410668	47642418	64766423	0.8558267	0	1	0.7541685	-34.6504
261688	cg1410856	29795429	13648308	0.5194591	0	1	0.3121332	-67.08037
261715	cg1411016	56687339	56687339	0.5612291	0	1	0.7936675	102.3236
261827	cg1411633	41652368	54719324	0.4961128	0	1	0.3688246	-27.35093
261840	cg1411676	30664401	39692389	0.1133416	0	1	0.0046312	-70.10843

261943	cg1412174	40715491	40715491	0.1777438	0	1	0.2796037	25.91095
261956	cg1412240	36711497	36711497	0.2251973	0	1	0.3701291	40.2873
261966	cg1412303	72770339	72770339	0.7866347	0	1	0.915963	68.21288
262147	cg1413262	19770390	19770390	0.5292098	0	1	0.6369699	21.58824
262159	cg1413310	27738492	27738492	0.4992857	0	1	0.612669	22.93008
262443	cg14148981	52708325	52708325	0.1435245	0	1	0.2579757	34.63021
262487	cg1415106	69684374	69684374	0.3345845	0	1	0.1006271	-122.4931
262515	cg1415246	26803312	26803312	0.568252	0	1	0.7019495	33.47089
262527	cg1415297	61620504	61620504	0.2806014	0	1	0.414321	32.14023
262631	cg1415752	32645447	32645447	0.543829	0	1	0.4120967	-28.72342
262647	cg1415855	49786440	49786440	0.588774	0	1	0.6966582	23.47967
262691	cg1416043	22798367	22798367	0.3733926	0	1	0.4927304	24.49743
262833	cg14166701	59676319	27655364	0.4337101	0	1	0.5640446	28.26036
262843	cg1416703	72735486	72735486	0.7820945	0	1	0.9346978	95.99923
262904	cg14170201	66762308	66762308	0.7185978	0	1	0.8804621	77.34793
262991	cg14174221	12618450	12618450	0.1636856	0	1	0.2663349	27.38311
263044	cg1417708	13644487	13644487		0	1		-4.34E-09
263104	cg1417928	57618362	57618362	0.3343967	0	1	0.1843696	-46.78915
263125	cg1418041	54715503	54715503	0.767092	0	1	0.8763618	42.68726
263233	cg1418495	18710350	18710350	0.6973331	0	1	0.8214221	40.52407
263298	cg1418781	38654363	38654363	0.5584601	0	1	0.4496821	-20.84642
263322	cg1418877	21618351	21618351	0.4084084	0	1	0.2995826	-22.41836
263330	cg1418911	57754348	57754348	0.5151849	0	1	0.6753632	43.59772
263341	cg1418953	16783506	16783506	0.6723546	0	1	0.7743348	25.67949
263353	cg1418978	48730327	48730327	0.3306698	0	1	0.4573836	27.8187
263416	cg1419229	66716342	54642479	0.8873494	0	1	0.7848228	-41.33937
263473	cg1419517	26730510	26730510	0.5760067	0	1	0.6912544	25.84501
263515	cg1419711	18656448	18656448	0.3245684	0	1	0.438543	23.49708
263529	cg14198221	55768438	55768438	0.3897829	0	1	0.5337019	33.56934
263594	cg1420142	33795429	24648384	0.5306402	0	1	0.6984327	48.72123
263660	cg14204081	63639347	63639347	0.2712959	0	1	0.145723	-39.63856
263786	cg1420951	40741482	40741482	0.3863198	0	1	0.533374	34.88596
263865	cg1421203	33638311	33638311	0.3616368	0	1	0.4999461	31.61075
263902	cg1421339	67685329	33758460	0.3490418	0	1	0.2373627	-25.82347
263937	cg1421473	54746417	31784456	0.1514847	0	1	0.0471719	-48.24405
263976	cg1421606	38746430	28745335	0.285497	0	1	0.4133002	29.63058
264165	cg14223671	38743305	38743305	0.3131503	0	1	0.2096144	-24.38812
264229	cg1422732	42669375	42669375	0.4631503	0	1	0.6032661	32.47551
264243	cg1422810	31747469	31747469	0.9070572	0	1	0.5302983	-310.7961
264381	cg1423491	14768483	14768483	0.3825736	0	1	0.4891114	20.24695
264446	cg1423812	69799509	69799509	0.2390862	0	1	0.5567071	374.3439
264480	cg1423965	15745447	15745447	0.3776328	0	1	0.2671524	-24.05542
264504	cg1424079	66778462	66778462	0.1694831	0	1	0.2829944	31.38856

264524	cg1424183	55738497	55738497	0.3668687	0	1	0.4951278	27.72904
264602	cg1424589	56606470	56606470	0.4976738	0	1	0.6039938	20.52704
264731	cg1425223	20612393	20612393	0.7968827	0	1	0.9191704	64.48829
264754	cg1425359	36807492	36807492	0.743337	0	1	0.5565782	-63.18744
264922	cg1426077	44645465	44645465	0.609821	0	1	0.5049901	-20.15322
265033	cg1426623	69689428	36775365	0.6926097	0	1	0.5075383	-57.30016
265105	cg1427000	69655308	36605363	0.8881696	0	1	0.7550253	-60.52542
265130	cg1427102	64732448	64732448	0.5776953	0	1	0.7489324	55.1841
265221	cg1427608	12607466	35645443	0.8452189	0	1	0.6983074	-57.48339
265248	cg1427729	28755433	28755433	0.5799425	0	1	0.7112358	33.02574
265319	cg1428103	65637437	65637437	0.3487586	0	1	0.4591554	21.8626
265384	cg1428364	50728485	50728485	0.3559449	0	1	0.4655093	21.48919
265387	cg1428375	10749446	42607466	0.238556	0	1	0.1326528	-32.03485
265493	cg1428804	27600478	27600478	0.6730114	0	1	0.7806712	28.43786
265544	cg1429007	13604340	13604340	0.4363575	0	1	0.5865431	36.36507
265609	cg1429367	29710310	29710310	0.4512209	0	1	0.8301659	374.3439
265634	cg1429495	42717353	42717353	0.4702838	0	1	0.6706018	64.36662
265635	cg14294971	27708424	27708424	0.7490953	0	1	0.5351524	-80.8025
265768	cg1430213	11677360	11677360	0.2539387	0	1	0.7158458	374.3439
265871	cg1430747	14724497	57715430	0.8528931	0	1	0.7217177	-50.00092
265887	cg14308311	58623424	58623424	0.2662575	0	1	0.3982834	32.13377
265899	cg1430864	38611396	38611396	0.6971207	0	1	0.8769147	88.86023
265938	cg1431087	55658463	55658463	0.4013088	0	1	0.2561323	-38.20879
266063	cg1431662	66809447	66809447	0.2612819	0	1	0.4285937	48.20387
266064	cg1431666	45791404	71766344	0.2851007	0	1	0.4453334	43.37456
266079	cg1431738	74681441	19676415	0.5954162	0	1	0.4903379	-20.02731
266194	cg1432320	16761452	16761452	0.5659432	0	1	0.4502995	-23.11004
266205	cg1432391	22757305	22757305	0.1948483	0	1	0.4408661	105.772
266224	cg1432481	42657509	42657509	0.4435144	0	1	0.3131405	-29.64815
266225	cg1432483	24619461	24619461	0.8175089	0	1	0.9388477	73.27152
266232	cg1432515	62672390	63721444	0.6780618	0	1	0.5421557	-33.14874
266235	cg1432518	27635449	25748318	0.7929899	0	1	0.6823524	-30.80896
266242	cg1432577	50772323	50772323	0.2481602	0	1	0.3512368	22.29229
266324	cg1432978	52733448	52733448	0.7419873	0	1	0.5385836	-73.02491
266327	cg1432988	38785507	32800433	0.6982418	0	1	0.8277644	44.31025
266351	cg1433086	63688403	63688403	0.4330111	0	1	0.5406998	20.44346
266359	cg1433120	35601349	35601349	0.8465849	0	1	0.6915289	-62.7523
266360	cg1433122	36734408	36734408	0.4483927	0	1	0.3032037	-35.90339
266526	cg1433946	37733330	37733330	0.4733411	0	1	0.6213549	36.10343
266549	cg1434046	66713386	66713386	0.3289846	0	1	0.4747267	35.29547
266559	cg1434092	43655507	43655507	0.3803439	0	1	0.2319891	-41.3177
266767	cg1435250	70794396	70794396	0.7082798	0	1	0.5889124	-28.16082
266854	cg1435691	39662411	39662411	0.2757204	0	1	0.3824396	22.46318

266921	cg1436125	20779300	43644329	0.6061346	0	1	0.4458355	-41.13301
267111	cg1437318	54713385	54713385	0.0449579	0	1		-4.34E-09
267246	cg1437856	49632458	49632458	0.3830594	0	1	0.2507172	-33.09151
267367	cg1438441	36707502	36707502	0.7392151	0	1	0.8418161	32.972
267438	cg1438823	21625490	21625490	0.2064538	0	1	0.0946117	-40.93117
267563	cg1439529	46769505	22755310	0.5467375	0	1	0.4197417	-26.97203
267708	cg1440222	60720388	60720388	0.2909254	0	1	0.3958434	21.39062
267822	cg14408831	71685333	71685333	0.693909	0	1	0.9464952	374.3439
267955	cg14414911	28722498	28722498	0.6358953	0	1	0.7518438	29.5163
268024	cg1441778	18609379	17793438	0.6379536	0	1	0.4905938	-36.30626
268096	cg1442071	40655403	40655403	0.8449991	0	1	0.9557542	74.71031
268125	cg1442224	28641377	28641377	0.3304976	0	1	0.4880102	40.33964
268136	cg1442250	64736341	64736341	0.473855	0	1	0.7031047	85.37443
268194	cg1442556	65709411	11727418	0.1914921	0	1	0.3200137	35.84457
268286	cg1442974	38615468	38615468	0.667946	0	1	0.9009311	143.7481
268337	cg1443157	17720381	17720381	0.4349861	0	1	0.5353531	18.21614
268349	cg14432251	73751357	73751357	0.3761774	0	1	0.4962313	24.71392
268389	cg1443475	67710342	67710342	0.6864648	0	1	0.794689	29.945
268402	cg1443555	10673464	18684454	0.6269901	0	1	0.5261468	-19.22838
268436	cg1443744	27759462	27759462	0.2546418	0	1	0.3608009	23.07051
268479	cg1444027	14740455	14740455	0.5337917	0	1	0.6751411	35.25216
268731	cg1445409	25606396	25606396	0.473458	0	1	0.6033274	28.5383
268787	cg1445745	28653324	28653324	0.8591209	0	1	0.9617472	71.71175
268891	cg1446240	22679490	22679490	0.1647421	0	1	0.280854	32.98922
268928	cg1446373	31733355	31733355	0.2282683	0	1	0.0705467	-76.17141
268991	cg1446701	53763328	53763328	0.118191	0	1	0.2240766	33.94419
268998	cg1446741	17628308	17628308	0.4789638	0	1	0.5915698	22.35926
269207	cg1447685	36706322	36706322	0.1048666	0	1	0.3274563	111.6404
269383	cg1448564	74770465	74770465	0.1790819	0	1	0.2809207	25.80062
269523	cg1449309	40603491	40603491	0.8639356	0	1	0.6869424	-82.22099
269603	cg1449764	38770382	38770382	0.6205413	0	1	0.8143981	79.84689
269656	cg1450048	70643436	26786310	0.6805371	0	1	0.5422706	-34.22951
269770	cg1450619	53678387	53678387	0.9054555	0	1	0.7396255	-90.59117
269976	cg1451536	57740498	21692339	0.8579797	0	1	0.7275575	-50.69371
270076	cg1451935	71655353	71655353	0.7077175	0	1	0.8078294	27.8039
270144	cg1452199	11608485	70606468		0	1		-4.34E-09
270156	cg14522441	38809464	64726319	0.6866211	0	1	0.583764	-21.41557
270232	cg1452539	54717343	54717343	0.1845204	0	1	0.3346226	46.80887
270387	cg1453109	48658334	23714502	0.912662	0	1	0.7650406	-80.21509
270462	cg1453498	67687408	15645431	0.2866144	0	1	0.1428361	-49.41331
270473	cg1453533	26651379	56756319	0.2783394	0	1	0.1723521	-27.98993
270735	cg14548901	45722301	45722301	0.3716836	0	1	0.5099393	31.45653
270764	cg1455006	67643448	67643448	0.3907734	0	1	0.2798792	-23.72873

270836	cg14553444	68711481	68711481	0.4240926	0	1	0.5387981	22.69755
270974	cg14559139	59614346	59614346	0.5723448	0	1	0.6943988	28.49276
271065	cg14562786	49608347	49608347	0.8109947	0	1	0.7083575	-29.20248
271201	cg14569423	25733453	25733453	0.4774488	0	1	0.6331053	39.74677
271284	cg14573817	56676465	56676465	0.6541107	0	1	0.5468007	-21.8656
271371	cg14577706	65723423	65723423	0.6727042	0	1	0.7794287	27.95433
271523	cg14583999	21607472	21607472	0.394039	0	1	0.649137	100.2271
271686	cg14592638	33702337	33702337	0.3333814	0	1	0.5600187	78.63268
271789	cg14597862	40691394	40691394	0.4094799	0	1	0.6022761	57.4521
271802	cg14598338	31791482	59746308	0.1382622	0	1	0.2845853	51.57705
271807	cg14598478	54608430	54608430	0.1217972	0	1	0.2846262	64.53538
271933	cg14604474	29608370	29608370	0.3689715	0	1	0.2577577	-24.69578
271936	cg14604522	48802381	62611436	0.6696108	0	1	0.8583446	88.68325
271952	cg14605357	29713486	29713486	0.2104319	0	1	0.3221306	27.39811
272022	cg14608770	49753305	39714411	0.7647989	0	1	0.6523743	-29.07649
272025	cg14609104	52683440	52683440	0.7111526	0	1	0.4837367	-84.96564
272069	cg14611455	52757336	52757336	0.5493169	0	1	0.6822329	32.13997
272155	cg14615266	69601336	40624490	0.3180754	0	1	0.1333303	-75.72861
272275	cg14621900	48627421	48627421	0.7078931	0	1	0.5555239	-41.99105
272339	cg14625636	10802457	10802457	0.7132637	0	1	0.5965301	-27.42793
272392	cg14629010	15711375	15711375	0.6539914	0	1	0.8442137	85.26231
272415	cg14630630	21656316	21656316	0.5739272	0	1	0.6745954	20.32117
272536	cg14636261	25713488	25713488	0.3710389	0	1	0.4955398	26.32363
272655	cg14642338	21795454	21795454	0.345681	0	1	0.4472888	19.17533
272675	cg14643264	24747360	24747360	0.3857371	0	1	0.487446	18.75965
272717	cg14645244	64690436	36600482	0.4349092	0	1	0.2802211	-41.07868
272748	cg14646641	67606429	67606429		0	1		-4.34E-09
272836	cg14651435	32620478	32620478	0.5473084	0	1	0.6630592	24.97389
272887	cg14653593	60626498	60626498	0.3450853	0	1	0.4674776	25.96679
272897	cg14654171	51679367	51679367	0.4736582	0	1	0.6003775	27.33481
273008	cg14659129	74709337	74709337	0.1474755	0	1	0.2540554	30.62715
273011	cg14659346	38621481	24713432	0.2848175	0	1	0.1799087	-26.94019
273017	cg14659662	52679362	47783399	0.3444168	0	1	0.4604881	23.80226
273019	cg14659698	13644387	66685405		0	1		-4.34E-09
273054	cg14661431	51625352	51625352	0.406243	0	1	0.2404309	-49.03829
273155	cg14666908	61604365	61604365	0.3933466	0	1	0.5480171	38.12434
273204	cg14669842	55635406	55635406	0.7717183	0	1	0.6134934	-51.05244
273206	cg14669863	52722450	17619465	0.3018773	0	1	0.4962214	60.00425
273211	cg14670092	72621416	72621416	0.2662963	0	1	0.420764	41.75839
273343	cg14679255	28650444	28650444	0.8410414	0	1	0.6094815	-115.2996
273439	cg14685946	17609450	17609450	0.4925787	0	1	0.6023154	21.57994
273444	cg14686042	23646341	23646341	0.2633644	0	1	0.7407238	374.3439
273463	cg14687298	15679356	67606421	0.3146757	0	1	0.1068815	-99.49695

273487	cg1468866	27700493	27700493	0.1564962	0	1	0.2760212	35.42366
273536	cg1469159	70786483	70786483	0.51829	0	1	0.6278555	21.97361
273625	cg14696601	62721321	62721321	0.5621378	0	1	0.6711928	22.94829
273648	cg1469823	33789329	33789329	0.7754866	0	1	0.8756339	37.44656
273669	cg1469925	45651331	28619402	0.2698505	0	1	0.1675121	-26.92634
273720	cg1470186	39801313	39801313	0.1941851	0	1	0.3395154	43.3592
273761	cg1470412	11634302	11634302	0.5863835	0	1	0.7198893	34.49076
273774	cg1470501	51719320	39673433	0.337536	0	1	0.4919545	38.77923
273832	cg14708411	48720320	40616345	0.4584895	0	1	0.3376932	-25.54982
273874	cg1471085	27638448	27638448	0.8266957	0	1	0.6847706	-50.80645
273883	cg1471124	18781419	18781419	0.231952	0	1	0.0730167	-76.12132
273954	cg1471569	46756442	66644400	0.6013563	0	1	0.8710731	374.3439
273980	cg1471712	16806408	16806408	0.3786618	0	1	0.7879277	374.3439
274187	cg1473146	20687329	20687329	0.6883	0	1	0.847442	65.51565
274249	cg1473608	48721339	48721339	0.8311306	0	1	0.7231991	-34.02399
274293	cg1473880	29643446	29643446	0.7083349	0	1	0.5605668	-39.92296
274317	cg1474097	28727498	28727498	0.5035692	0	1	0.6384467	31.25425
274351	cg1474244	39780473	39780473	0.5183096	0	1	0.6662767	37.65529
274353	cg1474261	14627388	14627388	0.3246969	0	1	0.2131141	-27.18065
274514	cg1475309	44624466	44624466	0.3751697	0	1	0.6023035	78.62325
274602	cg1475852	73712349	73712349	0.4744564	0	1	0.6419047	45.49614
274618	cg1475936	41780443	41780443	0.408395	0	1	0.2866919	-27.30709
274621	cg1475949	14686387	14686387	0.3962163	0	1	0.5225854	26.78535
274971	cg1478013	15659311	15659311	0.4517468	0	1	0.3509602	-18.85319
274979	cg1478046	61629303	19625435	0.2315567	0	1	0.3462225	27.24502
275030	cg1478255	50621445	50621445	0.3441009	0	1	0.1993556	-42.54236
275242	cg1479313	46638458	74760501	0.7636892	0	1	0.6204308	-42.58686
275292	cg1479525	25701421	58790505	0.1527366	0	1	0.0490328	-47.27384
275297	cg1479540	13644342	13644342		0	1	0.9281332	4.34E-09
275332	cg1479714	24788474	24788474	0.5231422	0	1	0.8227758	374.3439
275368	cg1479927	74607488	74607488	0.2125143	0	1	0.4892837	127.9083
275376	cg1479980	62630444	62630444	0.4690977	0	1	0.7479784	130.625
275438	cg1480490	47779475	47779475	0.4515153	0	1	0.6161584	43.36322
275508	cg14811011	62676339	62676339	0.2159809	0	1	0.3240038	25.66261
275509	cg1481101	69627345	69627345	0.2210358	0	1	0.3287652	25.26088
275567	cg14815891	59655461	24684340	0.4217027	0	1	0.5579849	30.48927
275599	cg1481827	46681424	46681424	0.6541591	0	1	0.7761948	34.11446
275602	cg1481841	70770367	70770367	0.5897468	0	1	0.4749664	-23.04998
275604	cg14818621	49708459	49708459	0.2815626	0	1	0.3917637	23.43485
275615	cg1481936	13644372	13644372		0	1		-4.34E-09
275727	cg1482585	17683414	17683414	0.7611327	0	1	0.6251812	-38.8975
275788	cg1482930	40753304	40753304	0.6010907	0	1	0.9093254	374.3439
275831	cg1483139	28714477	25660312	0.3929458	0	1	0.2554406	-34.95807

275847	cg14832352	73681385	73681385	0.1950233	0	1	0.3441515	45.12037
275855	cg14832904	22792504	22792504	0.2442318	0	1	0.3498992	23.35071
275886	cg14834300	36615392	36615392	0.8408129	0	1	0.7068557	-49.07571
275998	cg14839919	46686446	46686446	0.6294982	0	1	0.5291092	-19.13808
276017	cg14840848	42796501	17759429	0.5728108	0	1	0.6751133	20.85779
276233	cg14851460	45778357	45778357	0.4397212	0	1	0.5518877	21.89718
276239	cg14851544	53669497	53669497	0.3103178	0	1	0.4176516	21.65028
276315	cg14855378	58649403	58649403	0.579708	0	1	0.6933854	25.37308
276335	cg14856563	65740428	65740428	0.5975759	0	1	0.7278944	33.69515
276369	cg14858786	33709449	35701323	0.5214626	0	1	0.6234248	19.50259
276388	cg14859874	14694304	14694304	0.502335	0	1	0.3940264	-20.71729
276612	cg14873022	39715368	39715368	0.6401664	0	1	0.7960715	53.2735
276672	cg14877637	70646322	70646322	0.6412477	0	1	0.5384416	-20.11934
276678	cg14877834	28804443	28804443	0.2527637	0	1	0.4534916	67.08424
276757	cg14882966	42626317	31600403	0.1701885	0	1	0.0545772	-53.24293
276767	cg14883605	57691462	57691462	0.2292332	0	1	0.3474859	28.74979
276871	cg14891195	74756405	18734405	0.6263829	0	1	0.5187993	-21.30784
276900	cg14893857	25788482	25788482	0.3533182	0	1	0.2529225	-21.20502
276906	cg14894216	47779456	47779456	0.5179728	0	1	0.6387309	26.01656
276919	cg14895374	64717338	64717338	0.5532839	0	1	0.6617917	22.47474
277013	cg14900909	47622405	73707479	0.7180169	0	1	0.8932858	92.20353
277026	cg14902204	74772470	74772470	0.8792735	0	1	0.7780471	-38.79079
277154	cg14909614	36667507	36667507	0.2387392	0	1	0.3557332	27.72619
277267	cg14915878	47698493	71778502	0.3575494	0	1	0.2241495	-35.26356
277430	cg14926196	35619359	74680402	0.5695794	0	1	0.468958	-18.43505
277438	cg14926485	28731492	28731492	0.8547553	0	1	0.5259745	-215.9837
277455	cg14927745	56710417	64784332	0.7465494	0	1	0.6049225	-40.13873
277538	cg14931776	40692459	40692459	0.4795575	0	1	0.6357683	40.07955
277541	cg14931884	57642487	63670403	0.1957441	0	1	0.2994155	25.31319
277603	cg14936938	67655453	67655453	0.5120274	0	1	0.618138	20.68859
277625	cg14938419	51773359	40665371	0.8585226	0	1	0.7269951	-51.46165
277648	cg14939821	36751420	36751420	0.5560834	0	1	0.7076939	41.62743
277695	cg14943002	49717489	49717489	0.4253058	0	1	0.5307325	19.73394
277717	cg14944696	34806455	34806455	0.6361952	0	1	0.7440438	25.85574
277786	cg14949065	38663360	11652426	0.75594	0	1	0.6168943	-39.82117
277823	cg14951292	68654498	68654498	0.7713868	0	1	0.6702578	-25.13737
277850	cg14953379	73726329	73726329	0.730256	0	1	0.8523908	44.82435
277965	cg14960373	62676503	62676503	0.417033	0	1	0.5222617	19.67949
278121	cg14970273	18770301	18770301	0.636618	0	1	0.5359661	-19.35833
278221	cg14975347	11777315	11777315	0.746446	0	1	0.8485084	33.69691
278251	cg14977018	62660356	62660356	0.5863732	0	1	0.720856	34.9679
278315	cg14981468	30768379	30768379		0	1	0.8627156	4.34E-09
278340	cg14983135	52602503	12660507	0.8425899	0	1	0.7307357	-37.64853

278359	cg14983838	60699371	60699371	0.569271	0	1	0.451207	-23.94499
278371	cg14984341	43800433	55752431	0.5438069	0	1	0.4289097	-22.76761
278416	cg14986890	48640421	48640421	0.5473917	0	1	0.7398703	66.10843
278434	cg14987787	16646398	66768392	0.7820057	0	1	0.6793602	-26.53351
278474	cg14989977	17783337	17783337	0.2168143	0	1	0.3173974	22.92317
278535	cg14992972	21762414	21762414	0.6598659	0	1	0.7725611	29.81541
278624	cg14997132	63806388	63806388	0.4295923	0	1	0.5384129	20.79537
278633	cg14997592	25771491	25771491	0.5796251	0	1	0.4749421	-19.73411
278659	cg14999036	12701332	12701332	0.1852933	0	1	0.2936267	27.87835
278680	cg15000813	67606447	67606447	0.18625	0	1	0.2915319	26.60207
278752	cg15004787	28786454	28786454	0.8119246	0	1	0.925899	61.34002
278806	cg15007959	49757401	55726326	0.3008598	0	1	0.130415	-67.28383
278821	cg15009232	64739341	64739341	0.5148922	0	1	0.6192147	20.15145
278912	cg15014361	14649308	14649308	0.6041504	0	1	0.7647503	51.42089
279008	cg15020568	70810338	64604420	0.3101277	0	1	0.1813745	-36.93263
279047	cg15022609	55620414	19793382	0.5400599	0	1	0.3240196	-71.99827
279085	cg15025200	48763405	22691478	0.2923617	0	1	0.1473418	-49.34667
279140	cg15027721	22689478	22689478	0.314063	0	1	0.4238452	22.35445
279237	cg15033013	39655305	39655305	0.7940681	0	1	0.6172248	-64.91439
279251	cg15033552	74678456	74678456	0.4320931	0	1	0.5686673	30.65847
279423	cg15044146	38798388	38798388	0.9475304	0	1	0.8376011	-69.00249
279432	cg15044573	72727466	72727466	0.3499393	0	1	0.4583301	21.20418
279436	cg15044767	64648420	64648420	0.432609	0	1	0.3195578	-23.30379
279437	cg15044932	49637505	49637505	0.867865	0	1	0.7658162	-36.96303
279568	cg15054873	33754404	33754404	0.261564	0	1	0.3740487	24.98346
279586	cg15055782	61647408	61647408	0.4929564	0	1	0.61119	24.53286
279672	cg15059553	12650335	12650335	0.5477436	0	1	0.4420253	-19.85092
279682	cg15060081	66673325	30638301	0.3174776	0	1	0.4793259	42.7269
279690	cg15060599	73696342	72780487	0.1987519	0	1	0.0955848	-36.15641
279836	cg15068552	56712415	46733418	0.8065151	0	1	0.7054895	-28.05867
279932	cg15074709	39607394	23616423	0.3227798	0	1	0.0530335	-179.6317
280024	cg15079934	32752434	14738451	0.4082618	0	1	0.5240945	23.0865
280034	cg15080433	40634450	40634450	0.7131956	0	1	0.8885154	90.19691
280115	cg15084803	42709321	42709321	0.5044903	0	1	0.7387561	93.30235
280177	cg15087907	41711429	19799359	0.7181204	0	1	0.6129323	-23.48877
280257	cg15092219	41636348	41636348	0.2986402	0	1	0.1969954	-24.4727
280260	cg15092343	24699391	17737346	0.2370926	0	1	0.1219235	-37.93986
280352	cg15098643	37710373	37710373	0.5762125	0	1	0.6775874	20.638
280445	cg15104622	12797491	31705328	0.6809847	0	1	0.7948654	32.40652
280452	cg15105011	18792450	18792450	0.5597843	0	1	0.3881671	-46.04846
280654	cg15116095	69657441	69657441	0.7148057	0	1	0.5998309	-26.85208
280660	cg15116481	63633329	19609360	0.8195281	0	1	0.7096616	-33.41318
280671	cg15117754	27693398	27693398	0.6553584	0	1	0.4872814	-46.35828

280754	cg1512299	56723420	53652348	0.6586772	0	1	0.497493	-43.23799
280946	cg1513229	40628329	40628329	0.743957	0	1	0.8739604	54.37629
281002	cg1513516	56688395	56688395	0.6907663	0	1	0.8131198	38.49052
281007	cg1513528	26780484	26780484	0.1816819	0	1	0.2843361	25.92117
281014	cg1513576	14697311	44624470	0.3313319	0	1	0.4585824	27.99985
281050	cg1513828	48800482	48800482	0.2546221	0	1	0.5066262	101.7301
281129	cg1514269	16736447	23617466	0.8228424	0	1	0.6117935	-93.95747
281165	cg1514517	30645385	73619499	0.1179614	0	1	0.2238124	33.9603
281233	cg1514964	68604460	68604460	0.1448447	0	1	0.2789127	44.00752
281489	cg1516603	14662427	18800399	0.7012739	0	1	0.501335	-66.46135
281583	cg1517179	54705472	54705472	0.6390637	0	1	0.7746951	40.14685
281622	cg1517429	65800308	65800308	0.5614785	0	1	0.4369834	-26.12438
281685	cg1517761	37632356	48713472	0.3964663	0	1	0.2391833	-44.95192
281797	cg1518766	36727374	25731376	0.5057255	0	1	0.6403576	31.21594
281835	cg1519038	54644436	54644436	0.7044578	0	1	0.5778816	-30.74373
281871	cg1519313	25755329	31659427	0.6545675	0	1	0.5307515	-27.57944
281875	cg1519321	24717412	24717412	0.486775	0	1	0.590556	19.57318
281947	cg1519814	12726408	12726408	0.8095459	0	1	0.5737763	-108.9121
281973	cg1519998	18726423	18726423	0.4066938	0	1	0.5188763	21.89257
281974	cg1520000	30605453	30605453	0.1513813	0	1	0.2778662	39.32922
282058	cg1520542	67685347	41726414	0.7156742	0	1	0.6006703	-26.90821
282080	cg1520705	73778471	73778471	0.41982	0	1	0.5342778	22.61425
282225	cg1521534	72600300	65779478	0.2718959	0	1	0.1437625	-41.17289
282261	cg1521922	11753320	16794305		0	1		-4.34E-09
282359	cg1522634	58751381	58751381	0.8864602	0	1	0.6047232	-181.7855
282528	cg1523654	56680387	69765318	0.4647488	0	1	0.3127482	-38.46948
282642	cg1524385	56716505	30775414	0.2118992	0	1	0.099969	-39.96179
282675	cg1524613	37628397	37628397	0.8916965	0	1	0.7859694	-44.30798
282706	cg1524748	68781455	68781455	0.6622935	0	1	0.1068407	-371.3336
282740	cg1524934	35748431	35748431	0.5059884	0	1	0.6184062	22.71676
282756	cg1525063	26733393	16683386	0.1373376	0	1	0.274254	46.65878
282760	cg1525114	39710464	50745432	0.3412436	0	1	0.1582214	-69.31096
282767	cg1525138	43642427	65714457	0.2371556	0	1	0.1077025	-48.01125
282802	cg1525464	56711445	70679503	0.0405843	0	1	0.1596565	60.56231
282828	cg1525638	65765430	65765430	0.3996904	0	1	0.5351008	30.14538
283130	cg1527810	50758462	48714335	0.7365966	0	1	0.6194949	-28.928
283151	cg1527954	46670416	46670416	0.4312818	0	1	0.2621572	-49.04557
283193	cg1528297	10728416	10728416	0.1563554	0	1	0.328844	63.28057
283235	cg1528603	48760415	48760415	0.6565873	0	1	0.7849373	37.87111
283257	cg1528780	47793319	47793319	0.4537552	0	1	0.5703053	23.44373
283289	cg1529031	34647475	24790449	0.9021891	0	1	0.6305247	-181.2075
283310	cg1529209	57607317	57607317	0.4953502	0	1	0.6074794	22.4313
283314	cg1529235	21607304	21607304	0.8493967	0	1	0.6681601	-80.5832

283323	cg15293181	46700503	46700503	0.795612	0	1	0.6955823	-26.63084
283348	cg15295441	37744473	37744473	0.5072793	0	1	0.7067806	66.7029
283381	cg15298323	27651418	27651418	0.333419	0	1	0.2056415	-34.28796
283498	cg15309004	44725368	44725368	0.7400873	0	1	0.8909221	73.46546
283670	cg15320905	38807401	45758409	0.6096193	0	1	0.7548363	42.60964
283770	cg15326535	39665482	39665482	0.8883465	0	1	0.7881083	-40.24679
283788	cg15328131	12768428	12768428		0	1	0.385128	4.34E-09
283810	cg15329552	20721361	20721361	0.6546869	0	1	0.8613686	103.1033
283876	cg15334096	60662308	60662308	0.881725	0	1	0.7678078	-46.66662
283970	cg15340526	13611435	13611435	0.2531501	0	1	0.3584446	22.83698
284028	cg15345074	48773449	29760424	0.1909337	0	1	0.3635179	57.91338
284063	cg15347156	27772368	48705311	0.7841962	0	1	0.6716931	-30.76301
284224	cg15359321	23642399	23642399	0.4177842	0	1	0.5515418	29.49948
284232	cg15360181	48806320	48806320	0.0796393	0	1	0.1840415	39.89093
284234	cg15360451	33713458	69692479	0.6627392	0	1	0.7811483	33.00874
284253	cg15361697	68641388	54794394	0.7182375	0	1	0.5518184	-49.58957
284297	cg15364618	65807359	65807359	0.3776088	0	1	0.21049	-52.57658
284311	cg15365500	35642301	35642301	0.6788164	0	1	0.9350349	374.3439
284543	cg15381326	44630311	44630311	0.3359811	0	1	0.4414815	20.527
284584	cg15383633	21613480	21613480	0.6363997	0	1	0.5356039	-19.39762
284670	cg15389068	30747383	74746378	0.7770789	0	1	0.6680869	-28.67794
284673	cg15389191	17749315	17749315	0.6319572	0	1	0.7494153	29.94621
284731	cg15392147	28645389	28645389	0.3455479	0	1	0.540241	58.66245
284769	cg15393490	20622482	20622482	0.4377989	0	1	0.5414894	19.21683
284786	cg15394255	58728307	58728307	0.2606134	0	1	0.363442	21.71413
284814	cg15395971	51694313	51694313	0.4470171	0	1	0.5936782	34.9796
284901	cg15401477	10713410	10713410	0.2118614	0	1	0.3160815	24.5055
284932	cg15403517	31703427	31703427	0.30291	0	1	0.4612995	41.6974
284948	cg15404665	41703431	29770308	0.2440423	0	1	0.0561099	-104.9913
284960	cg15405432	18616329	18616329	0.4904562	0	1	0.3254337	-43.94165
285011	cg15408512	34757439	54742333	0.8930662	0	1	0.5538918	-250.5538
285038	cg15410411	39631417	32801472	0.5082831	0	1	0.3035472	-65.93059
285098	cg15414745	72610507	14768412	0.6402913	0	1	0.4866215	-39.10587
285162	cg15418499	31742425	31742425	0.4873055	0	1	0.6643266	51.25002
285261	cg15425276	35773437	35773437	0.4247049	0	1	0.6022211	49.33233
285297	cg15427793	60680371	60680371	0.7700835	0	1	0.9058024	68.58278
285341	cg15431659	48761366	24686486	0.8373002	0	1	0.7351916	-32.10971
285394	cg15435765	20696420	31691373	0.3983824	0	1	0.518989	24.74136
285413	cg15436955	56792351	56792351	0.4937544	0	1	0.0331296	-371.3336
285528	cg15443166	31604507	31604507	0.4733497	0	1	0.5874863	22.81069
285547	cg15444149	10800311	46618328	0.5561246	0	1	0.7282121	53.42755
285666	cg15450098	23785345	23785345	0.3784948	0	1	0.4905687	22.03179
285953	cg15465642	26715498	51783462	0.3997017	0	1	0.2939995	-21.55578

285980	cg1546695	21606362	21606362	0.5003697	0	1	0.6512119	38.26929
285992	cg1546783	24807351	55780486	0.896091	0	1	0.7915183	-44.76789
286163	cg1547704	44725479	44725479	0.2047078	0	1	0.3607564	47.51559
286390	cg1549143	57685373	57685373	0.2058202	0	1	0.3086824	24.36924
286478	cg1549840	15694411	15694411	0.3810802	0	1	0.5207084	31.90269
286511	cg1550152	58784502	16797443	0.5185298	0	1	0.3059831	-70.558
286566	cg1550561	35654344	42775501	0.7123709	0	1	0.6095983	-22.3938
286622	cg1550917	29713300	29713300	0.6672997	0	1	0.5484667	-26.20562
286662	cg1551271	67790443	67790443	0.635158	0	1	0.7552092	31.44119
286725	cg1551826	73628441	73628441	0.8949994	0	1	0.384464	-371.3336
286894	cg1553151	15600489	15600489	0.5152028	0	1	0.625874	22.29186
286906	cg1553264	57808427	30685341	0.5128649	0	1	0.6261412	23.15435
286972	cg1553785	38629356	38629356	0.5352216	0	1	0.6421579	21.4434
287031	cg1554117	26800467	26800467	0.1729881	0	1	0.283622	29.84712
287065	cg1554302	33733322	33733322	0.5389736	0	1	0.6392699	19.30552
287093	cg1554463	21638446	11751488	0.0162287	0	1	0.1612749	92.82227
287149	cg1554819	68666500	68666500	0.6070249	0	1	0.4914535	-23.56079
287285	cg1555496	12639475	12639475	0.7744004	0	1	0.8962258	55.7078
287402	cg1556149	45804321	45804321	0.7075087	0	1	0.8345642	44.16853
287495	cg1556736	45616309	45616309	0.3203527	0	1	0.6038721	123.7664
287504	cg1556807	21673461	21673461	0.6843171	0	1	0.4413901	-93.33034
287512	cg1556861	50717475	50717475	0.2661532	0	1	0.3707948	22.1106
287529	cg1557014	51775306	51775306	0.7407752	0	1	0.6232798	-29.35808
287602	cg1557443	46744474	42759335	0.4574795	0	1	0.3513491	-20.47412
287633	cg1557588	53732368	52664438	0.6845766	0	1	0.5743033	-23.82996
287741	cg1558194	56612410	56612410	0.5193249	0	1	0.7109004	62.46905
287799	cg1558479	15687443	40654329	0.7679191	0	1	0.6124419	-49.14602
287906	cg1559180	14631428	14631428	0.5576638	0	1	0.7351441	57.03144
287967	cg1559575	16787451	67647405	0.4055644	0	1	0.2632014	-36.57495
288025	cg1559966	26719502	26719502	0.2066782	0	1	0.3164281	26.89626
288040	cg1560043	36605384	36605384	0.4717503	0	1	0.6113617	32.43219
288094	cg1560267	47615484	47615484	0.3326941	0	1	0.490962	40.61762
288230	cg1560937	18690463	18690463	0.2927623	0	1	0.4011092	22.45722
288270	cg1561160	23664305	23664305	0.3455444	0	1	0.1958846	-45.28833
288416	cg1561937	46684424	46684424	0.2569408	0	1	0.3698053	25.3173
288496	cg1562348	13644384	35762463		0	1		-4.34E-09
288514	cg1562433	44808445	44808445	0.6039252	0	1	0.7451347	39.82019
288544	cg1562611	42735374	42735374	0.5241941	0	1	0.4229557	-18.47078
288681	cg1563391	46646406	46646406	0.3989604	0	1	0.5426677	33.44701
288684	cg1563408	38800332	62793370	0.2735491	0	1	0.4794303	68.46638
288829	cg1564285	39634377	61726325	0.6330839	0	1	0.3727773	-103.7732
288939	cg1564838	31797330	31797330	0.3708084	0	1	0.2660149	-22.16624
289017	cg1565253	15619492	15619492	0.7789949	0	1	0.458664	-178.3552

289063	cg15655097	24757507	24757507	0.7854072	0	1	0.8874848	41.11051
289206	cg15663948	21660393	21660393	0.5446236	0	1	0.3776046	-43.86933
289296	cg15671450	35775311	35775311	0.4335025	0	1	0.3173006	-24.42402
289409	cg15677681	50760476	50760476	0.9209419	0	1	0.5869254	-264.3651
289463	cg15680603	51706372	48692417	0.5279209	0	1	0.9219344	374.3439
289507	cg15682806	60729467	58645414	0.2308179	0	1	0.0937619	-55.58208
289508	cg15682807	29656395	71664408	0.3386456	0	1	0.2222958	-28.4366
289515	cg15683497	66639442	56773445	0.3656646	0	1	0.4804579	23.05847
289520	cg15683950	36756465	36756465	0.3988631	0	1	0.519715	24.82394
289534	cg15684661	61802507	61802507	0.313911	0	1	0.4189591	20.83512
289634	cg15690347	26736445	73634351	0.3847276	0	1	0.230592	-44.14248
289679	cg15692593	11651429	11651429	0.3591137	0	1	0.5016841	33.34788
289701	cg15693937	46625496	46625496	0.2390964	0	1	0.5342223	140.625
289800	cg15699085	35717465	35717465	0.4633707	0	1	0.3552838	-21.03025
289809	cg15699552	21738485	70790419	0.4202602	0	1	0.29074	-30.084
289909	cg15704280	65743393	65743393	0.4439898	0	1	0.3284844	-23.92549
289921	cg15704872	66726310	66726310	0.2194223	0	1	0.3821743	49.39448
289950	cg15706156	23704322	37737444	0.3191231	0	1	0.2083462	-27.18039
289957	cg15706568	47785393	47785393	0.6216803	0	1	0.3864862	-84.5145
290091	cg15714682	57675362	57675362	0.2857705	0	1	0.4077911	27.45741
290120	cg15716623	39768442	39768442	0.8639882	0	1	0.7491679	-43.13729
290138	cg15717617	60736362	60736362	0.5141554	0	1	0.7141826	67.73473
290271	cg15724876	62645487	62645487	0.5470525	0	1	0.6538692	21.69909
290293	cg15726123	31721364	31721364	0.4948838	0	1	0.5972829	19.23647
290347	cg15728692	12782313	12782313	0.3144147	0	1	0.4321859	25.03895
290352	cg15728909	34605452	34605452	0.1586832	0	1	0.2641679	29.01709
290391	cg15730931	17635330	17635330	0.4282073	0	1	0.302671	-28.1642
290415	cg15732107	60715449	60715449	0.8033203	0	1	0.6805111	-37.4389
290511	cg15737177	31610426	20809435	0.644744	0	1	0.488094	-40.59095
290559	cg15740507	60703439	60703439	0.6519967	0	1	0.814938	60.56478
290731	cg15752756	74780342	74780342	0.3042893	0	1	0.1663535	-42.99081
290805	cg15758008	42601307	42601307	0.7563968	0	1	0.8847801	56.40752
290884	cg15765638	43723466	43723466	0.9216133	0	1	0.7840503	-76.90823
290929	cg15768613	16680480	16680480	0.8726946	0	1	0.6982785	-83.42019
291036	cg15773974	44645334	16602440	0.4060423	0	1	0.6005511	58.38233
291129	cg15779891	50778398	50778398	0.0772562	0	1	0.2202654	63.93254
291139	cg15781156	66623406	66623406	0.3000196	0	1	0.164365	-42.12162
291177	cg15783848	30621385	30621385	0.2053292	0	1	0.4678118	117.0072
291210	cg15786827	26714352	50668485	0.4910823	0	1	0.3756546	-23.15709
291240	cg15788369	40613314	25712368	0.4105665	0	1	0.3038189	-21.6258
291259	cg15790184	32663490	32663490	0.3869713	0	1	0.5346084	35.12603
291295	cg15793258	63613330	63613330	0.6148902	0	1	0.8512756	123.008
291368	cg15798862	42764356	42764356	0.4842721	0	1	0.3686231	-23.30686

291401	cg1580134	14789485	14789485	0.3185924	0	1	0.2002862	-30.74318
291546	cg1581143	10741416	10741416	0.721324	0	1	0.5992697	-29.92173
291551	cg1581166	34771443	39796501	0.5819454	0	1	0.4531812	-27.8314
291557	cg1581202	19700315	69704377	0.3664055	0	1	0.2590937	-23.28341
291688	cg1581933	15621481	15621481	0.5375273	0	1	0.4169301	-24.69383
291795	cg1582443	59628421	59628421	0.5449327	0	1	0.6529014	22.04769
291800	cg1582470	19774392	25755347	0.258644	0	1	0.1398395	-37.1557
291851	cg1582681	22705486	22705486	0.3674149	0	1	0.5259826	40.05815
291899	cg1582908	60661444	58706346	0.3333934	0	1	0.0945684	-129.0717
291916	cg1582996	24632422	24632422	0.7869363	0	1	0.6837532	-27.15541
292089	cg1583794	38745406	38745406	0.4334455	0	1	0.3178242	-24.2127
292134	cg1584055	17633478	17633478	0.6542606	0	1	0.5366246	-25.3569
292203	cg1584441	24610482	24610482	0.2984421	0	1	0.4071066	22.39725
292227	cg1584536	68737498	68737498	0.3902594	0	1	0.4915276	18.59779
292254	cg1584727	43689412	43689412	0.3068841	0	1	0.4411722	31.35274
292318	cg1585073	33748413	33748413	0.4322317	0	1	0.5345231	18.78564
292343	cg1585244	33661343	33661343	0.2230374	0	1	0.326529	23.62165
292370	cg1585377	13754467	13754467	0.5221677	0	1	0.8267791	374.3439
292426	cg1585747	56623333	56623333	0.2959582	0	1	0.3993595	20.76337
292555	cg1586608	51799376	51799376	0.3527398	0	1	0.5224009	45.46056
292672	cg1587462	58630411	27706371	0.4265604	0	1	0.2542599	-51.22659
292677	cg1587470	60799356	60799356	0.2702819	0	1	0.3738493	21.60851
292718	cg1587752	37656439	23680318	0.0196109	0	1	0.2571143	374.3439
292779	cg1588179	17795419	17795419	0.419498	0	1	0.5259721	20.05973
292798	cg1588309	27730328	22789353	0.7549925	0	1	0.8878342	60.22037
292934	cg1589164	12768347	12768347		0	1	0.8536991	4.34E-09
292999	cg1589512	26673478	26673478	0.2039301	0	1	0.3122772	26.54153
293005	cg1589533	39716426	39716426	0.2067117	0	1	0.3952885	64.96644
293013	cg1589578	25801508	25801508	0.3740968	0	1	0.5319797	39.67484
293045	cg1589743	60706393	60706393	0.6563886	0	1	0.0305888	-371.3336
293082	cg1589980	37754400	37754400	0.2039615	0	1	0.4269547	87.34054
293242	cg1590897	22676328	22676328	0.6607521	0	1	0.5558169	-21.27987
293252	cg1590944	64786316	64786316	0.504548	0	1	0.7298574	85.76961
293287	cg1591116	66707467	66707467	0.3505954	0	1	0.4519971	19.04202
293289	cg1591132	50775463	50775463	0.5212218	0	1	0.408108	-22.19075
293392	cg1591981	57785429	57785429	0.553853	0	1	0.6805859	29.64871
293440	cg1592188	48629388	48629388	0.369014	0	1	0.4694181	18.52171
293489	cg1592456	34681444	34681444	0.6161091	0	1	0.768154	47.42164
293719	cg1593805	54774355	54774355	0.2697149	0	1	0.3976899	30.37136
293773	cg1594333	64668323	64668323	0.1599416	0	1	0.2600695	26.68869
293825	cg1594659	11734316	11734316	0.5885413	0	1	0.4273521	-41.25087
293857	cg1594841	13644396	13644396		0	1	0.8234274	4.34E-09
293861	cg1594856	31711352	26660377	0.3239217	0	1	0.217796	-24.85804

293871	cg1594955	61651509	61651509	0.2849879	0	1	0.4103867	28.74076
293895	cg1595146	62699310	62699310	0.4925581	0	1	0.3758554	-23.58013
293988	cg1595780	26701411	26701411	0.6662806	0	1	0.7886481	35.53431
293993	cg1595842	66711467	66711467	0.5585309	0	1	0.3466837	-68.77795
294010	cg1595946	59777444	59777444	0.3233137	0	1	0.6102071	126.8275
294080	cg1596398	15749386	15749386	0.639066	0	1	0.7692351	37.05794
294082	cg1596408	66682491	66682491	0.5572676	0	1	0.7726239	85.6431
294092	cg1596459	14786324	14786324	0.5823003	0	1	0.824546	118.4976
294109	cg1596538	64680473	64680473	0.5152832	0	1	0.6257485	22.22233
294331	cg1597849	23618398	23618398	0.832001	0	1	0.9382123	61.17387
294348	cg1597921	53601493	53601493	0.8891808	0	1	0.5955695	-195.7253
294420	cg1598398	33741381	33741381	0.7431206	0	1	0.846382	33.9628
294464	cg1598646	10602301	10602301	0.5310578	0	1	0.647926	24.90479
294491	cg1598828	22760510	22760510	0.1877936	0	1	0.2957126	27.52131
294498	cg1598856	68758493	68758493	0.0654411	0	1	0.2173734	74.0075
294557	cg1599147	59631436	14688462	0.8087332	0	1	0.5736487	-108.1572
294688	cg1599812	55707472	36666312	0.4533195	0	1	0.6213974	45.12617
294716	cg1599960	19649402	19649402	0.3155867	0	1	0.4252364	22.27452
294794	cg1600279	33698330	33698330	0.7177676	0	1	0.8592756	57.60218
294877	cg1600696	32687493	32687493	0.5198901	0	1	0.634483	23.78078
294927	cg1600955	74615493	74615493	0.519361	0	1	0.4172172	-18.74693
295035	cg1601603	34673336	34673336	0.6765033	0	1	0.776667	25.15268
295317	cg1603197	63740383	63740383	0.2272378	0	1	0.331606	23.71395
295363	cg16034991	67689422	67689422	0.3590652	0	1	0.6618293	143.1114
295384	cg1603604	20755439	20755439	0.3115329	0	1	0.4154709	20.54051
295420	cg1603914	51755452	51755452	0.5743988	0	1	0.6890345	25.53341
295460	cg1604179	54771465	54771465	0.2919096	0	1	0.4153656	27.76176
295464	cg1604209	73674391	73674391	0.3126736	0	1	0.4162007	20.38541
295590	cg1604891	74727377	74727377	0.4100622	0	1	0.5258941	23.0819
295614	cg1605032	73642398	73642398	0.800872	0	1	0.9091603	51.03382
295672	cg1605300	10756465	53707335	0.9604284	0	1	0.8430364	-83.66013
295751	cg1605827	73783407	73783407	0.4229881	0	1	0.571316	35.43279
295764	cg16059161	53712386	53712386	0.6506754	0	1	0.8240236	68.79951
295779	cg1606018	15760496	15760496	0.8178083	0	1	0.6886759	-42.527
295791	cg1606093	38683455	38683455	0.4404846	0	1	0.8351066	374.3439
295978	cg16074271	45695325	45695325	0.7848669	0	1	0.6098012	-62.2982
295986	cg1607499	40742491	40742491	0.6037436	0	1	0.8779263	374.3439
296021	cg1607749	13809348	13809348	0.538367	0	1	0.6416232	20.26772
296025	cg1607792	39679313	39679313	0.300071	0	1	0.429366	29.65985
296044	cg1607941	65692337	65692337	0.6691603	0	1	0.7802979	29.83696
296079	cg1608185	14675462	14675462	0.4923023	0	1	0.3289247	-43.06474
296093	cg1608269	35618508	61792419	0.5282061	0	1	0.6289619	19.23876
296103	cg1608355	58644371	58644371	0.6779037	0	1	0.9147054	156.5356

296112	cg1608419(	44650375	44650375	0.2165583	0	1	0.3827069	51.42514
296180	cg1608794(	45777327	18702508	0.7360705	0	1	0.602642	-35.60983
296229	cg16091952	65657362	49721438	0.8345875	0	1	0.7122411	-41.70685
296416	cg1610273(	43808361	43808361	0.5259605	0	1	0.6435567	25.03713
296461	cg1610556(	38611458	38611458	0.6105332	0	1	0.7709132	52.08637
296526	cg1610938l	32601352	32601352	0.341498	0	1	0.4868291	34.8135
296571	cg1611222(	27622453	32647322	0.460725	0	1	0.566128	19.84559
296578	cg1611288(	26722406	26722406	0.1070186	0	1	0.6581023	374.3439
296677	cg1611837(	21779474	21779474	0.3704955	0	1	0.5002744	28.2426
296837	cg1612768(	10784337	70648368	0.68599	0	1	0.3533891	-176.5426
296937	cg1613606(	69748499	69748499	0.4636084	0	1	0.5882282	26.40809
297053	cg1614290(	26759327	40629405	0.9596592	0	1	0.5679796	-371.3336
297070	cg1614365(	55661306	47767338	0.8162634	0	1	0.6817343	-45.06232
297104	cg1614518(	55618305	55618305	0.1897126	0	1	0.4727503	138.023
297187	cg1614992(	41734416	29799492	0.6931872	0	1	0.580834	-24.89487
297282	cg1615611(	70607365	73797430	0.8677649	0	1	0.4794197	-302.0879
297352	cg1616293(	33786330	68681333	0.1176563	0	1	0.5612452	374.3439
297428	cg1616756(	23663418	23663418	0.895403	0	1	0.7009342	-108.1169
297512	cg1617209(	42695463	57651379	0.3057898	0	1	0.442541	32.36049
297604	cg1617660(	15652470	15652470	0.3825884	0	1	0.4861941	19.35153
297629	cg1617773(	18663429	18663429	0.4307377	0	1	0.3204401	-22.37334
297634	cg1617783(	26746466	26746466	0.3759551	0	1	0.5044276	27.70184
297684	cg1618079(	30757342	47612460	0.3018042	0	1	0.1758615	-36.22601
297784	cg1618752(	34809454	34809454	0.8267871	0	1	0.9380893	65.02676
297813	cg1618964(	63781485	63781485	0.1666109	0	1	0.2711007	27.87654
297820	cg1618995(	45679329	45683363	0.7493176	0	1	0.6130059	-37.96711
297852	cg1619129(	59785357	59785357	0.804257	0	1	0.6788486	-38.7953
297864	cg1619257(	56802419	56802419	0.4782598	0	1	0.3554277	-25.94555
297979	cg1619974(	27783418	27783418	0.3008367	0	1	0.4369922	32.29897
298025	cg1620225(	61760497	15748418	0.8013321	0	1	0.9374048	84.20977
298086	cg1620481(	48789442	68603443	0.2700917	0	1	0.1682116	-26.68349
298146	cg1620805(	34695480	32786455	0.7619013	0	1	0.5333392	-92.95425
298187	cg1621035(	44803341	44803341	0.6491815	0	1	0.7598598	28.00613
298201	cg1621097(	27661497	27661497	0.4768126	0	1	0.6433909	45.13708
298240	cg1621415(	52613413	17673389	0.7426543	0	1	0.8447846	33.17427
298530	cg1623379(	19723383	19723383	0.3168474	0	1	0.5361595	74.35435
298537	cg1623433(	36711428	36711428	0.8675169	0	1	0.7627874	-38.32973
298556	cg1623570(	60718451	60718451	0.2543268	0	1	0.0757533	-89.16023
298936	cg1625566(	63743407	63636440	0.6610634	0	1	0.8870625	130.0716
298977	cg1625753(	12611483	12611483	0.543346	0	1	0.6921868	39.38009
299061	cg1626185(	71706473	71706473	0.6178725	0	1	0.7186968	22.01233
299084	cg1626318(	62685459	62685459	0.5023757	0	1	0.3496596	-37.76519
299280	cg1627305l	23623343	23623343	0.2626429	0	1	0.3763061	25.35659

299466	cg16284437	53698374	51644413	0.8543755	0	1	0.742242	-39.81041
299747	cg16300553	27665417	27665417	0.5107633	0	1	0.6154389	20.19589
299819	cg16306078	24761450	24761450	0.7118324	0	1	0.813684	29.14816
299897	cg16310003	57621323	57621323	0.1819182	0	1	0.295949	30.47712
299912	cg16310958	59700357	46809418	0.4202176	0	1	0.1944596	-90.85233
300028	cg16316472	64721346	10688333	0.2860854	0	1	0.1261556	-61.7923
300032	cg16316624	44670340	45663379	0.3008173	0	1	0.1814234	-32.79126
300122	cg16320888	26742496	49705394	0.6988859	0	1	0.516909	-56.10768
300305	cg16330146	30726435	17606402	0.3146737	0	1	0.2015186	-28.57712
300415	cg16336556	52782469	52782469	0.6450634	0	1	0.7686647	34.09024
300432	cg16337566	11661353	11661353	0.2116314	0	1	0.3173281	25.06113
300515	cg16342620	46759427	46759427	0.5894082	0	1	0.7625558	57.92387
300562	cg16345566	52757468	52757468	0.8610928	0	1	0.622734	-128.6332
300707	cg16354345	37758333	37758333	0.8550025	0	1	0.9588401	70.827
300726	cg16355591	27706301	27706301	0.4721243	0	1	0.6287096	40.02522
300807	cg16359799	63684417	63684417	0.612131	0	1	0.5057077	-20.6846
301019	cg16371229	49810458	49810458	0.1575115	0	1	0.2642069	29.64285
301045	cg16372632	15747371	25733311	0.3430685	0	1	0.4457642	19.54447
301105	cg16375820	56793477	56793477	0.3700885	0	1	0.5091652	31.79854
301296	cg16387046	49634405	49634405	0.4401257	0	1	0.6162294	48.9238
301409	cg16394018	35675418	38755351	0.3915149	0	1	0.2194849	-54.21147
301462	cg16397032	31606396	68796418	0.877056	0	1	0.7579713	-48.57305
301465	cg16397176	25706345	25706345	0.2848352	0	1	0.3934794	22.80201
301481	cg16397968	15795447	15795447	0.9461744	0	1	0.7680312	-125.7757
301482	cg16398051	67633365	34624302	0.2832056	0	1	0.4802187	62.57718
301493	cg16398581	54711381	54711381	0.193644	0	1	0.2945955	24.43346
301542	cg16400631	15771335	39755401	0.5615179	0	1	0.3870193	-47.48415
301647	cg16405432	66643403	66643403	0.3008986	0	1	0.4091407	22.19017
301676	cg16406892	43608374	43608374	0.4580687	0	1	0.6559061	62.08949
301798	cg16412745	68659506	68659506	0.7028409	0	1	0.8960948	107.4835
301819	cg16414030	58663492	58663492	0.6993729	0	1	0.5956667	-22.16922
301832	cg16414691	39688492	39688492	0.4985638	0	1	0.6126729	23.17031
301845	cg16415646	18638488	18638488	0.4440588	0	1	0.5630692	24.22421
301858	cg16416045	43706325	55629312		0	1		-4.34E-09
301899	cg16418183	63772319	63772319	0.3213491	0	1	0.4459097	27.26475
301936	cg16419584	46647457	74795414	0.4279406	0	1	0.2672607	-44.59674
301972	cg16421411	54701456	61679335	0.4070428	0	1	0.5421903	30.0289
302000	cg16423096	42782411	42782411	0.4565434	0	1	0.2738515	-55.25969
302055	cg16426293	63806360	18607354	0.5576801	0	1	0.378323	-49.98666
302095	cg16428357	12763437	12702443	0.7734976	0	1	0.5507129	-90.97511
302096	cg16428517	19643510	19643510	0.5066665	0	1	0.6443894	32.56012
302179	cg16432908	56670338	56670338	0.6633084	0	1	0.769434	26.92648
302231	cg16435686	63603337	63603337	0.7213338	0	1	0.5164245	-71.45725

302256	cg16436762	27747312	27747312	0.1962378	0	1	0.3071615	28.07812
302309	cg16440058	61623436	42729406	0.3308452	0	1	0.0536269	-186.7895
302465	cg16449636	11731360	11731360	0.2176924	0	1	0.329705	27.05786
302478	cg16450309	36715420	71656455	0.5377487	0	1	0.3972445	-32.15514
302492	cg16451306	74623409	74623409	0.1987959	0	1	0.3318265	37.18051
302533	cg16453056	59689453	59689453	0.5804921	0	1	0.3858415	-58.27675
302565	cg16455339	57651414	57651414	0.4614637	0	1	0.5655559	19.44292
302615	cg16458494	66632451	10603352	0.3382264	0	1	0.2259826	-26.65221
302646	cg16460383	61602507	61602507	0.7098797	0	1	0.6077645	-22.06393
302752	cg16467318	13644470	13644470		0	1		-4.34E-09
302901	cg16476432	53721323	53721323	0.8507974	0	1	0.7275891	-45.09935
302919	cg16477611	39660439	39660439	0.2845065	0	1	0.4756728	59.19325
302953	cg16479633	44641326	44641326	0.2809988	0	1	0.4079246	29.47717
302978	cg16481280	54714317	54714317	0.0884219	0	1	0.1898353	36.52767
303022	cg16484499	32709458	32709458	0.8626612	0	1	0.7244192	-56.4691
303112	cg16490124	62797474	62797474	0.2005358	0	1	0.4911712	142.7335
303174	cg16493238	66732473	66732473	0.4227222	0	1	0.5772014	38.12344
303193	cg16494625	73728435	73728435	0.6162831	0	1	0.9405329	374.3439
303298	cg16501561	73623317	73623317	0.3249343	0	1	0.4308199	20.85961
303394	cg16507569	31743395	31743395	0.7073681	0	1	0.5677001	-36.29979
303531	cg16514085	28678378	28678378	0.475455	0	1	0.2979321	-51.17556
303538	cg16514513	17773335	58738411	0.3385929	0	1	0.4418839	19.79904
303547	cg16515381	35604436	35604436	0.6460012	0	1	0.9054773	374.3439
303563	cg16516295	64797394	64797394	0.3171358	0	1	0.4210356	20.40195
303802	cg16527095	61749339	61749339	0.2368721	0	1	0.0880785	-64.43883
303821	cg16527629	21787337	21787337	0.4645038	0	1	0.610768	35.12384
303906	cg16531622	10689391	10689391	0.4064905	0	1	0.5249382	23.97155
303938	cg16533146	14607344	14607344	0.3827396	0	1	0.5137035	28.55811
303985	cg16535653	58647457	58647457	0.8529467	0	1	0.5995213	-138.3229
304078	cg16540590	61661377	61661377	0.2752401	0	1	0.4584503	55.44495
304228	cg16549644	69706449	55803491	0.5502781	0	1	0.6652904	24.78964
304238	cg16550264	70779475	43672350	0.2475024	0	1	0.3586972	25.14898
304413	cg16558994	54799486	54799486	0.4595723	0	1	0.231154	-87.23939
304527	cg16564828	11720494	11720494	0.8149909	0	1	0.929245	63.03281
304556	cg16566191	67803420	67803420	0.3910403	0	1	0.5354303	33.75585
304589	cg16568131	38617479	16743341	0.4062205	0	1	0.2888528	-25.67035
304636	cg16570885	40644306	40644306	0.9421397	0	1	0.8358577	-63.18084
304730	cg16575544	38718324	38718324	0.2267781	0	1	0.3739387	41.18276
304747	cg16576544	30685373	30685373	0.8808911	0	1	0.7794911	-39.23412
304757	cg16576930	15746497	15746497	0.7899035	0	1	0.9267425	78.92889
304892	cg16582419	31791419	56778505	0.1912797	0	1	0.3279531	39.56192
304916	cg16583552	40659477	53641413	0.6600785	0	1	0.3371151	-164.2329
305190	cg16596317	10704506	10704506	0.7506962	0	1	0.8574037	37.50733

305273	cg16600991	19676476	72679384	0.2252383	0	1	0.0710652	-73.51198
305298	cg16602316	11806443	46648400	0.4157865	0	1	0.2781084	-33.8511
305316	cg16603578	44617361	22607427	0.6547235	0	1	0.7649465	28.20552
305361	cg16606324	10633509	48719469	0.7597994	0	1	0.6188178	-41.10265
305434	cg16612072	21619432	21619432	0.0443862	0	1	0.1828281	72.85333
305483	cg16615357	26703479	26703479	0.5768176	0	1	0.4494686	-27.26311
305524	cg16617257	41734407	41734407	0.782349	0	1	0.9090788	63.54969
305631	cg16622899	22712323	39604492	0.2607599	0	1	0.3792334	27.18361
305632	cg16622906	32638312	13689444	0.294816	0	1	0.190916	-25.73115
305645	cg16623941	43748403	43748403	0.5894347	0	1	0.7088113	28.19176
305723	cg16627236	15764432	15764432	0.1191729	0	1	0.2219666	32.33538
305742	cg16627911	55773343	51629453	0.736227	0	1	0.8440018	35.82656
305902	cg16637458	33670508	33670508	0.2075808	0	1	0.3339121	33.51619
305979	cg16641638	42786453	54806449	0.4604594	0	1	0.3476726	-22.65611
306114	cg16649728	36757390	51722444	0.3434061	0	1	0.563465	74.05846
306145	cg16651314	37671494	37671494	0.2960402	0	1	0.4615102	45.30652
306189	cg16652920	40788502	40788502	0.2378091	0	1	0.0464104	-112.8698
306232	cg16655291	74683493	74683493	0.8658202	0	1	0.3885923	-371.3336
306236	cg16655343	66739312	66739312	0.6995358	0	1	0.5978683	-21.49688
306270	cg16656875	10784438	10784438	0.7918776	0	1	0.892424	41.40363
306304	cg16658460	20777316	20777316	0.3123513	0	1	0.4344998	26.63876
306337	cg16659773	41677386	41677386	0.2543658	0	1	0.4163984	46.10269
306352	cg16660494	57758504	57758504	0.5304791	0	1	0.656203	28.33627
306406	cg16662938	40787327	40787327	0.6420974	0	1	0.4811496	-42.44855
306456	cg16665310	57698390	25800460	0.844126	0	1	0.7240322	-42.16996
306590	cg16673522	49780451	49780451	0.5190889	0	1	0.6816107	45.05682
306675	cg16678159	42723496	42723496	0.3297348	0	1	0.433183	20.00537
306748	cg16681649	54754423	54754423	0.297895	0	1	0.4171609	26.04423
306779	cg16683060	42782316	42782316	0.3550943	0	1	0.5127164	39.82182
306819	cg16686135	12638432	12638432	0.4085988	0	1	0.5289063	24.6034
306935	cg16692735	16718443	33758489	0.4884665	0	1	0.3656879	-25.78051
307086	cg16700025	61810327	61810327		0	1		-4.34E-09
307151	cg16702660	16631322	16631322	0.2021059	0	1	0.5348747	374.3439
307162	cg16703135	46661465	72773385	0.5582091	0	1	0.3636516	-58.30186
307188	cg16704476	12688449	12688449	0.0817437	0	1	0.2097961	53.19697
307193	cg16704703	15797495	15797495	0.3770152	0	1	0.6409682	106.982
307233	cg16705827	54802377	54802377	0.8086214	0	1	0.6263986	-71.02461
307341	cg16711011	48686329	61723395	0.2168174	0	1	0.3428429	32.68825
307393	cg16713321	50792364	50792364	0.2860757	0	1	0.3891236	20.93171
307398	cg16713625	63809322	61685313	0.8455455	0	1	0.9582438	78.03788
307443	cg16716316	61673380	13651442	0.1714536	0	1	0.0689733	-41.17925
307514	cg16719517	46679337	32778503	0.0378919	0	1	0.1600098	63.81693
307580	cg16722884	32800508	32800508	0.3342546	0	1	0.4412891	21.04006

307582	cg1672294	30626503	30626503	0.6148582	0	1	0.5125078	-19.4743
307595	cg1672371	34633487	57732437	0.5850449	0	1	0.7472765	50.25274
307608	cg1672433	72634429	72634429	0.2595156	0	1	0.4067252	38.89855
307616	cg1672472	14750373	14750373	0.7990934	0	1	0.9046678	47.8469
307666	cg1672792	26754342	26754342	0.1344609	0	1	0.2439864	33.47785
307680	cg1672884	66656509	66656509	0.2045223	0	1	0.3068113	24.23813
307792	cg1673507	38734362	38734362	0.4532207	0	1	0.6243594	46.68914
307917	cg1674207	65711321	65711321	0.4979563	0	1	0.7718205	131.0456
307951	cg16744531	57607381	73703501	0.257453	0	1	0.1163693	-52.81129
307960	cg16744961	60757411	60757411	0.7245603	0	1	0.9075423	105.0645
308011	cg1674788	39769375	52600460	0.443316	0	1	0.5572358	22.49093
308012	cg1674792	74666366	74666366	0.4367957	0	1	0.5421858	19.73533
308016	cg1674808	67644496	67644496	0.4314348	0	1	0.3243737	-21.2435
308020	cg1674843	62647492	62647492	0.5719034	0	1	0.6731833	20.47256
308056	cg1675149	61726311	61726311	0.2452411	0	1	0.3712898	30.86982
308107	cg1675478	43663360	43663360	0.3248268	0	1	0.4470391	26.33488
308125	cg1675583	46701389	11653323	0.1524975	0	1	0.2664401	33.34221
308287	cg1676506	22662319	22662319	0.3019964	0	1	0.436637	31.65876
308330	cg1676788	49709439	30660451	0.9162823	0	1	0.7223555	-118.9578
308345	cg1676869	63725310	11665446	0.5231948	0	1	0.6249443	19.46543
308446	cg1677559	26788369	26788369	0.7435698	0	1	0.6005	-40.53691
308491	cg1677838	29686413	57612478	0.3670968	0	1	0.5224723	38.64037
308520	cg1678045	17718342	17718342	0.0984927	0	1	0.2153134	42.87732
308546	cg1678190	15780398	15780398	0.3298245	0	1	0.4573131	28.12286
308599	cg1678498	65766375	63699429	0.819681	0	1	0.6825874	-46.96021
308604	cg16785291	11645344	11645344	0.2530811	0	1	0.363526	24.62783
308652	cg1678735	19624446	19624446	0.3068649	0	1	0.4165805	22.51416
308661	cg1678809	10720331	70768333	0.166477	0	1	0.2864305	34.51417
308674	cg1678885	53651382	53651382	0.6149881	0	1	0.3540419	-103.9828
308681	cg1678910	39704468	45642388	0.3500941	0	1	0.2359237	-26.81894
308734	cg1679183	37644405	37644405	0.3776696	0	1	0.6674838	130.8536
308928	cg16802801	11725370	11725370	0.2910279	0	1	0.1611296	-39.73665
308956	cg1680384	29616304	61796314	0.4682773	0	1	0.3575729	-21.8313
309056	cg1681031	57768347	57768347	0.4410996	0	1	0.3279156	-23.15978
309120	cg1681468	11738460	11738460	0.6324946	0	1	0.286193	-192.0642
309232	cg1682257	73715405	21760444	0.4654938	0	1	0.3476109	-24.35985
309325	cg1682992	48698301	64800418	0.5834819	0	1	0.729309	40.59598
309398	cg16835531	10670397	10670397	0.7866992	0	1	0.915653	67.80871
309410	cg1683667	50727449	50727449	0.717431	0	1	0.8971791	97.38839
309451	cg1684101	22679452	22679452	0.3930252	0	1	0.5743163	50.97884
309550	cg16848221	61804390	61804390	0.3043615	0	1	0.6119846	147.5047
309614	cg1685236	37748353	37748353	0.7060506	0	1	0.831935	43.10379
309652	cg1685491	10729435	51693408	0.4490778	0	1	0.3345491	-23.47068

309654	cg16855352	43625305	72735337	0.9553673	0	1	0.8485118	-71.16553
309724	cg16860392	17760330	17760330	0.2437899	0	1	0.3507501	23.8213
309774	cg16863522	37648364	37648364	0.6484804	0	1	0.7648216	30.67758
309792	cg16864658	54668354	54668354	0.2375043	0	1	0.1175235	-41.09077
309834	cg16867584	44708468	23715328	0.2868857	0	1	0.1708175	-32.36101
309880	cg16871435	21642333	21642333	0.2895208	0	1	0.5709014	123.0877
309926	cg16874185	35752411	35752411	0.4697155	0	1	0.5721605	18.99507
309977	cg16877087	61683422	10674439	0.8488013	0	1	0.7204029	-47.57346
309982	cg16877681	46660353	46660353	0.5774596	0	1	0.7062239	31.71028
310172	cg16890563	27803308	27803308	0.3809054	0	1	0.5396811	40.01845
310289	cg16898193	33771462	33771462	0.3488662	0	1	0.1806671	-56.89983
310397	cg16904261	15693510	15693510	0.4986694	0	1	0.6484993	37.72736
310503	cg16908938	70749340	70749340	0.6024926	0	1	0.7669861	53.77276
310594	cg16914370	20636316	44607314	0.5624067	0	1	0.4115275	-36.47301
310633	cg16917903	44682343	44682343	0.5917243	0	1	0.9149014	374.3439
310692	cg16921727	35751384	35751384	0.4049443	0	1	0.2390969	-49.16751
310842	cg16929496	60667430	60667430	0.3992323	0	1	0.2893681	-23.06636
310845	cg16929739	15669433	15669433	0.6979161	0	1	0.8317567	47.30434
310871	cg16931770	70737340	51735392	0.2838404	0	1	0.4363847	39.93094
310873	cg16931822	45695381	45695381	0.6065266	0	1	0.7144932	24.29393
310892	cg16932827	42802482	42802482	0.1766343	0	1	0.2826393	27.63946
310942	cg16936421	71731399	46620479	0.7787382	0	1	0.8790859	38.26331
311321	cg16967578	35635502	35635502	0.7280852	0	1	0.6147336	-26.971
311460	cg16977510	33808376	33808376	0.2090309	0	1	0.0997078	-38.63337
311609	cg16988212	48614330	48614330	0.6057853	0	1	0.7603608	47.7957
311629	cg16989201	37653313	37653313	0.8342689	0	1	0.6999672	-48.01468
311801	cg16999994	30712357	30712357	0.8195337	0	1	0.9437702	78.41379
311926	cg17007628	30775418	30775418	0.7206043	0	1	0.5803663	-37.4313
311963	cg17009813	36691300	36691300	0.2850574	0	1	0.3863674	20.40832
312019	cg17013691	14613376	11784376	0.4846376	0	1	0.6648617	52.93319
312059	cg17015844	73809492	73809492	0.1552042	0	1		-4.34E-09
312108	cg17017591	25761437	55660322	0.5362527	0	1	0.3201582	-72.17139
312252	cg17025908	31682354	31682354	0.4540306	0	1	0.9278698	374.3439
312357	cg17032848	47601482	47601482	0.6734195	0	1	0.7902061	33.20308
312379	cg17033622	20651472	20651472	0.7138301	0	1	0.5950636	-28.22553
312384	cg17033891	55690443	55690443	0.6958938	0	1	0.7965619	26.97454
312553	cg17044529	12616427	12616427	0.637351	0	1	0.8567682	111.3117
312593	cg17047033	32799388	32799388	0.6155395	0	1	0.7214644	23.90956
312617	cg17048610	29783469	46791320	0.8098223	0	1	0.6869699	-38.2911
312644	cg17050806	11688438	11688438	0.2633587	0	1	0.1281915	-47.27519
312650	cg17051124	15719372	15719372	0.7618254	0	1	0.8727172	42.79929
312733	cg17055585	19643331	56656336	0.9522556	0	1	0.840888	-72.99932
312751	cg17056132	14802443	14802443	0.2745326	0	1	0.4125088	34.14316

312780	cg17058383	70617305	70617305	0.2349265	0	1	0.3622519	31.99718
312789	cg17059388	18662368	18662368	0.6210375	0	1	0.4222621	-61.2467
312868	cg17066275	12657472	12657472	0.2339485	0	1	0.3453608	25.9043
312941	cg17070988	27606354	71630392	0.6812385	0	1	0.5726216	-23.14277
312991	cg17074339	11762494	11762494	0.1817244	0	1	0.3711454	69.10555
313095	cg17080138	25603418	25603418	0.5520417	0	1	0.6911724	35.13004
313142	cg17082366	43632386	55654463	0.6797357	0	1	0.5235894	-41.96865
313187	cg17084358	58779333	58779333	0.7881279	0	1	0.8913883	42.75457
313324	cg17093485	22676510	32753378	0.1850691	0	1	0.0827493	-38.10448
313380	cg17096289	33628390	46699443	0.6084637	0	1	0.7585656	45.36456
313390	cg17097293	30690393	30690393	0.5719228	0	1	0.6901979	26.89802
313411	cg17098979	46633412	46633412	0.6726079	0	1	0.5181701	-40.81506
313430	cg17100047	14740471	14740471	0.2737275	0	1	0.3839539	23.7196
313650	cg17112812	23659497	64687370	0.1542993	0	1	0.2853813	41.18405
313828	cg17125742	58737438	50649421	0.4678189	0	1	0.2911248	-51.09901
313845	cg17126924	44698367	44698367	0.3454106	0	1	0.5655248	74.05824
313972	cg17133045	54744446	54744446	0.3173677	0	1	0.4232549	21.02234
314032	cg17137077	52762384	70634493	0.7828429	0	1	0.6597117	-35.26468
314133	cg17143179	61729372	61729372	0.5869079	0	1	0.6881887	20.95678
314253	cg17149911	20707449	20707449	0.3502455	0	1	0.2475593	-22.18562
314274	cg17151123	21770331	21770331	0.7294517	0	1	0.8515061	44.60593
314288	cg17152375	49763499	74665311	0.5732834	0	1	0.450019	-25.77177
314352	cg17155524	21615390	21615390	0.4247264	0	1	0.2205589	-72.628
314476	cg17162031	50706343	50706343	0.6594748	0	1	0.7654548	26.57577
314490	cg17162911	45807323	45807323	0.4370746	0	1	0.7390651	150.515
314512	cg17164093	55707310	55707310	0.4608911	0	1	0.5682883	20.47575
314516	cg17164345	60691426	60691426	0.4814672	0	1	0.5945619	22.557
314532	cg17165241	69692400	23810364	0.4058194	0	1	0.6309155	77.85081
314556	cg17166262	67633425	67633425	0.2363582	0	1	0.3891475	43.03986
314578	cg17167832	40617361	40617361	0.526028	0	1	0.6635563	33.17897
314605	cg17168875	13743444	13743444	0.9080226	0	1	0.7999794	-50.49981
314782	cg17178175	69748353	69748353	0.4883425	0	1	0.5944995	20.34852
314798	cg17178900	24757439	18682492	0.498817	0	1	0.37844	-24.80291
314832	cg17180633	60646378	60646378	0.2305414	0	1	0.3977483	50.60918
314854	cg17181941	40626314	40626314	0.8354923	0	1	0.9446734	66.80719
314939	cg17186103	43674488	43674488	0.3848926	0	1	0.5046564	24.53608
314977	cg17187785	26692361	26692361	0.9392979	0	1	0.7456157	-134.2347
315053	cg17193417	51661351	51661351	0.6275207	0	1	0.5107348	-24.36572
315078	cg17196051	58774337	58774337	0.3673225	0	1	0.5408107	47.11081
315079	cg17196155	24754456	24754456	0.4553932	0	1	0.2634436	-61.09358
315104	cg17198051	69694432	69694432	0.5403956	0	1	0.6477695	21.72118
315224	cg17205386	53759508	53759508	0.9279098	0	1	0.8139494	-62.21404
315252	cg17207064	36718408	36718408	0.5989796	0	1	0.6996297	21.16547

315265	cg17207724	38676425	64765509	0.5587221	0	1	0.4354554	-25.67554
315300	cg17209769	57677340	57677340	0.6388379	0	1	0.8686441	124.6407
315386	cg17214408	74666430	66699412	0.7335418	0	1	0.6210537	-26.96424
315421	cg17216092	34794502	34794502	0.2623729	0	1	0.3698858	23.22175
315499	cg17220055	70646350	70646350	0.5675711	0	1	0.6704938	20.91582
315502	cg17220237	73774471	73774471	0.7286312	0	1	0.5014601	-86.89155
315518	cg17221315	42636396	42636396	0.2417163	0	1	0.1352751	-31.95987
315595	cg17225604	66787301	66787301	0.547062	0	1	0.4312138	-23.09057
315786	cg17240198	28741440	28741440	0.5183623	0	1	0.6210603	19.68481
315818	cg17242351	34734432	65731463	0.309887	0	1	0.1822532	-36.33825
315885	cg17246929	28738380	28738380	0.7823387	0	1	0.9101256	64.70179
315897	cg17248267	55762375	55762375	0.3507597	0	1	0.5487017	60.4046
315915	cg17250082	47751472	47751472	0.3445971	0	1	0.2265216	-28.84521
315940	cg17251423	57779473	33693464	0.3362934	0	1	0.4737391	31.75559
315955	cg17253407	26789304	26789304	0.4790182	0	1	0.5863785	20.62759
315965	cg17253981	39748337	39748337	0.2525374	0	1	0.4157294	46.79807
316021	cg17257516	45621509	45621509	0.3996858	0	1	0.5209815	24.97415
316237	cg17272838	49706393	49706393	0.5756191	0	1	0.7173336	37.84914
316241	cg17273096	39645372	39645372	0.7340154	0	1	0.8704136	57.37006
316249	cg17273683	24688344	24688344	0.6154201	0	1	0.7484029	36.40722
316302	cg17276853	64668397	18768374	0.5530733	0	1	0.4367585	-23.26532
316305	cg17277199	44648340	74611303	0.5190808	0	1	0.3547378	-42.89906
316606	cg17292337	34808478	34808478	0.361363	0	1	0.1709611	-71.54261
316639	cg17294865	18639475	18639475	0.3305275	0	1	0.5502935	74.17619
316656	cg17295834	62803373	62803373	0.1444652	0	1	0.2635265	36.67221
316795	cg17302580	33720308	33720308	0.8750167	0	1	0.6803946	-99.18848
316949	cg17312546	69604352	69604352	0.4647867	0	1	0.579852	23.03453
317007	cg17316073	55632466	55632466	0.3441748	0	1	0.4555658	22.25906
317265	cg17330048	48702307	48702307	0.195129	0	1	0.328206	37.54128
317272	cg17330251	61784461	61784461	0.6078717	0	1	0.4697842	-31.75963
317305	cg17331757	28761395	28761395	0.8776218	0	1	0.694259	-91.76206
317345	cg17333767	61796381	61796381	0.1821711	0	1	0.2956882	30.24191
317351	cg17333973	60796449	60796449	0.1468582	0	1	0.2538436	30.87206
317357	cg17334266	64752491	65758332	0.7023993	0	1	0.8264081	41.24341
317374	cg17335001	70662462	70662462	0.498963	0	1	0.621905	26.3867
317491	cg17341345	52784434	52784434	0.4334098	0	1	0.5404131	20.22948
317533	cg17343184	62626346	62626346	0.4291308	0	1	0.6313007	63.53567
317564	cg17344932	37756330	38659340	0.4032894	0	1	0.5311553	27.3013
317565	cg17345036	50705397	55735450	0.5477233	0	1	0.427638	-24.52802
317575	cg17345450	35667417	35667417	0.2815877	0	1	0.4360527	40.90693
317606	cg17347178	65677341	65677341	0.5462165	0	1	0.4381846	-20.56333
317623	cg17348244	34619474	34619474	0.70469	0	1	0.4488943	-105.0591
317672	cg17351927	69628380	69628380	0.9051263	0	1	0.6971627	-124.3365

317737	cg1735587	32770399	32770399	0.8216988	0	1	0.6383107	-74.67133
317791	cg1736055	40713497	40713497	0.8668122	0	1	0.7439568	-48.32395
317893	cg1736781	44703447	44703447	0.2549354	0	1	0.4191778	47.13845
317923	cg1736969	59740473	59740473	0.0477143	0	1	0.2647149	133.794
317937	cg1737061	38638395	38638395	0.5760504	0	1	0.8337633	134.7172
318127	cg1738230	34648306	34648306	0.514142	0	1	0.6435462	29.30962
318169	cg1738412	14738462	14738462	0.6040882	0	1	0.7217646	28.24976
318181	cg1738476	12738359	12738359	0.6942544	0	1	0.8072348	33.36071
318205	cg1738570	72697330	72697330	0.9005679	0	1	0.7976526	-44.97609
318220	cg1738624	56635354	56635354	0.4652892	0	1	0.7341294	119.5755
318225	cg1738647	58756404	58756404	0.3918203	0	1	0.529277	30.97341
318261	cg1738877	42751448	42751448	0.8002326	0	1	0.3385616	-371.3336
318275	cg1738981	70801395	70801395	0.5726092	0	1	0.7516804	59.83557
318328	cg1739314	44749493	44749493	0.4870976	0	1	0.771948	140.9726
318364	cg1739555	13802506	13802506	0.1594226	0	1	0.2676848	30.12221
318426	cg1739928	60611360	63726326	0.5185749	0	1	0.4006864	-23.80233
318499	cg1740444	64711377	64711377	0.1780982	0	1	0.8940328	374.3439
318633	cg1741308	33798377	33798377	0.9032179	0	1	0.8017747	-44.80687
318663	cg1741532	57742313	57742313	0.5272639	0	1	0.6464673	25.67917
318666	cg17415381	38694432	38694432	0.7363901	0	1	0.6347489	-23.16039
318773	cg1742104	62610408	62610408	0.3787687	0	1	0.8002156	374.3439
318798	cg1742254	50708387	40618459	0.2792918	0	1	0.1688351	-30.15199
318804	cg1742291	54728465	54728465	0.4811867	0	1	0.6637718	54.11304
318834	cg1742506	40649492	40649492	0.6930914	0	1	0.819237	41.23119
318859	cg1742692	46713318	46713318	0.6871563	0	1	0.7988936	31.887
319092	cg1744219	63790401	63790401	0.5639232	0	1	0.691759	30.58777
319110	cg1744335	60715486	13669344	0.6261959	0	1	0.4969318	-28.78642
319156	cg1744576	43701337	61732401	0.3850749	0	1	0.272982	-24.39159
319220	cg1744995	31684386	22617405	0.5215914	0	1	0.4196442	-18.68473
319369	cg1745902	60658314	48644424	0.9362338	0	1	0.8108831	-75.00918
319397	cg1746036	56761388	56761388	0.911088	0	1	0.7285244	-106.6212
319557	cg1746845	66656324	66656324	0.1356811	0	1	0.2432187	32.41045
319660	cg1747371	49701335	49701335	0.2717582	0	1	0.4408355	48.38907
319684	cg1747478	19620473	19620473	0.6350321	0	1	0.5320301	-20.04622
319685	cg1747479	58636369	58636369	0.6840568	0	1	0.5197532	-46.05761
319733	cg1747757	42763346	42763346	0.5768563	0	1	0.7769432	76.2869
319817	cg1748211	46717450	40620377	0.2008136	0	1	0.3650017	52.12914
319826	cg1748242	16662422	16662422	0.7428482	0	1	0.8490774	35.85689
319938	cg1749019	35727500	35727500	0.2073877	0	1	0.3136049	25.51427
319957	cg1749130	54757498	54757498	0.2806529	0	1	0.4147887	32.30394
320193	cg17504791	21760487	21760487	0.354075	0	1	0.4714751	24.09091
320397	cg1751548	22677494	22677494	0.3620661	0	1	0.2371982	-30.86957
320419	cg1751624	55616388	55616388	0.1018966	0	1	0.2069097	36.02585

320438	cg17516997	20670464	20670464	0.5747991	0	1	0.6847063	23.70901
320483	cg17519156	13806418	13806418	0.3845546	0	1	0.4894503	19.72729
320667	cg17529386	53793338	59806471	0.8536293	0	1	0.6790617	-77.30141
320770	cg17536720	30749407	30749407	0.7884089	0	1	0.5484067	-106.8782
320779	cg17537073	60713348	12623339	0.025485	0	1	0.2123049	121.7978
320857	cg17543884	29697321	47758315	0.4321603	0	1	0.291725	-34.38303
320861	cg17544364	58678487	58678487	0.4909344	0	1	0.3664036	-26.39063
320862	cg17544584	61713469	61713469	0.7208605	0	1	0.8281993	33.34999
320901	cg17546649	56642318	56642318	0.4057481	0	1	0.270155	-33.38128
320988	cg17553149	50636422	40688384	0.4166142	0	1	0.3122639	-20.65311
321140	cg17564498	73792452	73792452	0.7568338	0	1	0.8598211	36.00212
321169	cg17566592	13668422	13668422	0.3731334	0	1	0.2482409	-30.24781
321214	cg17569842	47650435	47650435	0.2415787	0	1	0.3566008	26.8371
321365	cg17581485	31794477	31794477	0.2939709	0	1	0.4307061	32.78956
321402	cg17583957	61737317	61737317	0.1877052	0	1	0.3593203	57.81299
321450	cg17586885	24687467	20660370	0.2192692	0	1	0.3204122	22.99001
321484	cg17588704	11801433	11801433	0.6683885	0	1	0.9175507	374.3439
321488	cg17588812	33720486	49762315	0.8055172	0	1	0.9221388	61.65353
321513	cg17590135	46682420	64784322	0.7989658	0	1	0.9452695	97.66172
321566	cg17593342	63762391	63762391	0.5644003	0	1	0.6934122	31.13088
321620	cg17597639	32787408	32787408	0.2671093	0	1	0.1512168	-34.37271
321679	cg17601785	24640334	24640334	0.4396382	0	1	0.5668515	27.13306
321806	cg17611045	51783342	12662447	0.5262827	0	1	0.4256533	-18.28923
321822	cg17611936	70725376	53803433	0.2984665	0	1	0.1012902	-93.50549
321845	cg17613924	44667300	21715415	0.6294596	0	1	0.7621455	37.50827
321906	cg17619311	62762491	33638303	0.166312	0	1	0.0357217	-70.94254
321991	cg17626671	19642505	19642505	0.897045	0	1	0.6271537	-176.2052
322045	cg17631184	49774438	49774438	0.3615149	0	1	0.4919427	28.60144
322080	cg17633431	60767302	60767302	0.3928355	0	1	0.5109309	23.91256
322141	cg17639056	60754322	27808404	0.5927973	0	1	0.4899378	-19.32051
322202	cg17643624	10698454	10698454	0.4193567	0	1	0.5291328	21.09607
322240	cg17646499	21603415	21603415	0.9040995	0	1	0.7855889	-56.12054
322387	cg17655970	38694502	26658331	0.3223683	0	1	0.1735205	-47.55289
322440	cg17658874	38622405	38622405	0.8886123	0	1	0.7086577	-93.71603
322493	cg17662493	73732393	73732393	0.7414938	0	1	0.5539048	-63.4436
322808	cg17687367	46774480	46774480	0.5553201	0	1	0.676038	27.21032
322883	cg17694130	11600347	35689408	0.2398912	0	1	0.3603394	28.98125
322902	cg17695537	62691303	62691303	0.165698	0	1	0.2828199	33.33599
323032	cg17706972	40715497	40715497	0.2344802	0	1	0.3579162	30.46444
323037	cg17707274	29773376	29773376	0.2653793	0	1	0.4034644	34.65122
323047	cg17707870	43670432	43670432	0.2016619	0	1	0.5491044	374.3439
323093	cg17711541	57621337	57621337	0.5150888	0	1	0.3231969	-57.73568
323116	cg17713488	29754432	57727428	0.7593654	0	1	0.6153446	-42.49911

323143	cg1771486	39643303	48785319	0.9602498	0	1	0.7545544	-163.1745
323161	cg1771610	15612475	40706329	0.3110152	0	1	0.1865028	-34.54255
323281	cg1772320	20761434	20761434	0.0307993	0	1	0.2023662	105.5932
323401	cg1773197	50780340	11685308	0.6783835	0	1	0.9718837	374.3439
323458	cg1773559	61740315	61740315	0.5844696	0	1	0.4331921	-36.80703
323495	cg1773777	29669336	50711333	0.4376936	0	1	0.651701	71.56374
323507	cg1773852	64607510	64607510	0.6255415	0	1	0.7284933	23.21321
323508	cg1773861	33678338	33678338	0.288736	0	1	0.1093102	-78.48743
323561	cg1774144	15746504	15746504	0.4965869	0	1	0.3914568	-19.75024
323621	cg1774487	51762459	51762459	0.6005998	0	1	0.7913635	72.97719
323701	cg1774996	47763379	47763379	0.5499074	0	1	0.2503045	-143.4812
323776	cg1775447	12657385	72717470	0.9028391	0	1	0.7894499	-52.32525
323797	cg1775548	73631423	73631423	0.4016082	0	1	0.5381541	30.58023
323865	cg1775925	33732332	49729500	0.6568346	0	1	0.3430696	-154.1397
323875	cg1775959	69703437	69703437	0.8257265	0	1	0.9414295	70.22217
323896	cg1776126	70764415	70764415	0.7970147	0	1	0.9074135	51.85064
323926	cg1776356	44796313	44796313	0.7114335	0	1	0.8280375	37.78325
323936	cg1776483	29623345	29623345	0.6360726	0	1	0.7413979	24.76346
323939	cg1776499	38698498	38698498	0.1417339	0	1	0.2513158	32.61374
324096	cg1777657	30768498	42792354	0.5355801	0	1	0.4085654	-26.97957
324153	cg1778044	41752359	41752359	0.7228076	0	1	0.6220676	-22.17176
324206	cg1778369	24653317	24653317	0.5680506	0	1	0.676379	22.87674
324228	cg1778525	31652419	60723394	0.6837915	0	1	0.5587871	-29.12904
324363	cg1779481	58733440	39617452	0.4388123	0	1	0.332496	-20.84645
324413	cg1779794	54673319	54673319	0.2829642	0	1	0.4066657	28.18496
324492	cg1780326	12663410	12663410	0.915674	0	1	0.5688277	-276.4792
324505	cg1780411	71690317	21626456	0.4317781	0	1	0.2525479	-54.98187
324586	cg1780818	22641331	22641331	0.792326	0	1	0.8931251	41.72671
324677	cg1781243	20662375	20662375	0.9022205	0	1	0.6973413	-120.1381
324679	cg1781251	38646365	38646365	0.1052588	0	1	0.2347045	48.5097
324741	cg1781617	21802414	21802414	0.313087	0	1	0.4894513	49.91438
324758	cg1781752	74747366	74747366	0.7854325	0	1	0.6276235	-52.70511
324804	cg1782006	39603403	39603403	0.9172739	0	1	0.7221239	-120.586
324851	cg1782294	64808470	10634487	0.1896414	0	1	0.0542881	-66.64465
324931	cg1782689	42747303	42747303	0.3401022	0	1	0.4526045	22.69356
325005	cg1783117	69692402	69692402	0.3131219	0	1	0.187826	-34.76292
325040	cg1783303	49649482	49649482	0.4000603	0	1	0.2541733	-38.64313
325125	cg1783716	69810325	71724461	0.033033	0	1	0.3170331	374.3439
325144	cg1783816	10653390	10653390	0.5073164	0	1	0.3349075	-47.21096
325147	cg1783836	66669365	66669365	0.5236962	0	1	0.6976428	51.7824
325184	cg1783975	70682329	70682329	0.649311	0	1	0.4981505	-38.33473
325187	cg1784004	58761423	58761423	0.1363783	0	1	0.2572238	38.62074
325195	cg1784025	18672453	18672453	0.1448488	0	1	0.3784071	107.5617

325214	cg1784099	52603312	52603312	0.303921	0	1	0.4077063	20.67675
325261	cg1784341	42727506	33790411	0.9228884	0	1	0.7294632	-122.611
325291	cg1784568	70783337	70783337	0.3989882	0	1	0.2979477	-19.9684
325324	cg1784840	51725388	51725388	0.3740588	0	1	0.2667431	-22.9867
325377	cg1785127	36699438	36699438	0.6836915	0	1	0.4268135	-103.8609
325398	cg1785232	64767390	64767390	0.2582933	0	1	0.3610885	21.79103
325459	cg1785522	58603355	58603355	0.6387314	0	1	0.7923458	51.46498
325577	cg1786255	38697493	38697493	0.4930505	0	1	0.6110404	24.44695
325582	cg1786290	23774440	23774440	0.7566592	0	1	0.8600459	36.24775
325665	cg1786777	40605438	40605438	0.1656484	0	1	0.296393	39.59282
325734	cg17871621	35794392	35794392	0.3272966	0	1	0.135052	-80.28081
325777	cg1787410	52697443	52697443	0.2698337	0	1	0.3971476	30.10976
325812	cg1787629	40769337	40769337	0.2572168	0	1	0.459458	67.59248
325857	cg17878501	26600357	26600357	0.4745415	0	1	0.6128138	31.9327
325895	cg1788070	48690350	48690350	0.1781317	0	1	0.0682336	-45.73792
325935	cg1788306	67673459	67673459	0.6438505	0	1	0.7494093	25.3336
325955	cg1788476	31729411	31729411	0.6351568	0	1	0.7413357	25.07311
325975	cg1788579	61754331	61754331	0.5995224	0	1	0.7027656	22.14926
326112	cg1789436	65804408	65804408	0.5357352	0	1	0.7126201	54.52546
326114	cg1789457	64615429	64615429	0.3258317	0	1	0.5005	48.60221
326212	cg1790146	13609457	13609457		0	1		-4.34E-09
326237	cg1790350	46677482	46677482	0.4297263	0	1	0.573643	33.61986
326284	cg17906851	16669375	68732485	0.6368647	0	1	0.4785149	-41.07749
326332	cg17911021	73700473	73700473	0.5104893	0	1	0.3782211	-29.08702
326356	cg1791340	68658442	51785358	0.7570223	0	1	0.5597861	-71.28596
326377	cg1791567	23747310	16603441	0.6054266	0	1	0.4902424	-23.40548
326498	cg1792299	31729313	31729313	0.5947859	0	1	0.7419345	42.29226
326584	cg1792904	61732494	61785438	0.7620562	0	1	0.6482746	-29.41111
326599	cg1792963	42778478	24628430	0.8531438	0	1	0.4687246	-288.265
326641	cg1793209	54680411	71634319	0.6626226	0	1	0.5552987	-22.10926
326682	cg1793427	43775397	43775397	0.5506068	0	1	0.6932991	36.75787
326845	cg1794332	10725345	74710311	0.1885139	0	1	0.4167035	93.6544
326978	cg1795197	54721318	54721318	0.8117399	0	1	0.6897764	-38.11708
327066	cg1795851	26612425	26612425	0.4112897	0	1	0.5169094	19.81117
327134	cg1796263	57691346	48753432	0.5051364	0	1	0.3861735	-24.25251
327205	cg1796767	42652479	47683506	0.8227691	0	1	0.6176594	-89.68224
327290	cg1797201	55801377	55801377	0.2689267	0	1	0.374784	22.41515
327368	cg1797647	18628445	18628445	0.36827	0	1	0.5133007	34.21976
327603	cg1799191	48806380	48806380	0.745115	0	1	0.8558784	39.36042
327732	cg1800172	11803395	11803395	0.9324747	0	1	0.7035893	-161.0954
327959	cg1801385	14741457	14741457	0.6558623	0	1	0.8882308	136.2014
327982	cg1801503	55684336	53622345	0.5220813	0	1	0.3878506	-29.7513
327993	cg1801562	51612387	51612387	0.6552783	0	1	0.9136589	374.3439

328102	cg18021992	22634366	22634366	0.6073286	0	1	0.919933	374.3439
328180	cg18025438	39724429	53600384	0.6715711	0	1	0.7841678	30.8
328224	cg18027903	64659303	64659303	0.3681504	0	1	0.4956544	27.43761
328239	cg18029321	14773369	15627427	0.7255613	0	1	0.4581514	-117.0947
328579	cg18049365	20749317	20749317	0.5424312	0	1	0.1729926	-239.2113
328720	cg18058072	19698435	19698435	0.3559769	0	1	0.1258258	-110.4913
328852	cg18065195	56632432	56632432	0.7385838	0	1	0.8406996	32.58183
328853	cg18065318	57722402	28716370	0.3870311	0	1	0.2284116	-46.49788
328870	cg18066181	15764473	15764473	0.1366897	0	1	0.3119733	68.90778
328873	cg18066206	40766387	40766387	0.3223476	0	1	0.4537924	29.79138
328989	cg18073702	10662424	10662424	0.669277	0	1	0.7927245	36.47935
329023	cg18075691	44667386	40687509	0.2918113	0	1	0.4021236	23.14087
329052	cg18077580	65638428	55721395	0.4539678	0	1	0.3368681	-24.29167
329183	cg18085660	18797349	18797349	0.2738461	0	1	0.3758015	20.96334
329217	cg18087477	46682331	46682331	0.6687909	0	1	0.5329335	-32.72168
329223	cg18087694	61657497	61657497	0.4470513	0	1	0.5529236	19.91737
329248	cg18088906	67808397	67808397	0.6181261	0	1	0.7506824	36.41365
329262	cg18089380	35673462	35673462	0.771614	0	1	0.8862407	48.25889
329264	cg18089426	46749487	21664493	0.4136949	0	1	0.5797859	43.44143
329333	cg18093448	50789402	50789402	0.7058408	0	1	0.9039107	115.3988
329376	cg18096251	15772317	31766326	0.7620376	0	1	0.921666	94.05123
329414	cg18098433	46705300	46705300	0.6725715	0	1	0.773006	24.98884
329417	cg18098534	45759375	45759375	0.9307752	0	1	0.7033051	-158.4831
329470	cg18101138	56696302	33732501	0.5228491	0	1	0.3377454	-53.61557
329471	cg18101140	73696454	73696454	0.4866157	0	1	0.6423947	40.11497
329496	cg18102738	16785412	16785412	0.5329032	0	1	0.6338857	19.4034
329516	cg18104070	74644413	74644413	0.4603672	0	1	0.6187979	40.57762
329641	cg18109485	23629378	23629378	0.5455559	0	1	0.6547687	22.50678
329676	cg18111114	51629438	51629438	0.0620669	0	1	0.2592066	109.4242
329719	cg18113731	67743477	67743477	0.6131727	0	1	0.7134579	21.60113
329795	cg18116815	20656325	20656325	0.5948337	0	1	0.7261586	33.99726
329863	cg18120259	60660316	60660316	0.3415511	0	1	0.4837571	33.534
330015	cg18127410	18628506	30793406	0.2536401	0	1	0.1130748	-53.20357
330044	cg18128914	41774408	31634314	0.3630823	0	1	0.2143863	-42.97245
330054	cg18129296	52643353	52643353	0.5763842	0	1	0.744308	52.89544
330060	cg18129748	64665323	27793432	0.2068249	0	1	0.0968053	-39.53337
330068	cg18129996	27733307	27733307	0.5704463	0	1	0.6807162	23.68672
330108	cg18132363	59669394	59669394	0.1819256	0	1	0.2879196	27.21183
330192	cg18137779	16712471	16712471	0.5146382	0	1	0.814813	374.3439
330208	cg18138788	67667410	67667410	0.5968889	0	1	0.4934854	-19.53482
330271	cg18142730	17650424	17650424	0.794555	0	1	0.8955789	42.48196
330349	cg18146506	31784507	35749469	0.2029474	0	1	0.0680825	-61.49603
330734	cg18167946	49786505	49786505	0.2532676	0	1	0.3599224	23.29796

330748	cg1816892	65652445	65652445	0.4153726	0	1	0.2456307	-50.59873
330777	cg1817054	51703355	51703355	0.6886752	0	1	0.8262272	48.32701
330805	cg1817251	47666425	47666425	0.5411718	0	1	0.7493226	77.05352
330919	cg1817883	62753314	62753314	0.4095902	0	1	0.6350469	78.23401
330991	cg1818214	65806464	14759469	0.2349426	0	1	0.129494	-32.22064
331035	cg1818421	39675302	60713458	0.3297843	0	1	0.4691085	32.65948
331119	cg1818911	24641487	24641487	0.7844589	0	1	0.6536827	-38.94998
331169	cg1819174	39654422	39654422	0.1228601	0	1	0.299924	73.2854
331280	cg1819759	30777480	22606501	0.2519412	0	1	0.1337343	-37.70445
331424	cg1820685	71800437	71800437	0.9270024	0	1	0.8238518	-53.98529
331463	cg1820935	39698449	30614324	0.5474907	0	1	0.6502117	20.3019
331554	cg1821762	63639332	29753412	0.3872938	0	1	0.5075049	24.67137
331622	cg18221341	44712443	44712443	0.3612622	0	1	0.4615443	18.5715
331765	cg1822919	32720509	32720509	0.7262168	0	1	0.8535526	47.95888
331816	cg1823223	37622316	19617432	0.6227914	0	1	0.2371148	-249.4768
331893	cg1823574	74796359	74796359	0.3090369	0	1	0.4416434	30.62933
331908	cg1823658	56748399	56748399	0.8705037	0	1	0.7427638	-52.10413
331928	cg1823739	54606493	54606493		0	1		-4.34E-09
331940	cg1823773	59617323	59617323	0.2576567	0	1	0.3584348	21.14977
331970	cg18239511	31669324	31669324	0.3367223	0	1	0.0750041	-158.9736
331985	cg1824039	34758345	20710362	0.3867281	0	1	0.2778055	-23.13077
332008	cg1824155	36766333	36766333	0.2939816	0	1	0.4014543	22.13339
332046	cg1824384	59632301	59632301	0.1823622	0	1	0.2973554	30.84021
332249	cg1825694	70761332	18774336	0.2446699	0	1	0.3478301	22.4698
332349	cg1826316	32613407	32613407	0.4462654	0	1	0.5551614	20.86741
332368	cg1826409	51614455	51614455	0.3781452	0	1	0.4914354	22.42989
332724	cg1828533	62704331	62704331	0.4971197	0	1	0.674755	52.15304
332730	cg1828563	42663455	42663455	0.762631	0	1	0.8721916	41.93575
332773	cg1828853	12763351	24637492	0.4644081	0	1	0.31727	-36.22987
332937	cg1830246	63637364	63637364	0.4616836	0	1	0.5823407	24.95046
333075	cg1831063	22750426	22750426	0.4664827	0	1	0.5717211	19.83591
333109	cg1831309	20750478	20750478	0.4768206	0	1	0.5978334	25.27134
333121	cg1831341	56641438	56641438	0.3485189	0	1	0.4659309	24.18442
333227	cg1831936	59609370	59609370	0.2720201	0	1	0.3904886	26.69684
333275	cg1832192	38679509	38679509	0.4978177	0	1	0.6277736	29.08359
333278	cg1832202	73790449	73790449	0.5840138	0	1	0.4736582	-21.54704
333285	cg1832258	38604422	32672417	0.6616206	0	1	0.521342	-34.21996
333361	cg1832712	43622441	72679507	0.617547	0	1	0.4597647	-40.25459
333462	cg1833281	24660360	24660360	0.2006587	0	1	0.3648207	52.13344
333463	cg1833283	15750345	15750345	0.5299505	0	1	0.6790578	38.77109
333466	cg1833309	60758320	60758320	0.5469537	0	1	0.3751456	-46.20603
333678	cg1834663	25688486	25688486	0.2409003	0	1	0.4640827	82.50576
333872	cg1835921	63713492	63713492	0.6273652	0	1	0.9204257	374.3439

333900	cg1836142	38652398	38652398	0.5802251	0	1	0.7376639	46.86113
333934	cg1836391	44720423	72657405	0.5809868	0	1	0.4605991	-24.84319
334002	cg1836903	41755416	41755416	0.5188235	0	1	0.6829551	45.90808
334070	cg1837331	57639333	70647447	0.1586511	0	1	0.0559425	-44.63885
334213	cg1838398	59712332	62658412	0.5297996	0	1	0.4217538	-20.54801
334216	cg1838409	54661343	54661343		0	1	0.9023973	4.34E-09
334338	cg1839120	15607400	15607400	0.6794859	0	1	0.4953755	-55.85996
334419	cg1839535	50618432	50618432	0.349294	0	1	0.5077437	40.30328
334465	cg1839698	42719428	42719428	0.4713216	0	1	0.2630824	-70.73015
334477	cg1839745	71715420	39692388	0.1085773	0	1	0.2436864	51.0266
334522	cg1840028	44685449	44685449	0.5803683	0	1	0.7069605	30.88643
334575	cg1840367	35631307	35631307	0.6914436	0	1	0.3046201	-248.979
334655	cg1840827	67686379	67686379	0.2523736	0	1	0.3693584	27.02542
334732	cg1841321	62675325	62675325	0.5748795	0	1	0.4116848	-42.04519
334790	cg1841724	30753390	30753390	0.5773631	0	1	0.3736985	-63.53197
334797	cg1841762	22740372	22740372	0.2211267	0	1	0.1055472	-40.87598
334809	cg1841824	24632416	24632416	0.6130697	0	1	0.7323276	29.50067
334913	cg1842463	21718331	21718331	0.2222003	0	1	0.4209923	69.12391
335041	cg1843185	55604411	55604411	0.4874539	0	1	0.3493559	-31.73549
335090	cg1843435	72748422	72748422	0.311249	0	1	0.4275726	24.62288
335125	cg1843627	17740354	17740354	0.6840287	0	1	0.7866417	26.90134
335149	cg1843719	12788411	58659490	0.9166568	0	1	0.7912771	-65.6549
335154	cg1843755	10800325	10800325	0.7763751	0	1	0.9112698	70.23811
335259	cg1844374	22728380	22728380	0.4879939	0	1	0.2567246	-86.36403
335278	cg1844475	20699419	20699419	0.6357454	0	1	0.4463561	-56.4793
335300	cg1844644	42799423	42799423	0.2508439	0	1	0.3739151	29.40124
335513	cg1845680	47788300	47788300	0.3641312	0	1	0.5019262	31.37304
335545	cg1845835	22756322	22756322	0.3288077	0	1	0.4294206	19.15808
335851	cg1847653	74600356	44758432	0.1177651	0	1	0.2664365	56.91661
335853	cg1847656	30646465	30646465	0.2150702	0	1	0.3322968	29.24598
335933	cg1848065	70607379	70607379	0.6090241	0	1	0.7203102	25.77916
336036	cg1848623	52645457	52645457	0.6257808	0	1	0.7406336	28.31223
336122	cg1849294	17605353	17605353	0.322009	0	1	0.4451023	26.71923
336208	cg1849723	43603334	43603334	0.5575003	0	1	0.7156238	45.28109
336225	cg1849811	74803328	74803328	0.2931491	0	1	0.4099472	25.32565
336272	cg1850044	18746310	21703329	0.4411721	0	1	0.3325738	-21.56915
336305	cg1850223	14718442	14718442	0.3043486	0	1	0.4365979	30.64579
336340	cg1850382	35600395	35600395	0.7284465	0	1	0.8675171	58.24728
336353	cg1850498	35754305	35754305	0.2273823	0	1	0.3550819	32.64116
336411	cg1850952	36778350	36778350	0.5779159	0	1	0.4652705	-22.22292
336454	cg1851293	43642477	43642477	0.1674744	0	1	0.2716536	27.67437
336476	cg1851470	18775345	18775345	0.7691008	0	1	0.6474537	-33.28407
336663	cg1852614	31777387	31777387	0.2186918	0	1	0.3282776	26.08366

336740	cg18530748	27674480	27674480	0.1793423	0	1	0.3032573	34.96523
336877	cg18538668	57613469	57613469	0.2507402	0	1	0.4501088	66.46104
336910	cg18540674	47703489	34638494	0.4297531	0	1	0.5408131	21.51144
336977	cg18544888	56619423	56619423	0.5226663	0	1	0.6744429	39.71522
337048	cg18550212	47738353	47738353	0.3815666	0	1	0.5182855	30.75719
337182	cg18558968	24730370	62631352		0	1	0.9666369	4.34E-09
337183	cg18558969	32634441	32634441	0.825627	0	1	0.6433914	-74.85944
337202	cg18559901	33808339	33808339	0.6760721	0	1	0.3609682	-156.516
337230	cg18561676	23642315	25610431	0.4309056	0	1	0.25462	-53.26261
337322	cg18566555	69619467	69619467	0.149552	0	1	0.2674836	35.50874
337439	cg18574144	41738380	41738380	0.7078447	0	1	0.8261194	38.32595
337474	cg18576044	68603321	68603321	0.4571579	0	1	0.0373717	-371.3336
337519	cg18578974	44742476	44742476	0.5926932	0	1	0.7132407	28.8744
337651	cg18586886	59686310	25634375	0.2080168	0	1	0.3292081	31.3401
337664	cg18587476	66713393	16746438	0.5544955	0	1	0.4517375	-18.97999
337781	cg18594054	42643354	42643354	0.5350921	0	1	0.6470637	23.21458
337792	cg18594701	16771328	16771328	0.6014525	0	1	0.7027463	21.49806
337802	cg18595137	50743404	50743404	0.4119592	0	1	0.5141801	18.78131
337811	cg18595348	49600459	49600459	0.6660563	0	1	0.7780934	30.01722
337832	cg18596626	67608471	56619403	0.8078573	0	1	0.9683897	129.2439
337838	cg18596939	45791316	45791316	0.7087877	0	1	0.8272844	38.60769
337879	cg18599206	22725391	22725391	0.1128467	0	1	0.2500431	51.32253
338013	cg18609120	20639370	20639370	0.3443438	0	1	0.4562727	22.43129
338058	cg18612167	19683443	19683443	0.3164183	0	1	0.2072769	-26.62469
338088	cg18614735	72666418	72666418	0.5300609	0	1	0.4051636	-26.22366
338139	cg18618815	72789442	72789442	0.4979449	0	1	0.641177	34.68813
338172	cg18621672	54794373	54794373	0.1111756	0	1	0.3984346	374.3439
338175	cg18621852	49649455	49649455	0.6228728	0	1	0.521647	-19.26952
338219	cg18625305	38786353	38786353	0.5792021	0	1	0.4559498	-25.82249
338267	cg18628853	15752508	15752508	0.703895	0	1	0.8459558	54.78287
338290	cg18630644	30663428	71604489	0.7161348	0	1	0.6159772	-21.67374
338352	cg18634211	65675489	65675489	0.3896903	0	1	0.2860489	-21.12308
338535	cg18644703	24744359	42742445	0.5031127	0	1	0.3566819	-34.96992
338634	cg18650219	26727330	26727330	0.5911745	0	1	0.6923388	21.0648
338638	cg18650367	44770510	44770510	0.4788339	0	1	0.6502652	47.76966
338860	cg18667659	18600413	47657432	0.666698	0	1	0.5275189	-33.9793
338868	cg18668511	73803381	73803381	0.839918	0	1	0.7178983	-42.44349
338925	cg18672030	61724489	61724489	0.4350933	0	1	0.5587056	25.79738
338999	cg18676967	62800469	62800469	0.5141556	0	1	0.4140259	-18.15799
339023	cg18678645	30651474	30651474	0.6107293	0	1	0.4609037	-36.62037
339037	cg18679504	24634453	45682460	0.5097145	0	1	0.317655	-58.03375
339050	cg18680181	55777484	55777484	0.5718491	0	1	0.6848956	24.80572
339109	cg18684755	48604510	48604510	0.8967968	0	1		-4.34E-09

339311	cg1869879	71781488	71781488	0.6924856	0	1	0.9506763	374.3439
339327	cg1869974	17610311	50803478	0.4560803	0	1	0.1325455	-196.1432
339458	cg18707191	56623390	56623390	0.0690154	0	1	0.1694832	40.00816
339504	cg18709881	13716416	35614448	0.7732904	0	1	0.6627821	-28.98092
339506	cg1870990	36760466	36760466	0.8160102	0	1	0.9170898	48.89306
339507	cg1871005	57759456	30709321	0.4906814	0	1	0.3254094	-44.05994
339508	cg1871016	52787416	52787416	0.5618393	0	1	0.6757138	24.75216
339527	cg1871153	17630435	17630435	0.312102	0	1	0.4880378	49.7375
339592	cg1871519	55607332	55607332	0.7130747	0	1	0.8998646	104.1913
339664	cg1871956	62610332	42774428	0.8310128	0	1	0.716185	-37.34642
339690	cg1872080	36780455	36780455	0.675342	0	1	0.7821392	28.21136
339726	cg1872327	24728328	69768312	0.8015083	0	1	0.7006012	-27.52666
339836	cg1873086	44794322	44794322	0.3297567	0	1	0.4452925	23.90827
339929	cg1873683	62763467	62763467	0.7520989	0	1	0.859219	38.04821
340103	cg1874852	64734310	64734310	0.3576521	0	1	0.5143179	39.35141
340218	cg18755531	65673494	26705407	0.5984052	0	1	0.4351116	-42.36542
340249	cg18756771	58784415	58784415	0.5039467	0	1	0.604934	18.91495
340251	cg18756931	18673412	18673412	0.5907264	0	1	0.7360843	40.94159
340258	cg1875717	21604380	50633484	0.4023394	0	1	0.2966222	-21.48689
340266	cg1875781	46676349	46676349	0.7775643	0	1	0.5578411	-89.60294
340357	cg1876195	59759492	59759492	0.4988141	0	1	0.6791228	53.81607
340358	cg1876197	13705477	13705477	0.2161784	0	1	0.3663139	43.49307
340383	cg1876280	18783464	61769414	0.6268336	0	1	0.5148385	-22.74522
340406	cg1876416	54684365	54684365	0.5476578	0	1	0.6722691	28.50394
340418	cg18764771	23773404	23773404	0.1876915	0	1	0.2931187	26.5519
340431	cg1876556	30701412	69737303	0.2498166	0	1	0.1088734	-54.3348
340535	cg1877094	34736429	34736429	0.5636076	0	1	0.3805468	-51.91233
340549	cg1877155	30745384	30745384	0.6813283	0	1	0.5427824	-34.38305
340550	cg1877157	16795398	16795398	0.6085104	0	1	0.5018555	-20.69939
340560	cg1877193	45603442	45603442	0.8158631	0	1	0.619577	-81.82607
340593	cg1877393	66607479	66607479	0.5077007	0	1	0.6294277	26.12668
340597	cg1877417	15750484	15750484	0.6022393	0	1	0.7328125	34.14894
340633	cg1877646	59716352	59716352	0.3114254	0	1	0.5380567	79.39282
340722	cg1878260	33640410	69771399	0.1056854	0	1	0.2371849	49.58233
340778	cg1878622	15670369	15670369	0.2945916	0	1	0.4066034	23.62888
340856	cg1879034	21802416	21802416	0.4242682	0	1	0.5426084	23.92127
340897	cg1879253	59607453	37656490	0.6082008	0	1	0.0799996	-371.3336
340987	cg1879765	65706357	65706357	0.5074733	0	1	0.3948926	-22.07363
341051	cg1880150	29715318	29715318	0.9450908	0	1	0.7543037	-136.1507
341126	cg1880516	51795502	49795427	0.3752558	0	1	0.6670289	132.6617
341153	cg1880671	34733372	34733372	0.2818784	0	1	0.4097423	29.79938
341174	cg18808261	31775510	31775510	0.59395	0	1	0.4788505	-23.20922
341341	cg1881612	40800307	60804314	0.9207602	0	1	0.5098551	-371.3336

341344	cg1881639	63781395	63781395	0.1629016	0	1	0.2791756	33.25225
341438	cg1882295	39802455	39802455	0.9368634	0	1	0.8349522	-57.28105
341517	cg1882826	45742508	45742508	0.2439752	0	1	0.7971303	374.3439
341521	cg1882836	68786375	68786375	0.3416718	0	1	0.2171994	-32.01891
341585	cg1883224	32721320	32721320	0.3904626	0	1	0.5576096	43.87134
341589	cg1883261	64706315	64706315	0.6388124	0	1	0.459949	-51.03569
341734	cg1884235	62643339	62643339	0.1644395	0	1	0.2823857	33.83308
341746	cg1884325	23606377	23606377	0.3378499	0	1	0.1635622	-63.06949
341785	cg1884559	64729449	64729449	0.3377612	0	1	0.6101079	113.6044
341792	cg1884595	23655331	39745490	0.3955512	0	1	0.1239511	-146.4959
341814	cg1884759	37742467	37742467	0.3055763	0	1	0.698347	374.3439
342047	cg1886176	66694457	66694457	0.0460866	0	1	0.24395	118.4078
342058	cg1886221	30730442	30730442	0.2286949	0	1	0.3354132	24.47672
342092	cg1886412	54703465	54703465	0.6109429	0	1	0.7324404	30.39582
342141	cg1886621	71749347	71749347	0.2739121	0	1	0.404691	31.27517
342175	cg1886791	68708477	65731382	0.8815993	0	1	0.7386436	-64.87472
342223	cg1887201	14605399	14605399	0.1324742	0	1	0.2365406	31.22047
342243	cg1887350	40700434	40700434	0.7948557	0	1	0.5462527	-115.2495
342255	cg1887396	54692329	10612501	0.5603995	0	1	0.6972625	34.51647
342370	cg1887982	18622333	18622333	0.2638268	0	1	0.3738898	24.04198
342489	cg1888634	15615488	15615488	0.4835311	0	1	0.6294149	35.42814
342545	cg1888978	41772482	41772482	0.1315394	0	1	0.2345558	30.85814
342675	cg1889863	73652446	73652446	0.7906515	0	1	0.6760207	-32.30295
342751	cg1890455	57804445	57804445	0.5743998	0	1	0.6791028	21.76467
342859	cg1891220	12717429	33798456	0.2608026	0	1	0.1113885	-58.78545
342872	cg1891285	73627398	52719449	0.002572	0	1	0.1361168	92.37933
342886	cg1891384	27768316	27768316	0.8744255	0	1	0.7223496	-68.631
342899	cg1891475	22696464	22696464	0.5547554	0	1	0.6843486	30.92433
343015	cg1892198	26643444	18749330	0.1646645	0	1	0.0569132	-47.50388
343128	cg1893091	67639417	67639417	0.0848752	0	1	0.2309135	63.59873
343149	cg1893200	13771476	13771476	0.6524233	0	1	0.7766727	35.13924
343223	cg1893739	36698324	36698324	0.149874	0	1	0.2535601	29.12412
343239	cg1893890	28607449	28607449	0.2283611	0	1	0.0689299	-77.97769
343252	cg1894004	29738408	18643318	0.4791998	0	1	0.155589	-188.1278
343326	cg1894464	17610306	24766383	0.8880503	0	1	0.760206	-57.04758
343411	cg1894972	10737407	10737407	0.6438253	0	1	0.30303	-184.8848
343620	cg1896408	60705361	60705361	0.530683	0	1	0.3632746	-44.20829
343653	cg1896615	60689504	60689504	0.4500732	0	1	0.5670211	23.55267
343753	cg1897386	53621510	53621510	0.3522439	0	1	0.4550041	19.42788
343762	cg1897492	25750367	25750367	0.370111	0	1	0.5354228	43.1303
343861	cg1898292	73759472	73759472	0.2711289	0	1	0.3815999	23.9
343891	cg1898498	49726348	49726348	0.1999834	0	1	0.3118227	28.16782
343950	cg1898905	47798444	58669418	0.5833601	0	1	0.4568913	-27.01257

344075	cg1899791	73799498	73799498	0.7231702	0	1	0.6019103	-29.72041
344126	cg1900129	33738369	33738369	0.4687113	0	1	0.5779831	21.14305
344211	cg1900548	19753347	19753347	0.8921852	0	1	0.7586502	-62.09918
344414	cg1901755	12791403	12791403	0.3547769	0	1	0.4794676	26.61493
344513	cg1902457	66683313	66683313	0.6054035	0	1	0.716043	25.32605
344555	cg1902681	72688464	72688464	0.6165887	0	1	0.7851219	58.58451
344583	cg1902846	23709435	23709435	0.557274	0	1	0.6615548	21.09225
344766	cg1903992	18772410	18772410	0.9461599	0	1	0.8459435	-60.47986
344820	cg1904367	28634462	28634462	0.7961045	0	1	0.8999589	45.38864
344823	cg1904380	37690425	37690425	0.3567912	0	1	0.4817185	26.66774
344862	cg1904597	38642499	38642499	0.0471248	0	1	0.2019099	83.71507
344878	cg1904693	62747452	56669392	0.6215106	0	1	0.7252344	23.32111
344891	cg1904766	39632473	19788466	0.3610322	0	1	0.2594075	-21.36209
344941	cg1905055	53626330	53626330	0.5259252	0	1	0.6401757	23.80341
344996	cg1905415	50692499	38620328	0.542834	0	1	0.2977385	-93.08405
345088	cg1906169	16654445	16654445	0.4103339	0	1	0.5281713	23.75519
345120	cg1906430	16806431	16806431	0.5307276	0	1	0.6402273	22.22686
345165	cg1907008	51641443	51641443	0.1790844	0	1	0.3001517	33.73648
345253	cg1907749	59686444	59686444	0.4310313	0	1	0.5350038	19.29219
345301	cg1908157	39616332	64729355	0.4978321	0	1	0.6836219	57.04412
345343	cg1908403	22697405	22697405	0.3564303	0	1	0.4815475	26.74129
345358	cg1908462	15678303	21616417	0.8513207	0	1	0.7506846	-33.4257
345428	cg1908914	13650302	13650302	0.7258458	0	1	0.3828045	-193.2507
345636	cg1910156	41708499	41708499	0.7781229	0	1	0.8880597	45.89928
345662	cg1910317	69780387	55632318	0.6867411	0	1	0.8087891	37.77049
345719	cg1910693	70727507	13769303	0.2547971	0	1	0.0886437	-75.76921
345796	cg1911137	14791415	14791415	0.6177515	0	1	0.7265921	25.21908
345811	cg1911235	43715460	43715460	0.5891195	0	1	0.7551997	53.15914
345819	cg1911297	39655422	58802319	0.2873517	0	1	0.1720052	-31.93472
345830	cg1911368	62787444	52670483	0.7983441	0	1	0.6846814	-32.6776
345870	cg1911619	58774450	58774450	0.4579478	0	1	0.3509105	-20.76348
345948	cg1912198	17612323	29675408		0	1	0.001653	4.34E-09
346140	cg1913734	53769423	68711421	0.1099217	0	1	0.2368978	46.19777
346183	cg1914033	53809370	22730398	0.9241293	0	1	0.7467934	-109.8516
346186	cg1914042	20787496	63779377	0.5351521	0	1	0.4296679	-19.75355
346243	cg1914508	18765434	18765434	0.4379143	0	1	0.5380897	18.16394
346249	cg1914532	42631416	42631416	0.5327259	0	1	0.6978726	47.37252
346351	cg1915281	72749376	72749376	0.4879148	0	1	0.6024632	23.14774
346356	cg1915322	19720454	19720454	0.334826	0	1	0.4440714	21.73371
346387	cg1915593	43749462	39638415	0.7636027	0	1	0.6427932	-32.44465
346388	cg1915604	24621302	24621302	0.9019821	0	1	0.694625	-122.0847
346472	cg1916230	19617336	51760401	0.9306303	0	1	0.8027493	-74.02177
346490	cg1916339	14795356	14795356	0.7415662	0	1	0.9053119	88.9351

346495	cg1916393	32709467	37750441	0.5244855	0	1	0.6421119	25.00901
346664	cg1917850	70712376	70712376	0.6852968	0	1	0.7939534	30.05739
346685	cg1917991	74661377	74661377	0.8170305	0	1	0.9429965	79.35651
346710	cg1918152	25651436	10665457	0.7199677	0	1	0.5815146	-36.60868
346728	cg1918291	41702481	41702481	0.8010167	0	1	0.9091657	50.94361
346731	cg1918316	34778379	27645367	0.4098645	0	1	0.2864651	-27.93933
346737	cg1918339	69684305	69684305	0.5027539	0	1	0.283162	-76.35562
346808	cg1918820	64642350	64642350	0.7141111	0	1	0.829941	37.68201
346849	cg1919127	48655375	24616329	0.8679047	0	1	0.7385652	-52.41254
346874	cg1919262	32620442	32620442	0.3871397	0	1	0.5463077	40.15981
346906	cg1919464	63739487	63739487	0.4729598	0	1	0.5819008	21.0764
346925	cg1919640	28656499	64758359	0.5278646	0	1	0.3880638	-31.91908
346943	cg1919774	60653364	12766507	0.3287248	0	1	0.4346958	20.8104
346947	cg1919788	49737495	42794429	0.7288728	0	1	0.5496053	-57.3499
346985	cg1920058	18783416	21641317	0.5199971	0	1	0.3943134	-26.54863
346989	cg1920095	57715418	57715418	0.3219753	0	1	0.4376214	24.12082
346993	cg1920114	12668447	12668447	0.2430307	0	1	0.3481534	23.2162
347022	cg1920357	41729330	73749471	0.2963631	0	1	0.4026336	21.67315
347035	cg1920492	52618403	52618403	0.675272	0	1	0.8233931	53.65117
347212	cg1921808	46650473	58732404	0.6849413	0	1	0.7946587	30.57907
347269	cg1922239	53804325	53804325	0.8176125	0	1	0.9435779	79.70516
347327	cg1922595	62655484	62655484	0.7362891	0	1	0.8473971	38.05762
347370	cg1922921	41615359	41615359	0.2539107	0	1	0.3621078	23.80403
347408	cg1923238	57630337	48795476	0.4668184	0	1	0.3647776	-19.05366
347467	cg1923632	16618399	16618399	0.7605293	0	1	0.6529618	-26.83817
347474	cg1923667	39622372	39622372	0.8953814	0	1	0.6918275	-115.4642
347518	cg1923904	36808446	36808446	0.6975978	0	1	0.5938287	-22.12082
347587	cg1924261	72628304	72628304	0.6036165	0	1	0.9323199	374.3439
347613	cg1924403	27615359	27615359	0.1875402	0	1	0.3938206	78.79754
347653	cg1924594	59606503	59606503		0	1	0.091861	4.34E-09
347723	cg1924981	17795473	24793332	0.6501189	0	1	0.902716	374.3439
347839	cg1925582	69638391	46603391	0.1936795	0	1	0.0387996	-87.83546
347914	cg1925980	70606369	70606369	0.2379941	0	1	0.1298825	-33.40734
347974	cg1926360	43620445	43620445	0.4919423	0	1	0.3770297	-22.97308
348216	cg1927634	52623476	66609339	0.383164	0	1	0.264066	-27.26591
348220	cg1927673	74733353	20648379	0.3888207	0	1	0.2678044	-27.81206
348332	cg1928552	71768474	71768474	0.5275542	0	1	0.7486898	85.57989
348415	cg1929169	13748308	13748308	0.4340755	0	1	0.6840219	98.53712
348501	cg1930019	10720447	10720447	0.5302716	0	1	0.3668022	-42.30801
348504	cg1930040	38724489	38724489	0.5240074	0	1	0.9543688	374.3439
348509	cg1930054	18720498	18720498	0.5073093	0	1	0.6528649	36.06946
348535	cg1930189	29810355	29810355	0.4966694	0	1		-4.34E-09
348565	cg1930352	69647415	69647415	0.6976451	0	1	0.8268489	43.99157

348620	cg1930649	16807337	43714304	0.0138607	0	1	0.1269365	68.39566
348659	cg1930898	11636377	11636377	0.5244894	0	1	0.6603292	32.37516
348697	cg1931137	60640379	60640379	0.4570967	0	1	0.6190054	42.1665
348871	cg1932328	63752427	63752427	0.2672704	0	1	0.3994749	32.15527
348911	cg1932579	16661434	16661434	0.2305625	0	1	0.3476009	28.20349
348983	cg1933198	72621403	72621403	0.5616847	0	1	0.6957268	33.26957
349075	cg1934029	51696419	51696419	0.2988004	0	1	0.5532883	100.1433
349141	cg1934487	68703407	68703407	0.8292461	0	1	0.934038	58.16003
349254	cg1935305	23654413	23654413	0.8005702	0	1	0.9187729	61.39021
349382	cg1936021	48673335	48673335	0.838863	0	1	0.9555675	79.64574
349417	cg1936247	31614361	31614361	0.4262342	0	1	0.5361714	21.14724
349422	cg1936277	36649386	13798457	0.9296191	0	1	0.6476705	-211.6877
349495	cg1936717	35634328	28751497	0.9162455	0	1	0.7549093	-92.49089
349507	cg1936785	54795417	54795417	0.6909698	0	1	0.8257307	46.73871
349585	cg1937250	60705397	60705397	0.5682935	0	1	0.7477569	59.57161
349598	cg1937334	37624483	37624483	0.3148361	0	1	0.1878864	-35.486
349636	cg1937541	29773383	29773383	0.577149	0	1	0.7508991	56.78347
349678	cg1937760	74654306	74654306	0.4386761	0	1	0.5393689	18.31838
349715	cg1938015	62608399	62608399	0.611867	0	1	0.7247692	26.61591
349763	cg1938336	62758370	61672505	0.5624186	0	1	0.4360801	-26.78939
349845	cg1938937	60619466	59765345	0.3104758	0	1	0.201242	-27.06333
349899	cg1939255	35758373	35758373	0.4984325	0	1	0.3876206	-21.5513
349971	cg1939819	65712353	42639385	0.4426404	0	1	0.3380793	-20.19851
349976	cg1939845	71803437	71803437	0.4518004	0	1	0.5556688	19.31925
350062	cg1940331	38619467	38619467	0.3246903	0	1	0.4690594	34.84681
350117	cg1940588	28672500	28672500	0.3798882	0	1	0.4817419	18.84884
350175	cg1940857	22647322	26687438	0.1546063	0	1	0.0331254	-65.40038
350232	cg1941173	60751362	60751362	0.4250448	0	1	0.5450627	24.49942
350310	cg1941574	68625351	68625351	0.8363782	0	1	0.3269764	-371.3336
350345	cg1941831	60709383	60709383	0.584891	0	1	0.7527375	53.80909
350347	cg1941852	40631412	40631412	0.3058752	0	1	0.4106711	20.94796
350361	cg1941929	39699342	71736313	0.2410572	0	1	0.3581411	27.63547
350461	cg1942657	74655465	14802305	0.6304041	0	1	0.5127789	-24.71841
350495	cg1942860	46662383	46662383	0.7387386	0	1	0.8812075	64.42834
350726	cg1944264	52704394	74665486	0.3012405	0	1	0.1674446	-40.83788
350813	cg1944796	46763425	59680396	0.5186131	0	1	0.3660188	-37.44006
350814	cg1944796	24796508	24796508	0.3852843	0	1	0.5554172	45.32836
350848	cg1944994	66788487	66788487	0.1159313	0	1	0.2220608	34.38812
350863	cg1945081	30628447	30628447	0.5868224	0	1	0.7148337	31.90656
351047	cg1946319	69779335	69779335	0.4182004	0	1	0.5672503	35.71313
351138	cg1946944	19685405	19685405	0.2332562	0	1	0.3670471	34.78641
351154	cg1947081	50687414	50687414	0.4862108	0	1	0.5902572	19.65036
351168	cg1947146	44792377	44792377	0.7041777	0	1	0.5783191	-30.44658

351236	cg1947590	27728477	32691488	0.8813422	0	1	0.7612312	-50.29457
351258	cg1947678	35650493	46680357	0.6957105	0	1	0.5873402	-23.60865
351349	cg1948168	58680416	58680416	0.6507202	0	1	0.5426886	-22.01047
351379	cg1948409	25692469	25692469	0.7595271	0	1	0.4485192	-163.7903
351385	cg1948430	26682315	58741495	0.6224006	0	1	0.5188164	-19.98046
351433	cg1948786	61791398	21674385	0.3607469	0	1	0.234549	-31.56462
351483	cg19491221	43711300	43711300	0.9269265	0	1	0.7025824	-152.7557
351540	cg1949561	31707422	31707422	0.3589788	0	1	0.4853075	27.13781
351682	cg1950324	24659420	66736311	0.7938188	0	1	0.6661014	-38.6001
351732	cg1950625	15645445	15645445	0.3738861	0	1	0.4944787	24.92317
351798	cg1950939	37622407	20617345	0.7884414	0	1	0.6449326	-45.65047
351903	cg1951472	72789432	72789432	0.4238575	0	1	0.3081917	-24.47997
351943	cg19516921	32758486	32758486	0.4133815	0	1	0.5500488	30.62017
352008	cg1952023	65796424	65796424	0.2917739	0	1	0.5121564	76.30926
352028	cg1952161	37671427	54784313	0.445106	0	1	0.5587714	22.41541
352092	cg1952549	22736306	55730490	0.4451723	0	1	0.3302982	-23.6738
352159	cg1952970	53619307	36739481	0.9289843	0	1	0.8280843	-53.16954
352271	cg19536781	37640352	37640352	0.8003348	0	1	0.9007878	43.51513
352285	cg1953771	52694336	43710358	0.4123607	0	1	0.1913087	-88.10419
352323	cg1953998	12758378	12758378	0.7688085	0	1	0.8817844	46.12268
352418	cg1954593	59809335	59809335	0.4899275	0	1	0.3633187	-27.17657
352539	cg19553961	32663387	32663387	0.610834	0	1	0.7144191	22.76233
352582	cg1955677	10671472	27751496	0.1837201	0	1	0.0521546	-64.8221
352628	cg1956021	53731484	53731484	0.8176084	0	1	0.9335281	66.30752
352798	cg1957077	32771462	15679450	0.4752236	0	1	0.3656166	-21.37758
352939	cg1957921	66676426	62762448	0.6621752	0	1	0.4832683	-52.10698
353006	cg1958423	19601371	19601371	0.2578639	0	1	0.3655231	23.45268
353041	cg1958567	44725418	44725418	0.7684495	0	1	0.5950246	-58.88111
353278	cg1959687	71733384	71733384	0.5073517	0	1	0.7004678	62.41965
353427	cg1960541	42717455	42717455	0.7300584	0	1	0.8488812	42.35754
353479	cg1960943	37692420	37692420	0.2600009	0	1	0.40363	37.30289
353494	cg1961075	47697491	27663422	0.3465779	0	1	0.2464237	-21.38491
353719	cg1962362	13677339	54604468	0.4556975	0	1	0.3496732	-20.46584
353819	cg1962898	70743474	70743474	0.5100589	0	1	0.7046419	63.62652
353880	cg1963260	59792327	59792327	0.9010718	0	1	0.7874141	-51.93892
353921	cg19635401	68605351	68605351	0.470171	0	1	0.6071023	31.29222
353946	cg1963662	43728500	43728500	0.7061037	0	1	0.8485944	55.62983
354033	cg19640821	63719500	63719500	0.5716633	0	1	0.6903795	27.0677
354037	cg1964132	28633339	34644367	0.6260062	0	1	0.7345058	25.53182
354182	cg1965070	51600390	51600390	0.4947255	0	1	0.627492	30.13937
354187	cg1965111	65652432	65652432	0.4457499	0	1	0.2265889	-81.52558
354205	cg1965175	50649322	50649322	0.5569314	0	1	0.6825032	29.2886
354220	cg1965324	43737438	43737438	0.8258075	0	1	0.6170046	-93.15233

354269	cg1965642	41794410	41794410	0.8844773	0	1	0.5411072	-250.2995
354583	cg1967839	36727471	70710392	0.5349433	0	1	0.3471589	-54.82618
354664	cg1968341	53760422	53760422	0.4338461	0	1	0.5617643	27.35854
354666	cg1968349	50780489	50780489	0.3500599	0	1	0.5223153	46.775
354749	cg1968933	46677368	46677368	0.2902855	0	1	0.436756	36.97624
354758	cg1968987	31612432	31612432	0.6601417	0	1	0.7926125	40.72538
354781	cg1969126	36743375	36743375	0.2052592	0	1	0.3068822	23.95045
354882	cg1969679	34711400	34711400	0.2547052	0	1	0.3599685	22.76237
355034	cg1970521	32679304	32679304	0.428839	0	1	0.53843	21.03917
355076	cg1970765	57743487	57743487	0.5941113	0	1	0.728286	35.3541
355373	cg1972208	15638325	15638325	0.3529601	0	1	0.5285912	48.39274
355423	cg1972456	47774317	47774317	0.2833653	0	1	0.4295315	37.16263
355462	cg1972663	38736359	38736359	0.0405069	0	1	0.4224482	374.3439
355463	cg19726711	53789502	53789502	0.5217457	0	1	0.677107	41.46738
355491	cg1972822	63645353	63645353	0.4586281	0	1	0.357765	-18.78617
355517	cg1972993	20728450	20728450	0.4062992	0	1	0.2820609	-28.42054
355522	cg1973026	72622502	72622502	0.4244679	0	1	0.3226969	-19.62737
355581	cg1973373	63663437	63663437	0.3059203	0	1	0.4639537	41.41252
355627	cg19735421	44720402	44720402	0.8027945	0	1	0.6559876	-49.41541
355834	cg1974593	60730367	60730367	0.1459812	0	1	0.2613267	34.74383
355906	cg1974989	24694465	44652349	0.3271914	0	1	0.4369715	22.05781
355949	cg1975260	35665438	35665438	0.3419406	0	1	0.4499104	21.19945
355997	cg1975483	17683336	43763498	0.2840961	0	1	0.1776169	-27.7496
356017	cg1975581	10773369	26610429	0.9806752	0	1	0.7558216	-203.6608
356080	cg1975883	64717398	64717398	0.5498812	0	1	0.6631907	24.13405
356103	cg19759671	15716438	65697462	0.3092166	0	1	0.5101352	63.41466
356106	cg1975984	43696369	43696369	0.7844629	0	1	0.9039492	56.72085
356246	cg1976698	20616320	20616320	0.4341936	0	1	0.60885	48.02707
356312	cg19770671	19680502	19680502	0.4787757	0	1	0.6173392	32.14706
356385	cg1977468	50611302	50611302	0.0769861	0	1	0.3800698	374.3439
356404	cg1977576	22670481	73781407	0.7463527	0	1	0.6193709	-33.64829
356456	cg1977837	53777447	20734362	0.9415892	0	1	0.6747794	-205.905
356461	cg1977864	50607419	50607419	0.6174515	0	1	0.7208365	22.9897
356601	cg1978701	50641413	40741305	0.808175	0	1	0.5735565	-107.6446
356684	cg19791271	59625487	59625487	0.4609875	0	1	0.7243634	113.589
356799	cg19798881	10622317	42682438	0.1780426	0	1	0.3054575	36.66714
357092	cg1981607	31784354	31784354	0.7759207	0	1	0.8927818	51.46972
357319	cg1982787	67742337	31648360	0.2844851	0	1	0.3986211	24.68671
357361	cg1983037	21709404	60749337	0.9054318	0	1	0.8054129	-44.54776
357396	cg1983256	13755419	13755419	0.3325621	0	1	0.4667169	30.56514
357428	cg1983619	26695382	26695382	0.6577009	0	1	0.7586636	24.21389
357537	cg19843891	29795448	62706410	0.339476	0	1	0.1721078	-57.70022
357545	cg1984428	49775320	49775320	0.5495304	0	1	0.6550522	21.31301

357611	cg19847577	70786455	70786455	0.7311008	0	1	0.4375958	-141.1502
357634	cg19848732	22745427	22745427	0.695383	0	1	0.8381191	53.4955
357637	cg19848924	18686334	18686334	0.7609555	0	1	0.8824639	51.45022
357815	cg19858214	59655427	59655427	0.1437434	0	1	0.2566571	33.89427
357945	cg19864060	61679361	61679361	0.3893387	0	1	0.491991	19.01543
358118	cg19873923	17781439	17781439	0.7525593	0	1	0.6006301	-45.62813
358147	cg19876092	71761486	71761486	0.1732001	0	1	0.3180436	45.56104
358297	cg19885037	35712386	35712386	0.4663548	0	1	0.5875548	25.19805
358304	cg19885625	28772411	28772411	0.0763525	0	1	0.2351765	74.86142
358368	cg19889856	59725332	59725332	0.638928	0	1	0.757374	30.94861
358438	cg19894728	74609367	74609367	0.6650074	0	1	0.7891834	36.41729
358483	cg19897275	41718424	42744398	0.3122595	0	1	0.1580894	-52.57774
358491	cg19898108	11674459	11674459	0.624995	0	1	0.4696105	-39.38428
358511	cg19899539	42755505	42755505	0.4067885	0	1	0.2715148	-33.18473
358576	cg19903927	44719347	29742380	0.7733368	0	1	0.9570833	139.908
358589	cg19904352	31611431	31611431	0.4759423	0	1	0.3516021	-26.54203
358639	cg19907257	21714440	45748377	0.4632116	0	1	0.5723517	21.05267
358760	cg19912739	17667498	17667498	0.4637988	0	1	0.3568621	-20.6479
358915	cg19921651	42773329	42773329	0.339349	0	1	0.5022959	42.57971
359035	cg19927508	15756427	15756427	0.3133818	0	1	0.1619523	-50.5145
359088	cg19930004	17623415	17623415	0.3408652	0	1	0.443391	19.52811
359213	cg19937039	15742318	15742318	0.358866	0	1	0.4675586	21.17262
359215	cg19937061	31777487	56706476	0.1130607	0	1	0.2440193	47.78091
359381	cg19947463	53645471	53645471	0.3499853	0	1	0.4842319	30.23047
359494	cg19954234	44758434	44758434	0.5377216	0	1	0.6532055	24.57753
359566	cg19958593	45670346	45670346	0.350957	0	1	0.5246028	47.4423
359593	cg19960616	50669464	50669464	0.1966103	0	1	0.3375498	41.01741
359604	cg19961153	72760479	52661376	0.6799673	0	1	0.4400559	-90.786
359705	cg19967668	56696355	29681401	0.514884	0	1	0.3108659	-65.15995
359770	cg19972648	48651395	48651395	0.4463785	0	1	0.6431683	60.89179
359789	cg19974120	57652366	57652366	0.2775048	0	1	0.3780539	20.39569
359808	cg19975301	39678468	29753506	0.9147258	0	1	0.7943484	-61.30412
359822	cg19976037	23677489	23677489	0.5621706	0	1	0.7586873	71.08631
359826	cg19976449	44698394	44698394	0.8106945	0	1	0.6735854	-45.539
359874	cg19979108	45742455	45742455	0.1686136	0	1	0.3515968	67.39162
359926	cg19982031	70707453	70707453	0.4050255	0	1	0.5070317	18.73989
359954	cg19983948	63794307	63794307	0.1394307	0	1	0.2577879	36.99593
360008	cg19987900	72739359	72739359	0.2221246	0	1	0.3370514	27.8985
360152	cg19997062	59762379	22730465	0.3906364	0	1	0.2273391	-48.9185
360244	cg20002177	25675354	25675354	0.7767217	0	1	0.6694438	-27.95485
360255	cg20002901	18674314	73703502	0.3088954	0	1	0.4349969	28.17797
360310	cg20006652	60601461	55626498	0.8233851	0	1	0.6889071	-46.19022
360316	cg20007021	61733478	63671402	0.2331061	0	1	0.0567886	-95.57756

360532	cg2002014	32673453	68605367	0.3555678	0	1	0.0949914	-148.1468
360536	cg2002072	51764502	51764502	0.2856249	0	1	0.1796811	-27.36892
360550	cg2002203	44656440	44656440	0.8076671	0	1	0.559095	-118.6437
360616	cg2002636	55661387	55661387	0.7251983	0	1	0.6219346	-23.15829
360640	cg2002794	63760366	63760366	0.7971505	0	1	0.9245919	70.71347
360756	cg2003567	44729502	44729502	0.5144816	0	1	0.6920604	53.26024
360902	cg2004569	42794428	42794428	0.7612543	0	1	0.8869568	55.34857
360935	cg2004804	35687429	35687429	0.2714407	0	1	0.3792042	22.96475
360966	cg2005048	63714318	63714318	0.2239572	0	1	0.3295382	24.31927
361003	cg2005311	45641463	31810473	0.893038	0	1	0.7878139	-44.35354
361122	cg2006063	39792380	39792380	0.5603133	0	1	0.672946	24.2239
361182	cg2006415	49624409	49624409	0.4759908	0	1	0.3112196	-44.32398
361235	cg2006678	67725489	67725489	0.2229804	0	1	0.3260302	23.46799
361337	cg2007331	47630313	17625416	0.9606937	0	1	0.8160616	-107.9027
361384	cg2007612	49774361	49774361	0.3347906	0	1	0.4736753	32.35933
361391	cg2007651	41782446	41782446	0.3768478	0	1	0.4902939	22.49309
361421	cg2007864	66678384	66678384	0.1403305	0	1	0.2551729	35.21243
361423	cg2007880	66714495	66714495	0.321212	0	1	0.4444402	26.78789
361531	cg2008745	53631452	53631452	0.718343	0	1	0.8400479	42.30061
361532	cg2008751	10682449	49799315	0.5596287	0	1	0.3667906	-57.30722
361537	cg2008824	69751485	69751485	0.7719299	0	1	0.6534286	-32.19125
361555	cg2008979	37764504	37764504	0.4832535	0	1	0.6153803	29.61462
361558	cg2009006	41707350	41707350	0.7756066	0	1	0.6059618	-57.77951
361564	cg2009028	58795481	67686425	0.5000304	0	1	0.3894716	-21.45747
361624	cg2009434	27791426	27791426	0.383296	0	1	0.2356396	-40.71626
361816	cg2010607	49631492	49631492	0.4109924	0	1	0.9050019	374.3439
361931	cg2011452	72763473	72763473	0.7331464	0	1	0.8459559	38.68888
361950	cg2011615	33765311	59601326	0.5263703	0	1	0.4245509	-18.64247
362025	cg2011979	55721375	55721375	0.798093	0	1	0.6958864	-27.74577
362027	cg20119891	50617369	50617369	0.4276723	0	1	0.5676865	32.0039
362225	cg2013286	38701360	22791459	0.9859946	0	1	0.8650196	-110.28
362293	cg2013774	63661307	62647384	0.7394376	0	1	0.6302985	-26.05827
362348	cg2014139	63670429	25809507	0.2489433	0	1	0.3633007	26.22479
362373	cg2014276	73630387	73630387	0.4388228	0	1	0.2831319	-41.38373
362397	cg20144261	63723458	63723458	0.633904	0	1	0.7836271	48.18716
362735	cg20164601	24804471	68657454	0.4998106	0	1	0.3631192	-30.95735
362987	cg2018405	55689349	55689349	0.4925139	0	1	0.5962892	19.64013
363037	cg2018801	10758349	10758349	0.726352	0	1	0.8402475	38.30464
363038	cg2018821	12636503	12636503	0.3700344	0	1	0.1059147	-146.6745
363041	cg2018849	45773423	45773423	0.8491433	0	1	0.6738271	-76.49274
363050	cg2018924	41702417	58683406	0.227501	0	1	0.10935	-41.55076
363070	cg2019092	57708313	57708313	0.6630932	0	1	0.5629594	-19.82549
363251	cg2020518	29676313	29676313	0.4897632	0	1	0.7437349	108.9684

363276	cg2020732	15787404	15787404	0.6845664	0	1	0.7946008	30.70933
363300	cg2020860	74785399	74785399	0.5051143	0	1	0.405026	-18.17405
363364	cg2021291	45745470	45745470	0.437149	0	1	0.5601006	25.57155
363391	cg2021487	40789333	40789333	0.3446158	0	1	0.4847718	32.64444
363443	cg2021857	73790507	73790507		0	1	0.8059062	4.34E-09
363500	cg2022320	28672338	28672338	0.5201313	0	1	0.4110652	-20.88434
363507	cg2022368	42650326	16610447	0.7268397	0	1	0.8338968	33.98899
363614	cg2023129	36657311	36657311	0.7415528	0	1	0.8702478	52.61416
363769	cg2024288	15736503	71710493	0.4795277	0	1	0.2011996	-131.3751
363808	cg2024611	54789496	71748377	0.2933763	0	1	0.1383825	-56.42096
363867	cg2024932	11758417	11758417	0.0868917	0	1	0.3471197	151.7644
363887	cg2025034	67750401	67750401	0.213073	0	1	0.332092	30.09529
363989	cg2025537	26731480	30771301	0.6280044	0	1	0.1903462	-345.25
364092	cg2026233	47808302	47808302	0.4979733	0	1	0.3898217	-20.69468
364122	cg2026406	48676422	70637481	0.1693266	0	1	0.037984	-70.47643
364132	cg2026496	49718390	49718390	0.7517604	0	1	0.6499553	-24.09307
364163	cg2026732	41696395	41696395	0.6245784	0	1	0.8069725	70.7903
364197	cg2026904	33757366	20798360	0.151907	0	1	0.0310895	-65.82059
364258	cg2027264	41747302	41747302	0.2779222	0	1	0.4046048	29.5122
364267	cg2027326	67803443	67803443	0.3676986	0	1	0.4714323	19.53097
364331	cg2027678	49660309	49660309	0.8163517	0	1	0.6772324	-47.48735
364394	cg2028160	56683470	74788335	0.3917203	0	1	0.2503729	-36.89841
364405	cg2028255	43628367	30753492	0.3578856	0	1	0.2000047	-48.95467
364427	cg2028401	44796422	44796422	0.2865712	0	1	0.4074481	27.01026
364432	cg2028423	49746434	49746434	0.2414718	0	1	0.3653991	30.2468
364453	cg2028554	31603433	31603433	0.6583543	0	1	0.5556029	-20.51884
364486	cg2028793	60624477	60624477	0.7028851	0	1	0.8058474	28.81187
364499	cg2028861	50689426	50689426	0.4241486	0	1	0.5527808	27.5829
364520	cg2028985	48606406	48606406	0.3160733	0	1	0.441256	27.63232
364660	cg2029967	72697402	72697402	0.7407592	0	1	0.5411031	-70.54438
364680	cg2030051	53768450	53768450	0.3471187	0	1	0.0905595	-146.4888
364688	cg2030078	58697445	58697445	0.6126409	0	1	0.7347347	30.78685
364834	cg2031060	53748416	22764447	0.6748214	0	1	0.5450006	-30.59294
364842	cg2031100	67768324	67768324	0.5323716	0	1	0.7280303	66.60417
364856	cg2031167	48606478	48723444	0.7378013	0	1	0.6161256	-30.82652
364865	cg2031201	17683345	17683345	0.2382688	0	1	0.3827603	39.09198
364877	cg2031241	60802385	60802385	0.8112525	0	1	0.9211671	56.4715
365021	cg2032108	48745481	53754400	0.3280856	0	1	0.1948823	-37.62157
365091	cg2032557	39771403	39771403	0.7331306	0	1	0.8536687	44.20089
365125	cg2032784	24655434	41653386	0.2126275	0	1	0.3441429	35.33397
365168	cg2033115	58644321	58644321	0.2331734	0	1	0.3373554	23.35146
365190	cg2033250	45620310	45620310	0.5387569	0	1	0.6466264	21.85291
365215	cg2033411	33801340	33801340	0.5243319	0	1	0.6408646	24.59878

365246	cg2033601	58689457	58689457	0.6350965	0	1	0.9003653	374.3439
365282	cg2033799	28626323	28626323	0.3874956	0	1	0.2772626	-23.5947
365326	cg2034072	16728426	16728426	0.6305959	0	1	0.7435449	27.76396
365328	cg2034086	11678484	65669459	0.763635	0	1	0.6628905	-24.45696
365370	cg2034438	44636396	44636396	0.456428	0	1	0.5784769	25.39362
365414	cg2034766	68779491	14756391	0.2103894	0	1	0.0895374	-47.03036
365626	cg2036418	49676321	49676321	0.8583019	0	1	0.7317067	-48.55954
365714	cg2037018	70714459	70714459	0.3225039	0	1	0.196924	-34.07357
365742	cg20372591	61778393	61778393	0.4081773	0	1	0.5325401	26.02614
365747	cg2037274	67706308	12660310	0.536678	0	1	0.4117144	-26.23565
365806	cg2037730	39711501	16773420	0.2924596	0	1	0.1716644	-34.35033
365865	cg2038137	15777504	15777504	0.900367	0	1	0.608107	-201.3308
365929	cg2038462	19794463	64625488	0.6968254	0	1	0.8687511	80.29361
365993	cg2038777	13726478	13726478	0.2458639	0	1	0.3600912	26.32724
366013	cg2038873	67755386	67755386	0.1867404	0	1	0.2944283	27.51018
366047	cg20390711	56715415	53601482	0.9283862	0	1	0.7524211	-111.3614
366157	cg2039961	63653479	28680319	0.5416447	0	1	0.3931045	-35.47651
366185	cg2040154	66684405	66684405	0.0305556	0	1	0.1433082	60.15155
366206	cg2040278	66662387	33633366	0.8000922	0	1	0.3996026	-290.1862
366224	cg2040393	34752304	28762345	0.3533753	0	1	0.2092682	-41.28346
366296	cg2040975	48623369	48623369	0.5479506	0	1	0.7539557	76.35461
366320	cg2041155	25618398	25618398	0.6280798	0	1	0.7314377	23.50709
366427	cg2041852	64762372	39730349	0.1615125	0	1	0.2696716	29.87448
366531	cg2042627	36706349	36706349	0.7083478	0	1	0.9122332	124.9762
366664	cg2043385	17795371	17795371	0.3645118	0	1	0.482213	24.04554
366673	cg2043442	71609502	71609502	0.6005713	0	1	0.7203256	28.96648
366790	cg2044191	47727341	67792481	0.8645209	0	1	0.7579281	-38.75465
366916	cg20450471	12656497	38620431	0.531304	0	1	0.4252338	-19.93223
366964	cg20453861	63637430	63637430	0.4771613	0	1	0.6909537	74.04926
367013	cg20457051	74687328	74687328	0.2750336	0	1	0.4734294	63.92445
367053	cg2045903	27804461	27804461	0.0736094	0	1	0.2545153	91.73874
367150	cg2046415	27634393	27634393	0.242788	0	1	0.3428594	21.50889
367164	cg2046488	62676315	62676315	0.6096253	0	1	0.7191172	25.06603
367227	cg2046900	59735428	59735428	0.7180355	0	1	0.8215776	30.78043
367234	cg2046950	27692475	27692475	0.207376	0	1	0.3875124	60.02635
367352	cg2047770	37713507	37713507	0.5835086	0	1	0.4426894	-32.46484
367376	cg2047920	17633366	17633366	0.8864133	0	1	0.5910826	-195.8946
367514	cg2048867	16785488	16785488	0.5050418	0	1	0.6936952	59.35394
367614	cg2049477	42605490	42605490	0.403342	0	1	0.5081363	19.58563
367751	cg2050390	59775378	59775378	0.5820355	0	1	0.6856055	21.61382
367752	cg2050391	41745467	39679510	0.5518234	0	1	0.3953173	-38.93527
367790	cg2050680	21800380	46796390	0.8121165	0	1	0.9310523	67.39506
367794	cg2050727	25806371	25806371	0.1371507	0	1	0.3116933	68.34488

367816	cg2051003	11709493	11709493	0.3086593	0	1	0.4633425	39.80043
367875	cg2051341	68734497	68734497	0.6022296	0	1	0.7256293	30.71854
368004	cg2052239	20643447	20643447	0.3226169	0	1	0.4499399	28.24166
368080	cg2052878	28708301	28708301	0.4682872	0	1	0.6038607	30.7056
368106	cg2053084	47798492	47798492	0.6215444	0	1	0.3955756	-78.16257
368143	cg2053398	57741364	57741364	0.4454837	0	1	0.6138181	45.05351
368191	cg20536971	48795471	48795471	0.823164	0	1	0.6324422	-79.86642
368238	cg2054023	13606314	13606314	0.3864236	0	1	0.5776436	56.34305
368387	cg2054929	73796474	73796474	0.86693	0	1	0.4972611	-274.6334
368394	cg2055001	20688329	74727490	0.3226596	0	1	0.5984679	116.8173
368430	cg2055300	16702322	16702322	0.3078088	0	1	0.4239518	24.65475
368450	cg2055437	70636447	70636447	0.8012964	0	1	0.6956648	-29.4922
368537	cg2055921	33655451	33655451	0.8933825	0	1	0.7213682	-89.79781
368573	cg20561261	38732415	38732415	0.6388772	0	1	0.7757786	40.86765
368585	cg2056193	32730395	32730395	0.6492131	0	1	0.4922702	-40.894
368604	cg2056327	49686368	33708300	0.51098	0	1	0.3443833	-44.16901
368686	cg2056810	36666492	36666492	0.7237514	0	1	0.8372064	37.60322
368697	cg2056842	12740464	12740464	0.3875725	0	1	0.6624028	117.113
368722	cg2056980	59676454	59676454	0.2536941	0	1	0.3677706	25.8992
368817	cg2057659	58762444	58762444	0.3139131	0	1	0.4646403	37.87564
368865	cg2058085	13714328	13714328	0.7174707	0	1	0.8206776	30.52481
368875	cg2058187	71619415	65808494	0.5227512	0	1	0.4024395	-24.62281
368916	cg20584841	54797458	54797458	0.1910119	0	1	0.2979496	26.89661
368920	cg2058499	74778381	48629465	0.2646338	0	1	0.1315738	-45.57401
369018	cg2059201	11637351	15737394	0.7951246	0	1	0.6638162	-40.47712
369020	cg2059212	39750490	39750490	0.4480757	0	1	0.5680966	24.60332
369028	cg20592391	69708495	69708495	0.4732343	0	1	0.1725345	-159.0313
369036	cg2059283	43730356	43730356	0.2275112	0	1	0.3863622	46.69095
369111	cg2059677	36751506	36751506	0.7832219	0	1	0.8901384	44.62083
369302	cg2061045	62753398	39645307	0.4605663	0	1	0.3501312	-21.85352
369385	cg2061732	18710494	18710494	0.6883821	0	1	0.5605771	-30.41426
369625	cg2063381	73667326	73667326	0.2844774	0	1	0.1399638	-50.29267
369725	cg2063980	35692332	35692332	0.7453901	0	1	0.6106843	-36.91371
369740	cg2064037	18642456	31658443	0.5909355	0	1	0.8234947	110.3991
369764	cg2064167	10738373	10738373	0.5908806	0	1	0.7278492	36.5277
369791	cg2064344	42606486	42606486	0.4032811	0	1	0.5445696	32.45623
369915	cg2065164	47692461	47692461	0.4100075	0	1	0.5981528	54.83483
369941	cg2065312	32640330	32640330	0.721725	0	1	0.6017755	-29.12333
370012	cg2065770	12673404	12673404	0.3605098	0	1	0.483838	26.0444
370091	cg2066291	39793457	27705428	0.5238103	0	1	0.3881393	-30.30196
370096	cg2066304	73745465	73745465	0.2051051	0	1	0.3541026	44.00518
370125	cg2066444	44618449	49704310	0.7441545	0	1	0.8469439	33.81643
370345	cg2067625	24744337	24744337	0.4193999	0	1	0.5355781	23.18692

370395	cg20678835	50695330	50695330	0.3178956	0	1	0.4316968	23.59493
370396	cg20678988	63806509	63806509	0.8022	0	1	0.6224673	-68.18082
370404	cg20679403	43772339	43772339	0.7530649	0	1	0.8587273	37.19736
370475	cg20683445	62708473	54684413	0.3770518	0	1	0.494663	23.87366
370530	cg20686207	59637311	59637311	0.4110646	0	1	0.6007021	55.68552
370532	cg20686277	71638430	63712320	0.5740101	0	1	0.6759968	20.78404
370704	cg20695611	70661373	70661373	0.632953	0	1	0.7717505	41.32478
370787	cg20699274	71654483	71654483	0.2178302	0	1	0.3191064	23.11343
370847	cg20702205	28808505	28808505	0.23298	0	1	0.3350323	22.62085
370918	cg20704963	21621390	21621390	0.8898481	0	1	0.767545	-54.04811
370939	cg20705893	15653321	15653321	0.3942009	0	1	0.549243	38.28632
371113	cg20713810	69709355	13644459		0	1		-4.34E-09
371221	cg20720597	12740331	28690392	0.1480304	0	1	0.0341859	-59.42366
371272	cg20724032	59755484	59755484	0.6308751	0	1	0.760881	36.19055
371406	cg20731937	49698416	10682396	0.3242209	0	1	0.0659776	-160.6201
371447	cg20735069	28732348	28732348	0.6237399	0	1	0.5130704	-22.2484
371537	cg20741040	40687318	40687318	0.5077037	0	1	0.703177	64.01184
371550	cg20741528	34749417	34749417	0.2698487	0	1	0.1283455	-50.7054
371633	cg20746482	73669372	73669372	0.3653825	0	1	0.4730276	20.76175
371714	cg20751398	11652370	11652370	0.6424641	0	1	0.7551792	28.47068
371768	cg20756026	53647446	53647446	0.0693419	0	1	0.3836257	374.3439
371875	cg20764780	54722475	54722475	0.5702368	0	1	0.6794658	23.28741
371895	cg20767344	44648351	44648351	0.7314565	0	1	0.8434979	37.89013
371934	cg20769856	44637311	44637311	0.5748351	0	1	0.7436078	53.26729
371979	cg20773149	52728317	13657389	0.2683141	0	1	0.166472	-26.81504
372070	cg20778600	25686351	25686351	0.2213906	0	1	0.3339642	27.04593
372076	cg20778915	60629456	60629456	0.3230942	0	1	0.5327408	68.05485
372156	cg20783970	43801338	43801338	0.4333084	0	1	0.5613723	27.40962
372253	cg20789483	74659383	74659383	0.3413631	0	1	0.4492288	21.17628
372270	cg20790798	26770430	26770430	0.7772505	0	1	0.6539559	-34.77253
372275	cg20791291	71714440	71714440	0.6807304	0	1	0.3989983	-124.4246
372331	cg20795372	57723448	63695473	0.5361319	0	1	0.4190379	-23.49496
372333	cg20795417	63659363	63659363	0.8510549	0	1	0.5486093	-184.9206
372374	cg20798066	69666477	69666477	0.745583	0	1	0.9561924	374.3439
372583	cg20811755	53690493	53690493	0.7485319	0	1	0.6400557	-26.37507
372589	cg20811988	31628448	12625453	0.3505895	0	1	0.5084917	40.03162
372625	cg20814179	25742488	51751377	0.4847904	0	1	0.2574222	-83.61794
372718	cg20821042	48808387	48808387	0.4606748	0	1	0.5784018	23.90978
372731	cg20821713	57656364	57656364	0.6325151	0	1	0.747944	29.03136
372766	cg20823529	35605502	35605502	0.7449214	0	1	0.899561	79.60409
372827	cg20826740	47760413	47760413	0.0973814	0	1	0.2459202	61.70811
372843	cg20828284	31612369	74658363	0.9464626	0	1	0.7125244	-177.385
372907	cg20835708	39713425	39713425	0.4461663	0	1	0.547605	18.56023

372943	cg2083920	72782462	14649377	0.7056608	0	1	0.5669013	-35.80577
373011	cg20844861	31733489	31733489	0.5104797	0	1	0.3756302	-30.09262
373107	cg20850981	46766420	46766420	0.6188899	0	1	0.7514718	36.49307
373217	cg20859841	69633331	69633331	0.6460682	0	1	0.4987642	-36.5578
373269	cg2086421	37637493	29685483	0.2094389	0	1	0.3167073	25.77943
373416	cg2087676	39770411	39770411	0.2694902	0	1	0.1482706	-37.20943
373494	cg2088488	37803322	60728315	0.3482098	0	1	0.2461805	-22.02223
373525	cg2088736	25669327	47748497	0.5010105	0	1	0.3604377	-32.52478
373616	cg2089393	30740505	30740505	0.5520222	0	1	0.6663517	24.58766
373708	cg20899781	48636352	48636352	0.1554015	0	1	0.3018803	48.86944
373765	cg2090433	62603309	62603309	0.3503083	0	1	0.5946319	90.91823
373798	cg2090713	13706331	19607309	0.5039214	0	1	0.3531911	-36.8431
373800	cg2090740	33773300	33773300	0.597222	0	1	0.7049915	23.79107
373845	cg20910361	23728464	23728464	0.1766513	0	1	0.2916139	31.33624
373929	cg2091642	53682313	53682313	0.3926713	0	1	0.539799	34.88378
373937	cg2091707	17716311	17716311	0.3711587	0	1	0.4747123	19.43991
373944	cg20917491	70618476	70618476	0.0957924	0	1	0.3509225	142.9183
374027	cg2092442	30640339	30640339	0.2270145	0	1	0.3328826	24.2599
374067	cg2092739	13804374	13804374	0.1536907	0	1	0.2610944	30.33069
374075	cg2092765	13616379	13616379	0.4644907	0	1	0.5817881	23.79914
374290	cg2094118	58669414	58669414	0.5062119	0	1	0.6739523	47.13514
374359	cg2094508	40674373	29626407	0.3096278	0	1	0.1796362	-37.67699
374416	cg20948271	36623459	36623459	0.2721245	0	1	0.3752112	21.38795
374417	cg2094836	49686431	19704373	0.4046733	0	1	0.2839544	-27.04932
374473	cg2095164	51768470	51768470	0.9110554	0	1	0.798351	-54.63363
374618	cg2096032	58758453	58758453	0.5052844	0	1	0.7812403	135.1055
374766	cg20969151	30775370	30775370	0.1882567	0	1	0.3131646	34.55321
374933	cg2097819	49784457	49784457	0.2912995	0	1	0.4031204	23.66616
374944	cg2097892	68705431	13754460	0.5856816	0	1	0.7056855	28.26889
374952	cg2097915	38808325	71720494	0.3367828	0	1	0.4534932	24.16111
374956	cg2097938	40604470	40604470	0.1497533	0	1	0.3017707	52.74504
374998	cg2098116	67601502	67601502	0.2297492	0	1	0.4198263	63.11954
375006	cg20981451	11725350	40708411	0.2534209	0	1	0.137138	-36.31013
375095	cg2098683	72743474	72743474	0.537437	0	1	0.4231513	-22.55793
375110	cg20987431	63774318	63774318	0.3933614	0	1	0.4996003	20.07841
375157	cg2099115	38770375	38770375	0.4467304	0	1	0.6354177	56.08587
375232	cg2099508	14801411	35782396	0.4672849	0	1	0.5748456	20.57819
375252	cg20996351	13809302	61637328	0.577804	0	1	0.4553035	-25.54482
375391	cg2100551	35610381	44640449	0.8164231	0	1	0.6745073	-48.99407
375394	cg2100568	27653315	27653315	0.7954841	0	1	0.9283243	76.65974
375507	cg2101205	14677460	14677460	0.2304673	0	1	0.4113503	57.87186
375574	cg2101788	71619357	47602308	0.158208	0	1	0.2642565	29.30063
375699	cg2102831	71711491	71711491	0.4496761	0	1	0.7720986	374.3439

375778	cg2103256	19687445	50644406	0.4649571	0	1	0.0679255	-327.7817
375804	cg2103440	26684317	26684317	0.3573551	0	1	0.4630348	20.251
375908	cg2104009	70668361	70668361	0.2746461	0	1	0.380388	22.17517
375909	cg2104010	59656331	67614499	0.5618969	0	1	0.4602392	-18.69081
376001	cg2104557	10792451	10792451	0.1661726	0	1	0.2700827	27.67836
376051	cg2104870	59735421	59735421	0.0814998	0	1	0.2172677	58.03743
376064	cg2104939	71773502	71773502	0.4566918	0	1	0.6277366	46.74537
376116	cg2105276	51790432	70742444	0.2569605	0	1	0.3963489	35.66402
376153	cg2105491	63721486	63721486	0.5529037	0	1	0.4376485	-22.91208
376159	cg2105555	12765328	12765328	0.2246541	0	1	0.4536107	88.45956
376235	cg2106278	38635332	34689472	0.699432	0	1	0.5765367	-29.05499
376323	cg21070081	64787328	64787328	0.6777288	0	1	0.4227993	-101.854
376448	cg2107807	72651462	37638335	0.565383	0	1	0.2591555	-149.0719
376506	cg2108227	38628338	64679354	0.3044046	0	1	0.4064704	20.12523
376669	cg2109317	12741508	12741508	0.2572832	0	1	0.3816249	29.56263
376676	cg2109380	51790502	51609351	0.5027259	0	1	0.3905333	-21.97484
376726	cg2109778	58700335	58700335	0.1936137	0	1	0.3249343	36.89388
376842	cg2110587	34635360	37612334	0.5231825	0	1	0.4145033	-20.75504
376853	cg2110648	50801389	45649507	0.2378252	0	1	0.0772595	-75.7495
376981	cg2111472	10785309	39705421	0.6834013	0	1	0.92047	374.3439
377009	cg2111626	59722425	30706349	0.7542901	0	1	0.6491392	-25.49237
377100	cg2112160	23692348	23692348	0.3388166	0	1	0.4400185	19.16123
377177	cg2112662	56731381	56731381	0.4889053	0	1	0.3490507	-32.43571
377243	cg21130861	74646366	24683387	0.1479691	0	1	0.0315078	-62.43976
377373	cg2113979	27621380	27621380	0.8566965	0	1	0.4881204	-267.545
377454	cg2114406	26735430	26735430	0.6543867	0	1	0.5000661	-39.92746
377537	cg2114862	39620319	39620319	0.8426985	0	1	0.9428177	58.72391
377547	cg2114935	27800342	27800342	0.4641082	0	1	0.6278049	43.24257
377625	cg2115365	48737317	60749334	0.3227888	0	1	0.2166203	-24.9412
377675	cg2115638	62695318	38725337	0.4398873	0	1	0.3385229	-19.21503
377718	cg2115816	37710386	13616441	0.7674708	0	1	0.6088081	-50.7435
377724	cg21158501	51683349	24639308	0.092242	0	1	0.2148792	47.44757
377760	cg2116014	39644459	39644459	0.5118623	0	1	0.6270369	23.8087
377849	cg2116430	74616396	19793383	0.8873032	0	1	0.6991647	-99.39179
377920	cg2116740	36707329	28725425	0.3571028	0	1	0.1532683	-83.84389
377950	cg2116905	66643428	66643428	0.9185627	0	1	0.7980524	-62.95377
378064	cg2117568	33757409	33757409	0.7702675	0	1	0.893424	55.68649
378258	cg2118609	22682417	22682417	0.3134026	0	1	0.4308483	24.95283
378282	cg2118706	33657429	33657429	0.6744561	0	1	0.7765549	25.89251
378285	cg2118719	16608507	16608507	0.3741826	0	1	0.4786478	19.6863
378296	cg2118777	22600395	11635390	0.4634763	0	1	0.357877	-20.21932
378304	cg2118840	48623506	48623506	0.1674088	0	1	0.2749658	29.0695
378430	cg2119512	24682453	24682453	0.4021648	0	1	0.290966	-23.46583

378486	cg2119733	14633388	50615402	0.5152339	0	1	0.6310411	24.11183
378538	cg2119992	59607454	59607454	0.53951	0	1	0.6423208	20.14479
378593	cg2120227	54709323	54709323	0.5721923	0	1	0.8056337	106.0611
378610	cg2120324	16695486	16695486	0.862169	0	1	0.6002924	-149.9793
378711	cg2120795	28669333	35692508	0.3743521	0	1	0.2498522	-30.00757
378718	cg2120827	43681422	16804410	0.6676323	0	1	0.8214354	56.51179
378770	cg2121064	15645328	15645328	0.2412238	0	1	0.3893266	40.50805
378909	cg2121742	67633484	67633484	0.2783942	0	1	0.4678607	58.63872
378911	cg2121754	29667425	31734421	0.5704355	0	1	0.4693281	-18.58458
379003	cg2122184	11714457	17682427	0.8065147	0	1	0.6444941	-58.4539
379139	cg2122957	72766402	28702423	0.7845829	0	1	0.6825995	-26.47966
379193	cg2123248	13630343	40804496	0.2826405	0	1	0.1695181	-31.2188
379227	cg2123403	44734473	44734473	0.333533	0	1	0.4661657	29.95969
379229	cg2123408	14786388	14786388	0.8409468	0	1	0.43651	-313.0209
379406	cg2124244	17615461	17615461	0.3701061	0	1	0.2357294	-34.8674
379416	cg2124306	10697439	10697439	0.6933479	0	1	0.927962	374.3439
379444	cg2124413	42731360	68807439	0.4243203	0	1	0.2322551	-64.00304
379507	cg2124772	44771401	44771401	0.6571454	0	1	0.7724761	30.90167
379583	cg2125197	28692399	22688415	0.7265748	0	1	0.6041094	-30.40567
379656	cg2125729	11648326	11648326	0.4320303	0	1	0.5362517	19.36896
379730	cg2126554	22798463	22798463	0.5409839	0	1	0.6778569	33.53206
379736	cg2126591	54640409	37717456	0.8182366	0	1	0.9242337	54.90988
379811	cg2127227	54669345	54669345	0.320075	0	1	0.1856769	-39.07959
379920	cg2128032	38729303	38729303	0.4004499	0	1	0.2338137	-50.02277
380067	cg2129134	39752480	39752480	0.4933335	0	1	0.5939655	18.66874
380079	cg2129185	32715333	32715333	0.0726586	0	1	0.2543271	92.69468
380166	cg2129736	43669411	43669411	0.636556	0	1	0.8577464	113.0997
380208	cg2130099	10605381	14789475	0.4377831	0	1	0.325635	-22.86586
380214	cg21301341	16715416	16715416	0.494581	0	1	0.7622218	123.5931
380258	cg2130428	54764434	54764434	0.08041	0	1	0.1969225	46.63625
380457	cg2132310	50718335	50718335	0.5269397	0	1	0.6494748	26.95473
380563	cg2133181	39744307	14634387	0.5694107	0	1	0.463001	-20.17807
380568	cg2133230	26794493	26794493	0.2472155	0	1	0.3588535	25.32161
380672	cg2134032	63719354	44756317	0.7473341	0	1	0.8655586	45.38266
380738	cg2134594	66710318	21782313	0.391282	0	1	0.2900524	-20.23979
381213	cg2138531	72739466	72739466	0.7385551	0	1	0.5818486	-46.58456
381221	cg2138574	67616437	74709458	0.3127013	0	1	0.4712366	41.38017
381317	cg2139270	19729465	19729465	0.5061018	0	1	0.6454535	33.24783
381382	cg2139754	31744475	31744475	0.6120285	0	1	0.5116508	-18.83657
381428	cg21400851	43710318	43710318	0.5667462	0	1	0.7009485	33.62188
381486	cg2140493	60704396	51742335	0.4356173	0	1	0.2517625	-57.54124
381528	cg2140881	34738319	34738319	0.1793268	0	1	0.2906788	29.58987
381607	cg2141490	15671471	15671471	0.5318605	0	1	0.7014604	49.8501

381612	cg2141522	65715345	65715345	0.3690517	0	1	0.4983342	28.07698
381872	cg2143568	35794359	57688310	0.3148757	0	1	0.5275582	70.24121
381882	cg2143657	37779393	35648401	0.8135568	0	1	0.7065507	-31.40064
381890	cg2143741	29648403	29648403	0.9532442	0	1	0.8252435	-87.67958
381939	cg2144077	25778431	25778431	0.6077376	0	1	0.7459221	38.51339
381959	cg21442271	17615445	17615445	0.2083612	0	1	0.3706429	50.29139
381997	cg2144555	33647476	14602378	0.8135054	0	1	0.6710781	-48.78455
382017	cg2144677	69795464	69795464	0.3297055	0	1	0.5488153	73.77641
382021	cg21446981	69682374	69682374	0.4984247	0	1	0.6847051	57.3862
382077	cg2145022	46640502	46640502	0.2646748	0	1	0.4431548	53.66253
382083	cg2145062	74746464	74746464	0.6842768	0	1	0.793528	30.26908
382091	cg2145078	55615448	70740454	0.8390936	0	1	0.6860288	-59.77098
382250	cg21461981	21782468	21782468	0.5045523	0	1	0.6219769	24.46504
382391	cg2147158	11682463	40651448	0.9517016	0	1	0.8452525	-68.58543
382431	cg2147410	18751494	18751494	0.5114477	0	1	0.6169875	20.49031
382433	cg2147424	27742412	27742412	0.3055505	0	1	0.444332	33.1811
382571	cg2148247	69797492	61690493	0.5551158	0	1	0.4485449	-20.14217
382598	cg2148388	37804335	36737432	0.2030119	0	1	0.092603	-40.54747
382622	cg2148494	20628314	57756386	0.8087281	0	1	0.6880582	-37.10659
382706	cg21490751	19684498	19684498	0.5434406	0	1	0.6675751	28.14767
382757	cg21493951	27713418	48651339	0.3163006	0	1	0.2089939	-25.8216
382846	cg2149854	45773411	45773411	0.4046936	0	1	0.2276191	-56.08248
383089	cg2151380	32806307	32806307	0.9139432	0	1	0.7920648	-62.05159
383263	cg21524061	26665478	26665478	0.62954	0	1	0.4890992	-33.20207
383307	cg2152677	28675375	28675375	0.245747	0	1	0.3870318	37.16672
383309	cg2152707	42730477	47738478	0.5180364	0	1	0.6271521	21.81397
383317	cg2152761	38647423	38647423	0.3233624	0	1	0.4387503	24.00077
383331	cg2152892	14672460	14672460	0.3177842	0	1	0.4459455	28.68269
383337	cg2152947	71704423	71704423	0.238061	0	1	0.3460626	24.46118
383352	cg2153026	59617486	59617486	0.7641841	0	1	0.6199353	-43.11637
383367	cg2153138	41625395	41625395	0.50995	0	1	0.6356765	27.72216
383459	cg2153594	39635363	52656337	0.3649332	0	1	0.2409752	-30.28738
383476	cg2153718	24764306	24764306	0.5230716	0	1	0.646555	27.21066
383587	cg2154343	25663371	25663371	0.7885462	0	1	0.9215078	73.39178
383718	cg2154895	60786424	38790471	0.7019211	0	1	0.5815402	-28.22297
383787	cg2155230	17661452	17661452	0.3295024	0	1	0.4326042	19.90311
383858	cg2155714	62615452	62615452	0.6616296	0	1	0.5547407	-21.93803
383926	cg21561701	32757473	44642452	0.4339457	0	1	0.3102345	-27.26304
384000	cg2156643	50669491	50669491	0.0818867	0	1	0.5758676	374.3439
384123	cg21574271	50724467	50724467	0.4306052	0	1	0.5419146	21.59336
384139	cg2157482	12645459	12645459	0.5924169	0	1	0.727861	35.86868
384208	cg2157845	62623454	62623454	0.3685702	0	1	0.5081815	32.02871
384213	cg2157864	11631406	11631406	0.6822707	0	1	0.9342765	374.3439

384277	cg2158211	52731499	52731499	0.7060221	0	1	0.8070317	28.10305
384360	cg2158615	42654505	16670326	0.5039039	0	1	0.3694088	-30.02771
384370	cg2158700	66612314	66612314	0.908246	0	1	0.7890509	-58.03677
384401	cg2158941	22623481	22623481	0.5462348	0	1	0.6908527	37.45011
384451	cg2159315	25634351	25634351	0.6945642	0	1	0.4776676	-76.34172
384455	cg2159340	12716411	12716411	0.5546481	0	1	0.4350744	-24.3743
384464	cg2159367	50643403	50643403	0.4832044	0	1	0.3804051	-19.12692
384487	cg2159470	46660491	46660491	0.2380165	0	1	0.4746043	92.15779
384538	cg2159848	17665351	17665351	0.9286903	0	1	0.8170953	-60.8172
384654	cg21605781	36656336	36656336	0.3959877	0	1	0.5096107	22.40682
384726	cg2160958	52647497	52647497	0.5920748	0	1	0.7136725	29.3032
384752	cg2161083	55730303	55730303	0.3893993	0	1	0.5096477	24.66927
384756	cg2161092	19687435	19687435	0.6110108	0	1	0.88429	374.3439
384791	cg2161362	10728413	10728413	0.2127492	0	1	0.3472142	36.61018
384798	cg21614201	42692387	42692387	0.4486778	0	1	0.5957739	35.1929
384851	cg2161735	49799346	49799346	0.6553689	0	1	0.7635642	27.3015
384963	cg2162344	31708474	31708474	0.5095599	0	1	0.6365659	28.21589
385069	cg2163084	13610445	13610445	0.8721364	0	1	0.5886596	-175.6861
385122	cg2163494	38617440	58629367		0	1	0.5200669	4.34E-09
385137	cg2163587	52726337	47718377	0.5398147	0	1	0.3779134	-41.46774
385234	cg2164205	46765335	46765335	0.6276009	0	1	0.8940746	374.3439
385259	cg2164326	28801369	28801369	0.4971504	0	1	0.5984914	18.93473
385308	cg2164526	58727386	58727386	0.6648075	0	1	0.5623981	-20.58713
385315	cg2164575	48612396	48612396	0.6836433	0	1	0.8379678	60.27367
385331	cg2164639	72635404	72635404	0.592128	0	1	0.6944864	21.53428
385340	cg2164718	72714356	72714356	0.2955058	0	1	0.4664361	47.98236
385368	cg2164837	28640480	14658488	0.5704911	0	1	0.4589818	-21.79244
385470	cg21655171	71731387	71731387	0.7956847	0	1	0.9160053	61.77373
385687	cg2167071	22640468	22640468	0.4124421	0	1	0.5254679	22.15185
385721	cg2167299	74799351	74799351	0.5522996	0	1	0.6583636	21.57758
385771	cg2167946	39808413	39808413	0.5360777	0	1	0.7012492	47.62571
385922	cg2169045	59707422	59707422	0.4381943	0	1	0.3307441	-21.23848
385936	cg21690921	14715322	14715322	0.4482821	0	1	0.5845949	30.70556
385959	cg2169262	65690437	49801463	0.446779	0	1	0.3160846	-29.68262
386003	cg2169637	46777321	46777321	0.2683593	0	1	0.4144535	37.89903
386021	cg2169776	72804500	72804500	0.9188037	0	1	0.7353595	-111.7129
386180	cg2171237	29754329	29754329	0.4539242	0	1	0.5768455	25.68315
386234	cg2171772	71663496	71663496	0.502512	0	1	0.3368187	-43.92754
386305	cg2172279	60720343	28699467	0.6377958	0	1	0.4752564	-43.03029
386431	cg21733531	33698309	73719447	0.3637859	0	1	0.2534342	-24.57933
386452	cg2173506	37686370	37686370	0.3669812	0	1	0.589389	75.38398
386531	cg2174128	42783350	70787499	0.7555836	0	1	0.643563	-28.2256
386532	cg2174151	32773475	32773475	0.3388011	0	1	0.5933025	98.83263

386539	cg21741998	38683447	38683447	0.5126107	0	1	0.6247501	22.74969
386663	cg21749951	72665489	72665489	0.3256211	0	1	0.4827499	40.31129
386671	cg21750589	62758508	62758508	0.6273454	0	1	0.7495726	31.90542
386874	cg21762589	63757329	63757329	0.6525785	0	1	0.534913	-25.31677
386943	cg21767657	60616459	60616459	0.5126514	0	1	0.6167845	20.05116
386988	cg21770393	66640321	66640321	0.5767751	0	1	0.7439848	52.4846
387103	cg21777188	40634335	40634335	0.3724647	0	1	0.2327768	-37.36037
387127	cg21778987	15666369	15666369	0.455241	0	1	0.5975516	33.25746
387142	cg21780600	15696410	15696410	0.7813752	0	1	0.9127911	68.37259
387192	cg21783442	12680303	12680303	0.6612715	0	1	0.7819543	34.0845
387195	cg21783672	60644498	60644498	0.6488736	0	1	0.5103934	-33.01344
387356	cg21792983	35623406	35623406	0.3364492	0	1	0.4539744	24.44505
387377	cg21794767	56615495	56615495	0.6119439	0	1	0.7210701	25.03346
387505	cg21805731	50674364	50674364	0.4780728	0	1	0.6181568	32.77024
387509	cg21805880	36696500	36696500	0.2679195	0	1	0.3837601	25.9154
387584	cg21809927	47711327	23679433	0.445282	0	1	0.2326858	-76.4931
387596	cg21810411	29679377	29679377	0.6695027	0	1	0.8130513	49.31119
387612	cg21811911	48689493	48689493	0.8624361	0	1	0.6365853	-118.7363
387620	cg21812850	39717419	39717419	0.8578901	0	1	0.7448976	-40.9238
387644	cg21814550	16735421	16735421	0.5561947	0	1	0.6968258	36.07794
387769	cg21823426	60751458	60751458	0.5939209	0	1	0.7035225	24.36785
387852	cg21829038	46608371	13645391	0.9619265	0	1	0.675687	-246.0255
387886	cg21830932	31754304	31754304	0.8978418	0	1	0.5960483	-209.9961
387891	cg21831183	65707402	65707402	0.5384276	0	1	0.6587961	26.46807
387938	cg21833776	73772414	73772414	0.4088507	0	1	0.5949272	53.67606
388026	cg21839504	44680459	47676368	0.5419165	0	1	0.6787891	33.57524
388055	cg21841632	55683413	55683413	0.4418806	0	1	0.5885237	34.8998
388076	cg21842920	66777402	66777402	0.1957162	0	1	0.3285809	37.39048
388153	cg21847118	37664311	37664311	0.4201423	0	1	0.5245898	19.43704
388271	cg21854332	11607314	11607314	0.2830375	0	1	0.4011841	26.15402
388290	cg21855211	12780345	12780345	0.2878896	0	1	0.1877429	-24.5291
388366	cg21859562	19654372	19654372	0.3305122	0	1	0.4407046	22.12351
388385	cg21860675	50647478	50647478	0.2873109	0	1	0.4621946	50.3835
388400	cg21862099	56698492	56698492	0.1692422	0	1	0.3224739	50.41677
388427	cg21864016	40755448	40755448	0.7998523	0	1	0.9089205	51.47
388511	cg21870038	37664451	37664451	0.6818969	0	1	0.8006335	35.22054
388742	cg21881798	61795328	61795328	0.2803326	0	1	0.3877998	22.55662
388784	cg21885112	73753465	56694324	0.3967316	0	1	0.6252814	80.00337
389026	cg21902325	60770320	60770320	0.545566	0	1	0.7223028	55.32927
389029	cg21902394	70630496	70630496	0.7401372	0	1	0.617349	-31.4411
389050	cg21903646	42616369	58643484	0.6006899	0	1	0.4913183	-21.44015
389182	cg21911276	15730437	15730437	0.4452923	0	1	0.3259387	-25.3028
389221	cg21913335	26716330	71672317	0.6522397	0	1	0.8731586	119.2334

389271	cg2191591	53602438	24619471	0.7952899	0	1	0.6689677	-38.11767
389355	cg2192056	47651462	47651462	0.8695798	0	1	0.7548887	-44.26131
389444	cg2192680	41692372	41692372	0.6695535	0	1	0.5633219	-21.95982
389458	cg21927991	25632330	25632330	0.7188519	0	1	0.4794983	-94.29424
389523	cg2193171	24684390	25616423	0.244835	0	1	0.0575984	-103.7091
389530	cg2193198	73685456	73685456	0.3277007	0	1	0.4375556	22.07149
389538	cg2193236	26719328	25696394	0.4556391	0	1	0.276607	-53.14886
389618	cg2193739	69623491	69623491	0.5673686	0	1	0.4649624	-18.94836
389640	cg21938541	69691430	69691430	0.1673111	0	1	0.2770787	30.00361
389741	cg2194563	30642361	56781505	0.1318616	0	1	0.2784276	52.87147
389755	cg21946631	56710498	56710498	0.7161047	0	1	0.8546822	54.72126
389835	cg2195172	42767403	25663443	0.7858915	0	1	0.6531447	-40.04715
389876	cg2195465	24766355	24766355	0.7266713	0	1	0.5708987	-45.05479
389909	cg2195839	46665387	46665387	0.9457412	0	1	0.8379295	-66.29672
390076	cg2196979	63779384	44754485	0.7223597	0	1	0.6019791	-29.32832
390160	cg2197813	11782505	11782505	0.868534	0	1	0.7171817	-66.34566
390317	cg2199481	16603301	16603301	0.4639165	0	1	0.6140305	36.81647
390329	cg2199565	63727351	63727351	0.3217861	0	1	0.4835386	42.53592
390338	cg2199606	29712302	29712302	0.5826002	0	1	0.4627176	-24.68662
390366	cg2199772	55681501	70735507	0.2737002	0	1	0.4685799	61.99565
390470	cg2200721	13793461	13793461	0.606807	0	1	0.7990023	75.39091
390581	cg2201411	31741504	18749447	0.2595527	0	1	0.3877769	30.96108
390650	cg2201808	18651414	18651414	0.4416873	0	1	0.2700908	-49.75398
390778	cg2202608	60740480	60740480	0.5244514	0	1	0.6806412	42.03872
390829	cg2202901	40750308	10720446	0.6523764	0	1	0.8303252	73.22053
390845	cg2202987	29656450	29656450	0.6645311	0	1	0.8044388	46.04729
390883	cg2203202	62667465	62667465	0.7347248	0	1	0.8477833	39.12802
390972	cg2203724	44755506	44755506	0.2072686	0	1	0.5461969	374.3439
391015	cg2204020	27756392	27756392	0.4925843	0	1	0.328835	-43.24052
391210	cg2205163	32731457	32731457	0.7864084	0	1	0.9153653	67.68819
391264	cg2205491	18731335	18731335	0.3265512	0	1	0.5122464	54.26177
391390	cg2206404	72703306	72703306	0.3198975	0	1	0.4214014	19.60261
391447	cg2206840	66663338	27656445	0.4065561	0	1	0.2292086	-56.0711
391472	cg22069441	74738411	27704357	0.3107005	0	1	0.1933163	-30.91493
391551	cg2207642	61764309	61764309	0.5305853	0	1	0.6905497	44.38602
391554	cg2207661	12701365	12701365	0.6117725	0	1	0.879005	374.3439
391569	cg2207731	39626373	39626373	0.3504719	0	1	0.4676178	24.06195
391585	cg2207845	53692421	53692421	0.4650132	0	1	0.5926638	27.55758
391663	cg2208280	11799427	20794463	0.6037244	0	1	0.5027791	-18.88571
391700	cg2208505	24730483	57749407	0.0076213	0	1		-4.34E-09
391718	cg2208735	12768443	12768443		0	1		-4.34E-09
391813	cg2209492	37642502	37642502	0.8893602	0	1	0.5107641	-301.0478
391818	cg2209526	30706332	30706332	0.4571128	0	1	0.5675039	21.41249

391928	cg22105162	56718419	56718419	0.2230967	0	1	0.3414874	29.18129
391940	cg22106220	37606332	37606332	0.6611301	0	1	0.4385616	-77.5645
392000	cg22110158	56661428	56661428	0.2209299	0	1	0.34209	30.41842
392026	cg22111167	47652314	47652314	0.4971386	0	1	0.5992229	19.1666
392031	cg22111694	60693421	60693421	0.4264863	0	1	0.320739	-20.90411
392138	cg22117893	59706422	59706422	0.628781	0	1	0.4436828	-53.93056
392149	cg22118297	15809455	15809455	0.3258458	0	1	0.426147	19.11947
392184	cg22121557	41734419	40791476	0.6478111	0	1	0.4841326	-43.93885
392294	cg22127309	27724371	27724371	0.265956	0	1	0.4196291	41.41535
392499	cg22140866	53785452	53785452	0.5868223	0	1	0.7028897	26.66371
392516	cg22142142	37691483	37691483	0.5221379	0	1	0.6725561	39.01986
392530	cg22143285	74665360	74665360	0.4640823	0	1	0.3406687	-26.41272
392559	cg22144900	73794378	38745448	0.8431126	0	1	0.7407187	-33.05861
392584	cg22147163	47795484	47795484	0.8345392	0	1	0.7282333	-33.71973
392650	cg22151773	33752365	33752365	0.3934784	0	1	0.5128102	24.32918
392657	cg22152229	11755402	12615500	0.540364	0	1	0.3923529	-35.25611
392798	cg22159647	10709400	10709400	0.2923031	0	1	0.4343028	35.00548
392831	cg22161115	38611463	38611463	0.6686098	0	1	0.7772945	28.57095
392890	cg22164009	49680432	49680432	0.497942	0	1	0.6223635	26.9256
393018	cg22172057	43740344	43740344	0.6897797	0	1	0.5417866	-38.86484
393173	cg22185043	38609393	50609306	0.3150868	0	1	0.2106594	-24.65228
393238	cg22189786	50767389	72751456	0.529862	0	1	0.3268077	-63.97519
393240	cg22190023	37667321	37667321	0.5651157	0	1	0.3738992	-56.35646
393351	cg22198853	61682431	12810408	0.9576421	0	1	0.787721	-127.9035
393368	cg22199969	73764363	45746334	0.5801442	0	1	0.4527359	-27.31763
393403	cg22202381	73628497	73628497	0.4234029	0	1	0.5235379	18.145
393424	cg22203829	67639510	67639510		0	1		-4.34E-09
393493	cg22209918	30609421	30609421	0.5738113	0	1	0.6840573	23.80117
393503	cg22210497	24779331	24779331	0.7535822	0	1	0.608466	-42.43679
393563	cg22214800	62789388	62789388	0.4209014	0	1	0.5352613	22.58179
393589	cg22216196	69605422	58784418	0.2528209	0	1	0.3606713	23.73027
393682	cg22222799	47789410	47789410	0.7538859	0	1	0.8809336	54.45669
393686	cg22223119	39794491	39794491	0.6680666	0	1	0.7729544	26.70783
393829	cg22231758	13740491	69793339	0.5695213	0	1	0.6821657	24.56065
393887	cg22234930	32803418	32803418	0.4595907	0	1	0.6059874	35.08157
393908	cg22236066	25762347	25762347	0.0966936	0	1	0.2060309	39.19136
393923	cg22237018	27797434	27797434	0.8677745	0	1	0.6944856	-80.91566
393933	cg22237495	59714316	59714316	0.897593	0	1	0.7241391	-92.75117
393935	cg22237644	15786353	15786353	0.5486476	0	1	0.7086782	45.66673
394017	cg22242857	61748404	61748404	0.8463085	0	1	0.7315392	-39.76161
394022	cg22243109	39666377	19677413	0.7398638	0	1	0.6191919	-30.56381
394089	cg22247748	20605478	20605478	0.2915501	0	1	0.3928439	20.21837
394147	cg22251684	59672310	59672310	0.1642183	0	1	0.2883654	36.66763

394276	cg2226089	17786473	17786473	0.5932368	0	1	0.7438729	44.13392
394340	cg2226498	15656323	15656323	0.585569	0	1	0.7273147	38.59277
394449	cg2227411	33784443	33784443	0.0866306	0	1	0.186678	36.13745
394516	cg2227808	56639356	56639356	0.1430186	0	1	0.2461135	29.58649
394567	cg2228208	48656396	48656396	0.4592757	0	1	0.5870127	27.515
394680	cg2229014	28751506	70754366	0.5060711	0	1	0.6296974	26.80999
394755	cg2229658	57770413	57770413	0.5842465	0	1	0.4800978	-19.61664
394844	cg2230451	53635488	53635488	0.727563	0	1	0.4516998	-124.5926
394869	cg2230600	71772431	71772431	0.107305	0	1	0.2528046	57.38768
394995	cg22316451	36810353	36810353	0.6041884	0	1	0.7213249	28.01875
394997	cg2231661	34764306	67739463	0.3303131	0	1	0.1289549	-88.11882
395053	cg2232132	49710463	49710463	0.3448649	0	1	0.4474706	19.48914
395119	cg2232582	43632388	43632388	0.5197949	0	1	0.4018997	-23.79969
395284	cg2233580	39743399	34757343	0.294188	0	1	0.4407007	36.82543
395306	cg2233686	55637506	55637506	0.417793	0	1	0.7252919	153.5253
395319	cg2233762	36714448	36714448	0.4395871	0	1	0.6082395	45.07973
395354	cg2234050	12808405	24758434	0.3189943	0	1	0.153841	-59.43993
395365	cg2234131	70701466	70701466	0.4163271	0	1	0.1784419	-102.8048
395389	cg2234372	26622337	59671385	0.688758	0	1	0.5729918	-25.92671
395519	cg2235277	47718389	47718389	0.4095892	0	1	0.2822137	-29.59905
395636	cg2236110	63806459	63806459	0.5290551	0	1	0.4176068	-21.63307
395685	cg2236489	57682467	57682467	0.7673901	0	1	0.8891818	53.52679
395744	cg2236770	65647306	59700369	0.2388867	0	1	0.0894386	-64.46755
395751	cg22367981	25645372	25645372	0.2067226	0	1	0.3233875	29.60057
395835	cg2237309	35685405	35685405	0.5118611	0	1	0.7477524	95.86665
396134	cg2239004	59608335	59608335	0.1960288	0	1	0.3012995	25.90017
396288	cg22402121	23779301	34774468	0.2331417	0	1	0.9273968	374.3439
396358	cg2240810	60731414	60731414	0.7600778	0	1	0.874113	44.90738
396394	cg2241118	47682498	47682498	0.8807091	0	1	0.768483	-45.4156
396488	cg2242051	17693448	17693448	0.5207446	0	1	0.6432045	26.74476
396498	cg22422251	73660487	73660487	0.5997406	0	1	0.7349595	36.30106
396565	cg22428691	51644345	51644345	0.4560167	0	1	0.5787671	25.64179
396685	cg2243740	36771482	36771482	0.2126433	0	1	0.330143	29.51863
396747	cg2244261	62754307	62754307	0.2092905	0	1	0.355444	42.24211
396758	cg2244321	65611468	65611468	0.107955	0	1	0.6172995	374.3439
396849	cg2245040	27629332	27629332	0.3507572	0	1	0.5009546	36.66162
396881	cg2245223	11725483	42645456	0.6526007	0	1	0.5283438	-27.6778
396936	cg2245566	52783348	41720477	0.1430792	0	1	0.0309836	-59.49481
397167	cg2247333	27676319	27676319	0.3208358	0	1	0.436088	24.01411
397272	cg2248116	66810335	19775311	0.2412609	0	1	0.1343764	-32.2716
397633	cg2250230	47810318	47810318	0.4530943	0	1	0.7278968	123.7207
397722	cg2250814	59700445	59700445	0.6779606	0	1	0.932094	374.3439
397736	cg2250893	73600419	73600419	0.5603319	0	1	0.6805413	27.20263

397746	cg2250911	58605415	63801383	0.5281082	0	1	0.4111552	-23.45507
398085	cg2253023	48703391	48703391	0.5252491	0	1	0.6356975	22.43133
398150	cg2253428	44735506	51738369	0.4006284	0	1	0.2899755	-23.31262
398271	cg2254125	14721442	14721442	0.5544266	0	1	0.4215063	-29.188
398298	cg22542451	17773359	17773359	0.7257101	0	1	0.8930556	86.18604
398315	cg2254337	59706414	59706414	0.3229509	0	1	0.4255982	19.89114
398320	cg2254392	63771360	63771360	0.8821498	0	1	0.6541543	-129.3412
398342	cg22545121	62657346	49710451	0.4686458	0	1	0.6420097	48.38554
398440	cg2255081	72640301	72640301	0.6362981	0	1	0.7520379	29.44688
398572	cg2256179	43675403	43675403	0.6537064	0	1	0.7738301	33.05916
398608	cg2256381	35731370	35731370	0.3734113	0	1	0.5192848	34.50652
398663	cg2256949	61810439	10741321	0.5460708	0	1	0.3929165	-37.46013
398754	cg2257626	46701454	46701454	0.432646	0	1	0.5530805	24.66429
398766	cg2257760	53709439	53709439	0.4109952	0	1	0.288844	-27.39261
398781	cg2257907	55763419	55763419	0.402379	0	1	0.5070975	19.56662
398871	cg2258595	29749339	29749339	0.3614897	0	1	0.2332549	-32.47409
398894	cg2258760	30659497	30659497	0.1385621	0	1	0.2535598	35.51274
398900	cg2258814	12768471	16693306		0	1		-4.34E-09
398920	cg2258972	73648503	73648503	0.5669671	0	1	0.4597178	-20.42045
398923	cg2258982	63618321	63618321	0.3860058	0	1	0.4963299	21.4076
399014	cg2259721	43696442	43696442	0.2803876	0	1	0.3820498	20.66087
399072	cg2260141	54726304	54726304	0.6965978	0	1	0.8031746	30.08775
399091	cg2260326	27673429	27673429	0.6202497	0	1	0.72391	23.23365
399231	cg2261112	23694300	23694300	0.652833	0	1	0.7734557	33.2401
399247	cg2261244	44674486	13747358	0.6181902	0	1	0.721445	22.97352
399369	cg2262068	48767360	48767360	0.8574259	0	1	0.7506029	-37.57136
399416	cg2262289	38644415	38644415	0.7889528	0	1	0.673421	-32.52495
399443	cg2262490	30641306	30641306	0.1148328	0	1	0.270674	61.87379
399481	cg2262702	35617474	36799401	0.1110105	0	1	0.2242578	38.71111
399557	cg2263161	49803433	49803433	0.3084199	0	1	0.4100789	19.90278
399566	cg2263252	35766468	37606499	0.6466745	0	1	0.4914203	-40.03856
399603	cg2263463	18779345	18779345	0.3934869	0	1	0.4972397	19.31973
399617	cg22635491	63726451	34610498	0.7026443	0	1	0.8197427	36.85211
399650	cg22637941	67726462	67726462	0.5657488	0	1	0.6947085	31.17534
399682	cg2264081	20771450	20771450	0.1485164	0	1	0.2487768	27.80837
399780	cg2264768	16783379	16783379	0.8225724	0	1	0.9338099	62.89035
399851	cg2265314	62627395	48804333	0.2485758	0	1	0.3742824	30.54918
399860	cg2265395	39672463	52765451	0.7602082	0	1	0.5820993	-60.39845
399912	cg2265705	31653389	31653389	0.5225477	0	1	0.3572705	-43.29248
399945	cg2265926	64795501	35739490	0.6143383	0	1	0.5000042	-23.27489
399979	cg2266093	47756478	13763395	0.5795959	0	1	0.4755512	-19.53982
400028	cg2266429	29680347	29680347	0.2046121	0	1	0.4982116	144.7747
400139	cg2267260	11633459	57720491	0.2263758	0	1	0.1176263	-35.4159

400154	cg2267354	55723396	55723396	0.8467442	0	1	0.6182954	-114.8167
400208	cg2267607	36774424	49760474	0.3224717	0	1	0.2145406	-25.71458
400254	cg2267867	32674499	46613423	0.4188183	0	1	0.5307453	21.78675
400257	cg2267873	10612410	10612410	0.3043341	0	1	0.4057745	19.93251
400264	cg2267901	27807312	27807312	0.4432468	0	1	0.3352423	-21.32926
400310	cg2268170	46668356	46668356	0.5580103	0	1	0.4579555	-18.19724
400317	cg2268194	49730486	49730486	0.4705071	0	1	0.2528313	-77.62176
400324	cg2268220	58691497	58691497	0.5287536	0	1	0.632605	20.2595
400344	cg2268301	57666362	57666362	0.4279085	0	1	0.5334265	19.76275
400347	cg2268303	19808382	19808382	0.5020616	0	1	0.3786345	-25.86367
400365	cg2268437	13609479	44713442	0.365845	0	1	0.4762663	21.63443
400598	cg2269654	17676435	17676435	0.7069091	0	1	0.5433004	-47.27618
400657	cg2269931	66748409	66748409	0.2602775	0	1	0.4256188	47.30188
400664	cg2269962	49665394	49665394	0.2546527	0	1	0.3817325	30.76368
400669	cg2270001	22767393	52774327	0.6341645	0	1	0.4727607	-42.38141
400688	cg2270079	67694374	53774307	0.3516768	0	1	0.1982048	-46.92708
400689	cg2270082	22648488	22648488	0.2089493	0	1	0.3172039	26.18103
400769	cg2270595	53786440	53786440	0.5595616	0	1	0.4451371	-22.66852
400830	cg22708961	54703456	70629384	0.3889982	0	1	0.5033663	22.69427
400873	cg2271167	55697508	55697508	0.2849548	0	1	0.3999608	24.97387
400946	cg2271626	70793361	70793361	0.4887291	0	1	0.589566	18.67958
400967	cg2271723	23800358	23800358	0.5190328	0	1	0.9133399	374.3439
400970	cg2271747	45700416	37802319	0.9718113	0	1	0.7891722	-153.2203
401126	cg2272743	16809362	16809362	0.8069081	0	1	0.9092528	47.17641
401167	cg2273002	12650394	12650394	0.54175	0	1	0.6517867	22.69731
401169	cg2273004	73676317	15721361	0.076341	0	1	0.2704524	100.6052
401214	cg2273212	27620327	27620327	0.2127259	0	1	0.3204437	25.7449
401343	cg2274159	26754377	26754377	0.088413	0	1	0.3251755	129.965
401376	cg2274510	66648508	66648508	0.4698934	0	1	0.3510989	-24.61278
401387	cg2274562	70606419	70606419	0.260825	0	1	0.3657812	22.41577
401405	cg2274686	60650501	60650501	0.6269367	0	1	0.7442753	29.53448
401416	cg2274765	63759321	63759321	0.2101037	0	1	0.091838	-45.05052
401578	cg22759261	31682388	31682388	0.4565946	0	1	0.5610119	19.51341
401632	cg2276359	41798424	41798424	0.3467341	0	1	0.4745324	27.87757
401652	cg22764591	19801466	58622419	0.0170441	0	1	0.2887755	374.3439
401736	cg2277175	63691435	63691435	0.1494712	0	1	0.4610172	374.3439
401786	cg2277560	69745429	69745429	0.4759787	0	1	0.6214755	35.05423
401822	cg2277756	14786382	14786382	0.5782979	0	1	0.8557957	374.3439
401879	cg2278176	27713505	27713505	0.5736598	0	1	0.2815925	-133.3938
401951	cg2278647	13717427	13717427	0.7077832	0	1	0.852942	58.25275
401958	cg2278674	49745403	49745403	0.216578	0	1	0.3429044	32.83078
401996	cg2278931	70685378	22676408	0.8090419	0	1	0.6603194	-51.44699
402005	cg2278998	31797416	59652457	0.5732009	0	1	0.4693339	-19.43068

402016	cg2279087	46786313	46786313	0.7351894	0	1	0.8467144	38.15707
402040	cg2279198	67764353	57737497	0.611158	0	1	0.4906131	-25.3291
402068	cg2279306	57707436	15678323	0.3210981	0	1	0.2187277	-23.453
402112	cg2279534	41687317	15801383	0.9168879	0	1	0.7973307	-61.58786
402267	cg2280189	31802445	31802445	0.6071253	0	1	0.4170686	-56.02983
402273	cg2280201	74740492	74740492	0.8197045	0	1	0.9310946	61.74411
402280	cg2280229	17684406	17684406	0.6024109	0	1	0.4934837	-21.32358
402324	cg2280452	39610321	39610321	0.3889289	0	1	0.5013361	22.05514
402330	cg2280480	24717506	24717506	0.8104162	0	1	0.6323479	-68.80047
402470	cg2281261	12751429	12751429	0.4576235	0	1	0.5791595	25.22183
402498	cg2281402	27604327	36741365	0.7947008	0	1	0.8997124	46.03905
402543	cg2281646	30630456	13682306	0.9749551	0	1	0.8593658	-93.9101
402718	cg2282657	48779380	19609302	0.2441453	0	1	0.0917659	-65.68613
402765	cg2282918	30777395	30777395	0.5691448	0	1	0.4332213	-30.40987
402833	cg2283347	69655472	69655472	0.5026202	0	1	0.630422	28.34856
402842	cg2283414	39767488	39767488	0.2639292	0	1	0.4363217	50.56999
402850	cg2283454	73755435	73755435	0.2710541	0	1	0.392123	27.69173
402860	cg2283563	30777385	30777385	0.6449029	0	1	0.5208532	-27.36785
403112	cg2285194	27650394	27650394	0.7048311	0	1	0.5669025	-35.40279
403196	cg2285632	60663333	18745388	0.7359005	0	1	0.6352671	-22.7802
403304	cg2286235	13670335	13670335	0.3340984	0	1	0.2268503	-24.76525
403331	cg2286370	14810313	36777310	0.6281462	0	1	0.4360677	-57.68891
403839	cg2289106	67760498	37743313	0.3429458	0	1	0.2295505	-26.88062
403973	cg2290047	47648350	47648350	0.5262498	0	1	0.636961	22.54665
404050	cg2290440	63689409	63689409	0.4986194	0	1	0.6411074	34.37992
404065	cg22905511	10777300	62767353	0.4578744	0	1	0.1804948	-134.9608
404095	cg2290729	25656423	25656423	0.339082	0	1	0.4773924	32.03207
404116	cg2290908	31672308	31672308	0.6356965	0	1	0.51118	-27.28237
404227	cg2291734	33807428	33807428	0.0678821	0	1	0.2285792	79.27639
404236	cg2291804	56689381	56689381	0.0737593	0	1	0.1790572	41.69405
404358	cg2292686	21730447	21730447	0.034012	0	1	0.2559091	146.9932
404425	cg22931151	44794321	44794321	0.7672557	0	1	0.8925456	56.79327
404432	cg2293145	33604408	33604408	0.3262543	0	1	0.4328881	21.069
404477	cg2293380	53623508	53623508	0.3018807	0	1	0.586898	125.7221
404506	cg2293542	58611458	58611458	0.6777628	0	1	0.7924351	32.50271
404521	cg2293625	29744499	29744499	0.2011374	0	1	0.321553	31.54587
404529	cg2293735	10764462	10764462	0.4331809	0	1	0.5434399	21.25992
404567	cg2293970	11632479	11632479	0.6508896	0	1	0.759137	27.00324
404656	cg2294480	24604355	24604355	0.2227187	0	1	0.3498428	32.72346
404748	cg2294976	42718400	42718400	0.5336661	0	1	0.4190356	-22.67155
404766	cg22950831	38624309	38624309	0.7962929	0	1	0.91638	61.75909
404812	cg2295368	59715476	59715476	0.4974471	0	1	0.6157031	24.62435
404865	cg2295663	25629423	41654421	0.7643586	0	1	0.9308435	105.0237

405086	cg2296910	51682366	51682366	0.5488732	0	1	0.6556907	21.74841
405099	cg2297000	18714369	18714369	0.4216271	0	1	0.1991566	-87.75455
405112	cg2297121	27643360	27643360	0.1552408	0	1	0.0475179	-50.36032
405136	cg2297280	46726489	43680309	0.3594392	0	1	0.5914609	81.9668
405267	cg2297978	67806326	24759318	0.6952532	0	1	0.5799178	-26.04873
405350	cg2298458	37602338	29733506	0.7487687	0	1	0.9055986	83.85537
405383	cg2298666	32810386	62806350	0.4182539	0	1	0.2389602	-56.18943
405460	cg2299132	23775482	19733510	0.6932528	0	1	0.5928341	-20.85518
405483	cg2299249	46762356	46762356	0.5851631	0	1	0.4726355	-22.25858
405489	cg2299273	48680468	23639303	0.2679135	0	1	0.1638046	-27.96982
405494	cg2299319	44704364	22743479	0.3569202	0	1	0.1993746	-48.85432
405561	cg2299676	43608419	43608419	0.2216651	0	1	0.8172901	374.3439
405609	cg2299962	31727365	47793449	0.6551377	0	1	0.7575078	24.66117
405692	cg2300510	68655481	54730315	0.8904874	0	1	0.5312217	-274.8357
405737	cg2300856	41675351	38711325	0.27444	0	1	0.1715488	-26.81053
405752	cg2300909	59611434	51731434	0.6217211	0	1	0.8494292	115.1996
405788	cg2301062	35619380	35619380	0.880191	0	1	0.7744509	-41.53605
405810	cg2301231	50664382	30761362	0.1911133	0	1	0.3349106	42.9482
405818	cg2301265	12657463	12657463	0.6693857	0	1	0.8574325	87.88558
405934	cg2301958	31615444	31615444	0.5326928	0	1	0.2966114	-86.64081
405975	cg2302205	67711384	67711384	0.6779407	0	1	0.8653693	90.17036
406084	cg2302874	49756401	49756401	0.3752483	0	1	0.5624151	54.13054
406123	cg2303020	37721486	37721486	0.2462409	0	1	0.3592704	25.8714
406203	cg2303492	43682329	43682329	0.2753926	0	1	0.1595287	-33.42877
406253	cg2303726	36602441	36602441	0.8864704	0	1	0.7753057	-46.22697
406392	cg2304527	61622368	61622368	0.7498	0	1	0.8557931	36.85576
406526	cg2305192	39676303	39676303	0.4899846	0	1	0.6955611	69.34681
406561	cg2305350	68659434	44808484	0.3923484	0	1	0.6660577	116.3678
406676	cg2305831	36693466	67652467	0.4881247	0	1	0.7964069	374.3439
406732	cg2306111	46647510	28752344	0.5608889	0	1	0.4581231	-19.01504
406745	cg2306179	73733463	73733463	0.4400916	0	1	0.6590264	75.08199
406816	cg2306628	72707452	57736329	0.5146871	0	1	0.7234434	74.09391
406866	cg2306904	53733425	53733425	0.5938032	0	1	0.7180648	30.59912
406949	cg2307493	28749411	28749411	0.4435288	0	1	0.2792615	-45.59734
406972	cg2307561	56645475	56645475	0.3138284	0	1	0.4198433	21.14365
407022	cg2307906	39756485	39756485	0.4045087	0	1	0.553867	35.80553
407120	cg2308450	33767397	33767397	0.3060832	0	1	0.4318568	28.14348
407129	cg2308514	27684492	27684492	0.6816314	0	1	0.5505707	-31.37639
407220	cg2309020	47796459	47796459	0.0375157	0	1	0.1466564	54.80779
407389	cg2309806	12711505	12711505	0.4073636	0	1	0.5598912	37.1791
407401	cg2309878	23786356	23786356	0.918372	0	1	0.8015773	-60.22606
407514	cg2310604	27662435	27662435	0.6790217	0	1	0.5595299	-26.87975
407570	cg2310986	68739412	57770329	0.7792131	0	1	0.6738903	-27.37338

407638	cg2311461	67614345	58772358	0.6297095	0	1	0.5170289	-23.03304
407672	cg2311738	39656417	39656417	0.6692849	0	1	0.5430461	-28.99939
407766	cg2312325	26689339	64768303	0.4219213	0	1	0.2797489	-35.638
407832	cg2312851	34773406	34773406	0.7029406	0	1	0.4295192	-119.3035
407866	cg2313083	41611411	41611411	0.6045898	0	1	0.7320585	32.79783
407916	cg2313674	17660464	66795481	0.8493093	0	1	0.7236713	-46.14299
407977	cg23141851	72804303	72804303	0.7146705	0	1	0.6086539	-23.61623
408189	cg2315650	69727490	69727490	0.2838677	0	1	0.3843736	20.18928
408213	cg2315818	32629444	12713425	0.0764463	0	1	0.1889563	45.24425
408243	cg2315997	72704311	72704311	0.0505989	0	1	0.6187553	374.3439
408284	cg2316259	59687470	59687470	0.7915626	0	1	0.8968646	45.42547
408379	cg2316742	59770497	59770497	0.7969657	0	1	0.6902326	-29.5336
408398	cg2316852	67794317	67794317	0.9243932	0	1	0.7882752	-77.18129
408444	cg2317110	19799376	19799376	0.3715729	0	1	0.4759429	19.6833
408477	cg2317340	61624403	63721342	0.5890236	0	1	0.4857697	-19.3964
408484	cg2317368	18794419	62765313	0.436703	0	1	0.3113373	-27.83432
408510	cg2317557	51749314	51749314	0.4114062	0	1	0.5246253	22.21699
408530	cg2317661	59602301	59602301	0.2649701	0	1	0.3748109	23.9196
408621	cg2318284	34670367	65739445	0.5966171	0	1	0.4664963	-28.52278
408682	cg2318731	59663416	59663416	0.5200337	0	1	0.3754832	-33.9397
408699	cg2318868	63604477	25783483	0.4166218	0	1	0.2532879	-46.81284
408819	cg2319576	44748359	44748359	0.473251	0	1	0.7668971	148.0846
408955	cg2320272	12694323	12694323	0.4498016	0	1	0.5570878	20.37318
409097	cg2320935	59758416	59758416	0.8164232	0	1	0.936599	71.14987
409106	cg23209941	37721439	37721439	0.2608064	0	1	0.378354	26.84088
409126	cg23210521	49695350	49695350	0.3616306	0	1	0.4948979	29.66535
409156	cg2321244	74799377	74799377	0.270762	0	1	0.3915617	27.60443
409197	cg2321443	57770404	57770404	0.7806518	0	1	0.9075493	63.07859
409203	cg2321476	62803315	22614428	0.4572536	0	1	0.349868	-20.88827
409265	cg2321835	60646428	18724379	0.3631931	0	1	0.219869	-39.99086
409266	cg2321836	70727307	70727307	0.2907658	0	1	0.455511	45.21601
409272	cg2321855	45740474	35708392	0.2045929	0	1	0.0318337	-105.9518
409280	cg2321895	58717327	58717327	0.3110724	0	1	0.4602566	37.31065
409285	cg2321925	26748333	26748333	0.470418	0	1	0.5896092	24.53152
409392	cg2322435	55717393	30647326	0.3586785	0	1	0.2361708	-29.99686
409432	cg2322691	23658400	43769447	0.4413859	0	1	0.2995992	-34.62477
409465	cg2322852	12778419	49678399	0.2993798	0	1	0.1529483	-49.21822
409502	cg2323083	54682481	54682481	0.0991077	0	1	0.2499453	62.69104
409516	cg23231631	39659445	39659445	0.8383591	0	1	0.6487145	-83.1618
409551	cg2323341	15758300	15758300	0.2990346	0	1	0.0828666	-115.2362
409658	cg2323879	13741416	64642364	0.423135	0	1	0.3226537	-19.23573
409730	cg2324214	36799442	62803492	0.051834	0	1		-4.34E-09
409795	cg2324491	70620478	16603329	0.4106607	0	1	0.2956852	-24.60962

409860	cg2324794	46605301	54684461	0.6336008	0	1	0.495542	-32.36415
409871	cg2324842	33740452	33740452	0.7350959	0	1	0.8473252	38.62151
409916	cg2325057	40613384	62690339	0.3800264	0	1	0.2787434	-20.59078
410036	cg2325648	71759373	63640366	0.6790089	0	1	0.7960313	33.92554
410094	cg2325954	29766366	29766366	0.6705192	0	1	0.5430772	-29.50326
410134	cg2326117	18708502	18708502	0.3641255	0	1	0.4759429	22.10423
410252	cg2326863	63735467	63735467	0.147345	0	1	0.2605409	33.59543
410483	cg2328152	59606390	43696426		0	1		-4.34E-09
410615	cg2328883	68682381	68682381	0.5050247	0	1	0.6559646	38.50173
410619	cg2328902	58802339	58802339	0.3187782	0	1	0.2019565	-30.01216
410630	cg2328985	23752376	23752376	0.6625121	0	1	0.5537215	-22.58972
410639	cg2329031	48724355	48724355	0.2716139	0	1	0.4337552	45.02586
410730	cg2329679	72682370	72682370	0.7161036	0	1	0.9392219	374.3439
410750	cg2329886	11700305	34632345	0.7162685	0	1	0.8465955	48.20394
410767	cg2329991	19700344	20734385	0.5667751	0	1	0.2778776	-130.707
410817	cg2330274	44725301	44725301	0.4619423	0	1	0.6046678	33.54959
410823	cg2330299	10626312	10626312	0.4840671	0	1	0.5920718	20.89471
410853	cg2330512	31657469	23720345	0.5801985	0	1	0.4418301	-31.4581
410863	cg2330589	64730380	73795306	0.3881381	0	1	0.6078414	73.75003
411252	cg2333143	24708349	24708349	0.2624297	0	1	0.6023744	374.3439
411288	cg2333349	58633483	58633483	0.2113734	0	1	0.3999341	64.36359
411336	cg2333648	21771471	21771471	0.5947858	0	1	0.48952	-20.07709
411362	cg2333765	59667438	59667438	0.6248285	0	1	0.5221506	-19.7465
411371	cg2333838	49774469	49774469	0.7878324	0	1	0.9441579	105.3765
411498	cg2334550	42759326	42759326	0.3213141	0	1	0.4921148	46.84631
411570	cg2334897	31695334	42783446	0.816954	0	1	0.6963251	-38.17688
411619	cg2335170	21606469	21606469	0.5823336	0	1	0.6937031	24.5699
411632	cg2335224	44763338	73707305	0.7036446	0	1	0.885105	93.36764
411818	cg2336404	42654436	56704416	0.7802071	0	1	0.6439341	-41.06988
411937	cg2337147	46780375	46780375	0.5006839	0	1	0.6572651	41.06365
411940	cg2337158	61718377	61718377	0.339848	0	1	0.1392402	-84.93283
412033	cg2337655	41759380	41759380	0.3261724	0	1	0.2012501	-33.42837
412200	cg2339011	14778329	13618360	0.743937	0	1	0.6089664	-36.90956
412232	cg2339238	29658437	29658437	0.042246	0	1	0.6463042	374.3439
412350	cg2340044	53742492	53742492	0.2395868	0	1	0.3570669	27.86403
412376	cg2340179	41668374	31702423	0.3483804	0	1	0.4504424	19.27205
412380	cg2340230	44670458	44670458	0.6762795	0	1	0.8232073	52.94579
412426	cg2340473	33614370	33614370	0.5486036	0	1	0.7836565	102.0218
412597	cg2341486	60804361	49684479	0.7740956	0	1	0.6596086	-30.68946
412647	cg2341807	63758467	63758467	0.1178929	0	1	0.2743414	61.53361
412667	cg2341896	22654362	22654362	0.2532986	0	1	0.3812241	31.16965
412699	cg2342139	14675470	14675470	0.5209352	0	1	0.7834492	123.9444
412704	cg2342189	49705387	49705387	0.5168497	0	1	0.8257315	374.3439

412817	cg2342974	52632490	52632490	0.2909951	0	1	0.4290864	33.45576
412950	cg2343851	50695345	50695345	0.0628152	0	1	0.531554	374.3439
412974	cg2344038	18738325	18738325	0.8276032	0	1	0.9318193	56.75747
412987	cg2344124	59728457	59728457	0.2783223	0	1	0.4389344	43.9147
412999	cg2344219	23739407	62718433	0.7770117	0	1	0.6602638	-31.90382
413278	cg2346230	74612343	74612343	0.5395398	0	1	0.6469489	21.71198
413305	cg2346368	22625473	22625473	0.828022	0	1	0.6100127	-100.5683
413327	cg2346474	51804485	51804485	0.4751216	0	1	0.318157	-40.47815
413519	cg2347687	66602389	66725344	0.2070992	0	1	0.0527307	-80.88664
413583	cg2348102	16732386	16732386	0.5445687	0	1	0.6568854	23.60398
413597	cg2348186	74770344	74770344	0.3704439	0	1	0.4854752	23.08103
413737	cg2349016	59606495	34632365	0.3573621	0	1	0.173942	-66.74618
413834	cg2349617	69629438	69629438	0.841947	0	1	0.5855051	-136.6214
413853	cg2349730	38764414	53764352	0.5745441	0	1	0.4595755	-22.95312
413858	cg2349756	45679428	45679428	0.2303428	0	1	0.4089997	56.66803
413921	cg2350100	20681329	20681329	0.7005769	0	1	0.8073478	30.61017
413991	cg2350504	20795336	16688394	0.550159	0	1	0.6538691	20.70466
414035	cg2350820	50687494	50687494	0.3462586	0	1	0.466013	25.02528
414108	cg2351301	42775378	42775378	0.5132069	0	1	0.7345982	83.73095
414161	cg2351549	63698447	63698447	0.1252269	0	1	0.2870123	63.11938
414198	cg2351711	25611479	25611479	0.77143	0	1	0.5657279	-78.96844
414215	cg2351794	62643304	23765336	0.6057912	0	1	0.3989413	-65.66019
414264	cg2352114	52617473	47673385	0.2708308	0	1	0.3918105	27.66814
414308	cg2352335	40683383	40683383	0.960352	0	1	0.6430051	-279.8178
414652	cg2354348	13689325	13689325	0.1351722	0	1	0.2398814	31.18806
414762	cg2354990	36622495	65717441	0.4193697	0	1	0.2819422	-33.57387
414772	cg2355070	34740420	34740420	0.222442	0	1	0.3290791	24.78344
414784	cg2355172	73611464	73611464	0.6930503	0	1	0.5539377	-35.2243
414928	cg2356447	57798316	57798316	0.5426093	0	1	0.9224377	374.3439
414963	cg2356712	36634317	36634317	0.7653452	0	1	0.6467417	-31.66287
415112	cg2357953	26799415	26799415	0.4150767	0	1	0.6074977	57.33886
415145	cg2358350	31753327	31753327	0.7955022	0	1	0.9160056	61.90332
415181	cg2358627	54606442	54606442		0	1		-4.34E-09
415209	cg2358804	51692442	51692442	0.2394031	0	1	0.1272278	-35.69553
415251	cg2359038	65610329	52657479	0.3177719	0	1	0.6174315	139.2117
415267	cg2359146	18644450	18644450	0.3924322	0	1	0.2250394	-51.2225
415270	cg2359160	65720370	65720370	0.667514	0	1	0.7818643	31.33038
415317	cg2359530	11609369	11609369	0.9154767	0	1	0.7988142	-58.99099
415329	cg2359612	24660376	24660376	0.6632485	0	1	0.5058149	-41.71988
415479	cg2360399	14792375	14792375	0.604601	0	1	0.7064872	21.84562
415565	cg2361037	27760360	14661413	0.2687388	0	1	0.1108674	-64.07973
415583	cg2361169	50719487	50719487	0.448086	0	1	0.5692701	25.01318
415644	cg2361604	53728375	53728375	0.4272054	0	1	0.323627	-20.16509

415757	cg2362236	15693488	67650322	0.1325192	0	1	0.0260707	-57.47629
415908	cg2363017	14642480	14642480	0.7870033	0	1	0.9025965	53.6888
415931	cg2363132	50666408	50666408	0.6696314	0	1	0.5695119	-20.00238
415994	cg2363434	45738341	24724448	0.6453202	0	1	0.5269899	-25.34092
416038	cg2363657	41790318	41790318	0.4594063	0	1	0.6657149	67.61595
416064	cg2363804	54804489	54804489	0.7037724	0	1	0.5820832	-28.81219
416077	cg2363864	73647450	51656335	0.8973888	0	1	0.7908015	-46.36449
416155	cg2364227	48642510	48642510	0.6744662	0	1	0.7800616	27.55196
416272	cg2364908	27711488	29791450	0.34688	0	1	0.54238	59.08913
416394	cg2365608	49691371	66651389	0.8112246	0	1	0.7084604	-29.2816
416457	cg2365905	48605322	48605322	0.5029818	0	1	0.6192636	24.02159
416546	cg2366438	50730307	50730307	0.9573924	0	1		-4.34E-09
416553	cg2366477	29803410	29803410		0	1		-4.34E-09
416678	cg2367063	39727415	71635485	0.5609783	0	1	0.4444904	-23.3605
416725	cg2367339	56774429	56774429	0.8180048	0	1	0.9220538	52.70138
416842	cg2367934	31602493	31602493	0.7013369	0	1	0.8058393	29.46915
416843	cg2367937	57767364	57767364	0.625455	0	1	0.7321705	24.74896
416898	cg2368174	65620344	25792325	0.7253829	0	1	0.6066417	-28.87078
416899	cg2368186	25694317	25694317	0.4345615	0	1	0.3105775	-27.35207
416919	cg2368301	66739327	21636467	0.5742405	0	1	0.4595079	-22.87257
416934	cg2368380	72631320	72631320	0.4428604	0	1	0.6247308	52.10767
417014	cg2368743	65801402	65801402	0.352777	0	1	0.5978715	91.48782
417097	cg2369141	68601485	68601485	0.7826467	0	1	0.6633879	-33.52665
417151	cg2369449	15604455	15604455	0.285001	0	1	0.4764034	59.29432
417226	cg2369827	70810465	70810465	0.7830689	0	1	0.5135919	-129.8387
417341	cg2370515	51728396	51728396	0.1811913	0	1	0.2960157	30.87174
417439	cg2371201	41796445	17703398	0.0164757	0	1	0.1349236	71.22602
417479	cg2371390	53693410	53693410	0.7625609	0	1	0.6134407	-45.31707
417680	cg2372707	29693481	29693481	0.820823	0	1	0.716691	-30.95638
417737	cg2373060	11773436	10627324	0.2622694	0	1	0.3708334	23.58615
417784	cg2373262	27652365	27652365	0.5906639	0	1	0.4829431	-20.78882
417801	cg2373339	35610394	35610394	0.5356974	0	1	0.3912756	-33.76778
417856	cg2373719	63690442	30723353	0.6157725	0	1	0.5061908	-21.7474
417933	cg2374223	56640382	56640382	0.1372763	0	1	0.2752788	47.24438
418137	cg2375882	64672430	66743443	0.3354949	0	1	0.4733751	31.94526
418286	cg2377222	52666371	52666371	0.3395952	0	1	0.4469625	21.04916
418526	cg2379321	10789310	53791392	0.3416052	0	1	0.5092372	44.72596
418528	cg2379333	67739465	67739465	0.3071046	0	1	0.4494537	34.57897
418771	cg2381248	14714457	14714457	0.9111463	0	1	0.6210684	-206.3551
418789	cg2381339	59678432	59678432	0.3485412	0	1	0.1986297	-45.11705
418888	cg2381902	70699431	70699431	0.7260419	0	1	0.8538713	48.30541
418999	cg2382795	64759481	60656358	0.3887801	0	1	0.6008584	68.79803
419012	cg2382868	49800321	49800321	0.463702	0	1	0.3295974	-30.61887

419122	cg23835894	64778312	28624444		0	1		-4.34E-09
419123	cg23835923	36600420	36600420	0.6658716	0	1	0.9250589	374.3439
419167	cg23838005	29808339	29808339	0.4761305	0	1	0.5788486	19.13303
419412	cg23853861	46628393	19687406	0.5912781	0	1	0.3899554	-62.18856
419431	cg23855392	19709465	19709465	0.1799533	0	1	0.0629381	-51.57814
419453	cg23856611	37808387	37808387	0.4869511	0	1	0.6567374	47.25306
419555	cg23863670	43604369	43604369	0.3201162	0	1	0.4765087	40.1565
419564	cg23864202	57781427	57781427	0.4023894	0	1	0.5129126	21.37525
419622	cg23869232	28782332	28782332	0.7423873	0	1	0.8824259	63.21717
419684	cg23873996	17694510	17694510	0.5802777	0	1	0.6948656	25.76237
419716	cg23876149	63806393	64756379	0.8326911	0	1	0.6300744	-90.65371
419752	cg23878260	60638333	60638333	0.5145155	0	1	0.6377395	26.86978
419816	cg23881926	30680503	42733395	0.3013908	0	1	0.4022216	19.81602
419914	cg23887839	48673495	48673495	0.7270508	0	1	0.929018	134.1052
420007	cg23892766	48640474	48640474	0.53948	0	1	0.852127	374.3439
420064	cg23895439	67722339	67722339	0.5533514	0	1	0.6648383	23.5648
420133	cg23899527	21750485	21750485	0.8000174	0	1	0.9362794	83.70341
420232	cg23905789	48748494	48748494	0.2643935	0	1	0.6148587	374.3439
420234	cg23905908	35718450	59743342	0.3453174	0	1	0.2328684	-26.34448
420307	cg23910458	12614492	12614492	0.5049515	0	1	0.6154627	22.04139
420393	cg23915527	32806360	32806360	0.6090512	0	1	0.5030289	-20.51043
420438	cg23918315	36794403	36794403	0.4680055	0	1	0.3641157	-19.61871
420555	cg23924370	63705465	47704307	0.5104815	0	1	0.4088333	-18.62009
420593	cg23926439	69633370	54786464	0.798215	0	1	0.6537491	-47.49752
420626	cg23928165	56691490	34772365	0.156641	0	1	0.0561036	-43.25957
420639	cg23928763	30742476	40630333	0.9066724	0	1	0.7885545	-56.74693
420644	cg23929036	13644375	13644375		0	1	0.891229	4.34E-09
420664	cg23930313	52704340	52704340	0.4796336	0	1	0.3644286	-23.21029
420791	cg23937295	72720393	72720393	0.4497683	0	1	0.592779	33.46727
420820	cg23939001	38746305	51725359	0.5325723	0	1	0.3419122	-56.50654
420880	cg23942717	16778433	34674323	0.8781595	0	1	0.7632461	-46.37606
420956	cg23947654	71638364	71638364	0.4277216	0	1	0.7884097	374.3439
420968	cg23948391	44670393	44670393	0.5840508	0	1	0.448614	-30.36117
420974	cg23948811	37602467	74744491	0.4732455	0	1	0.5791942	20.11773
420979	cg23948993	39790306	12633348	0.3772372	0	1	0.2707287	-22.56819
421174	cg23958704	47736360	47736360	0.4527365	0	1	0.6405335	55.8012
421195	cg23959772	61661388	61661388	0.0822329	0	1	0.1997402	46.78356
421293	cg23966361	22690431	22690431	0.7501104	0	1	0.8800197	55.98884
421383	cg23971182	54750474	54750474	0.1739336	0	1	0.2763604	26.43238
421451	cg23974473	63659338	63659338	0.7170482	0	1	0.6019621	-27.01137
421493	cg23976981	29800510	29800510	0.3038432	0	1	0.4697619	45.16967
421572	cg23981702	22734320	22734320	0.5922344	0	1	0.6937067	21.21469
421645	cg23985370	59733300	33766476	0.3354442	0	1	0.2184089	-28.95065

421709	cg2398802	32618471	42732388	0.1469051	0	1	0.3535088	87.21752
421925	cg2400021	65621380	39740461	0.429673	0	1	0.2990466	-30.20393
422093	cg2400792	29756506	46755377	0.3906341	0	1	0.6475239	101.5603
422118	cg2400906	72650436	72650436	0.1005246	0	1	0.208475	37.77154
422191	cg2401358	26810484	26810484	0.3473829	0	1	0.2400745	-24.11786
422206	cg2401455	44688390	44688390	0.0694317	0	1	0.3102201	142.7335
422244	cg2401685	26718464	26718464	0.4052657	0	1	0.6293454	77.12507
422253	cg2401814	73806350	73806350	0.632293	0	1	0.7574753	33.78683
422502	cg2403244	17682431	17682431	0.5762355	0	1	0.7209205	39.42892
422514	cg2403310	32630505	22792481	0.9197221	0	1	0.8153231	-52.07969
422515	cg2403312	13790358	13790358	0.4583613	0	1	0.3366232	-25.90205
422521	cg2403350	12682383	13644361	0.9891426	0	1		-4.34E-09
422596	cg24036791	12614397	47768375	0.5467736	0	1	0.7810282	100.853
422761	cg2404608	53665466	59795326	0.3095572	0	1	0.2082422	-23.66252
422772	cg2404661	72694474	72694474	0.3015756	0	1	0.4262219	27.87151
422846	cg2405123	52757446	52757446	0.6916249	0	1	0.5386493	-41.20709
422854	cg2405174	70679390	70679390	0.6069399	0	1	0.4925652	-23.16082
422957	cg2405755	71674454	71674454	0.7460133	0	1	0.9531683	156.5356
423018	cg2406091	24667399	24667399	0.3963813	0	1	0.2752166	-27.55394
423033	cg2406238	70637368	70637368	0.2002918	0	1	0.5127901	374.3439
423080	cg24065641	25672361	25672361	0.7085683	0	1	0.5552901	-42.45999
423269	cg2407658	31766373	31766373	0.2865832	0	1	0.386935	20.06214
423272	cg2407674	22733497	22733497	0.3093601	0	1	0.4314503	26.70339
423289	cg24077401	42744339	42744339	0.5029694	0	1	0.1725564	-190.7101
423333	cg2408012	67640506	67640506	0.2214338	0	1	0.0598441	-83.1515
423369	cg2408268	51756305	51756305	0.5007183	0	1	0.3449548	-39.19734
423418	cg2408492	47735449	47735449	0.6192105	0	1	0.4643906	-38.98057
423621	cg2409709	63650427	63650427	0.6178524	0	1	0.4676195	-36.95755
423666	cg2410029	62648337	62648337	0.9358381	0	1	0.832675	-57.75484
423668	cg2410035	38660364	59766507	0.6941081	0	1	0.525584	-48.78091
423677	cg24100841	54650349	54650349	0.6373392	0	1	0.7520853	29.05366
423716	cg2410304	31723420	31723420	0.4918921	0	1	0.6332058	33.65831
423880	cg2411401	54677411	59640472	0.6970059	0	1	0.4545008	-94.1768
423901	cg2411501	64600307	64600307	0.3415529	0	1	0.4585597	24.17018
423925	cg2411638	18614375	18614375	0.5249069	0	1	0.6321126	21.30488
423947	cg2411750	56702336	56702336	0.9453554	0	1	0.8442572	-60.76154
424000	cg2412021	27697486	71668435	0.9893587	0	1	0.8749177	-107.6527
424121	cg2412684	70700395	37676493	0.8577062	0	1	0.7364435	-45.41896
424140	cg2412741	42665471	42665471	0.7804796	0	1	0.6352309	-45.50239
424198	cg2413028	41607326	41607326	0.6296816	0	1	0.5144298	-23.89297
424270	cg2413418	47714360	47714360	0.5111234	0	1	0.6307524	25.42071
424385	cg2413987	59650333	59650333	0.5873879	0	1	0.7755133	68.55569
424443	cg2414277	29730323	54661507	0.5343676	0	1	0.3695934	-42.88363

424667	cg2415485	54680357	72777479	0.5448244	0	1	0.7818443	103.1153
424691	cg2415618	35765340	35765340	0.4404821	0	1	0.5556592	22.89771
424752	cg2415887	73610478	73610478	0.5219744	0	1	0.663644	34.87644
424789	cg2416042	41739424	41739424	0.5958748	0	1	0.4645746	-28.95074
424891	cg2416691	13752399	13752399	0.4080535	0	1	0.2029158	-75.63499
424930	cg2416948	47650434	47650434	0.7432355	0	1	0.8713068	52.50742
424941	cg2417008	55767342	20663507	0.4962695	0	1	0.612398	23.84035
425097	cg2418117	60718359	60718359	0.319342	0	1	0.451883	30.29272
425107	cg2418166	72677445	72677445	0.5574719	0	1	0.6776661	27.08251
425142	cg2418350	47684365	47684365	0.1111033	0	1	0.2537913	54.86249
425150	cg2418402	22600456	71690340	0.8802173	0	1	0.7781592	-39.45778
425176	cg2418565	56687360	55750345	0.9004197	0	1	0.7719917	-61.50823
425261	cg2419255	54676328	72666434	0.81131	0	1	0.6804951	-42.41639
425264	cg2419266	40765501	62705329	0.2084554	0	1	0.092632	-43.51542
425375	cg2419938	29724343	29724343	0.5169359	0	1	0.6498379	30.84556
425460	cg2420504	22657328	22657328	0.3776284	0	1	0.4966642	24.35113
425505	cg2420858	52723466	52723466	0.5111631	0	1	0.6561134	35.94062
425528	cg2421081	37769364	37769364	0.2182821	0	1	0.3346363	28.69254
425837	cg2423367	60729308	60729308	0.2161503	0	1	0.3182211	23.48653
425895	cg2423840	13672463	13672463	0.6603431	0	1	0.7826724	34.8882
426221	cg2426423	51699370	51699370	0.9446412	0	1	0.8244122	-75.67595
426235	cg2426572	30724305	30724305	0.9315115	0	1	0.7619342	-108.0203
426415	cg2428083	57670475	16687490	0.7685197	0	1	0.6674572	-24.90934
426463	cg2428446	16800439	16800439	0.1311756	0	1	0.2383453	32.80274
426465	cg2428453	18760487	54751387	0.7874968	0	1	0.5395584	-112.9113
426500	cg2428721	17713396	17713396	0.6871635	0	1	0.574159	-24.87995
426515	cg2428945	30605485	63790501	0.8574162	0	1	0.7372429	-44.75303
426609	cg2429618	21741468	21741468	0.6550065	0	1	0.7622727	26.84556
426658	cg2429908	38674411	38674411	0.3046153	0	1	0.566089	105.3796
426662	cg2429930	44711379	44711379	0.5360461	0	1	0.7170058	57.11234
426745	cg2430461	73697392	73697392	0.3578403	0	1	0.4610003	19.47414
426830	cg2430976	31759311	31759311	0.3887808	0	1	0.9079667	374.3439
426870	cg2431164	56688344	56688344	0.4796391	0	1	0.6021166	25.84916
426889	cg2431252	27670303	27670303	0.5268342	0	1	0.626975	19.01636
427006	cg2432003	59641444	47739385	0.7805722	0	1	0.929999	90.61403
427033	cg2432197	62765508	62765508	0.3575049	0	1	0.5237774	43.75755
427074	cg2432483	15742383	13698310	0.8648215	0	1	0.7338532	-52.62548
427091	cg2432599	31734427	31734427	0.2929767	0	1	0.1793943	-30.50964
427162	cg2433045	40790492	71730422	0.2083076	0	1	0.405611	69.98405
427438	cg2434343	28716473	28716473	0.5702672	0	1	0.6909187	27.80739
427639	cg2435518	71711502	12653509	0.7254062	0	1	0.5582771	-50.58678
427694	cg2435992	20672497	20672497	0.5935822	0	1	0.7808861	68.94727
427710	cg2436087	71656418	71656418	0.351813	0	1	0.4702139	24.46663

427762	cg2436339	31666380	31666380	0.5309336	0	1	0.6692184	33.72146
427764	cg2436362	48790407	48790407	0.5658991	0	1	0.4574936	-20.77397
427839	cg2436784	48762444	37767480	0.7599493	0	1	0.6537801	-26.25868
427841	cg2436795	47744433	47744433	0.2136128	0	1	0.351129	37.89092
428092	cg2438424	27644355	36635317	0.1219311	0	1	0.011783	-67.19733
428209	cg2439293	57755443	57755443	0.765264	0	1	0.8722441	40.50816
428217	cg2439331	64658453	28662378	0.7167686	0	1	0.5729082	-38.75908
428326	cg2439934	68718419	55710367	0.4256148	0	1	0.30268	-27.21068
428452	cg2440624	67648488	67648488	0.667045	0	1	0.7766506	28.89218
428486	cg2440820	44687303	44687303	0.715891	0	1	0.8443062	46.69154
428624	cg2441715	72680508	72680508	0.8393643	0	1	0.4293944	-321.2908
428659	cg2441960	59679345	59679345	0.6717174	0	1	0.7778278	27.57614
428694	cg2442190	43631335	43631335	0.2426685	0	1	0.1134844	-46.72201
428750	cg2442597	73741498	73741498	0.6031618	0	1	0.7087306	23.19223
429001	cg2443968	53698457	53698457	0.5495297	0	1	0.6723212	27.82933
429013	cg2444065	20731321	52792477	0.7968475	0	1	0.6057312	-74.26487
429156	cg2445011	52684506	52684506	0.8696845	0	1	0.6777682	-95.06404
429184	cg2445187	39659345	39659345	0.3125602	0	1	0.6274981	156.5356
429199	cg2445245	14612502	58778375	0.6032935	0	1	0.3779329	-77.43323
429271	cg2445711	23806421	23806421	0.481265	0	1	0.6094553	28.02936
429325	cg2446012	22710467	12605372	0.696664	0	1	0.576318	-27.95672
429343	cg2446130	37723323	37723323	0.5627677	0	1	0.4577534	-19.70538
429398	cg2446450	48775334	48775334	0.1562209	0	1	0.271339	33.45571
429413	cg2446532	60633364	60633364	0.6026046	0	1	0.7723279	57.3549
429494	cg2447046	22782397	22782397	0.5529487	0	1	0.8338605	156.5356
429507	cg2447121	26675310	26675310	0.483148	0	1	0.3211208	-42.68491
429571	cg2447603	58697331	28755447	0.3422766	0	1	0.1681041	-62.23445
429602	cg2447812	64749312	64749312	0.7128827	0	1	0.8746982	75.30563
429626	cg2447938	54699405	54699405	0.6047888	0	1	0.7313121	32.35649
429736	cg2448592	50692366	50692366	0.5761124	0	1	0.1813818	-273.5412
429873	cg2449449	27809338	27809338	0.5116601	0	1	0.6138297	19.403
430089	cg2450622	61722487	69724377	0.2603967	0	1	0.0414393	-139.3636
430115	cg2450776	68607444	68607444	0.3668048	0	1	0.4688478	19.03176
430128	cg2450842	66660332	36656493	0.466139	0	1	0.1356327	-202.9142
430358	cg2452276	34629506	34629506	0.5623847	0	1	0.742954	59.61814
430448	cg2452709	19792331	19792331	0.2685748	0	1	0.1517991	-34.70868
430575	cg2453309	71673405	71673405	0.8008708	0	1	0.6868418	-33.11504
430645	cg2453634	21699463	21699463	0.4941041	0	1	0.6077223	22.92348
430654	cg2453678	11672327	35767456	0.6036297	0	1	0.4579052	-34.75807
430702	cg2453959	41691439	41691439	0.2846917	0	1	0.4050912	26.90575
430736	cg2454155	40673371	40673371	0.2229853	0	1	0.3321646	25.68388
430888	cg2455021	45679347	47717394	0.7230719	0	1	0.505564	-79.68359
430982	cg2455675	33642301	33642301	0.5883245	0	1	0.7263451	36.87562

431108	cg24567694	42736321	42736321	0.0683409	0	1	0.2146657	69.08398
431152	cg24571110	59631496	59631496	0.2487747	0	1	0.1268356	-40.5848
431246	cg24577594	35619362	35619362	0.2311009	0	1	0.4489712	80.11201
431374	cg24585418	12692438	59677393	0.7508775	0	1	0.6433305	-26.17474
431390	cg24586205	21656447	21656447	0.4294519	0	1	0.5528096	25.68353
431406	cg24587185	39810504	39810504	0.2871378	0	1	0.4315884	36.25702
431498	cg24592527	70651325	40737350	0.2118817	0	1	0.1055755	-36.07478
431500	cg24592576	21710401	21710401	0.160239	0	1	0.2603185	26.64286
431527	cg24593918	61624328	61624328	0.4482469	0	1	0.3189949	-29.05633
431540	cg24594633	52750506	52750506	0.7698184	0	1	0.871524	37.47903
431590	cg24597825	35631360	74648484	0.4715577	0	1	0.6364305	44.07395
431631	cg24599709	30746490	30746490	0.7911801	0	1	0.8912351	40.82504
431766	cg24607859	52763510	52626476	0.4355897	0	1	0.3110229	-27.55129
431784	cg24609101	50675301	50675301	0.4757461	0	1	0.605557	28.5557
431851	cg24613956	61737472	61737472	0.4426045	0	1	0.6112996	45.1676
432011	cg24625984	22730469	22730469	0.4839095	0	1	0.58792	19.61342
432057	cg24629232	16694492	16694492	0.6649213	0	1	0.7673293	25.33674
432192	cg24636332	22607313	74769447	0.3506465	0	1	0.6285958	118.6285
432205	cg24636969	10804440	12717471	0.0954677	0	1	0.2237142	49.95558
432209	cg24637044	28656357	39746472	0.1410471	0	1	0.3142425	66.68298
432397	cg24648384	31751309	31751309	0.1146638	0	1	0.2203247	34.34624
432400	cg24648715	71797347	71797347	0.3449329	0	1	0.2397102	-23.40335
432424	cg24650913	65768461	65768461	0.4367266	0	1	0.6131625	49.01543
432446	cg24652615	52635432	74687433	0.8562945	0	1	0.6429561	-106.3579
432495	cg24655706	20762315	20762315	0.2309112	0	1	0.3398248	25.15279
432573	cg24661168	59699382	59699382	0.6584959	0	1	0.7728188	30.51083
432576	cg24661236	30641453	35761407	0.6707745	0	1	0.5408635	-30.46068
432733	cg24670453	28689388	55775453	0.6342115	0	1	0.5329277	-19.50171
432771	cg24672777	55760423	48672464	0.6386265	0	1	0.7412767	23.78658
432801	cg24674504	11728364	29619326	0.6779678	0	1	0.5699834	-22.81538
432933	cg24680632	11688465	71701313	0.4197045	0	1	0.261173	-43.96722
432934	cg24680646	12746311	12746311	0.6632105	0	1	0.5277832	-32.32297
432936	cg24680742	27802424	27802424	0.7371216	0	1	0.9315445	129.2521
433055	cg24686551	68782416	68782416	0.582108	0	1	0.7160385	34.41767
433056	cg24686553	36667388	36667388	0.3039209	0	1	0.4084801	20.92198
433093	cg24687805	48707310	48707310	0.6809006	0	1	0.7919785	30.89849
433129	cg24689026	23719446	23719446	0.4780685	0	1	0.2209961	-110.0103
433150	cg24690094	30685388	12747325	0.2220275	0	1	0.0775884	-64.76555
433176	cg24691167	23766456	54758300	0.5399093	0	1	0.3278257	-69.39436
433178	cg24691330	45715405	45715405	0.6986918	0	1	0.5346751	-46.8768
433231	cg24693551	47721303	47721303	0.2265873	0	1	0.0980939	-49.50785
433260	cg24694833	20694418	20694418	0.2314072	0	1	0.7661498	374.3439
433297	cg24697433	54700308	54700308	0.3292851	0	1	0.1924592	-39.51419

433431	cg2470422	54634418	54634418	0.7908504	0	1	0.9263266	77.66559
433494	cg2470748	30779434	29621508	0.3746507	0	1	0.4773461	19.14715
433496	cg2470757	37737351	22726360	0.6218021	0	1	0.4894086	-29.85883
433525	cg24709001	60731329	16657340	0.917455	0	1	0.7818339	-73.4894
433752	cg2472105	28716403	28716403	0.7165061	0	1	0.820792	31.02195
433779	cg2472257	50656303	50656303	0.3523208	0	1	0.6301333	118.5305
433835	cg2472552	32785398	32785398	0.2342462	0	1	0.3880309	43.67691
433917	cg2472983	59719371	59719371	0.3077301	0	1	0.5020243	59.69727
434026	cg2473673	60699433	60699433	0.3054082	0	1	0.4371571	30.41742
434099	cg2474051	19624417	74651303	0.9788163	0	1	0.8585284	-102.033
434237	cg2474936	39680485	18799420	0.7334564	0	1	0.560442	-54.4437
434297	cg2475309	74793327	74793327	0.456947	0	1	0.5870433	28.38162
434303	cg2475376	10639318	10639318	0.6748121	0	1	0.5357586	-34.28469
434325	cg2475513	39620346	39620346	0.3691555	0	1	0.5329384	42.4253
434331	cg2475545	24624480	55695461	0.4196704	0	1	0.5251786	19.76178
434412	cg24760581	69733370	69733370	0.0164815	0	1	0.410164	374.3439
434490	cg2476578	52708465	52708465	0.8270739	0	1	0.9419154	69.80421
434565	cg24769381	24754359	24754359	0.542365	0	1	0.8297019	374.3439
434762	cg2478197	32606446	32606446	0.2896307	0	1	0.4175237	29.50483
434809	cg2478617	41677319	41677319	0.5141038	0	1	0.6577026	35.43709
434836	cg2478759	42792334	42792334	0.6731968	0	1	0.9461449	374.3439
434899	cg2479121	29765492	56755477	0.1622688	0	1	0.0242253	-82.42976
434985	cg2479664	22726355	17683424	0.8846592	0	1	0.7498575	-60.49847
435052	cg2480022	64678343	64678343	0.9081283	0	1	0.6901755	-134.6751
435209	cg2480926	50603507	50603507	0.4568333	0	1	0.5902379	29.66272
435231	cg2481073	41786312	59756367	0.1458601	0	1	0.2562411	32.49406
435339	cg2481926	15679456	15679456	0.5800502	0	1	0.6881329	23.21397
435355	cg2482067	50789471	18647489	0.5821205	0	1	0.4769471	-19.90781
435398	cg24824371	12641307	12641307	0.47652	0	1	0.5889721	22.27764
435400	cg2482447	46719372	46719372	0.3525546	0	1	0.4548506	19.28344
435418	cg2482533	24658347	46787365	0.1736389	0	1	0.0199365	-97.60558
435574	cg2483439	10618304	10618304	0.5193468	0	1	0.6522864	30.94287
435617	cg2483682	22686440	17725391	0.8236086	0	1	0.4437848	-267.8958
435641	cg2483806	38702310	31642452	0.8128767	0	1	0.6543378	-57.61354
435648	cg2483831	27744377	27744377	0.5883106	0	1	0.4765627	-22.04182
435774	cg2484593	71800302	71800302	0.1016439	0	1	0.2076396	36.5702
435776	cg2484600	16757458	16757458	0.4368075	0	1	0.6464221	68.5943
435811	cg2484784	57762353	62768401	0.2855425	0	1	0.0783531	-109.9785
435960	cg2485638	28806483	28806483	0.3840616	0	1	0.2493312	-34.15719
435966	cg2485667	25747460	25747460	0.4483499	0	1	0.2753453	-50.13119
436005	cg2485922	69663383	69663383	0.1509795	0	1	0.2634327	32.84376
436020	cg2485964	12639454	12639454	0.0526396	0	1	0.2055684	79.86792
436058	cg2486139	16740353	16740353	0.0756329	0	1	0.2173088	63.56615

436066	cg24861747	28663414	28663414	0.1451371	0	1	0.2477863	29.16836
436139	cg24865482	48699411	48699411	0.798363	0	1	0.9230827	67.9864
436164	cg24866764	29671350	29671350	0.4736431	0	1	0.5880393	22.90262
436176	cg24867279	36727436	28609422	0.4662425	0	1	0.2614207	-68.78515
436237	cg24870391	44690397	44690397	0.374653	0	1	0.5013304	27.06316
436272	cg24872173	59689343	59689343	0.7188997	0	1	0.2796595	-341.8894
436311	cg24873924	29785495	29785495	0.8800977	0	1	0.6997616	-90.4962
436388	cg24877509	52639464	52639464	0.5835879	0	1	0.4653718	-24.12882
436399	cg24877964	66606448	66606448	0.4308363	0	1	0.5387061	20.49697
436498	cg24882709	60703325	60703325	0.603376	0	1	0.7281274	31.42158
436503	cg24883219	44800449	44800449	0.5149643	0	1	0.3464096	-45.05679
436588	cg24886788	14800312	14800312	0.3456224	0	1	0.4503436	20.12426
436604	cg24888257	43667408	38600394	0.7056611	0	1	0.5993813	-23.30392
436688	cg24893378	44810332	44810332	0.1929983	0	1	0.3819018	67.05425
436727	cg24896460	70722452	70722452	0.5736765	0	1	0.7255338	43.09238
436742	cg24897392	59659411	59659411	0.4991262	0	1	0.6322967	30.41993
436779	cg24900563	53796500	53796500	0.5823953	0	1	0.6830264	20.57421
436882	cg24906015	47620370	47620370	0.6206981	0	1	0.5004875	-25.39966
436907	cg24908198	58770325	17807473	0.9068198	0	1	0.7983664	-50.38023
436947	cg24911283	55669478	55669478	0.5995697	0	1	0.7036223	22.45707
436957	cg24911837	36781471	36781471	0.3828944	0	1	0.5257683	33.18923
436962	cg24912023	25801336	25801336	0.5061952	0	1	0.6094078	19.65086
436970	cg24912560	47689501	47689501	0.8588834	0	1	0.7331163	-48.21364
436978	cg24913168	64614493	59706366	0.4293315	0	1	0.5308102	18.54093
437033	cg24917131	33787301	33787301	0.583049	0	1	0.8577305	374.3439
437113	cg24923430	17678303	63754349	0.6499183	0	1	0.466263	-53.9906
437130	cg24923931	38724324	55774308	0.4985497	0	1	0.3510643	-35.51058
437159	cg24925741	20633404	20633404	0.3347109	0	1	0.4400429	20.49731
437170	cg24926185	62631457	62631457	0.4491606	0	1	0.5574181	20.67774
437197	cg24927769	57729426	57729426	0.783623	0	1	0.8967263	50.2573
437315	cg24933157	32625369	32625369	0.3559769	0	1	0.4640142	21.005
437456	cg24940951	38653505	38653505	0.3042475	0	1	0.4057006	19.93859
437468	cg24941469	15772351	15772351	0.1927107	0	1	0.6167701	374.3439
437470	cg24941603	69621483	10765423	0.6156996	0	1	0.7189992	22.87375
437522	cg24946117	46801340	46801340	0.6147243	0	1	0.8984246	374.3439
437554	cg24947637	72609377	19674510	0.5621516	0	1	0.7663849	77.16189
437569	cg24948743	22636366	15613336	0.6269843	0	1	0.5196031	-21.25541
437691	cg24955829	13663506	13663506	0.7568595	0	1	0.5395678	-84.24699
437694	cg24955955	20670468	20670468	0.5432607	0	1	0.7688479	92.08909
437709	cg24957518	67780307	67780307	0.6064682	0	1	0.7834708	63.20399
437723	cg24958687	10629423	10629423	0.5436311	0	1	0.3249099	-73.67802
437745	cg24960960	17612325	37779367	0.2692963	0	1	0.0904147	-84.02534
437748	cg24961286	72637374	72637374	0.6540124	0	1	0.7548794	23.9411

437814	cg2496636	49617431	49617431	0.4213721	0	1	0.5745832	37.54813
437843	cg2496886	19687446	19687446	0.792824	0	1	0.8957974	43.71581
437853	cg2496949	15736439	15736439	0.415989	0	1	0.7593192	374.3439
437926	cg2497472	28661329	20728454	0.7063808	0	1	0.5343077	-51.49058
437931	cg2497521	18722400	18722400	0.3773249	0	1	0.4810376	19.4287
437983	cg2497916	44756319	44756319	0.2549458	0	1	0.4136929	44.48614
438426	cg2500624	42722446	55680418	0.5111055	0	1	0.3591882	-37.24884
438454	cg2500772	69692414	68723455	0.5060306	0	1	0.3445486	-41.78151
438577	cg2501375	25682361	25682361	0.3582745	0	1	0.5403031	51.57389
438587	cg2501422	49645350	49645350	0.2501087	0	1	0.3637929	25.92409
438595	cg2501503	67632390	67632390	0.5745226	0	1	0.6774984	21.14978
438632	cg2501722	29608371	46697347	0.2658209	0	1	0.3953486	31.16314
438640	cg2501762	27739443	28777354	0.267693	0	1	0.0373741	-152.283
438646	cg2501797	47616304	59810484		0	1	0.0233081	4.34E-09
438849	cg2502699	72730386	38693418	0.5268467	0	1	0.3373101	-56.00875
438895	cg2502944	37766331	37766331	0.8214604	0	1	0.7206747	-29.53924
438992	cg2503494	48777493	48777493	0.4957087	0	1	0.5998652	19.80258
439005	cg2503563	61738421	30677325	0.3224285	0	1	0.1483453	-65.74887
439162	cg2504657	23646384	23646384	0.2424391	0	1	0.4125378	51.0449
439332	cg2505940	42669397	42669397	0.7258658	0	1	0.835012	35.15285
439340	cg2505969	61613414	61613414	0.4564468	0	1	0.5829772	27.03048
439421	cg2506513	12621490	12621490	0.4352489	0	1	0.5542101	24.16312
439439	cg2506666	11755371	38749389	0.8693908	0	1	0.7020925	-77.29882
439701	cg2508536	57758371	57758371	0.5348002	0	1	0.3827832	-37.01841
439894	cg2509909	19746429	19746429	0.8096299	0	1	0.525535	-150.5824
439966	cg2510341	40688342	40688342	0.2883688	0	1	0.4136531	28.56902
439982	cg2510423	26625304	26625304	0.3851286	0	1	0.5923899	65.74813
440161	cg2511418	24629421	24629421	0.2022981	0	1	0.3034057	23.94188
440308	cg2512356	37785319	37785319	0.3688177	0	1	0.4856403	23.69677
440362	cg2512630	24616484	24616484	0.5109201	0	1	0.9138074	374.3439
440393	cg2512912	27730408	41638407	0.4255294	0	1	0.3248375	-19.25685
440489	cg2513464	21646334	21646334	0.7026598	0	1	0.5384678	-47.24674
440574	cg2513875	39780366	11757314	0.530273	0	1	0.6340232	20.25727
440600	cg2514021	60681365	60681365	0.2968062	0	1	0.4877058	58.34538
440840	cg2515375	57695325	57695325	0.36934	0	1	0.2520459	-27.15576
440976	cg2516307	21787372	21787372	0.8152897	0	1	0.69151	-39.48505
441007	cg2516554	18794378	49604510		0	1	0.7137342	4.34E-09
441062	cg2517111	19601447	19601447	0.3572235	0	1	0.4707863	22.76479
441092	cg2517411	42628414	42628414	0.654606	0	1	0.5171468	-32.80758
441096	cg2517433	24627320	24627320	0.8053802	0	1	0.9101354	49.02666
441104	cg2517460	67697330	21705410	0.3268157	0	1	0.4478187	25.85972
441174	cg2518117	45797474	45797474	0.3434794	0	1	0.4514919	21.18716
441241	cg2518614	71800390	71800390	0.7457542	0	1	0.8575065	40.1866

441381	cg2519482	29809481	29809481	0.3189672	0	1	0.4374059	25.15355
441418	cg2519671	64647415	64647415	0.49019	0	1	0.383335	-20.33892
441516	cg2520236	61615420	61615420	0.6467357	0	1	0.4726614	-48.92993
441536	cg2520324	67684364	67684364	0.8040926	0	1	0.701293	-28.56787
441578	cg2520543	18792373	18792373	0.8075005	0	1	0.6464034	-58.1007
441772	cg2521727	63639328	63639328	0.2173328	0	1	0.3837542	51.487
441807	cg2521949	71607444	71607444	0.4080805	0	1	0.5427735	29.85281
441813	cg2522006	30798484	26616353	0.2988595	0	1	0.0942669	-101.5495
441904	cg2522515	46784473	11652474	0.7991213	0	1	0.6357303	-57.94611
441934	cg25226891	74719354	74719354	0.4646975	0	1	0.3562166	-21.14157
441944	cg2522780	65744387	65744387	0.2556835	0	1	0.359805	22.3366
442118	cg2524242	57751408	57751408	0.3125382	0	1	0.4132217	19.50891
442130	cg2524308	55626484	43698461	0.6757144	0	1	0.5427124	-31.87951
442191	cg2524689	12721379	12721379	0.7382994	0	1	0.4957897	-99.287
442207	cg2524768	23714413	23714413	0.7710787	0	1	0.5831565	-67.72445
442232	cg2524928	36623314	71712407	0.3614733	0	1	0.4881682	27.23363
442235	cg2524936	17794346	17794346	0.6820153	0	1	0.8293214	54.33202
442273	cg2525201	36690375	36690375	0.6317003	0	1	0.7320586	22.48777
442274	cg2525219	42767506	42767506	0.1280498	0	1	0.2331236	32.23116
442339	cg25257671	57675383	36743314	0.7362666	0	1	0.590201	-41.28479
442513	cg2527089	54630401	54630401	0.9299902	0	1	0.8254924	-56.18255
442618	cg2527780	17760506	17760506	0.5489025	0	1	0.4387609	-21.23718
442675	cg2528184	53728444	53728444	0.2501398	0	1	0.3517545	21.71946
442701	cg2528333	20702363	20702363	0.2890834	0	1	0.7795317	374.3439
442803	cg2529022	65797502	65797502	0.5625722	0	1	0.4553191	-20.39312
442821	cg2529125	32617420	32617420	0.8354344	0	1	0.7047634	-46.25608
442891	cg2529693	39603442	39603442	0.3914981	0	1	0.5004312	20.92891
442908	cg2529831	46643482	51700386	0.3660332	0	1	0.0400202	-250.5329
443037	cg2530733	20611310	20611310	0.3846082	0	1	0.5188726	29.78759
443134	cg2531205	48710475	48710475	0.4436822	0	1	0.5524824	20.82575
443152	cg2531297	14611497	14611497	0.5476474	0	1	0.6546655	21.78573
443271	cg2531927	11772429	11772429	0.80401	0	1	0.6803386	-37.93377
443370	cg2532559	19657413	15603304	0.6379317	0	1	0.5282031	-22.24753
443384	cg2532628	69638390	20604404	0.2096539	0	1	0.3226596	27.95491
443396	cg2532699	52608434	46762308	0.1892742	0	1	0.0817915	-41.15245
443523	cg2533689	12802321	12802321	0.527218	0	1	0.719062	63.41651
443561	cg2533905	74719359	74719359	0.3779716	0	1	0.6271452	94.89543
443587	cg2534068	53782363	38662399	0.5679961	0	1	0.4494896	-24.08553
443689	cg2534573	41694346	41694346	0.123933	0	1	0.225194	30.9979
443889	cg2535646	40666356	40666356	0.5842804	0	1	0.7309638	41.12482
443909	cg2535766	67661507	67661507	0.7107604	0	1	0.8253083	36.38985
444047	cg2536593	33620336	59714368	0.4120016	0	1	0.2996636	-23.58803
444121	cg2536926	60723452	60723452	0.2218748	0	1	0.3262241	23.98937

444150	cg2537126	46633425	46633425	0.5636074	0	1	0.6740328	23.5055
444182	cg2537229	66787371	66810354	0.2719322	0	1	0.4419784	48.85971
444227	cg2537516	65732308	65732308	0.4181897	0	1	0.5757074	39.45872
444243	cg2537603	45623463	19763424	0.6777091	0	1	0.8005341	37.10494
444318	cg2538125	28714405	28714405	0.7257973	0	1	0.9222565	124.8037
444348	cg25382821	26632370	26632370	0.6074413	0	1	0.7125075	23.18671
444446	cg2538895	24657323	24657323	0.9474273	0	1	0.7030855	-188.4031
444552	cg2539554	21733385	21733385	0.510325	0	1	0.4100101	-18.22313
444608	cg2539930	59792335	59792335	0.5264575	0	1	0.4081033	-23.93549
444626	cg2540037	25778421	42739471	0.1296988	0	1	0.2378024	33.4275
444777	cg2540896	67762367	67762367	0.6933988	0	1	0.8785393	93.4474
444809	cg2541078	19742358	19742358	0.5206456	0	1	0.7136461	63.54901
444904	cg2541767	46678372	48657349	0.3828187	0	1	0.268193	-25.46983
444939	cg25420101	65616357	65616357	0.4184394	0	1	0.6430004	77.95456
445004	cg2542307	53686471	70602466	0.9058185	0	1	0.7748805	-65.22946
445030	cg2542427	44730478	44730478	0.2872234	0	1	0.4286197	34.97222
445055	cg2542599	55685434	55685434	0.4689274	0	1	0.3660949	-19.27648
445157	cg2543280	58726341	73736305	0.8814739	0	1	0.780819	-38.9419
445180	cg2543486	63772451	59708488	0.7542831	0	1	0.8922827	65.12864
445198	cg2543624	60784379	51657370	0.7368808	0	1		-4.34E-09
445223	cg2543788	14705510	14705510	0.6798612	0	1	0.7881452	29.35366
445237	cg2543887	46644374	46644374	0.376186	0	1	0.4787887	19.10506
445325	cg25445671	38619346	38619346	0.3295415	0	1	0.4888403	41.17265
445343	cg2544646	25720424	25720424	0.7079348	0	1	0.809203	28.43067
445411	cg25450121	23733451	23733451	0.1152491	0	1	0.2372686	42.54676
445447	cg2545216	58610460	10801428	0.8708485	0	1	0.7181571	-67.92208
445491	cg2545540	56705368	56705368	0.5632918	0	1	0.666102	20.75125
445616	cg2546285	19638351	19638351	0.1557525	0	1	0.2675084	32.01286
445684	cg2546783	56651484	56651484	0.5010929	0	1	0.6783146	52.15614
445703	cg2546861	69778302	23627486	0.7239861	0	1	0.5532198	-52.33312
445714	cg2546892	31686334	31686334	0.9349387	0	1	0.8341333	-55.59692
445726	cg2546941	47711344	68633335	0.1779492	0	1	0.2872099	28.84875
445747	cg2547075	73769489	72647366	0.5809531	0	1	0.4117401	-44.94452
445908	cg2548116	13663473	13663473	0.2669095	0	1	0.3748578	23.19532
445949	cg2548390	22723355	22723355	0.4808907	0	1	0.599512	24.47301
446017	cg2548828	57793476	57793476	0.811076	0	1	0.9121003	47.2133
446173	cg25498731	73789377	73789377	0.3123357	0	1	0.5473514	85.10367
446458	cg2551680	41793409	41793409	0.3785068	0	1	0.2314516	-40.76235
446640	cg2553122	19725311	19725311	0.718525	0	1	0.5516859	-49.82681
446653	cg25532201	26658455	52798333	0.5220832	0	1	0.393838	-27.47878
446703	cg2553598	14607324	14607324	0.3621943	0	1	0.5170528	38.48122
446712	cg2553646	34807466	34807466	0.4085344	0	1	0.6359653	79.59093
446740	cg25538571	64636442	64636442	0.3733552	0	1	0.5177575	33.90163

446800	cg2554231	49701389	49701389	0.4498976	0	1	0.5856267	30.49245
446807	cg2554287	56757475	22721337	0.3985451	0	1	0.5137158	22.90279
446827	cg2554438	16604387	16604387	0.2081208	0	1	0.321507	28.20652
446854	cg2554648	53758452	53758452	0.3787972	0	1	0.4826246	19.4503
446861	cg2554713	23714488	23714488	0.4790661	0	1	0.5908168	22.07263
446933	cg2555169	13644385	13644385		0	1		-4.34E-09
447007	cg2555600	48631359	48631359	0.5278742	0	1	0.6454979	25.09951
447051	cg2555840	49637374	11728357	0.3553143	0	1	0.2531143	-21.79519
447196	cg25568241	55683481	55683481	0.6874784	0	1	0.8070474	36.37588
447212	cg2556946	66638340	66638340	0.8206583	0	1	0.6552387	-63.19321
447213	cg2556948	54634366	66626421	0.7744395	0	1	0.6626862	-29.58595
447330	cg25576711	53674496	53674496	0.2602204	0	1	0.1416761	-36.78827
447334	cg25576961	67768472	67768472	0.7957621	0	1	0.4414288	-223.2663
447466	cg2558481	56767305	31807363	0.8505689	0	1	0.7218968	-48.0887
447468	cg2558493	19769332	19769332	0.4504659	0	1	0.1808995	-127.9737
447531	cg2558884	27759392	27759392	0.3317982	0	1	0.439577	21.32254
447605	cg2559319	33751503	33751503	0.5880287	0	1	0.4098297	-49.47576
447639	cg2559482	27779474	27779474	0.5261412	0	1	0.4061425	-24.50307
447665	cg2559628	35611367	35611367	0.39066	0	1	0.5454519	38.18669
447680	cg2559711	58743426	58743426	0.5344508	0	1	0.688991	41.76344
447693	cg2559762	32647412	32647412	0.2917382	0	1	0.3996586	22.34694
447696	cg2559774	43678384	43678384	0.5165083	0	1	0.3983612	-23.9003
447725	cg2559871	14714508	14714508	0.9066262	0	1	0.7022567	-122.1437
447791	cg2560170	25670452	25670452	0.8470733	0	1	0.64788	-92.54516
447860	cg2560531	43703500	43703500	0.7474386	0	1	0.6383031	-26.55494
447885	cg2560678	13640314	35797396	0.8940859	0	1	0.7721385	-55.11167
447896	cg2560721	47759413	47759413	0.3746516	0	1	0.4912356	23.55264
447950	cg2561051	14744466	13797329	0.3701088	0	1	0.2289015	-38.31791
447956	cg2561105	52649309	45790361	0.6149713	0	1	0.7630723	44.87158
447984	cg25613061	23731348	38682366	0.1967606	0	1	0.3043537	26.74025
448001	cg2561425	12786346	70791391	0.4617485	0	1	0.6508133	56.93473
448073	cg2561855	67639508	67639508	0.4535331	0	1	0.5914935	31.43595
448077	cg25618731	19602485	19602485	0.4494013	0	1	0.3131578	-31.91652
448211	cg2562647	56619478	56619478	0.3582218	0	1	0.5399784	51.43297
448229	cg2562767	13775313	13775313	0.837808	0	1	0.6705902	-68.19366
448328	cg2563306	72743407	72743407	0.8005056	0	1	0.9254932	69.30048
448351	cg2563500	13644333	13644333		0	1	0.8853487	4.34E-09
448373	cg2563646	54810503	54810503	0.2111749	0	1	0.3420571	35.17649
448449	cg2564151	10757490	10757490	0.2510192	0	1	0.3557293	22.72669
448471	cg2564295	33807370	33807370	0.6507074	0	1	0.7825602	39.24107
448486	cg2564409	61724465	61724465	0.6921556	0	1	0.5894439	-21.56493
448497	cg2564447	35724359	35724359	0.4578074	0	1	0.641721	53.77596
448561	cg2564951	25669495	25669495	0.2708427	0	1	0.6586671	374.3439

448609	cg2565275	25660390	25660390	0.1595973	0	1	0.2696927	30.89137
448670	cg2565548	41648465	41648465	0.9276263	0	1	0.7315214	-128.0261
448714	cg2565990	32630357	32630357	0.5042471	0	1	0.6069688	19.46546
448778	cg2566405	50613420	50613420	0.5746399	0	1	0.6844012	23.6476
448804	cg2566621	13665497	13665497	0.4215521	0	1	0.6142181	57.6215
448873	cg2567124	26733308	26733308	0.6542093	0	1	0.7593099	25.80691
448918	cg2567402	35754413	35754413	0.8196559	0	1	0.6994819	-38.33115
448925	cg2567488	24782425	24782425	0.3769865	0	1	0.5001368	25.78228
448952	cg2567739	43683426	43683426	0.5572107	0	1	0.72374	50.12905
449099	cg2568787	33636301	33636301	0.5085342	0	1	0.6165398	21.25783
449136	cg2569095	18631435	50701307	0.410479	0	1	0.3016442	-22.36423
449160	cg2569213	26791369	26791369	0.5789675	0	1	0.723433	39.51816
449177	cg2569292	29610437	29610437	0.3169485	0	1	0.545288	80.31303
449197	cg2569479	66718303	66718303	0.1857533	0	1	0.2887913	25.76914
449201	cg2569502	20753405	34643314	0.2968803	0	1	0.1884046	-27.69505
449232	cg2569772	66760371	35687481	0.6072488	0	1	0.3543063	-97.53401
449282	cg2570164	20738426	20738426	0.3298644	0	1	0.4649318	30.984
449331	cg2570549	42733480	11778350	0.0888154	0	1	0.2090859	46.85942
449371	cg2570774	43624350	43624350	0.3980955	0	1	0.5063811	20.68777
449396	cg2570933	29620365	29620365	0.677015	0	1	0.8011093	37.77287
449409	cg2571029	31786453	31786453	0.4388989	0	1	0.5606223	25.14473
449534	cg2571874	34656411	34656411	0.5304308	0	1	0.6414839	22.76735
449820	cg2573549	58601483	28662440	0.1580191	0	1	0.3387406	67.93367
449832	cg2573625	63709335	50624488	0.7713711	0	1	0.5634732	-80.40267
449843	cg2573698	42624311	42624311	0.3207346	0	1	0.1885771	-37.75693
449867	cg2573817	31778309	31778309	0.2437517	0	1	0.3572333	26.1588
450021	cg2574613	45616428	71657317	0.735022	0	1	0.6295438	-24.45761
450045	cg2574767	54620484	54620484	0.6124183	0	1	0.760487	44.5739
450070	cg2574925	65713432	65713432	0.6246313	0	1	0.7357012	26.55838
450137	cg2575363	22639435	43710382	0.6548347	0	1	0.5493541	-21.29402
450139	cg2575372	32777378	32777378	0.1588749	0	1	0.2755531	33.86413
450178	cg2575585	57716321	57716321	0.3463332	0	1	0.4603226	23.07449
450208	cg2575714	55763352	55763352	0.7919567	0	1	0.6115489	-66.68143
450293	cg2576321	40639344	40639344	0.7404023	0	1	0.8453119	34.61017
450333	cg2576519	10671490	10671490	0.671647	0	1	0.796388	37.50579
450414	cg2577105	13616491	13616491	0.6830693	0	1	0.8532966	74.28949
450416	cg2577111	48691468	48691468	0.3754372	0	1	0.487609	22.09271
450430	cg2577185	36780433	36780433	0.8609775	0	1	0.6443484	-110.7184
450530	cg2578002	73614460	73614460	0.2012322	0	1	0.3103269	27.01031
450554	cg2578175	67767325	67767325	0.1668594	0	1	0.3238076	52.74796
450598	cg2578398	13644438	13644438		0	1	0.8719878	4.34E-09
450603	cg2578428	20699410	20699410	0.3320479	0	1	0.439359	21.16918
450661	cg2578879	68742426	68742426	0.3917991	0	1	0.5362904	33.79387

450677	cg2579013	24628433	24628433	0.2295408	0	1	0.3439857	27.27605
450888	cg2580435	56611493	56611493	0.7205114	0	1	0.5758775	-39.37574
451073	cg2581750	31787453	31787453	0.8078796	0	1	0.6822978	-39.35303
451207	cg2582562	69600381	69600381	0.7092423	0	1	0.8130499	29.93099
451243	cg2582767	53622440	53622440	0.2802672	0	1	0.4384772	42.68883
451265	cg2582896	72722475	72722475	0.1327973	0	1	0.2392302	32.25962
451312	cg2583241	54781444	42720419	0.6166686	0	1	0.4569475	-41.10725
451322	cg2583292	43714394	36726440	0.2799495	0	1	0.1594002	-35.5606
451548	cg2584803	69774465	29642457	0.4950904	0	1	0.3852165	-21.27057
451644	cg2585609	22744405	22744405	0.5814615	0	1	0.7850433	80.05802
451818	cg2587351	27674380	27674380	0.7657608	0	1	0.8915457	56.80021
451890	cg2587939	28614346	28614346	0.7434925	0	1	0.3158891	-322.374
451914	cg2588095	50802381	50802381	0.449187	0	1	0.689494	91.87236
452009	cg2588647	65601307	44698438	0.7500027	0	1	0.6054411	-41.82633
452031	cg2588886	16784456	16784456	0.5977738	0	1	0.4772047	-25.11667
452078	cg2589258	57739357	57739357	0.3186263	0	1	0.441425	26.70101
452119	cg2589660	41801497	48769415	0.628756	0	1	0.5183764	-22.25658
452128	cg2589704	11768491	11768491	0.7326587	0	1	0.5904273	-39.22984
452278	cg25910261	15796467	15796467	0.4373412	0	1	0.241752	-65.08949
452301	cg2591200	47703395	47703395	0.4898535	0	1	0.6124887	26.08645
452330	cg2591452	27699304	27699304	0.48274	0	1	0.6759387	60.62719
452401	cg2591992	37687374	18734419	0.1737643	0	1	0.0193367	-98.58508
452582	cg2592939	14621300	14621300	0.4191144	0	1	0.0276528	-349.2962
452640	cg2593286	72731368	14691388	0.3083745	0	1	0.4600335	38.47936
452712	cg2593721	64668503	31790314	0.9387382	0	1	0.7759559	-107.0919
452715	cg25937451	41673508	41673508	0.279543	0	1	0.4038485	28.54623
452980	cg2595121	33737452	37624370	0.7913222	0	1	0.6834554	-29.47314
452989	cg2595171	14715421	14715421	0.927412	0	1	0.7421162	-118.6018
453043	cg2595426	73614359	73614359	0.3322673	0	1	0.4383008	20.76192
453047	cg2595453	70697407	70697407	0.7812776	0	1	0.6238726	-51.89884
453070	cg2595608	32617505	32617505	0.3593568	0	1	0.4617875	19.23495
453072	cg2595610	33647352	33647352	0.3021441	0	1	0.4040059	20.11765
453110	cg25959131	39609353	39609353	0.4260786	0	1	0.581329	38.50097
453194	cg2596421	74775451	74775451	0.5734528	0	1	0.7305108	46.01398
453233	cg2596690	40606387	40606387	0.4932174	0	1	0.3516026	-33.09159
453426	cg2597776	66729380	66729380	0.1508845	0	1	0.299482	50.70055
453471	cg2598063	46736398	19772372	0.5302351	0	1	0.4124193	-23.74422
453503	cg2598338	67706311	71663305	0.3046974	0	1	0.1634418	-45.02779
453539	cg2598535	18673434	24707378	0.5126501	0	1	0.3879403	-26.24054
453541	cg2598545	57639456	57639456	0.4187259	0	1	0.6698399	98.33933
453578	cg2598745	27789451	10603416	0.543075	0	1	0.4014615	-32.59023
453689	cg25996061	26777302	26777302	0.803418	0	1	0.909972	50.15628
453690	cg2599607	14794347	14794347	0.0832583	0	1	0.187919	39.28132

453712	cg2599730	67738491	67738491	0.2008994	0	1	0.3038986	24.7253
453754	cg2600054	13707418	13707418	0.4215916	0	1	0.2464036	-53.35111
453756	cg2600061	49723391	32777403	0.1978384	0	1	0.0591244	-67.1687
453830	cg2600477	43686443	49758509	0.4413912	0	1	0.3152336	-28.01296
453975	cg2601302	17626301	41699495	0.8866869	0	1	0.7625947	-54.24926
454097	cg2601968	27660307	58793389	0.2691893	0	1	0.1673258	-26.75132
454202	cg2602705	15694442	15694442	0.4776487	0	1	0.5782254	18.4911
454210	cg2602766	67758452	36725493		0	1	0.0355917	4.34E-09
454322	cg2603431	51738305	51738305	0.5324259	0	1	0.6720646	34.40134
454339	cg2603507	30783484	30783484	0.3344671	0	1	0.8626972	374.3439
454352	cg2603563	61612472	61612472	0.4511722	0	1	0.3335597	-24.53387
454389	cg2603793	22744448	22744448	0.3792316	0	1	0.5270568	35.26214
454399	cg2603851	11809492	11809492	0.4001659	0	1	0.6256903	77.97603
454585	cg2605329	18687306	60664323	0.394046	0	1	0.2242251	-52.56351
454801	cg2606709	71710417	71710417	0.3124903	0	1	0.4606517	36.8238
454831	cg2606904	12603426	12603426	0.40095	0	1	0.5248661	25.88811
454842	cg2606953	31662423	31662423	0.3301698	0	1	0.4746491	34.74027
454852	cg2606997	46804344	46804344	0.6123749	0	1	0.7146379	22.3201
454971	cg2607623	44657335	44657335	0.4961496	0	1	0.3208193	-49.10336
454992	cg2607713	10724432	10724432	0.5187843	0	1	0.3995114	-24.27809
455130	cg2608690	55766497	21660459	0.1986502	0	1	0.3419667	41.93422
455148	cg2608829	60663334	73801426	0.6425626	0	1	0.5060837	-32.00818
455169	cg2608970	62735412	62735412	0.583429	0	1	0.7281102	39.97725
455353	cg2610098	30670307	30670307	0.6974872	0	1	0.5900663	-23.35417
455401	cg2610317	47663399	47663399	0.30622	0	1	0.4232006	24.9894
455402	cg2610330	59764449	59764449	0.5959872	0	1	0.7782497	65.46835
455630	cg2611437	31604358	39695312	0.3106791	0	1	0.1839608	-35.75967
455646	cg2611521	38731321	55617402	0.858871	0	1	0.7063819	-64.32678
455663	cg2611632	25741478	25741478	0.1389962	0	1	0.2576449	37.19402
455763	cg2612090	64650457	64650457	0.4218938	0	1	0.5441847	25.2884
455822	cg2612459	57687319	57687319	0.5117643	0	1	0.7000284	59.64408
455849	cg2612629	25720316	25720316	0.2610918	0	1	0.3687847	23.33392
455881	cg2612783	32679334	32679334	0.2653538	0	1	0.161568	-28.03921
456030	cg2613557	52734438	32772485	0.8041048	0	1	0.6577423	-49.38221
456059	cg2613741	49642328	49642328	0.7614554	0	1	0.5717822	-67.32548
456110	cg2614047	42804422	42804422	0.1034957	0	1	0.2447789	55.76197
456173	cg2614456	23648361	37618434	0.3387147	0	1	0.4406692	19.39011
456442	cg2615827	45735423	45735423	0.1285971	0	1	0.2493193	39.69935
456506	cg2616105	16681300	16681300	0.2641151	0	1	0.3811444	26.50578
456621	cg2616685	22682412	22682412	0.2703612	0	1	0.4405727	49.04201
456669	cg2616978	21710418	21710418	0.1915323	0	1	0.3154753	33.83815
456683	cg2617056	68740498	52687301	0.2833878	0	1	0.1802527	-26.21647
456729	cg2617377	55714323	64648378	0.3113224	0	1	0.564155	98.26444

456747	cg2617465	53648435	53648435	0.2811906	0	1	0.4320756	39.32589
456760	cg2617544	67607446	67607446	0.3870369	0	1	0.5335267	34.64615
456783	cg26177041	21601334	21601334	0.209334	0	1	0.3483855	38.94976
456784	cg2617709	34651357	34651357	0.4824789	0	1	0.6254478	34.11657
456813	cg2617940	24615388	24615388	0.9161152	0	1	0.7918727	-64.61189
456848	cg26181731	39672354	39672354	0.1267223	0	1	0.2796175	57.50088
456897	cg2618476	55672420	55672420	0.9580349	0	1	0.8540938	-70.39412
456978	cg26188621	61802303	61802303	0.4865208	0	1	0.6342611	36.35091
457121	cg2619793	23737425	23737425	0.8865655	0	1	0.7835912	-41.41427
457162	cg2620159	30699308	30699308	0.6450452	0	1	0.7469154	23.82813
457293	cg2620967	24801488	24801488	0.159748	0	1	0.2602482	26.85698
457324	cg2621172	16665412	16665412	0.5668288	0	1	0.3306991	-85.25916
457458	cg2622011	59617342	59617342	0.7503647	0	1	0.8542628	35.52598
457598	cg2622722	11801364	70688369	0.5212397	0	1	0.1090402	-328.5496
457615	cg2622812	38777402	13800396	0.235375	0	1	0.1129069	-43.20112
458016	cg2625158	33790464	33790464	0.5465709	0	1	0.7117989	48.45827
458241	cg2626476	12612401	12612401	0.2806867	0	1	0.3809875	20.2193
458469	cg26276301	58641425	58641425	0.4145022	0	1	0.5221066	20.41814
458470	cg2627632	69759301	69759301	0.3278179	0	1	0.2207669	-25.02765
458521	cg2627898	57773508	57773508	0.8727414	0	1	0.7647633	-41.16799
458599	cg2628279	50743508	35771465	0.19051	0	1	0.3115988	32.70448
458667	cg2628683	56743399	52663310	0.4695551	0	1	0.6084437	32.08654
458672	cg2628708	70697461	70697461	0.584962	0	1	0.8620189	374.3439
458674	cg2628715	28777449	28777449	0.8176677	0	1	0.9330938	65.7206
458678	cg26287521	48732370	48732370	0.9404292	0	1	0.7183041	-161.0438
458797	cg2629495	71770374	71770374	0.2324823	0	1	0.3425268	25.4814
458812	cg2629577	27637485	27637485	0.6523969	0	1	0.5136898	-33.22895
458823	cg26296371	32610338	32610338	0.4451529	0	1	0.7459268	150.515
459085	cg2631025	19693331	19693331	0.3923037	0	1	0.2625624	-31.40843
459089	cg2631042	66734380	50763482	0.8090089	0	1	0.9285548	66.66373
459092	cg26310551	26661506	36664364	0.2197306	0	1	0.0712646	-69.52829
459222	cg2631694	45600479	45600479	0.5506961	0	1	0.4486329	-18.7567
459310	cg2632273	60620301	60620301	0.2908681	0	1	0.4934297	65.33379
459326	cg2632379	57763307	58702312	0.5100664	0	1	0.3065289	-65.07499
459392	cg2632863	30791406	17743418	0.5956609	0	1	0.4606053	-30.3705
459437	cg2633080	63768469	63768469	0.6198224	0	1	0.7575938	39.39201
459521	cg2633451	40773309	40773309	0.2747751	0	1	0.4485495	50.55668
459639	cg2634000	23653500	13707336	0.3076309	0	1	0.1900161	-31.28259
459743	cg2634520	24719508	24719508	0.6653395	0	1	0.7797087	31.13984
459891	cg2635265	25639317	25639317	0.7502463	0	1	0.6495618	-23.59497
459910	cg2635359	56697335	56697335	0.4720878	0	1	0.6050292	29.71991
459955	cg2635575	26645385	26645385	0.2469071	0	1	0.1324594	-36.06394
460055	cg2636143	26635492	26635492	0.3397738	0	1	0.4747276	30.7072

460058	cg26361533	38608410	38608410	0.4262078	0	1	0.6073621	51.29596
460197	cg26368752	71640387	16671344	0.4024936	0	1	0.2769355	-29.12598
460286	cg26373733	30695325	45787391	0.3141225	0	1	0.212056	-23.71378
460358	cg26379258	38675371	61735303	0.699258	0	1	0.586956	-25.13607
460494	cg26387458	44610504	44610504	0.4575473	0	1	0.1159996	-224.1818
460510	cg26388509	37715492	37715492	0.5434363	0	1	0.6444257	19.62959
460567	cg26391794	61735467	61735467	0.3310822	0	1	0.5053777	48.25304
460606	cg26393629	63741303	63741303	0.5314956	0	1	0.4088782	-25.40734
460637	cg26394788	51750435	65769395	0.487191	0	1	0.669552	54.3175
460654	cg26395694	65681467	65681467	0.3206315	0	1	0.4420576	26.15995
460655	cg26395761	52649436	52649436	0.2806206	0	1	0.4012477	27.14226
460690	cg26398228	32682322	32682322	0.7947065	0	1	0.6216758	-62.76493
460818	cg26406176	59727345	59727345	0.4083213	0	1	0.3065502	-19.9817
460873	cg26409826	12685507	12685507	0.6866149	0	1	0.8620221	80.48644
460930	cg26413192	33663333	33663333	0.1995356	0	1	0.3112733	28.15995
461015	cg26419287	45633360	45633360	0.8826764	0	1	0.7763126	-42.46534
461076	cg26422465	50734334	50734334	0.2143522	0	1	0.4732714	112.5449
461084	cg26422762	39603443	39603443	0.2055696	0	1	0.3122146	25.78972
461199	cg26429017	38702376	38702376	0.7006841	0	1	0.8097247	31.87391
461200	cg26429022	34655409	34655409	0.4892434	0	1	0.6368251	36.36396
461384	cg26440059	59636307	59636307	0.3761652	0	1	0.5158364	31.96578
461385	cg26440142	57664313	57664313	0.4073588	0	1	0.5231922	23.08919
461407	cg26441877	71732460	71732460	0.4440356	0	1	0.589184	34.29033
461433	cg26444097	58806385	58806385	0.578476	0	1	0.6788645	20.36377
461459	cg26445985	44800343	44800343	0.168704	0	1	0.066091	-41.9464
461513	cg26450149	69747316	69747316	0.4865548	0	1	0.59159	19.96768
461519	cg26450259	23687451	51794485	0.727327	0	1	0.8980404	90.87402
461541	cg26451345	74750436	74750436	0.542206	0	1	0.7242417	58.40152
461548	cg26451735	47622446	16697437	0.5823957	0	1	0.4280691	-38.10598
461609	cg26456183	59694308	59694308	0.3847494	0	1	0.2350389	-41.70668
461630	cg26457160	43639448	43639448	0.5711594	0	1	0.4378035	-29.44211
461661	cg26458748	18645396	18645396	0.4919968	0	1	0.6291469	31.88185
461698	cg26461267	58808317	58808317	0.2714072	0	1	0.3771466	22.28713
461710	cg26461710	47652340	47652340	0.8286428	0	1	0.9352425	60.06337
461717	cg26462055	48657505	48657505	0.3257207	0	1	0.4981574	47.50028
461780	cg26465155	22688368	22688368	0.7682354	0	1	0.9269488	96.30986
461796	cg26465602	15791438	11686361	0.1541998	0	1	0.2832462	40.20321
461875	cg26469387	55800379	55800379	0.2200035	0	1	0.4149799	67.09354
461884	cg26469895	18752376	18752376	0.4728953	0	1	0.5915743	24.38171
461936	cg26472636	51751360	39664404	0.3691081	0	1	0.1763361	-72.07888
461998	cg26476502	48690435	48690435	0.5583146	0	1	0.4243476	-29.59939
462010	cg26477117	24774328	24774328	0.7895786	0	1	0.4725711	-177.6891
462275	cg26494916	43673381	43673381	0.3881784	0	1	0.4937826	19.91717

462322	cg2649763	49677468	49677468	0.1946703	0	1	0.3336752	40.30596
462335	cg2649896	34658301	55807442	0.1964179	0	1	0.2975804	24.33113
462369	cg2650081	69624364	69624364	0.057124	0	1		-4.34E-09
462436	cg2650426	69779320	69779320	0.2272524	0	1	0.3576086	33.75317
462444	cg2650461	54705308	54705308	0.3916058	0	1	0.5710781	50.02446
462487	cg2650742	19698378	19698378	0.5624205	0	1	0.441226	-24.97109
462491	cg2650763	53661308	62741421	0.8928398	0	1	0.7634498	-59.56969
462574	cg2651246	38741327	41740366	0.7502131	0	1	0.6035997	-42.81844
462596	cg2651374	30608337	30608337	0.9230144	0	1	0.7332752	-119.5555
462630	cg2651568	30779505	30779505	0.8817914	0	1	0.6573837	-126.1163
462709	cg2652001	21677360	23712417	0.4171472	0	1	0.3066634	-22.77318
462823	cg2652546	25746318	25746318	0.5800183	0	1	0.6848242	21.99392
462936	cg2653123	34794479	34794479	0.6991495	0	1	0.8323922	47.09525
462942	cg2653170	49604443	49604443	0.3280978	0	1	0.2129418	-28.57418
463079	cg2653932	64633410	44747338	0.8151851	0	1	0.6292304	-74.83304
463260	cg2654781	55630445	55630445	0.4083208	0	1	0.5376492	27.82823
463279	cg2654841	13797473	13797473	0.8615659	0	1	0.6940563	-74.93964
463325	cg2655086	65611427	60674478	0.7602031	0	1	0.6513026	-27.33329
463405	cg2655505	55781355	56735502	0.4211623	0	1	0.5658683	33.89164
463428	cg2655633	39802498	39802498	0.8685749	0	1	0.7655866	-37.59882
463446	cg2655727	57621386	57621386	0.2584664	0	1	0.3744254	26.36549
463455	cg2655775	55671425	55671425	0.2075353	0	1	0.3223357	28.80228
463610	cg2656618	51692407	51692407	0.4470692	0	1	0.0961874	-245.5379
463630	cg2656738	35810338	35810338	0.7865394	0	1	0.9138371	65.85504
463637	cg2656773	46682415	46682415	0.3375166	0	1	0.459772	26.06598
463685	cg2657071	31716491	31716491	0.7071573	0	1	0.5890477	-27.62988
463692	cg2657090	71802374	49785337	0.526945	0	1	0.3703399	-39.1448
463806	cg2657635	11695399	11695399	0.7508217	0	1	0.6400986	-27.38716
463923	cg2658334	33799355	36642399	0.4844858	0	1	0.3523984	-29.36766
464019	cg2659008	24751415	24751415	0.2847196	0	1	0.1145986	-70.89518
464020	cg2659010	61648332	61648332	0.2221794	0	1	0.4313095	75.55077
464132	cg2659987	46766455	46766455	0.269745	0	1	0.3963172	29.82766
464148	cg2660118	34774405	48758480	0.5347347	0	1	0.4235112	-21.55855
464175	cg2660327	56671362	56671362	0.5764431	0	1	0.6836433	22.75067
464233	cg2660658	29720320	58680349	0.510499	0	1	0.4100764	-18.25453
464241	cg2660703	53770489	53770489	0.2736636	0	1	0.3855493	24.2941
464250	cg2660762	65650307	74790425	0.6029274	0	1	0.4193684	-52.46578
464424	cg2661844	44629409	44629409	0.4193768	0	1	0.2920028	-29.21953
464468	cg2662053	72664469	62672337	0.5859732	0	1	0.3298015	-100.2993
464770	cg2664092	55773392	55773392	0.4791974	0	1	0.6279535	36.59499
464790	cg2664277	71617460	71617460	0.5996879	0	1	0.8048208	85.25845
464810	cg2664396	22660445	65702504	0.4811074	0	1	0.3629702	-24.21339
464812	cg2664404	50714320	56650334	0.2923621	0	1	0.1618079	-39.96765

464818	cg2664467	35767342	35767342	0.5126967	0	1	0.6283602	24.00278
464834	cg2664543	61731305	61731305	0.1365575	0	1	0.3254521	77.68653
464894	cg2664818	69716389	69716389	0.5026507	0	1	0.6124254	21.75145
464952	cg2665128	21716506	21716506	0.6428679	0	1	0.8766773	131.7069
464954	cg2665130	69748313	57691326	0.5355802	0	1	0.6866323	40.04563
465087	cg2665850	17793361	17793361	0.6717535	0	1	0.8160079	50.18817
465104	cg2665980	67781376	70743379	0.1330239	0	1	0.0300226	-53.3782
465197	cg2666503	32769455	73635397	0.6761742	0	1		-4.34E-09
465240	cg2666709	58684433	58684433	0.7938002	0	1	0.6816176	-31.55615
465382	cg2667364	20643483	20643483	0.5358475	0	1	0.7246571	62.2494
465423	cg2667533	25790323	25790323	0.7093742	0	1	0.8364338	44.49883
465449	cg2667644	29735503	29735503	0.6180683	0	1	0.7213076	22.96158
465502	cg2667900	24802369	37789498	0.3172181	0	1	0.1705321	-46.84028
465539	cg2668060	29604349	29604349	0.533429	0	1	0.6628928	29.98239
465634	cg2668436	50792331	19714383	0.4476502	0	1	0.2848537	-44.59229
465697	cg2668717	60616472	60616472	0.5096417	0	1	0.3893771	-24.67498
465769	cg2669040	41734414	41734414	0.088329	0	1	0.5863634	374.3439
465820	cg2669332	56719484	56719484	0.2102468	0	1	0.1041498	-36.20279
465929	cg2670091	54775355	54775355	0.6029847	0	1	0.7140504	25.38129
466003	cg2670559	44686317	44686317	0.0615172	0	1	0.2057635	70.11072
466007	cg2670576	56712347	55669349	0.5201651	0	1	0.6910145	49.73338
466169	cg2671555	19747404	16738355	0.6195966	0	1	0.4354482	-53.15301
466183	cg2671690	47627353	66605321	0.4667596	0	1	0.3031831	-44.08859
466193	cg2671755	42807306	54764402	0.1927466	0	1	0.0396371	-86.04832
466328	cg2672502	19733366	10692372	0.1992208	0	1	0.0663621	-60.73236
466410	cg2673054	60736495	60736495	0.4425139	0	1	0.5700766	27.28311
466461	cg2673424	51800501	51800501	0.4960846	0	1	0.3728518	-25.85464
466519	cg2673802	21643304	21643304	0.5748709	0	1	0.7087717	33.95289
466536	cg2673914	57760454	20729387	0.532464	0	1	0.4298697	-18.87473
466540	cg2673932	15674421	15674421	0.8188916	0	1	0.6008221	-98.0136
466621	cg2674468	25706443	32762320	0.4779202	0	1	0.2717919	-68.74731
466725	cg2675164	43756408	56742483	0.2294457	0	1	0.0996384	-49.92181
466756	cg2675390	45736477	19683378	0.8359046	0	1	0.7094229	-44.09849
466798	cg2675722	52677329	52677329	0.9072421	0	1	0.7370458	-94.8213
466871	cg2676394	21756503	21756503	0.5435055	0	1	0.6468631	20.42051
466937	cg2676797	69641403	69641403	0.1830597	0	1	0.2864293	26.09578
467004	cg2677238	47753436	47753436	0.6021035	0	1	0.7252483	30.59301
467036	cg2677512	44723436	44723436	0.6214463	0	1	0.4747091	-35.5699
467061	cg2677678	29600381	29600381	0.3962818	0	1	0.6344377	86.9821
467185	cg2678420	38639415	29731349	0.6121998	0	1	0.5099773	-19.39331
467239	cg2678661	41696393	41696393	0.4121014	0	1	0.6818519	114.1571
467258	cg2678738	18622475	38648505	0.4937791	0	1	0.3863368	-20.49808
467274	cg2678821	63738432	63738432	0.2526861	0	1	0.3574739	22.68373

467328	cg26791257	25630315	64734485	0.5189366	0	1	0.4093952	-21.03898
467393	cg26794700	25603505	25603505	0.6013666	0	1	0.7062845	22.8629
467426	cg26796043	51642431	66716324	0.8315139	0	1	0.9826413	135.4976
467429	cg26796083	70615357	70615357	0.4029786	0	1	0.5816132	49.6409
467526	cg26800883	38756410	38756410	0.1627276	0	1	0.2659621	27.70746
467536	cg26801241	35631475	35631475	0.4199775	0	1	0.560981	32.36438
467553	cg26802063	64604428	71645485	0.3038473	0	1	0.1632446	-44.72494
467574	cg26803268	21803377	47640414	0.3882493	0	1	0.2869738	-20.34166
467705	cg26809868	40618348	40618348	0.3422519	0	1	0.4624062	25.23708
467743	cg26811705	14659426	30701330	0.2742469	0	1	0.4270062	40.52684
467773	cg26813483	58803504	58803504	0.0555665	0	1	0.1981449	71.21186
467804	cg26815032	10657320	10657320	0.4970047	0	1	0.693324	63.67137
467857	cg26817755	38804485	38804485	0.5616929	0	1	0.6723583	23.53051
467878	cg26818786	13611506	13611506	0.2116449	0	1	0.3148978	24.16603
467915	cg26820259	40647335	40647335	0.7928856	0	1	0.6700979	-36.194
467956	cg26822175	43780356	43780356	0.7682899	0	1	0.6647125	-25.8526
468033	cg26826183	38808475	38808475	0.3599725	0	1	0.49838	31.67455
468080	cg26828599	55632485	55632485	0.2927101	0	1	0.5063658	71.96589
468323	cg26841048	10786344	10786344	0.4967498	0	1	0.3813044	-23.1101
468387	cg26843807	74679492	74679492	0.3654743	0	1	0.4934614	27.64792
468562	cg26854588	20690445	20690445	0.5683381	0	1	0.7136328	39.1782
468563	cg26855015	34739493	34739493	0.710413	0	1	0.8414311	47.56784
468599	cg26856631	31766367	31766367	0.3519212	0	1	0.2470596	-22.94751
468744	cg26864826	14772371	14772371	0.2210127	0	1	0.4129451	65.1735
468843	cg26871180	67801384	67801384	0.3942535	0	1	0.5175299	25.69332
468897	cg26873880	65743318	65743318	0.8473133	0	1	0.7104147	-52.08136
468902	cg26874229	66674405	42694358	0.74232	0	1	0.6152386	-33.38008
469019	cg26879644	72640510	72640510	0.5129722	0	1	0.6373462	27.27444
469058	cg26881268	42661402	42661402	0.4168494	0	1	0.2364482	-57.02462
469088	cg26882525	14744359	14744359	0.474404	0	1	0.2781773	-62.45633
469646	cg26915799	21626380	21626380	0.6014811	0	1	0.7208102	28.8301
469650	cg26915952	30713425	36747372	0.5628749	0	1	0.4596944	-19.1511
469860	cg26925980	23688339	23688339	0.4984899	0	1	0.6298445	29.66284
469890	cg26927544	17756352	60699427	0.890152	0	1	0.7719354	-51.55801
469908	cg26928789	60716382	60716382	0.0420629	0	1	0.1875691	79.11317
469935	cg26929925	48754322	25803318	0.5174887	0	1	0.3732188	-33.84893
469943	cg26930498	36600316	36600316	0.8601365	0	1	0.7288915	-51.67023
470059	cg26936989	69669477	69669477	0.8868213	0	1	0.7097054	-90.82958
470117	cg26939946	22713399	22713399	0.1800686	0	1	0.2845006	26.73948
470131	cg26940725	67799462	67799462		0	1	0.0760833	4.34E-09
470144	cg26941787	70637510	70637510	0.7212012	0	1	0.064938	-371.3336
470147	cg26941870	63650347	65750312	0.9371387	0	1	0.8282544	-62.698
470163	cg26942829	24618335	24618335	0.6151276	0	1	0.7424989	33.51572

470226	cg2694597	21758419	21758419	0.5991247	0	1	0.7126305	26.19884
470286	cg2694905	59707352	59707352	0.510498	0	1	0.6405457	29.46334
470328	cg2695170	42739502	49667370	0.1705284	0	1	0.883224	374.3439
470400	cg2695529	38625407	38625407	0.3918009	0	1	0.4987584	20.31002
470416	cg2695588	63760457	63760457	0.2840147	0	1	0.1473875	-44.94025
470632	cg2696837	17663376	17663376	0.7263461	0	1	0.613721	-26.60035
470660	cg2697004	43685411	43685411	0.294686	0	1	0.4208013	28.64967
470693	cg2697255	16777377	16777377	0.6155992	0	1	0.499868	-23.76535
470733	cg2697518	57631400	36712464	0.723347	0	1	0.8296869	33.0781
470792	cg2697837	22712463	22712463	0.6147664	0	1	0.8429322	113.2359
470827	cg2698015	59747386	59747386	0.5825824	0	1	0.7182892	35.31535
470836	cg2698093	24794368	24794368	0.4204075	0	1	0.5374599	23.48099
470873	cg2698260	50742459	23730422	0.7102292	0	1	0.601233	-24.45789
470990	cg2698792	16658418	16658418	0.4872152	0	1	0.6319625	35.02923
471047	cg2699157	42649388	18632350	0.6435825	0	1	0.5231168	-26.04406
471118	cg2699550	39753355	39753355	0.2142281	0	1	0.5506265	374.3439
471181	cg2700023	73632481	73632481	0.7148778	0	1	0.8478277	49.93367
471185	cg2700049	55698357	66762343	0.8027424	0	1	0.6698967	-42.2276
471186	cg2700050	74713304	74713304	0.6434106	0	1	0.889303	148.7541
471258	cg2700511	39757339	39757339	0.4808498	0	1	0.6330995	38.24883
471336	cg2701015	74726465	74726465	0.5639297	0	1	0.6897745	29.72116
471393	cg2701443	43626331	43626331	0.5291834	0	1	0.6383536	22.07552
471462	cg2701830	30775481	30775481	0.6608894	0	1	0.7688682	27.61395
471471	cg2701898	55730337	55730337	0.2492103	0	1	0.7153928	374.3439
471500	cg2702034	37797354	21763385	0.9093664	0	1	0.6751305	-149.9869
471551	cg2702336	29785438	37634479	0.7463422	0	1	0.6066685	-39.22553
471563	cg2702387	37744504	37744504	0.8420811	0	1	0.6692869	-72.87234
471578	cg2702440	40638350	40638350	0.368018	0	1	0.4837921	23.3556
471612	cg2702619	40729374	40729374	0.2487208	0	1	0.3604716	25.29137
471701	cg2703214	60613493	22725397	0.4482486	0	1	0.3193854	-28.90006
471755	cg2703599	58804463	58804463	0.8146815	0	1	0.9156724	48.35574
471990	cg2704959	56651508	56651508	0.3921471	0	1	0.5098249	23.77566
471991	cg2704964	65639453	36691449	0.3744866	0	1	0.0785343	-191.2851
472006	cg2705040	72697501	72697501	0.4621366	0	1	0.5822592	24.7654
472065	cg2705329	61762319	21655443	0.6330103	0	1	0.4782489	-39.3471
472165	cg2705848	71679446	71679446	0.656011	0	1	0.5495279	-21.64874
472225	cg2706179	49754427	49754427	0.5112742	0	1	0.6251848	23.3455
472363	cg2706942	52798451	14672356	0.5620713	0	1	0.4052102	-39.09737
472376	cg2707039	16613327	16613327	0.8145192	0	1	0.6778355	-45.91053
472386	cg2707115	49759419	74642481	0.2513356	0	1	0.147114	-29.63952
472430	cg2707334	28774445	28774445	0.5364553	0	1	0.6802009	36.50883
472438	cg2707417	42657472	53774367	0.5990794	0	1	0.4116417	-54.46663
472443	cg2707450	63669414	63669414	0.6452407	0	1	0.7484017	24.3859

472452	cg27074995	25671495	25671495	0.3665757	0	1	0.4770725	21.64992
472525	cg27079096	18698302	18698302	0.7155995	0	1	0.5234082	-63.27229
472528	cg27079194	22628361	22628361	0.4259663	0	1	0.6204415	58.79035
472546	cg27080348	23660470	67760433	0.8278413	0	1	0.6798989	-54.40378
472555	cg27081243	33704307	13644439		0	1		-4.34E-09
472576	cg27083087	26697460	69671508	0.5207891	0	1	0.6543442	31.25407
472597	cg27084028	33774509	33774509	0.3479825	0	1	0.4801289	29.4699
472600	cg27084232	55610395	55610395	0.7367988	0	1	0.8412686	33.79373
472626	cg27086157	40698319	40698319	0.4054468	0	1	0.5742245	44.68752
472627	cg27086308	55662450	55662450	0.0762081	0	1	0.1933797	48.05889
472740	cg27092248	58623436	58623436	0.3779662	0	1	0.5658135	54.48849
472827	cg27097438	26787346	56786397	0.3943252	0	1	0.1843031	-81.82818
472869	cg27100140	41639327	41639327	0.5384663	0	1	0.656572	25.59284
472987	cg27107292	33650305	33650305	0.653266	0	1	0.8833083	131.6642
472995	cg27107963	61804348	61804348	0.6137342	0	1	0.7441629	34.94736
473108	cg27112983	22625499	38637352	0.948352	0	1	0.4945295	-371.3336
473147	cg27115863	22626378	14698339	0.2744685	0	1	0.4829434	69.97648
473213	cg27119318	47786401	49631300	0.1556783	0	1	0.0455351	-52.6227
473235	cg27120543	62612508	62612508	0.170834	0	1	0.2812442	29.9484
473269	cg27122706	44638414	44638414	0.4372748	0	1	0.5580679	24.80904
473471	cg27134251	54780387	54780387	0.6259891	0	1	0.4804124	-35.20536
473498	cg27135799	38624406	38624406	0.6961677	0	1	0.9072369	128.1914
473522	cg27137258	40786356	16786492	0.442646	0	1	0.3088668	-31.08908
473538	cg27138088	25769382	23785427	0.3721734	0	1	0.1972291	-58.39659
473572	cg27140058	20615401	35637328	0.3360263	0	1	0.221503	-27.78181
473601	cg27141751	69713489	69713489	0.5569783	0	1	0.710283	42.59526
473603	cg27141807	55690505	55690505	0.8175783	0	1	0.331204	-371.3336
473679	cg27145347	33750455	33750455	0.5814308	0	1	0.7487887	53.09442
473682	cg27145458	56637356	56637356	0.376381	0	1	0.5215699	34.193
473709	cg27147556	67807427	29706375	0.2591509	0	1	0.3703953	24.64728
473728	cg27149073	11611421	11611421	0.4604256	0	1	0.2315561	-87.50206
473744	cg27149973	40726435	40726435	0.3641795	0	1	0.5097877	34.51276
473772	cg27151677	44778424	44778424	0.2500113	0	1	0.3573981	23.69097
473774	cg27151770	30703368	64807415	0.8991746	0	1	0.7783437	-56.01089
473783	cg27152219	48629373	11693393	0.4299943	0	1	0.3281509	-19.54337
473831	cg27156510	73639456	73639456	0.6134913	0	1	0.7650948	46.84022
473862	cg27158572	33730338	39658484	0.7896887	0	1	0.6829184	-28.86449
473885	cg27159987	14676344	14676344	0.424045	0	1	0.5420973	23.82277
473973	cg27166177	72774459	72774459	0.5809637	0	1	0.6866862	22.36488
473981	cg27166673	68632365	44726414	0.3580844	0	1	0.2290351	-33.08722
474104	cg27173148	18733325	35674409	0.3032802	0	1	0.4274666	27.64808
474141	cg27175112	18779347	18779347	0.3712738	0	1	0.4973964	26.90071
474183	cg27177158	20601316	20601316	0.336081	0	1	0.4468276	22.19484

474205	cg2717829	25683343	25683343	0.3038762	0	1	0.1878237	-30.81573
474225	cg2717937	42797416	64680471	0.806002	0	1	0.6619074	-48.47364
474235	cg2717981	53803352	53803352	0.2213047	0	1	0.3301382	25.65207
474274	cg2718137	69721302	55727389	0.0701657	0	1	0.1865908	49.18149
474312	cg2718303	71680393	71680393	0.6060561	0	1	0.7451934	38.88082
474366	cg2718651	58668500	58668500	0.3799189	0	1	0.5079635	27.50696
474404	cg2719002	53748501	53748501	0.2996215	0	1	0.419524	26.21602
474550	cg2719969	41754334	41754334	0.5512347	0	1	0.6936901	36.67837
474562	cg2720025	58746331	58746331	0.4958464	0	1	0.6079493	22.43035
474574	cg2720089	66639482	66639482	0.2175691	0	1	0.3298394	27.16343
474600	cg2720291	29707314	29707314	0.3893447	0	1	0.1540373	-106.4897
474781	cg2721496	27609506	15718384	0.2246604	0	1	0.3268245	23.069
474843	cg2721918	57769383	57769383	0.4864779	0	1	0.626011	32.74377
474965	cg2722614	16780412	38724384	0.135556	0	1	0.2756251	48.6395
474998	cg2722774	31712431	37619383	0.2449484	0	1	0.1252896	-39.67231
475009	cg2722827	25764475	25764475	0.3722155	0	1	0.4973722	26.54382
475055	cg2723076	49780490	49780490	0.3650911	0	1	0.4852826	24.88825
475084	cg2723236	27709322	27709322	0.2337672	0	1	0.3502915	27.82345
475093	cg27233151	13736483	13736483	0.1670715	0	1	0.3215551	51.3924
475251	cg2724497	74728376	33694484	0.6404576	0	1	0.4101748	-81.70122
475288	cg2724769	44759351	31768322	0.0904623	0	1	0.205772	43.68424
475308	cg2724858	16718309	16718309	0.4324445	0	1	0.3306483	-19.48265
475343	cg2725115	37707300	12721408	0.6473841	0	1	0.4106952	-86.45903
475352	cg2725192	43694332	52770307	0.4373225	0	1	0.3239358	-23.31472
475374	cg2725348	66610377	66610377	0.4729127	0	1	0.3454184	-27.79122
475442	cg2725798	20738498	20738498	0.4723905	0	1	0.7828887	374.3439
475454	cg27258561	65616364	65616364	0.5269969	0	1	0.4109381	-23.15577
475501	cg2726173	54743425	54743425	0.6382905	0	1	0.463028	-49.19096
475537	cg2726399	19633313	19633313	0.4635296	0	1	0.5757963	22.08084
475544	cg2726432	39635355	46659312	0.9652267	0	1	0.7944688	-135.5835
475615	cg2726883	74723367	74723367	0.2037286	0	1	0.3068616	24.5972
475675	cg2727224	35664454	35664454	0.8527514	0	1	0.6437397	-101.7537
475692	cg2727322	45740413	45740413	0.61983	0	1	0.8574861	126.5399
475845	cg2728239	14747339	14747339	0.3001115	0	1	0.4062	21.5113
475865	cg2728412	64691332	64691332	0.3998019	0	1	0.5061655	20.08214
475866	cg2728419	47622464	47622464	0.6865138	0	1	0.5316443	-41.76806
475966	cg2729130	33710361	33710361	0.2675749	0	1	0.1577269	-30.97403
475968	cg2729146	51768317	51768317	0.3228096	0	1	0.4306893	21.53812
475978	cg2729209	72810314	72810314	0.6053461	0	1	0.7301877	31.59373
475981	cg2729222	41607394	41607394	0.6200283	0	1	0.7538734	37.26595
476054	cg2729565	29685464	29685464	0.7776478	0	1	0.8780116	38.04894
476097	cg2729755	25602349	25602349	0.2584012	0	1	0.3829918	29.603
476119	cg2729834	26760337	39706440	0.5490946	0	1	0.3652275	-52.44751

476330	cg27307781	26809452	58752493	0.0027164	0	1	0.1191962	77.77986
476357	cg27308738	33793335	33793335	0.418588	0	1	0.7443705	374.3439
476739	cg27326620	66679486	63773438	0.4771303	0	1	0.346495	-28.93093
476776	cg27328673	11704424	11704424	0.739526	0	1	0.5801822	-47.98954
476794	cg27330006	14736422	14736422	0.9231387	0	1	0.8028324	-64.76322
476809	cg27331292	54688488	54688488	0.3382758	0	1	0.4446487	20.75927
476891	cg27336587	12720447	71636304	0.0760711	0	1	0.1818823	41.46307
476931	cg27338836	13644452	13644452		0	1		-4.34E-09
476991	cg27342919	33666436	15745448	0.4938667	0	1	0.2469567	-98.69467
477068	cg27347523	61768307	42802448	0.3149559	0	1	0.5412835	79.03873
477082	cg27348515	66743491	58797317	0.3476132	0	1	0.2148526	-35.69656
477112	cg27350579	16797429	16797429	0.4837574	0	1	0.589301	20.0974
477191	cg27355713	60743476	60743476	0.4860043	0	1	0.6025745	23.82461
477289	cg27362525	44659426	29653431	0.320819	0	1	0.1627293	-53.99532
477294	cg27362989	63766336	63766336	0.3147332	0	1	0.5123168	61.25398
477297	cg27363141	27793347	21680509	0.5078914	0	1	0.6171039	21.65271
477345	cg27365991	20770382	20770382	0.2444026	0	1	0.4209388	54.23112
477358	cg27366766	21651349	14699327	0.7098462	0	1	0.5187926	-62.07313
477412	cg27369096	46808467	44740455	0.455086	0	1	0.3359542	-25.00688
477450	cg27371456	11810404	11810404	0.6126637	0	1	0.7127938	21.52104
477463	cg27372452	18690453	19678397	0.67098	0	1	0.5620077	-22.9137
477557	cg27378537	31615459	31615459	0.3887984	0	1	0.1702539	-90.37083
477569	cg27379407	44699377	48766488	0.8468719	0	1	0.7334294	-39.17054
477651	cg27383418	29768342	29768342	0.3815296	0	1	0.2702782	-24.20201
477797	cg27391816	54750357	56763451	0.1462727	0	1	0.2560247	32.16477
477819	cg27392904	71676300	71676300	0.2796624	0	1	0.3871301	22.57915
478023	cg27405400	59651484	70740307	0.8838141	0	1	0.7814126	-40.44855
478037	cg27406070	59665410	59665410	0.7234855	0	1	0.8509437	47.48512
478063	cg27408171	39791422	12749411	0.4434051	0	1	0.6660975	77.94891
478132	cg27412857	28717352	28717352	0.4128891	0	1	0.5300817	23.53293
478167	cg27414868	44664477	21610445	0.4466959	0	1	0.8606907	374.3439
478186	cg27416337	71665371	71665371	0.3081909	0	1	0.4413012	30.85146
478279	cg27422345	53700466	53700466	0.4598596	0	1	0.5679919	20.70292
478394	cg27427743	16749426	30747495	0.8774992	0	1	0.7479622	-55.04924
478452	cg27431049	26641373	32768334		0	1		-4.34E-09
478490	cg27433479	42614354	42614354	0.6775389	0	1	0.9234161	374.3439
478504	cg27434368	42682384	42682384	0.7251097	0	1	0.6088726	-27.89226
478594	cg27440866	56672320	56672320	0.1053516	0	1	0.2099182	35.23546
478606	cg27441354	14756460	14756460	0.7072533	0	1	0.5944551	-25.67897
478635	cg27443332	28752456	28752456	0.1274147	0	1	0.2312843	31.75619
478767	cg27450744	50802392	50802392	0.2285548	0	1	0.6767671	374.3439
478775	cg27451362	24611496	24611496	0.6543968	0	1	0.513674	-34.12096
478796	cg27452255	58690410	58690410	0.8902772	0	1	0.7877361	-42.05327

478806	cg2745292	55621476	40702446	0.6632386	0	1	0.5566679	-21.88083
478822	cg2745410	73724445	73724445	0.3097949	0	1	0.4240102	23.94117
478920	cg2746125	62610464	62610464	0.5879353	0	1	0.726187	36.96496
479011	cg2746787	14632431	14632431	0.2009788	0	1	0.0431793	-87.8899
479026	cg2746888	29620403	12793431	0.6566043	0	1	0.9369063	374.3439
479041	cg2746973	38713346	31774471	0.8091847	0	1	0.6876946	-37.55527
479217	cg2748142	44744456	44744456	0.4895775	0	1	0.7638177	129.6336
479269	cg2748466	21666391	11780432	0.7278507	0	1	0.8388299	36.62023
479275	cg2748510	17605506	20768326	0.4244875	0	1	0.3036002	-26.44408
479345	cg27488741	48773302	48773302	0.731518	0	1	0.834564	32.18213
479433	cg2749416	20717367	20632490	0.3408422	0	1	0.45177	22.16658
479445	cg2749489	61748336	61748336	0.2771873	0	1	0.4254063	38.35656
479569	cg2750229	62806352	62687463	0.6436923	0	1	0.901582	374.3439
479589	cg2750395	45729369	45729369	0.7967566	0	1	0.696515	-26.81828
479675	cg2750818	42743387	42743387	0.6903453	0	1	0.8091993	36.30849
479693	cg2750912	34691381	34691381	0.5489126	0	1	0.6493522	19.57408
479707	cg2750996	30789337	30789337	0.1487208	0	1	0.3723611	99.01151
479793	cg2751403	50745409	46671445	0.9437393	0	1	0.7637284	-125.5406
479801	cg2751433	39653495	39653495	0.6316997	0	1	0.7502524	30.44968
479840	cg2751692	19682423	19682423	0.9341912	0	1	0.62705	-243.2921
479851	cg2751756	45782402	45698475	0.7236221	0	1	0.6119495	-26.09712
479911	cg2752054	67703307	67703307	0.4542818	0	1	0.5729957	24.19508
479920	cg2752116	34808321	50637434	0.6222686	0	1	0.9510186	374.3439
479994	cg2752642	10643372	64765396		0	1	0.6920689	4.34E-09
480000	cg2752677	30783419	30783419	0.303263	0	1	0.408354	21.10818
480133	cg2753385	34615334	34615334	0.7408047	0	1	0.8769957	59.08617
480195	cg2753719	17804389	17804389	0.512873	0	1	0.3920116	-24.86371
480275	cg2754189	73804305	73804305	0.7262226	0	1	0.5730417	-43.77585
480281	cg27542341	72691401	52700469	0.20769	0	1	0.3092656	23.78897
480293	cg2754304	11634337	11634337	0.5570147	0	1	0.3330365	-76.86561
480331	cg2754467	66683447	66683447	0.2178459	0	1	0.3309973	27.48253
480355	cg2754611	35768310	35768310	0.6210355	0	1	0.4496898	-46.69542
480415	cg2754918	60697329	60697329	0.3773793	0	1	0.6588255	122.7299
480440	cg2755066	32793334	54606331		0	1		-4.34E-09
480503	cg2755392	12790451	64639473	0.4206991	0	1	0.3168731	-20.38465
480563	cg2755778	19616307	19616307	0.8642442	0	1	0.6814982	-86.39791
480749	cg2756758	42654353	42654353	0.0586664	0	1	0.2058143	73.22786
480827	cg2757212	19647409	51674379	0.5820965	0	1	0.4205936	-41.32235
480892	cg2757562	15736467	15736467	0.7735316	0	1	0.9099112	70.73605
480920	cg2757714	16659309	44767473	0.6248013	0	1	0.5151716	-21.93246
481021	cg2758232	14704347	14704347	0.1393097	0	1	0.2410011	29.37763
481047	cg2758330	27634389	32665472	0.3459871	0	1	0.2050426	-40.20573
481082	cg2758514	24620463	24620463	0.4433997	0	1	0.5565931	22.25048

481137	cg2758835	48702341	48702341	0.2576218	0	1	0.3732775	26.29324
481272	cg2759810	72641436	72641436	0.3968972	0	1	0.5260394	27.79281
481324	cg2760157	26690489	26690489	0.5875124	0	1	0.6999018	25.19558
481482	cg2761232	51801389	51801389	0.3402431	0	1	0.1777217	-54.19957
481522	cg2761448	62601359	47732508	0.5380088	0	1	0.4030845	-29.94905
481632	cg2762172	62733489	62733489	0.3228862	0	1	0.4709342	36.43872
481639	cg2762199	41605444	41605444	0.4156277	0	1	0.5252444	21.04958
481685	cg2762513	15722311	15722311	0.767724	0	1	0.4598527	-162.4123
481704	cg2762618	16807466	66634378	0.1143765	0	1	0.3425046	112.6678
481966	cg2763919	49621366	49621366	0.7869173	0	1	0.686281	-26.1359
481989	cg2764025	73669303	73669303	0.5763307	0	1	0.6821095	22.22181
482028	cg2764247	58749395	48615364	0.6613992	0	1	0.4864583	-50.04103
482109	cg2764821	25667382	25667382	0.3983145	0	1	0.5080811	21.15334
482112	cg2764827	67670425	67670425	0.4815387	0	1	0.587833	20.3125
482208	cg2765521	27784335	25657320	0.283587	0	1	0.1403717	-49.52032
482283	cg2765904	50766426	51699366	0.7458662	0	1	0.6434876	-23.95097
482296	cg2765979	58690368	58690368	0.225704	0	1	0.4109862	60.81833
484258	ch.22.4827	62659432	62659432	0.1691802	0	1	0.045637	-61.72841
485513	rs10033147	53636471	37774439	0.6182185	0	1	0.4890457	-28.56932
485514	rs1019916	43769491	43769491	0.3735388	0	1	0.5216559	35.44028
485516	rs10457834	15748350	15748350	0.9695354	0	1	0.8480659	-94.54636
485517	rs10774834	22788456	30718329	0.6346762	0	1	0.3352349	-138.9381
485518	rs10796216	14622465	41635319	0.3364213	0	1	0.1695455	-57.81847
485520	rs10882854	47771383	39668349	0.4810969	0	1	0.7757474	151.7644
485521	rs10936224	34619331	30630453	0.76804	0	1	0.6245472	-43.17172
485522	rs11034952	58692423	44652497	0.1902064	0	1	0.0371009	-87.33179
485523	rs11249206	60753422	60753422	0.5155119	0	1	0.3411648	-48.00545
485524	rs13369115	44627385	74780462	0.5035905	0	1	0.345103	-40.40899
485525	rs133860	52724359	52724359	0.8465078	0	1	0.6601176	-83.27675
485526	rs1414097	23759362	39621311	0.7912084	0	1	0.9320854	84.98336
485527	rs1416770	28667385	28667385	0.8580264	0	1	0.6352852	-114.4526
485528	rs1467387	45739435	45739435	0.5543295	0	1	0.6637531	22.83754
485529	rs1484127	33780375	33780375	0.9717023	0	1	0.655333	-290.7561
485532	rs1510480	69633374	69633374	0.5190102	0	1	0.3614534	-39.68781
485534	rs1941955	33709340	33709340	0.500488	0	1	0.8212647	374.3439
485536	rs2032088	63663495	63663495	0.6841089	0	1	0.2068664	-371.3336
485537	rs2125573	25698376	25698376	0.7132156	0	1	0.3832534	-176.2696
485538	rs213028	10622451	24684377	0.639438	0	1	0.3323443	-146.7529
485539	rs2208123	12714403	19761497	0.1791884	0	1	0.4754308	153.5253
485540	rs2235751	17621345	17621345	0.8264972	0	1	0.5399352	-158.7121
485541	rs2385226	46691371	17623494	0.4607706	0	1	0.7682423	374.3439
485542	rs2468330	23632464	23632464	0.6958199	0	1	0.3528791	-189.5658
485543	rs2521373	12625304	12625304	0.5063571	0	1	0.6690394	44.44134

485544	rs264581	52695345	52695345	0.6711646	0	1	0.3841269	-128.5183
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485546	rs2857639	23793421	23793421	0.5595321	0	1	0.4548768	-19.57744
485550	rs3936238	42802473	29627504	0.2996688	0	1	0.6114528	151.7644
485551	rs4331560	10654345	10654345	0.5533861	0	1	0.6969407	37.34011
485553	rs4742386	34623456	34623456	0.4267532	0	1	0.5944017	44.35028
485555	rs5931272	39615340	39615340	0.5126834	0	1	0.9819773	374.3439
485559	rs6471533	11697340	55602361	0.3647898	0	1	0.2173016	-42.13958
485560	rs654498	36707408	15665335	0.3428003	0	1	0.2399364	-22.57817
485562	rs6626309	15806372	69767339	0.6416932	0	1	0.7914119	49.26139
485569	rs798149	48789496	48789496	0.8004849	0	1	0.6402367	-56.39805
485570	rs845016	37661486	37661486	0.3433668	0	1	0.4997139	39.49137
485571	rs877309	54760445	54760445	0.393485	0	1	0.0252833	-317.2814
485572	rs9292570	48712372	14806497	0.1782431	0	1	0.3370402	52.12325
485573	rs9363764	36689314	36689314	0.8294031	0	1	0.9573595	90.60218
485574	rs939290	70759471	70759471	0.6131538	0	1	0.7430084	34.60989
485575	rs951295	11711409	39778441	0.8075045	0	1	0.3545702	-371.3336
485576	rs966367	16795360	16795360	0.0352012	0	1	0.2056667	102.114

PCOS.Delta	ILMNID	NAME	ADDRESS	ALLELEA_	ADDRESSB	ALLELEB_	INFINIUM	NEXT_BAS
0.1824424	cg00004073	cg00004073	38766357	TTAAAAAACCAAAAACCATCA			II	
-0.114829	cg00006815	cg00006815	18804378	CACCTCCTCCCCRATACAATCA			II	
0.1075888	cg00009306	cg00009306	74728390	CACACTTACATAACCCATTTTA			II	
-0.498723	cg00009523	cg00009523	42761437	TACCRACAACAACRCTCATTAA			II	
0.1200536	cg00013655	cg00013655	44675355	CCCCCTA	31736405	CCCCCTA	I	A
-0.145023	cg00017157	cg00017157	53626407	AATACAATTTCTAAAACTATCC			II	
-0.128469	cg00022997	cg00022997	43668467	ATAATTC	31767442	ATAATTC	I	A
0.1741403	cg00023024	cg00023024	37787505	ACCTAAAAAAACCRCRAACTA			II	
0.1136433	cg00024516	cg00024516	15677432	TTTTAAAAAACCTAAACCAACT			II	
-0.133283	cg00027155	cg00027155	36681337	CTAACTAAATAACCACCTAAA			II	
0.1056348	cg00028299	cg00028299	38749489	ATTACCATAAATCCTCCCCTAT			II	
-0.106365	cg00028308	cg00028308	58620505	AAAAAAAATCCTCTCCCCCTCT			II	
-0.15843	cg00033209	cg00033209	35667425	AACCCCTATACCTAACCAAAA			II	
0.1595896	cg00033213	cg00033213	73611364	AAAAATACRATAAACRCCRAA			II	
0.1698296	cg00033490	cg00033490	67770302	ACTATATCATATCATAAAAAAC			II	
-0.161146	cg00035449	cg00035449	51625403	CTCCRATAAAAACCRTCAATAA			II	
0.1002302	cg00036137	cg00036137	62807489	AAAAAAAACCATCRAAAACAA			II	
0.1374837	cg00038020	cg00038020	71732358	CTCTTTCTCTATATAAATTACC			II	
0.1103506	cg00039489	cg00039489	26722425	CCTAAAACTCCCCCTACAATCC			II	
-0.138292	cg00040103	cg00040103	63772389	TCATACAAAATTCCCTACAATT			II	
0.2251326	cg00040530	cg00040530	34668426	ACCCATAACCTACAAAACTAA			II	
0.1024121	cg00045070	cg00045070	61760432	AAAAAACTAAACTTATACCTAC			II	
0.1042157	cg00047694	cg00047694	54689478	ATTACAAAACAAAAAACACAAA			II	
-0.363685	cg00051154	cg00051154	70761365	TACCCTATTTTTTAAATACTAA			II	
-0.121884	cg00056433	cg00056433	13810448	ACTACAATAATTTCCACCAAAA			II	
-0.110892	cg00058009	cg00058009	47670413	ACCCTTC	34681339	ACCCTTC	I	C
0.1575409	cg00061551	cg00061551	72748427	AACCATAATAAAAATTTAATAT			II	
0.1187444	cg00063982	cg00063982	53716300	AAAAAATAAATCACTCTATCTT			II	
0.1071726	cg00066239	cg00066239	46751326	ATAAAAATAAAATTATACAAA			II	
-0.293885	cg00069771	cg00069771	30764342	CACAACATACAATCCCCACAAT			II	
0.112421	cg00083790	cg00083790	46801467	TACACAA	13659322	TACACAA	I	C
0.1164489	cg00084271	cg00084271	36640339	CACCTTCCTATAAACCTTACRA			II	
-0.119091	cg00093478	cg00093478	16757450	CTAAAAT	14611473	CTAAAAT	I	A
0.1357238	cg00095259	cg00095259	60656333	AAATCCAAAAACTTAAAAAAA			II	
0.3647068	cg00098182	cg00098182	47651469	TCCTCTTC	50685321	TCCTCTTC	I	C
0.1252292	cg00101154	cg00101154	30746351	AATTAATCTTAAACTTAACCCC			II	
0.1098738	cg00101227	cg00101227	59747444	ACATTACAAACTTCTTAAAATA			II	
0.1020973	cg00101602	cg00101602	33735361	ACAAATAATTACTTATCAAATA			II	
0.1303455	cg00106565	cg00106565	74721382	CATCCTCAATATCAAACTCRTA			II	
-0.102595	cg00108944	cg00108944	24657395	ACRAAACAAAACTTACTTACRT			II	
0.1258031	cg00118783	cg00118783	71730440	ATAACCA	30680362	ATAACCG	I	A

0.1336879	cg00119778	cg00119778	65649460	CTCTTTCTCTCTCTCACACTTT			II	
0.139879	cg00121626	cg00121626	19779393	AAAACTAATAAAAATAACTTA			II	
0.1602222	cg00121876	cg00121876	11641490	AATAACATTATAAAACAATTC			II	
0.200882	cg00122779	cg00122779	50730351	TCTTAAATTCAAATCAAAAAA			II	
0.1181042	cg00123214	cg00123214	16683390	TATCACTCAATTTCCTCATCAA			II	
-0.146608	cg00124902	cg00124902	66794348	TAACCAAAAATACACCAATTC			II	
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-0.107074	cg00125893	cg00125893	31787444	CCAAATCAATATACAATCAAA			II	
-0.209826	cg00128718	cg00128718	64701377	AAAAAATAATCCACACCTTAC			II	
0.176604	cg00136547	cg00136547	12733385	ACAAATAATATACTAATAACT			II	
-0.366904	cg00146240	cg00146240	44697466	AATACTCCACRATAAACCACT			II	
0.1050526	cg00149537	cg00149537	28618375	CTTCCAT	52810459	CTTCCGT	I	A
0.1547821	cg00154902	cg00154902	59771461	TTTCATA	71747396	TTTCATA	I	A
-0.118692	cg00156497	cg00156497	74780459	ACTCAAAACTCACTATAAAAC			II	
0.1478863	cg00157016	cg00157016	54695379	CAAATCTTAAACACTCACATT			II	
0.2536919	cg00157199	cg00157199	67794389	AACTCTT	67704375	AACTCTT	I	C
0.155105	cg00163702	cg00163702	59703408	AATTCAAATTTCCTAACTTTAT			II	
-0.141063	cg00166722	cg00166722	55760432	ACCTACT	14676335	ACCTACT	I	T
-0.154305	cg00167248	cg00167248	69734324	AACAAAATTTTACATTCAAAA			II	
0.1303501	cg00167670	cg00167670	47678333	ATCCTTATTAAATTCTTATCAA			II	
0.1412137	cg00167913	cg00167913	34621465	ACCATACCTATCCACCTACCT			II	
0.1020706	cg00171092	cg00171092	47771303	AAAACTAACCTCATATTACAC			II	
-0.110827	cg00172603	cg00172603	50632452	AAAAATT	73639386	AAAAATT	I	A
0.1523787	cg00182893	cg00182893	64744407	CTAAAAAAAACAACTACAATA			II	
-0.240073	cg00187244	cg00187244	54743510	CATAAAAATATAAAAACTACA			II	
0.1030963	cg00192882	cg00192882	58670408	TTCTTAACAAACCTAAAACAT			II	
0.1869919	cg00204802	cg00204802	64623441	CCCCAAA	47756405	CCCCGAA	I	T
0.1246974	cg00206507	cg00206507	70732476	TTTCACATATTTACCCTAAACT			II	
0.1466873	cg00209612	cg00209612	27678431	CTTAAAACAAACATTTATTAC			II	
0.1051298	cg00210856	cg00210856	12772328	CTCTTCCCTAAATCATTCTACA			II	
-0.327772	cg00211215	cg00211215	12790319	CTACAAA	39622342	CTACAAA	I	C
0.2390722	cg00212031	cg00212031	29674443	CCCAATT	38703326	CCCAATT	I	T
-0.126467	cg00213805	cg00213805	71737411	AACACAATATTAAACTAAACR			II	
0.1720481	cg00218628	cg00218628	60625336	TTCCAAATACATCCAAATACR			II	
0.123006	cg00221185	cg00221185	54678344	AACAACT	24788422	AACAACT	I	A
-0.108605	cg00222015	cg00222015	17719383	CCCTCTCATAACCCAACCACC			II	
0.1302324	cg00223245	cg00223245	50693357	ATCTAAAAAACTCCAAATACA			II	
0.1018733	cg00230120	cg00230120	14662484	ACCCAAA	19720437	ACCCGAA	I	C
0.3416751	cg00231519	cg00231519	19627374	CCTACTCTAATAATAAATTTCT			II	
0.2771948	cg00232388	cg00232388	35709315	TCATTTAAATCTTCRTTCAAAA			II	
0.1210151	cg00234370	cg00234370	48684425	ATATATTCTCTCCCTAAATTAT			II	
0.1018026	cg00235754	cg00235754	28719502	AAAACTAACAAATCCAACRTT			II	
0.1192852	cg00239742	cg00239742	51742392	AAAATAAACTCCTTAAATACT			II	

0.1324437	cg0024100	cg0024100	54771452	ATAAAAC	57737407	ATAAAAC	I	T
-0.126427	cg0024190	cg0024190	43619318	AACTTTA	10732399	AACTTTA	I	C
-0.189757	cg0024492	cg0024492	47710335	TTAAACATTTACCCTATAACA			II	
0.2170968	cg0024709	cg0024709	22631327	CRCTAAAAACTATAAAACTAA			II	
0.2659728	cg0024886	cg0024886	64710346	CAAACAACTTAACTAATTCCA			II	
-0.16564	cg0025373	cg0025373	60729344	AAAAAAAAAATTTCCRTCTAA			II	
0.2127221	cg0025409	cg0025409	69780487	TAACTCCAAACCTTCTAAACC			II	
-0.110238	cg0025430	cg0025430	54748461	CCATTTC	17645336	CCGTTTC	I	A
-0.110721	cg0025588	cg0025588	63789443	TACTACRAATAAACRTACTAT			II	
0.1379045	cg0025604	cg0025604	73700305	AACCCAAAATTTATACTAAAA			II	
0.1065856	cg0025632	cg0025632	34663423	ATTATTATATCTACRATATCCA			II	
0.2416773	cg0025984	cg0025984	15806472	TTTTATCTACRCTAAAAATCTA			II	
0.2390068	cg0026972	cg0026972	67766493	AAATTCCTAAACTTCAAATAA			II	
-0.103467	cg0026980	cg0026980	61752345	ATAAAAAAAATCTTTCAAAAA			II	
0.2057893	cg0027187	cg0027187	11808416	CRCCAAATTTATTCAAACTTCT			II	
0.1118558	cg0027279	cg0027279	74632377	RCCACCTAATATCTACTAAAA			II	
0.103954	cg0027290	cg0027290	41724510	ATTAATAAAAATTTACTAACA			II	
-0.150959	cg0027464	cg0027464	47758438	AAACCCTTCRAAAAAACCRAA			II	
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	cg0027975	cg0027975	13644355	AATACAAAACCCTTCCACAAA			II	
-0.123238	cg0028183	cg0028183	56772418	AAAATAAAAACRACCTAAACC			II	
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-0.182411	cg0028784	cg0028784	34718404	CATTCATCTTTAAACCTACCAA			II	
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-0.264662	cg0029060	cg0029060	64718396	CTCCTTC	62628499	CTCCTTC	I	A
	cg0029266	cg0029266	13644450	AACCCRAATAAAACCAAAACC			II	
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0.1696367	cg0029541	cg0029541	41681387	TACTAAAATAATTTTAAATAC			II	
0.1040363	cg0029690	cg0029690	27749328	ATTATAATTCTAACTCCTCCCC			II	
-0.222302	cg0029787	cg0029787	24757500	CAAATTCRCTCAATAAAAATA			II	
0.1057237	cg0030276	cg0030276	60641446	ACAATTAATTCTCTTAACTATC			II	
0.1097211	cg0030452	cg0030452	27747375	AACTACC	37645353	AACTACC	I	T
0.1265446	cg0031188	cg0031188	43616362	CTTATTA	62666317	CTTATTA	I	A
0.1097369	cg0031400	cg0031400	54769436	ATTCAATATACATTAAAATCT			II	
-0.111965	cg0031816	cg0031816	30729329	TACTAAATCCTAAAAATAAAA			II	
-0.128941	cg0031863	cg0031863	64702450	ACTATAATACCCATAAAAAAT			II	
0.100657	cg0032100	cg0032100	34743356	ACCTCTCAATACCAAATCCAA			II	
0.1546537	cg0032170	cg0032170	29758495	CTCTAAAACAACAACAATACC			II	
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-0.165935	cg0032512	cg0032512	73798400	TATTTAC	39785417	TATTTAC	I	C
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0.1541798	cg0032591	cg0032591	14694367	TCATAAAATTCCTAAAAATAC			II	
0.1595393	cg0032821	cg0032821	72703382	TTTTATAATTATTTTAATTTAT			II	

0.1107691	cg00328597	cg00328597	38675330	AAAAAAAATCCTAATCATAAT			II	
-0.151364	cg00328916	cg00328916	72644443	TAATAAATATTAATTTATACC			II	
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0.1241249	cg00347620	cg00347620	51782356	TTCCAAA	65801309	TTCCAAA	I	C
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0.122436	cg00352576	cg00352576	46794399	CTCTCACTACCATATTCCAATA			II	
-0.126273	cg00353407	cg00353407	29767306	CTCTCTAAACTTTTCAAAAATA			II	
0.1677401	cg00354381	cg00354381	53661303	TAATTAATCAATACAATCTAAC			II	
	cg00363750	cg00363750	73802349	CCCTATACTCTATCCACTTTCC			II	
0.1729915	cg00366603	cg00366603	71632347	TACTATCTACATAAAATTAAAT			II	
0.109563	cg00369056	cg00369056	22723346	CCTCATATTATAAATTTCCAAA			II	
0.1078323	cg00370414	cg00370414	68769470	TCRATAAAAAACCCTACAAAC			II	
0.1004608	cg00371061	cg00371061	70750478	CRTATCTAACCTCCCCAATACT			II	
0.1692826	cg00373436	cg00373436	35689309	TCTACCAACCCATTCTTAAACC			II	
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-0.140437	cg00384701	cg00384701	45767476	CRAAAAAAACRTCTTTCTCCRT			II	
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	cg00394712	cg00394712	24737432	TTAATATTATACCCATAAATCA			II	
0.1287061	cg00398048	cg00398048	15783450	CTAAACAAACATTCCAAACAC			II	
0.105296	cg00399951	cg00399951	24614302	TATACAAAATCCAACCCCCCR			II	
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-0.13246	cg00404187	cg00404187	59806369	CAAACTACATATTATAATATTA			II	
0.1135794	cg00406010	cg00406010	60735327	AATCTCRTATTAATAAAAATAT			II	
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-0.135403	cg00410898	cg00410898	41650376	AACTTTTACAAACTAAAAACC			II	
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-0.156608	cg00436969	cg00436969	51693491	ATCAAAAATAATAAAATAAAC			II	
0.1154762	cg00440797	cg00440797	46608309	TTAATCCAACTAACTCCCTAAA			II	
0.1938849	cg00450029	cg00450029	70611456	AAATAAATATATCCTATACATT			II	
-0.316587	cg00456343	cg00456343	16712478	CTCAATACCTTAAAAAACCRA			II	
0.1202003	cg00458932	cg00458932	69765306	ATTCCTATTATAACTATCAAAA			II	
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0.2371812	cg00466116	cg00466116	36716493	AAAAAACATTCAAATCTAAAT			II	
0.154954	cg00467278	cg00467278	57640486	TCCACAA	71694449	TCCACGA	I	A
0.1578017	cg00472840	cg00472840	20810380	AACTTTATATCCCCRACAATAA			II	
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0.1191266	cg0048625	cg0048625	67693416	CTTCCAACAAATATAACACCT			II	
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0.1205994	cg0049790	cg0049790	62600457	CTATACAACTCAATCAAAACT			II	
0.1267453	cg0049913	cg0049913	38801390	TCTATAACTTTCTCATCCCTAA			II	
0.1150294	cg0050002	cg0050002	48607448	CTAAACTTCAAAAAACTTCAA			II	
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0.1065352	cg0051071	cg0051071	38763374	CTCRAAATAATAACACTTCCT			II	
0.1184269	cg0051133	cg0051133	20665459	CTCACCRAAAAACAACAACAA			II	
0.1018859	cg0052360	cg0052360	70747313	CCAAAACAACAATTATAATAT			II	
0.1524791	cg0052362	cg0052362	39768400	AAAAATAAACACCATTAAAAT			II	
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-0.277315	cg0054029	cg0054029	37809366	AAAAATAAAAAATCTACCCAA			II	
0.150685	cg0054403	cg0054403	23632499	AATAAAATTATACTAAATACT			II	
0.375331	cg0054675	cg0054675	74625369	AATTTATCAATCTTCCTATAAA			II	
0.1035224	cg0055508	cg0055508	42616447	AATACTAAAAACTTTACTCC			II	
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0.163762	cg0057564	cg0057564	16668481	CTAATACTTTATCCACRAATC			II	
0.1013348	cg0057613	cg0057613	22668323	TACTTCCTAAAATTTCCRACA			II	
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0.1014317	cg00587301	cg00587301	23781313	AATATTCAACAAATCAATAAA			II	
0.1003872	cg0058734	cg0058734	39716491	AAAACCTAAAAAAAAACCAC			II	

0.2600051	cg00587941	cg00587941	55710466	CTACAAA	28715476	CTACAAA	I	A
0.1410605	cg0058892	cg0058892	70627410	TTAAATCCTCCAAACTTCTTAA			II	
-0.117416	cg00595051	cg00595051	15623412	TTCATTCTAAAAACCRTTCCAT			II	
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0.1164856	cg00635343	cg00635343	45612424	CCTAATAATATACTTCTTAACT			II	
0.1182786	cg00636194	cg00636194	62744391	CCTCTCTCTTCTTTCRTATATA			II	
0.1193676	cg00638021	cg00638021	71783431	CTATATTCTCTCCTTCCAAAAT			II	
-0.167911	cg00639615	cg00639615	64697321	AAAAAACAAAAATTTCTAACT			II	
0.1049242	cg00655552	cg00655552	27604337	AAATCATATATATCCCTCCAT			II	
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0.1547226	cg00668212	cg00668212	47690491	CAAAACACATCTACCTAAAAA			II	
0.113979	cg0067533	cg0067533	68697397	TCTTCCTACTTTCCAATATCCC			II	
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0.1421484	cg0069404	cg0069404	56600501	CAAAATTAAATAATCRTCTAT			II	
0.1861162	cg00694353	cg00694353	61688483	ACTCAATAATTAAATCRAAAA			II	
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-0.354203	cg00702561	cg00702561	19740489	TTTTTCTAAACTACTTACATAA			II	
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0.1181018	cg00725145	cg00725145	49647457	AAAAAAA	13676315	AAAAAAA	I	C
0.1473785	cg00727777	cg00727777	72788303	TAACCATTCCAAATACTATCAA			II	
0.1164738	cg00729708	cg00729708	15681478	RTAAAAACCCACRAAAATAAT			II	
0.1545759	cg00733978	cg00733978	58790502	AATAATTACTTAAAACTCAACT			II	
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0.1032431	cg0074747	cg0074747	73744465	TCAACCATTTCCACAAAACCA			II	
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0.1265295	cg0075354	cg0075354	23677356	AAATAAATATTCCTCCATATTC			II	
0.1281634	cg0075392	cg0075392	13628431	ACCTATAAACATAAACACTAA			II	
0.1165502	cg0075498	cg0075498	16601458	TATCTAATTTTTAAATTAAAAA			II	
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0.1034604	cg0076817	cg0076817	17658469	AAACRCAATCCAATTATAATA			II	
0.1468759	cg0077756	cg0077756	58611311	ATAAACTTCTATACTAAAATC			II	
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0.1523997	cg0079393	cg0079393	36619332	TTTAAAC	72628509	TTTAAAC	I	A
-0.184425	cg0079399	cg0079399	29629398	AAAATAATAAAAATTTCAACC			II	
0.1681027	cg00794911	cg00794911	25661471	AAAAAATACCRTCAAAACAAA			II	
0.1118464	cg0079520	cg0079520	56635320	AACTTACTACTAAAATATAAA			II	
0.1028429	cg0080424	cg0080424	54773334	TCCTAAA	45725488	TCCTAAA	I	A
0.2390398	cg0081421	cg0081421	64602355	TAACRTATATACATAAAAAAC			II	
0.1227916	cg0081651	cg0081651	14806404	TCAAATCCTCAATTTTAAAAA			II	
-0.198072	cg0082118	cg0082118	70683476	AAACAAAACTCCACTATACRA			II	
-0.132721	cg0082203	cg0082203	18798349	AAAACTC	10688394	AAAACTC	I	A
0.1044073	cg0082964	cg0082964	61646498	ATCCAAA	38687433	GTCCAAA	I	A
0.1015578	cg0083213	cg0083213	62629352	ATCACAAATATTACCAAAATA			II	
0.1670972	cg00836101	cg00836101	33668367	ACCRCAAATAACTTACAAATC			II	
0.11423	cg0083789	cg0083789	55725467	AAACTCCAAAACAACAAATAA			II	
0.107611	cg0083842	cg0083842	16654482	AAACRAAAAACATTATCCTAC			II	
-0.10402	cg0084363	cg0084363	68647386	AAACACAACACTAAACATAAC			II	
0.102256	cg0084837	cg0084837	19743484	ATTTAATAATATTTTCATCAAA			II	
0.1161994	cg0085151	cg0085151	47624412	AAAACRAAAAAACCRAAACCC			II	
0.1027896	cg0085260	cg0085260	47669404	AAACAAA	30621348	AAACGAA	I	A
0.1325734	cg0085394	cg0085394	60716487	AAAATAACCAAATTAAATATT			II	
0.2223739	cg0085987	cg0085987	32640506	TCAACTCCTAATAAAATAATA			II	
0.1865849	cg0086121	cg0086121	49625401	CCCCAATCTTTTTAACACCTAA			II	
-0.137516	cg00864171	cg00864171	52799325	CAACAAATAAACAACCTCCCC			II	
-0.223575	cg0086930	cg0086930	71621326	ATATAACRAAATACCATACTC			II	
-0.158724	cg00873601	cg00873601	18668468	ATACCTT	60679306	ATACCTT	I	A
-0.100771	cg0087675	cg0087675	43778390	AAAACAA	41784387	AAAACGA	I	A
-0.137596	cg0087816	cg0087816	39764486	ATCAAAA	58726385	ATCGAAA	I	A

-0.113931	cg0087921	cg0087921	19790496	RCATTATCAAAACTCTCAAAC			II	
	cg0087949	cg0087949	49788354	TATCCAC	13644469	TATCCGC	I	A
0.2036033	cg0087954	cg0087954	47671476	TAAAATTATATATTTTAACCA			II	
0.4914707	cg0088189	cg0088189	68677465	ATTCCTTTTCCCCTCATCCTTA			II	
0.1185193	cg0088657	cg0088657	15612500	CAAAAACTATACTAAAAACCC			II	
0.1098151	cg0088875	cg0088875	24721332	CCTAAAAAAAACCATTATTCC			II	
0.1008365	cg0089007	cg0089007	63730395	TAACATCATACCATCCATATT			II	
-0.105769	cg0089236	cg0089236	48731416	AATCCAC	51671432	AATCCGC	I	A
0.1123998	cg0090073	cg0090073	29702359	TCCAATT	14789326	TCCGATT	I	T
0.1084806	cg0090531	cg0090531	64770334	TACCAAAAACTAAACACTTAC			II	
-0.129192	cg0090552	cg0090552	33623413	TAACACA	24656365	TAACACA	I	C
-0.106461	cg0090574	cg0090574	62698386	AAACCTAAAAATCCAAAAAAC			II	
-0.102257	cg0090860	cg0090860	70794326	ACACTTCCCCACTCCAATCTA			II	
0.1540623	cg0091395	cg0091395	72679382	CCCCTTCTATCCAAACAAAAA			II	
-0.356263	cg0091818	cg0091818	70622484	AAATACACAAACCCRAAAAAT			II	
0.1143639	cg0091912	cg0091912	14642320	AAAACACCCTTTACCTTAAAA			II	
0.1234062	cg0092066	cg0092066	36693338	CACCCAA	23620361	CACCCGA	I	T
0.1348595	cg0092508	cg0092508	70796393	CTTTACCACAAATATTAAAAC			II	
0.1536998	cg0092642	cg0092642	61804339	ATAATTA	73696387	ATAATTA	I	T
0.2038003	cg0093968	cg0093968	23660333	CAAAAACCAATCTTCTTAATA			II	
0.2610922	cg0094463	cg0094463	33644501	ACTCATTCTCATATATCTTAAA			II	
0.1448193	cg0094778	cg0094778	22655509	ACAACAC	11725434	ACAACGC	I	T
-0.112344	cg0094998	cg0094998	23653380	ACACCAT	50799380	ACACCAT	I	A
0.1214544	cg0095278	cg0095278	20734465	CAAAAAAAATCCTACTCACAC			II	
-0.138874	cg0095578	cg0095578	48794300	TTAAAAAAATATAAACRTATC			II	
-0.103909	cg0095649	cg0095649	30773316	RATACTACTAAAATATATTCT			II	
0.152703	cg0095769	cg0095769	27697394	TAATAAAAACTAACATAAAC			II	
0.1097345	cg0096816	cg0096816	41790387	AAACTCCTTATTTAAAAAAAT			II	
-0.100932	cg0096877	cg0096877	64794380	CTATACC	16624467	CTATACC	I	A
-0.135772	cg0097027	cg0097027	38750401	ACAAAAT	43783437	ACGAAAT	I	C
0.1110156	cg0097452	cg0097452	12731470	AAACTTCTCCCCTATATATATC			II	
-0.107359	cg0097457	cg0097457	37653347	CATAAAAATCRACTTTAAAAC			II	
0.1652674	cg0097574	cg0097574	57691312	TAATAATAAACATAATTACCT			II	
0.1732812	cg0097884	cg0097884	52680431	ATTCCTCAAATCCACTCTAAA			II	
-0.13577	cg0097928	cg0097928	64652323	CCAACAC	10616422	CCAACAC	I	A
-0.180338	cg0098187	cg0098187	15731476	AAATACC	28704329	AAATACC	I	C
-0.134868	cg0098298	cg0098298	48702333	AAAAAAACCCCAAAATATACA			II	
0.1219094	cg0098369	cg0098369	51787353	ACAAAAAAACAAACTAAACA			II	
0.1101105	cg0098370	cg0098370	22623502	CRCTCCAAACAACACTAACTA			II	
0.1005041	cg0098538	cg0098538	36700401	CCTACACTTAAAAAATACTTC			II	
-0.202152	cg0098805	cg0098805	37707449	AAAAAA	31720502	AAAAAA	I	A
0.1080514	cg0099076	cg0099076	68787438	AAACCCCTCACTACCTAAAAC			II	
0.1017399	cg0099383	cg0099383	67633457	TAATTTAAAATAATATTCCTTT			II	

-0.113426	cg0099390	cg0099390	26725474	CCTTTTTCCTCAAAATTTTATT			II	
-0.157505	cg0099536	cg0099536	49810395	ACCTATATCAACTTATCCCCCT			II	
0.1046425	cg0099725	cg0099725	40617310	TTACATTAACTAATTACTCACC			II	
0.1628344	cg0099916	cg0099916	34802473	ACCAACA	57752377	ACCGACC	I	C
-0.108109	cg0099963	cg0099963	58704438	TAAATATTACAACTCTTAAAA			II	
-0.130151	cg0100065	cg0100065	67673486	AAAAAA	35768392	AAAAAA	I	A
0.1214254	cg0100131	cg0100131	49793311	ACTTAAACCTAAAACCTTCTA			II	
-0.101604	cg0100195	cg0100195	57762422	CTTTACACTCTTCTACCTTCCC			II	
0.1059879	cg0100518	cg0100518	72747446	AACCTAAATCATAACTATAAA			II	
0.1286917	cg0100542	cg0100542	13730504	TTTTTCTTTTTAATTTCACAAA			II	
-0.106747	cg0100548	cg0100548	49765459	AAAACAAAAACTACTCTTAAC			II	
-0.107685	cg0100680	cg0100680	39651497	AAATTAA	64691402	AAATTAA	I	A
0.2150862	cg0101303	cg0101303	35631361	AAATTAC	35690419	AAATTAC	I	C
-0.186061	cg0101566	cg0101566	21666465	TTATAAA	26648376	TTATAAA	I	C
-0.172106	cg0101609	cg0101609	21694469	CCCACTCTAATCCTTAATTTTC			II	
0.1008208	cg0102211	cg0102211	17782395	AAATACC	42638353	AAATACC	I	A
-0.115597	cg0102218	cg0102218	25786466	AAATCTAAAAAAAATCCCTTA			II	
0.167631	cg0102267	cg0102267	15660474	CTAATAACTCAACCAATATAC			II	
-0.112289	cg0102324	cg0102324	67743501	TCCCTTTTAAAAATAACATCC			II	
0.1071486	cg0102370	cg0102370	33783394	AAACTTAAAACAAAACTAAAA			II	
-0.157893	cg0102509	cg0102509	68672467	CTATTAA	64763345	CTATTAA	I	C
-0.202844	cg0102933	cg0102933	73787312	CACATTA	14657451	CACATTA	I	C
-0.102368	cg0102968	cg0102968	63766436	AATATTTCTTCAAAAATTCAA			II	
0.1164579	cg0103131	cg0103131	11690361	TAAAAAAATTCCAATACTACT			II	
0.1480042	cg0103481	cg0103481	28693312	TACCTTTCCRTAAACAATAAA			II	
-0.175848	cg0104220	cg0104220	43649477	ACCATCA	21654418	ACCATCG	I	T
-0.125421	cg0104827	cg0104827	66719465	TAACCATTTATCTTTTAACTTT			II	
0.1095443	cg0105569	cg0105569	63796358	CAATAACCTTATCTAATTTATC			II	
-0.108077	cg0105569	cg0105569	51629480	AATAACC	25614359	AATAACC	I	C
-0.131384	cg0105646	cg0105646	10629329	CAAAACA	16649394	CAAAACC	I	C
-0.159218	cg0105911	cg0105911	69731430	AACTTTCATTTCCTATTCCAAT			II	
-0.142821	cg0105938	cg0105938	61780487	ACAAAAAACCCRAAACAAAA			II	
-0.101791	cg0105943	cg0105943	37645427	ATCAAAC	38781310	ATCGAAC	I	A
0.1509777	cg0106116	cg0106116	34769367	ATCTAAA	25702481	ATCTAAA	I	T
-0.118267	cg0106152	cg0106152	61760464	TAACCTATAAATAAACRAAAA			II	
0.1024155	cg0106253	cg0106253	57764394	TACATAA	21718483	TACGTAA	I	T
0.1416259	cg0106294	cg0106294	52752434	AAAAACTTCRCRATTACCTAA			II	
0.1409029	cg0106308	cg0106308	53684349	CTTCCRAAAACAACRACRATA			II	
-0.14839	cg0106426	cg0106426	58621422	ATACAAA	51611437	ATACAAA	I	A
0.119834	cg0107238	cg0107238	62787373	ATAATACTTTCCACATAAAAA			II	
0.2315002	cg0107408	cg0107408	17770500	ACTCTAATCTTCTACTAAAAA			II	
-0.469878	cg0108158	cg0108158	63773393	ATACCTATTTATACAAAACTCC			II	
0.1284347	cg0108539	cg0108539	34667319	ATTCAAATAACTTACTAAAAT			II	

	cg0109744	cg0109744	13617312	AAAAAA	37610325	AAAAAA	I	A
-0.128466	cg0110166	cg0110166	57773374	CCACCACCAAATAAACAATAA			II	
0.1173881	cg0110167	cg0110167	35652338	CATTTCTAAAACATCTCCCAA			II	
-0.400459	cg0110540	cg0110540	58625305	CRCTAAAACCATTTTCTATCCC			II	
0.1156125	cg0110863	cg0110863	52758389	TTAAAATCAAAAACTACTTTT			II	
0.1487882	cg0111413	cg0111413	71625399	CTACTAAATACCRTAAAACAC			II	
-0.164344	cg0111727	cg0111727	24632368	AAATAAAAACTTTAAAAAACC			II	
-0.281204	cg0111864	cg0111864	72739319	TAAAAATCAAAAATCTAAAAT			II	
-0.119206	cg0112413	cg0112413	53638343	ATTAAATACTATATAAAATTA			II	
-0.145984	cg0112760	cg0112760	24715331	TACTTCCRAAATCRAAAACTA			II	
0.1207551	cg0112804	cg0112804	18724455	AAATCTATTCTCAACATTTACT			II	
0.2399866	cg0113969	cg0113969	45607388	TCCTACCTTAATCTCCCTCAAA			II	
0.1067752	cg0113969	cg0113969	16700378	ACAACTATTTATTAAATAACC			II	
0.1332062	cg0115262	cg0115262	32644411	TTTCCATTTCACTAAATACTTC			II	
0.2167035	cg0115337	cg0115337	45738320	CAAAAA	50626330	CAAAAA	I	A
0.1145931	cg0115433	cg0115433	44652369	AAAATAACCATACTCTTCTCC			II	
0.1335649	cg0116105	cg0116105	62747307	TTCCAAACACTAACTATATTTT			II	
0.1163456	cg0116590	cg0116590	35653429	ACATAAAATCCTAACTAACTA			II	
-0.237185	cg0117514	cg0117514	47769365	AACTAAAATACAACCTTAAAA			II	
0.1170594	cg0118207	cg0118207	37774380	TCRATAAAAAATATAACTATA			II	
0.1173925	cg0118564	cg0118564	22706469	TTCTATTTTCACRATACTAATA			II	
0.1338679	cg0119091	cg0119091	14707477	AAAACC	27750351	AAAACC	I	A
0.1153925	cg0119115	cg0119115	50612384	TAAAAAACCAAACAACTCACC			II	
-0.132302	cg0119336	cg0119336	21647360	AAAATA	26755371	AAAATA	I	A
0.109475	cg0119407	cg0119407	72697401	AAACCA	32694336	AAACCG	I	T
0.1183261	cg0119476	cg0119476	24770508	AAAAATCATAATTAATTTCTA			II	
0.1012988	cg0119633	cg0119633	64764433	ACAAAAAAAAACCTACCTCCT			II	
-0.132959	cg0120251	cg0120251	59676304	TAAAAA	47600463	TAAAAA	I	C
0.1177978	cg0120376	cg0120376	74635411	AACAAAACCCTAATCCCTTTA			II	
-0.119595	cg01215761	cg01215761	23623339	CAAATA	62672339	CAAATA	I	C
-0.205462	cg0122158	cg0122158	24784320	ACCTAACCTACCRAATAAAAT			II	
-0.293126	cg01228941	cg01228941	55600356	AATCAA	35613357	AATCAA	I	A
0.2914732	cg0123032	cg0123032	18649346	TAAAACCAATCAAAATTTTAA			II	
0.1364021	cg0123063	cg0123063	72809365	TTTTTTATTTTAAACATATCAA			II	
-0.113418	cg01231921	cg01231921	35765480	RACCCRACAAACACCATAACC			II	
0.1679514	cg01232331	cg01232331	11624391	AACCTACATAAACTAACTAAA			II	
-0.11084	cg01232511	cg01232511	34701365	AAACCA	35621479	AAACCG	I	C
0.1552874	cg0123656	cg0123656	38743488	TCAAAATTTCTTTCTACTTTAT			II	
0.1624808	cg0124522	cg0124522	70663375	AAAAATACCATAACAATATCC			II	
-0.138841	cg0124874	cg0124874	44690486	TTCCRAAATCAAAATCTAAAA			II	
0.2978484	cg0125430	cg0125430	32766403	CTACAAA	50639305	CTACGA	I	A
0.1137398	cg0125778	cg0125778	25672372	CTACTTCCCACCATAAAAAAA			II	
0.1911996	cg0126491	cg0126491	73763380	ACTTCCCRACATACCRCTAAA			II	

0.1242095	cg0126921	cg0126921	37698464	RACCCTACAAAAATACATTAT			II	
-0.116436	cg0127000	cg0127000	52631391	TAAACTC	43650379	TAAACTC	I	C
-0.167414	cg0127490	cg0127490	52722315	TAAAAAAACATTTACTATATT			II	
-0.121921	cg0128333	cg0128333	61774489	ACAAACACTTTAATTTTCCTCC			II	
0.2141066	cg0128428	cg0128428	64720495	CAAACATAACTCATTATATAT			II	
-0.106353	cg0128550	cg0128550	50703500	AACCCTAACCTTAAACTATAA			II	
-0.113453	cg0128592	cg0128592	28747346	CAATCAA	62630489	CAATCAA	I	C
0.1183712	cg0128668	cg0128668	67740487	CCTAAAA	61726375	CCTAAAA	I	C
-0.100332	cg0128700	cg0128700	71733390	ACCATTA	38620464	ACCGTTA	I	A
-0.104305	cg0128954	cg0128954	36615507	AATTTTTCTACCTACCTACAAA			II	
0.1202017	cg0128987	cg0128987	24806427	TAAAAAAATACCTTTAATTAA			II	
0.1113836	cg0129253	cg0129253	68748466	CRAAACATTTTCTAAACAAAC			II	
0.1217001	cg0129281	cg0129281	50683422	TTAAAAACTAAAAATATTACT			II	
0.114005	cg0129428	cg0129428	63706392	AATAACRAAAAACRACTAATT			II	
-0.118378	cg0129564	cg0129564	63606406	CCAAAAATAAATAAACAAAA			II	
0.1465809	cg0129810	cg0129810	35734489	TTTCCTCCCCCTTCTACTACCT			II	
0.1081485	cg0129867	cg0129867	12736491	CRTAAAAAACATAATTTCATA			II	
-0.264291	cg0129891	cg0129891	35809352	ACRTACTAAATAAACRTACTA			II	
-0.118624	cg0130128	cg0130128	10771424	CRTAAATATTTATTTACTACCT			II	
-0.112596	cg0131647	cg0131647	67705342	CCAAATTCTTCCCAAACRAAC			II	
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-0.132743	cg0132057	cg0132057	46731406	ACCTCCC	41796418	GCCTCCC	I	A
0.148701	cg0132196	cg0132196	47774394	TTAATCCACATATATCCCAAA			II	
0.1382241	cg0132426	cg0132426	30671344	CAAACRCRATAACTCACACCT			II	
0.1136073	cg0132546	cg0132546	40647340	CATCTAATACATTTAAACCAT			II	
-0.186718	cg0132642	cg0132642	32630496	TTAAATATTCTAATAATTAAT			II	
0.18383	cg0132969	cg0132969	30690303	ACCATACCAACTACTCRTTAT			II	
0.1723318	cg0134180	cg0134180	23754361	ATCTAATACTTTTACAAACAA			II	
0.1283213	cg0134858	cg0134858	55740334	CAACCAA	17663399	CAACCAA	I	C
0.2766204	cg0135080	cg0135080	47628373	TTAAAAACTTTAATTTTTACAT			II	
0.1141881	cg0135478	cg0135478	34742332	CTAATCACCAAAAAAACCAAC			II	
0.1013616	cg0135982	cg0135982	28651441	ACAATAA	46697474	ACGATAA	I	A
-0.15861	cg0136922	cg0136922	20742450	AATTAATCTAAACAATAAAAC			II	
0.1021779	cg0136989	cg0136989	55620332	AAATATCCTAAAAAAATTTTT			II	
0.101056	cg0137142	cg0137142	44612418	TAATAACTCCTACCTTCTCATA			II	
0.1073404	cg0137726	cg0137726	55689445	CCATCAA	71681318	CCGTCGA	I	A
0.1334915	cg0138182	cg0138182	15732482	AAAAACTTACTTACTTACTATT			II	
-0.149393	cg0138286	cg0138286	19729390	CAACAAA	55803378	CGACGAA	I	A
0.1612814	cg0138595	cg0138595	28748320	TCAAAATAAATATTATATACC			II	
0.1092978	cg0138790	cg0138790	36640437	AACACCTAAAACTTAAAATC			II	
-0.186837	cg0138869	cg0138869	49677502	AAACCAATACCAAATAATATC			II	
0.2296487	cg0139416	cg0139416	12717498	TCTCAAACACCTAAAACTTTT			II	
0.2437959	cg0139554	cg0139554	62685325	ACAACAACTTACTCTCCCATA			II	

0.3555591	cg0139749	cg0139749	73746324	CCATCCTTCACTTCTTTCAATA			II	
-0.183637	cg0139931	cg0139931	13760327	TAACTAA	70639478	TAACTAA	I	C
0.1151507	cg0140004	cg0140004	49616453	ATAACRTAAACTAATTATTCAT			II	
0.121896	cg0140744	cg0140744	43638467	ACCCTAATACATTTTTTTAACT			II	
0.1080483	cg0140934	cg0140934	55651304	CATTTCAAAAATACCTAAAAA			II	
0.1365083	cg0140970	cg0140970	70799373	TTACCTAAAAATATAAACACT			II	
0.175768	cg0141092	cg0141092	56726407	TTTCATTCTTACATTCTTTAAC			II	
0.1021615	cg0141240	cg0141240	49660476	CRACAAAATCTCTTTCTTCACT			II	
-0.122583	cg0141241	cg0141241	72610302	TCACCCT	69694413	TCGCCCT	I	A
-0.129539	cg0141297	cg0141297	57688456	CCAATTT	12650324	CCGATTT	I	C
0.1066035	cg0141358	cg0141358	32689494	CTCAAAAACCAAAACCTCCAA			II	
-0.110291	cg0141384	cg0141384	38718438	ACCATAA	40801417	ACCATAA	I	A
-0.111489	cg0141418	cg0141418	57719415	TTAATCT	39804430	TTAATCT	I	A
-0.154489	cg0141656	cg0141656	12766393	CTACTCT	31702477	CTACTCT	I	T
-0.167021	cg0142837	cg0142837	39602445	CACAAA	61800414	CACAAA	I	T
-0.113868	cg0142944	cg0142944	48610458	TTATTCA	38713324	TTATTCG	I	C
0.1160814	cg0144048	cg0144048	67620425	ACAAACATACAAAATTATAAC			II	
0.1015121	cg0144284	cg0144284	62673347	CTACCAAAAAAAACAACTACT			II	
0.1017079	cg0144568	cg0144568	17793335	ACTAAAA	37710470	ACTAAAA	I	A
-0.175389	cg0144579	cg0144579	46745432	CAAATCC	29695498	CAAATCC	I	T
-0.127556	cg0144856	cg0144856	10771502	ATCCTCA	27630358	ATCCTCG	I	A
0.1006401	cg0145110	cg0145110	39754340	ATCTCCCCAAAACCAATAATA			II	
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0.1139171	cg0146043	cg0146043	61777484	AATCTACAACCTTTTCAAATTT			II	
0.1171566	cg0146272	cg0146272	58768363	AAAAACAAAACTTTAAAACTC			II	
-0.121734	cg0146311	cg0146311	10715421	AAAAATACATATAAATACCCC			II	
0.1625134	cg0146406	cg0146406	49746427	AAAACCTTTATAAACCCTAAA			II	
-0.132512	cg0146986	cg0146986	10809390	RAAAAAAAACAAATAATCCCC			II	
-0.292838	cg0147468	cg0147468	10701448	TACTTTTACCAACCAAATTCAA			II	
-0.107607	cg0147538	cg0147538	20620412	CTCCCCT	53605402	CTCCCCT	I	C
-0.145776	cg0147817	cg0147817	69693345	ACTTCTACTCCTTCTCTTCCAA			II	
-0.189438	cg0148365	cg0148365	70649496	TTTCTTCACTCAACCCAACAAC			II	
0.1930621	cg0148484	cg0148484	23790396	TACTTTCTCATCCTCAAACTAA			II	
0.1919336	cg0149009	cg0149009	53695420	AATCCRAACCTCTCTAACTCCT			II	
0.1484562	cg0149142	cg0149142	15709507	ACCTCCTAAAACAAAAACTCC			II	
0.1438841	cg0149300	cg0149300	12753507	AAAACTTATATATATATTACA			II	
-0.172185	cg0149981	cg0149981	57646393	CAACACA	43678317	CAACACC	I	C
0.1394424	cg0150246	cg0150246	54808314	TAAAAATTTATCTCTTAATACC			II	
-0.11955	cg0151822	cg0151822	50676477	CTAAAAA	19679386	CTAAAAA	I	A
-0.244071	cg0151922	cg0151922	64745443	ATCTAACACCCTCCAAATAAT			II	
-0.10593	cg0151950	cg0151950	36802474	CAAACCT	67694477	CGAACCT	I	A
0.1847731	cg0152302	cg0152302	18756452	CRTCTTAAACACCTTACRTTTC			II	
0.1073898	cg0153425	cg0153425	27658321	AAACACATTAACTAAAAAATA			II	

-0.224409	cg0154358	cg0154358	33710356	AAAAATCAACACTTACCAAAA			II	
-0.272719	cg0154681	cg0154681	53787464	ATAACTATAATATTAACTTAC			II	
0.1075603	cg0154846	cg0154846	66707495	TTCCATATATTAAATACACCC			II	
0.1093484	cg0154922	cg0154922	16643509	CATAAACTCACAATCAAACTC			II	
0.119344	cg0155034	cg0155034	57800438	ATTATATTCACCAACTCCACA			II	
0.4091769	cg0155138	cg0155138	59663305	RTACTATTAATAAATTCCAAC			II	
0.1756893	cg0155477	cg0155477	29748349	AAATACTATTAAAACCAAAAT			II	
0.1044712	cg0155930	cg0155930	21687389	AAAACAATAATAAACRTAAAA			II	
-0.115929	cg0156087	cg0156087	16674376	AAATAAAACTAACTATAATAA			II	
0.4024945	cg0156175	cg0156175	53619391	AATCACCATAAAAATTAAAAC			II	
-0.103267	cg0156186	cg0156186	48704344	TCACCAATAACTTTAAATCTC			II	
0.1040084	cg0156281	cg0156281	21632448	AAAAACTCCCAACRATAAAAA			II	
-0.137293	cg0156998	cg0156998	42778479	ATCTCAAAACCCTTTACACTC			II	
0.100654	cg0157960	cg0157960	67692433	TCCTCTTTAAATAAATTTAACT			II	
0.1243966	cg0158022	cg0158022	26693475	AACTACAATATACTCTTACAA			II	
0.1072579	cg0158103	cg0158103	35778319	TAAAACTAAAAACCCTATTAA			II	
-0.141529	cg0158134	cg0158134	45618385	TAACATAATATTATCAAAAAT			II	
0.1152306	cg0158206	cg0158206	61600338	CAACCTATAACACACTTTAAA			II	
-0.178611	cg0158572	cg0158572	34695470	ATTCCAAATACACAAACTACC			II	
-0.308765	cg0159134	cg0159134	35649365	AAAAAATATTTATTTTAACTT			II	
0.1056913	cg0159235	cg0159235	74631308	AAACTAACACACCATATACAC			II	
0.2220894	cg0160171	cg0160171	22645432	AAAAAAACTCACTCTTTAACT			II	
0.1317395	cg0160400	cg0160400	56664402	TAAAAATTTACTTAAATCCCA			II	
-0.16395	cg0161229	cg0161229	38678327	TCAACCT	60736393	TCGACCT	I	C
0.1039007	cg0161265	cg0161265	33661463	ACTCCTC	14650472	ACTCCTC	I	C
-0.114108	cg0161410	cg0161410	66709389	CAAAAA	51669418	CAAAAA	I	A
0.1200047	cg01620701	cg01620701	45739403	ATAAATACTACCTACTAAAAC			II	
0.1362019	cg0162139	cg0162139	23710488	AAATCACTCATAATACAAACC			II	
0.1049234	cg0162900	cg0162900	29673359	ATCRACCATCAAACCATACTA			II	
0.1043318	cg0163133	cg0163133	58620420	AAACTACCAATCATTCTCATA			II	
0.1078006	cg0163657	cg0163657	66756369	ATTTTACTATTTCACATTTCTT			II	
0.2076519	cg0163687	cg0163687	50613508	TCATCAA	13770417	TCGTCAA	I	T
0.1136358	cg0163724	cg0163724	14719443	AACTACACCTTCTCCCATTAC			II	
0.1005611	cg0163748	cg0163748	31720477	ACTTTAACTTTAATAATCTATC			II	
0.1812492	cg0163778	cg0163778	63665456	ACAACACCCCCTATAAACAAA			II	
0.1119457	cg0163822	cg0163822	51719450	ACAAACT	43603388	ACGAACT	I	C
0.1548951	cg0164794	cg0164794	29767500	AATCCTAAACTTAAATTACCA			II	
0.2066977	cg01649611	cg01649611	69642419	TAAAAAATAACCAATAAACTA			II	
0.1632643	cg0165116	cg0165116	18772368	TCTAAAATAAATCATCATAAA			II	
-0.103878	cg0165224	cg0165224	20802475	AAACTTT	26638420	AAACTTT	I	C
-0.37287	cg0165565	cg0165565	14611329	ACTAAAACACTACRATACTAA			II	
0.1016076	cg01655721	cg01655721	42695500	CATCAAA	61791376	CATCAAA	I	C
-0.174981	cg0166865	cg0166865	34664417	AACCCTC	57628330	AACCCTC	I	C

-0.14805	cg01678701	cg01678701	12684333	ACTACCC	14738326	ACTACCC	I	C
0.1088333	cg01681863	cg01681863	38675349	CACAAATAAAAAAACCCCCTC			II	
-0.138686	cg01685883	cg01685883	49689328	TCCATAACTATTATATTAACCT			II	
0.125554	cg01693328	cg01693328	52662346	CAAACAAAAATACCTACATTT			II	
0.1297629	cg01695994	cg01695994	26726427	AACCAACACCRTATTAACTCAT			II	
-0.101979	cg01699880	cg01699880	10749443	CTAAAACATAAAACTCCAATCT			II	
0.3063267	cg01702501	cg01702501	66667497	AAAATAATATCATTTCRTTTCA			II	
0.1091681	cg01708377	cg01708377	50717377	TTAACCATCATTCTCTACAAAA			II	
-0.171111	cg01710670	cg01710670	14745317	TCCCACA	42785427	TCCCGCA	I	C
-0.193987	cg01713505	cg01713505	66622481	CATACCRTTTCCTTAACACCTC			II	
0.118728	cg01717482	cg01717482	71740418	AAATCRACCRAAATAAAAAAC			II	
-0.102639	cg01737026	cg01737026	66789447	AACAAA	66618329	AACAAA	I	C
-0.237695	cg01740135	cg01740135	69676427	TCATTAACTTTCAAAAACCATT			II	
-0.138553	cg01741056	cg01741056	70642504	CAATTCT	16632414	CAATTCT	I	A
0.176612	cg01741372	cg01741372	49677332	AAAAAAATATCCTACCACRTT			II	
-0.117197	cg01744396	cg01744396	37747425	CRAATCCTAACACTAAAATTTA			II	
0.1041586	cg01748757	cg01748757	24802426	AAATAAAACCAACTTTCCCTCT			II	
	cg01750375	cg01750375	37724327	ACAACCT	13644489	ACGACCT	I	A
0.1494735	cg01754423	cg01754423	68737322	ATCRTATCTCTTAACCCACAAA			II	
-0.205741	cg01754525	cg01754525	18686381	AACAAA	21736365	AACGAA	I	A
-0.123472	cg01759674	cg01759674	23650393	ACAACAAAAACTAAATTCCRA			II	
-0.170022	cg01760090	cg01760090	33662376	CCATTACATTCACACCTATACT			II	
0.3139232	cg01763947	cg01763947	32688424	TTTTCCCACTAAAACRATATTA			II	
0.101058	cg01765322	cg01765322	16704479	AAAATATCACTACCTCCAACC			II	
0.184473	cg01786704	cg01786704	56664461	TTATACA	32808388	TTATACG	I	C
-0.101617	cg01792601	cg01792601	34798432	ACACRAAAACTCTAAAAACTCT			II	
0.123678	cg01796223	cg01796223	65731500	AAACTCTTTATAAATACAACTT			II	
0.1518078	cg01797371	cg01797371	52795419	AACAATT	10640304	AACAATT	I	T
-0.109344	cg01797652	cg01797652	23670458	CACCAAAATTATACATTTATTA			II	
0.205142	cg01801090	cg01801090	59654474	TACTAATATAATATCTCTATTA			II	
-0.103184	cg01804934	cg01804934	30652499	ACTAAATCTCCRAAAAACTAA			II	
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	cg01813738	cg01813738	70692408	TCRTTCCAACAAAACTATTAA			II	
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-0.194622	cg01818369	cg01818369	48799312	CAAATAAAATATCATCTTTACT			II	
-0.167396	cg01820273	cg01820273	37709389	CACAAAA	66738353	CGCGAAA	I	C
-0.282585	cg01823585	cg01823585	54804382	RAATAACRAAAACTCTACACCT			II	
0.1082076	cg01824063	cg01824063	43696400	ACCTAATCCACCCTCAATCTA			II	
0.112628	cg01829632	cg01829632	74607370	AAACTATAAAAATCAACTTAA			II	
0.1143788	cg01835922	cg01835922	21638313	TTCTATACCAACRCTTCAACTA			II	
0.120975	cg01836455	cg01836455	27725379	TTAAATTTTTTATAAAAACAAA			II	
-0.146876	cg01838004	cg01838004	62755506	CCCCRAAAAACATAACAAAAT			II	
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0.3122706	cg01842774	cg01842774	44678464	ACCAAAA	17673382	ACCAAAA	I	A
0.1574313	cg01843264	cg01843264	27791413	TAAAAACAAACCCTACRAAAA			II	
0.2842354	cg01847062	cg01847062	74642468	CCRTACAACTTTATATAACCCC			II	
0.103129	cg01855010	cg01855010	51601347	CATTCTCCTTAAACCACATATA			II	
0.151453	cg01857151	cg01857151	24772402	ACRTCAATACTTTATTACAACT			II	
0.1145085	cg01857838	cg01857838	36653390	AAAAAAACATAACATATAATA			II	
0.1229424	cg01858712	cg01858712	38792447	AATTTCCTAAATCTAAACCCAA			II	
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-0.103058	cg01862688	cg01862688	36734461	TAAAACA	45740407	TAAAACC	I	C
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0.1431783	cg01875467	cg01875467	26673508	CTCACCTAAACCTAAAATCTAA			II	
0.1164951	cg01876338	cg01876338	43725462	TAATACCTCTAATCCTACATCA			II	
0.1017063	cg01880569	cg01880569	54806507	TAATAAAAAAAATCTTTTTACA			II	
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0.1001445	cg01882084	cg01882084	44622465	AATTTTATAAACTAACCTAAAT			II	
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0.1167212	cg01889893	cg01889893	13602332	CTAAAAACCAATCTTACCCTAC			II	
0.1091149	cg01889956	cg01889956	41802369	AATAACAAATAAAAATCAAAA			II	
-0.27241	cg01891583	cg01891583	60666352	CAACAATCCAAAAATCCAACR			II	
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0.1051775	cg01905478	cg01905478	34688463	CTAAACCTTAAATAAACCAAA			II	
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0.3016931	cg01916697	cg01916697	35690442	AATTTACTCATCTATAAAATAA			II	
0.2085481	cg01918604	cg01918604	26687384	AATACCTCATAAACCCATAAA			II	
0.1589421	cg01919941	cg01919941	33759365	ATATCRCRTATAAATACRACAA			II	
0.2750817	cg01921484	cg01921484	24711510	RCACTAAAATAACAACAAAAT			II	
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-0.122931	cg01926813	cg01926813	48794458	CRAACAACRAAATCCTTTTTAA			II	
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0.2547298	cg01930745	cg01930745	24720508	CCTCCCCAACRAAATAACTAA			II	
0.1032234	cg01931222	cg01931222	23666344	TATTTATTTCCTACCATAAAAA			II	

0.1103286	cg0194158	cg0194158	61651486	CTTTCTTTAACCCTTACCTTCT			II	
0.1058438	cg0194255	cg0194255	57796400	TAATTTTTTCAACTATAAAAT			II	
0.3108529	cg0194609	cg0194609	31608438	AACTAAAAAATATCATCATTT			II	
0.1137094	cg0194821	cg0194821	66810339	ATACAACCTAAAAAACTCRCA			II	
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0.1717602	cg0195818	cg0195818	26702322	AACCATAAATATCCTAATACT			II	
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0.1677675	cg0196692	cg0196692	27633458	TTTAAATAAAACCCTACAATA			II	
0.120087	cg0197033	cg0197033	73637467	CTCCCTCATAATTTAACCTACC			II	
0.1893138	cg0197454	cg0197454	33705326	TACTCTTAAAATAAACCTTTTC			II	
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0.1050991	cg0197823	cg0197823	29660412	AAATATCCTTAAACRTCATTA			II	
0.1020476	cg0197870	cg0197870	27711305	TTACAAA	69625371	TTACAAA	I	A
0.1044592	cg0198920	cg0198920	11611407	CTATATATTCCCCATTACTCAT			II	
0.2926548	cg0199174	cg0199174	60789496	CACAATCTAATTCTACCCRAA			II	
0.1561316	cg0199355	cg0199355	15679463	TCACTTCCTATCCAAATAAAC			II	
-0.112111	cg0199741	cg0199741	48680440	AAAAAA	22726367	AAAAAA	I	C
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0.1483069	cg0199788	cg0199788	22666461	TCTATTACTCATTTAACTTTAT			II	
0.1053485	cg0200106	cg0200106	66717351	TAACCTCCAACACCTTTTATTT			II	
-0.163883	cg02004401	cg02004401	14658436	AATACCT	25690377	AATACCT	I	C
-0.116649	cg0201139	cg0201139	63759488	AATCTCTACATTACCTCCCAC			II	
-0.106419	cg0201172	cg0201172	73613315	CTAAAAC	54669365	CTAAAAC	I	C
0.21898	cg0201237	cg0201237	30653507	ACACCTATAAATCAATATCAA			II	
-0.148053	cg02012821	cg02012821	54691403	TACTAAATAAAACTATTATTT			II	
0.1768294	cg0201439	cg0201439	72718380	TTCTCCTTCACCCTTCACCTTA			II	
0.1212699	cg02018291	cg02018291	31768427	AATATAACCCAAATCTACCAA			II	
0.1197931	cg0202038	cg0202038	41641503	AAATATAAACTTTTAAACAAC			II	
0.1352229	cg0202191	cg0202191	66773311	CACCACTATAACTTACCACAA			II	
0.1101283	cg02031121	cg02031121	43772385	CAATAAATCTATAACCAAATT			II	
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0.1561927	cg0205313	cg0205313	40754486	CACCCATAAAACAAAACCTCC			II	
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0.111109	cg0206959	cg0206959	11701350	TCAATATAAAATACATAAAAA			II	
0.1281525	cg0207346	cg0207346	18787317	ACAAAAACTACTAAATAAAAA			II	
0.1099135	cg02075791	cg02075791	35650440	RCTTTATTACTCACTAATTTT			II	

0.1003167	cg0208798	cg0208798	44624356	TTTTACTTTAAACCTAACTAAA			II	
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0.1211777	cg02095601	cg02095601	71613376	TACCAACATACTCCCAAACAT			II	
0.1311229	cg0209622	cg0209622	38701337	TCCTTTTCCTCTTACATCCCTA			II	
0.105191	cg0210207	cg0210207	42690304	TAAATCATCTTCCRTAACAAA			II	
0.2848869	cg0210607	cg0210607	67692407	TCTACAATCCTATCAAAAATT			II	
-0.278494	cg0211305	cg0211305	22668459	TAAAACAATACTAAAAACCCC			II	
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-0.28394	cg0212689	cg0212689	21603365	CAAAAACAAAAAAACAAAAC			II	
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0.4257554	cg0213205	cg0213205	46729363	TAAAACCCRCCAAAATCATTA			II	
0.124758	cg0213402	cg0213402	49760428	TCACTACCCAATATCCCATAC			II	
0.1022882	cg0213512	cg0213512	57807302	CATTATTTCAATCCCATAACC			II	
0.1153394	cg0214057	cg0214057	26657344	CCTAACTAAACAAAAATAACA			II	
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0.1083152	cg0215672	cg0215672	14803389	CAAATATACTTTAATCATCTA			II	
0.1117669	cg0215762	cg0215762	53781451	CRTTTCCCCRAAAAACCCCAA			II	
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-0.10467	cg0216228	cg0216228	12807354	TCAATAA	56601450	TCGATAA	I	A
0.1032495	cg0216858	cg0216858	26797508	TAAACCTTAATTTCCTCAATAT			II	
-0.130708	cg0216971	cg0216971	72641379	TACCCTCAAATATCCCTTAACT			II	
0.1054188	cg0217010	cg0217010	39697472	TATCCATATACTTAAATCAAA			II	
0.1070331	cg0217288	cg0217288	49699431	AAAAACCCCTTTACAATACCA			II	
-0.1581	cg0217306	cg0217306	36681393	ACAACTA	26757342	ACGACTA	I	C
-0.114711	cg0217409	cg0217409	15664467	TAACAAA	72608378	TAACAAA	I	A
0.1121801	cg0218422	cg0218422	37622508	CATTACTCTTAATACTAACAA			II	
-0.295149	cg0218454	cg0218454	42771474	ACAAATTTAAACAAACTAAAT			II	
0.1130801	cg0218500	cg0218500	72694378	TTTCTCTAAACATCTTCTCAAT			II	
-0.333021	cg0218814	cg0218814	44745437	AAAAAAAATTTAAATTTAAAC			II	
0.1790994	cg0218866	cg0218866	10787450	CCCATAAAACACAAAAAACRA			II	
0.109087	cg0219252	cg0219252	64801367	TAACTACTACTAAAACCAAAA			II	
0.1372477	cg0219380	cg0219380	59631353	CAATTTTACCCTAAACAAACC			II	
-0.172117	cg0219490	cg0219490	38687336	AAAAAA	48773344	AAAAAA	I	A
0.1185326	cg0219625	cg0219625	37619333	ATAAAAAAAACTTACCCACTA			II	
-0.115273	cg0219762	cg0219762	19743370	AAAACA	41784469	AAAACG	I	A
0.3886147	cg0220175	cg0220175	46662451	ATTCTTACCTTACCRACCTAAA			II	

0.1070819	cg02203761	cg02203761	43722355	ACTAAATTTATACAAAAAAT			II	
-0.108967	cg02205962	cg02205962	38789501	RAAACCRAAACTACTATAAAA			II	
-0.138656	cg02214597	cg02214597	46607504	ACAAACA	63775303	ACAAACC	I	C
-0.107472	cg02217247	cg02217247	28616345	ACAAAACAAAATCACTCCCCA			II	
	cg02218932	cg02218932	13644467	AAAAATAAATAACCCCTAATT			II	
0.1003582	cg02220418	cg02220418	18675470	TAAAAAA	51631381	TAAAAAA	I	A
-0.114028	cg02222362	cg02222362	34644438	AAAAAAAACCCRCACAAAATA			II	
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-0.126908	cg02224314	cg02224314	54760479	CACCTTA	33722311	CACCTTA	I	C
0.1015476	cg02227879	cg02227879	58654437	TATATACTAAAATCATCTCAA			II	
0.1027737	cg02233197	cg02233197	26765412	CACACRCTAAAACTACTACTC			II	
0.1126048	cg02235843	cg02235843	11800397	AAAACATAAAACRACACTAAA			II	
0.138279	cg02243386	cg02243386	16646325	CAACAAAACTCTATAATTTTCA			II	
-0.104803	cg02243630	cg02243630	59795312	CAAATCCAAAATCTAACATCT			II	
-0.123874	cg02249577	cg02249577	19661302	CTAAAAA	16740379	CTAAAAA	I	A
0.1827217	cg02251771	cg02251771	14751370	AAATCCTCCCCACTTTTAATAT			II	
-0.124858	cg02254774	cg02254774	32607413	TACCAAT	54600312	TACCGAT	I	C
-0.267003	cg02262167	cg02262167	45666375	TTTAAAC	70666403	TTTAAAC	I	A
0.2246636	cg02262553	cg02262553	12658476	ACAACATCCCAACTATATAAC			II	
-0.130547	cg02267270	cg02267270	60657497	AACCTAAACCTATAAAAAAC			II	
-0.103593	cg02268561	cg02268561	13671358	CATTTACCCTTCTTACAAAATT			II	
-0.194094	cg02275226	cg02275226	65730497	CTCACAACRATAACRTATATA			II	
-0.113164	cg02286623	cg02286623	72747447	ATTATAC	27628432	ATTATAC	I	T
-0.115239	cg02286642	cg02286642	26615326	AAAAATCCTAACATCTTAACT			II	
-0.171475	cg02287371	cg02287371	10605360	ACCACACRTACACAACRACAT			II	
0.14842	cg02288345	cg02288345	19809433	TCTAAAATCTATCCATCAAAT			II	
0.1100012	cg02291561	cg02291561	15691331	TAAAAATTTCAACTAAAATCR			II	
-0.108566	cg02293501	cg02293501	28714496	AATCACTACRTATAACCACAC			II	
0.1087275	cg02295509	cg02295509	45796496	TAATTTTAACAATATCTTTTAT			II	
0.1273972	cg02295574	cg02295574	26612374	ATAAAAATACTTATCCTTTAA			II	
0.1504112	cg02296931	cg02296931	39721443	ATACCTA	24783471	ATACCTA	I	A
0.367502	cg02299007	cg02299007	57603479	ATCACCAAACAACTATTTTAA			II	
0.1018741	cg02300652	cg02300652	30661432	CAAAAACAAATCCCAAATAAC			II	
0.2372498	cg02301920	cg02301920	24763311	ACTCTCTCTACTTCCRCRACTT			II	
0.1137466	cg02303209	cg02303209	34697354	AATTCCATTTCTACAAAATAA			II	
-0.286574	cg02304092	cg02304092	47773302	CTAAAAT	48721351	CTAAAAT	I	A
-0.15922	cg02304584	cg02304584	30626500	AAAATTACCCTAAAAAATCCR			II	
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	cg02311337	cg02311337	70681353	CAATATTAAATCRACCTTAAA			II	
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0.1125451	cg02313379	cg02313379	22653369	ATTTATA	51809345	ATTTATA	I	T
0.1131413	cg02315732	cg02315732	23732351	TTACCATCTAAACTAAATTAA			II	
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-0.183465	cg0231982	cg0231982	46797387	ATAATAACAATAACTAAAATA			II	
0.1033667	cg0231986	cg0231986	63707303	CACCATCCCATTCAATCCCAC			II	
-0.105817	cg0232656	cg0232656	37675446	ACAACRACATCATATAACTTC			II	
0.1105387	cg0233050	cg0233050	53770462	ACTCACAAATAATCTAATTCA			II	
0.1237034	cg0233525	cg0233525	67807477	CCTCTTAATACTATTTAACTT			II	
	cg0233884	cg0233884	58657370	AAAACATTTTTAATACCCTCT			II	
0.1211588	cg0234009	cg0234009	19620379	ATCATAATAATAATCACCTCA			II	
-0.175413	cg0234275	cg0234275	41775434	TTTTCCCTTCTTTAAAATTATC			II	
0.2070957	cg0234575	cg0234575	37710395	ATAACCCCCCTAACTTAATAA			II	
0.1461118	cg0234843	cg0234843	47783343	ACTCATATCTAAAAACCTATT			II	
0.1167719	cg0235127	cg0235127	33786418	CTACCCTTTAAATCACACCAA			II	
0.1105085	cg0235263	cg0235263	32803433	TCCACCRCRAATAATAATAAA			II	
-0.238896	cg0235580	cg0235580	29764301	TTCCATTCATCATTACTAAAA			II	
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0.1601282	cg0236359	cg0236359	62732492	TAAATCATAAACTCCTCTTAT			II	
-0.302812	cg0237240	cg0237240	33619327	ATAATTATACCAAAAACCAAC			II	
0.1397086	cg0237498	cg0237498	62778419	ACRAAACACTTTTTAAAATCC			II	
-0.133169	cg0237691	cg0237691	22802390	ATTCCTTATTCCTTTAACRCAA			II	
-0.243346	cg0237954	cg0237954	52684309	AAACCATATATAAAAACATTT			II	
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0.1242858	cg0238185	cg0238185	43676505	CAATAAATCCACACACAAATT			II	
-0.192647	cg0238904	cg0238904	74604407	AAAAAAAATTACCCTAAAAAA			II	
0.1264679	cg0238918	cg0238918	30634354	AATAAACTACAATTAACAATT			II	
0.2171699	cg0238931	cg0238931	61663314	AAAACAACAAATTCATTTAAA			II	
0.1193126	cg0238963	cg0238963	56808505	AAAACTACTTAACATAAAAAA			II	
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0.1563676	cg0239424	cg0239424	19662495	AAAACCTTTCCTCCCAAACCT			II	
0.1973158	cg0239848	cg0239848	27722479	CCTTCCTCCTCTCTTACTAAAA			II	
0.1099623	cg0240077	cg0240077	67767450	ATAATTAAAAACCCCTAAAAC			II	
-0.128478	cg0240135	cg0240135	19620448	AACAAAAACCCTTCCTCCCTT			II	
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-0.107147	cg0241505	cg0241505	47715360	AATTAAC	39807380	AATTAAC	I	A
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0.1347415	cg0242757	cg0242757	56689398	AATAATAACATAACAATAACA			II	
-0.102522	cg0243455	cg0243455	73652409	AACCTATCRAAAAAAACTTAC			II	
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0.1313525	cg0244829	cg0244829	21728441	AACRCCCTATAAAATTACCAT			II	
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0.122077	cg0244893	cg0244893	43770317	AATAAAATACACAAATATATA			II	
0.2973689	cg0244967	cg0244967	21667300	AAAAACTAACTTTACTCATCR			II	
-0.238636	cg0245241	cg0245241	22803434	TAAAAAACRCCAAAAAAAATA			II	
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0.1031537	cg0245534	cg0245534	49740456	AATCCTTAACCTACCAACCTA			II	
	cg0245803	cg0245803	70648417	CCCACAA	18723357	CCCACGA	I	A
0.1209881	cg0245818	cg0245818	32715306	AACAAAAATTATAACTACCRT			II	
-0.376261	cg0246219	cg0246219	34754444	TCCCTTACTCCCAACCCACTA			II	
0.107573	cg0246266	cg0246266	52800491	CCACATTTATTTATCTAAAACT			II	
0.224478	cg0246445	cg0246445	35647474	ATAACTAAATTAAAACCAACC			II	
0.1386248	cg0246448	cg0246448	41709400	AAACTTTAATTCRATAACTCA			II	
-0.192436	cg0246480	cg0246480	26621487	AAATAATTCTCTAAATACATA			II	
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0.1900756	cg0247836	cg0247836	62778410	AACAATCCAAAACTAATACAA			II	
0.1351225	cg0247902	cg0247902	28787373	TTATCTAATCCCRAATAACAA			II	
0.1040623	cg0247930	cg0247930	73614314	TACTCRAAAATCCTATAATTCT			II	
0.1057028	cg0248032	cg0248032	55675493	CTCAAACCRAATAAAACTAAA			II	
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0.1773434	cg0249194	cg0249194	21602370	AATATTAAAATTACCTCTTTTT			II	
0.1468478	cg0249576	cg0249576	45745344	ACTTTACAAACCAATTAAATA			II	
0.1046141	cg0249930	cg0249930	62710352	TAAAACACTCCCAATAAACCA			II	
0.1024688	cg0249964	cg0249964	72752352	AACATATCTCACCRAAAATAA			II	
0.1943824	cg0250214	cg0250214	13619464	TAAAAAAATCATAACTCACTA			II	
0.1468692	cg0250595	cg0250595	60701359	TACAATCATTATCCATAAACA			II	
0.114093	cg0250672	cg0250672	65732360	TAAACRCRCAATCCAAACAAA			II	
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0.1469981	cg0250718	cg0250718	29708358	AACATATCCCTCRTACTACTA			II	
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0.1052738	cg0251521	cg0251521	57774402	TATTTTTTTATCAAATCCTACC			II	
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-0.236915	cg0252293	cg0252293	29680371	CAATTTAATTCCTTACTACTCT			II	
0.1044444	cg0252423	cg0252423	33677426	AAACCATTCCTACAACCTAAA			II	
0.1045096	cg0252781	cg0252781	41782488	AAAACCTACTAATAACAACCA			II	
0.1016939	cg0253264	cg0253264	46751358	AACAAA	31767336	AACGAA	I	T
-0.144669	cg0253372	cg0253372	37758449	AACATTAAAATAAACAATTAA			II	
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0.1123581	cg0254281	cg0254281	47704302	TAATTAAATATACTTTCTACCA			II	
-0.10837	cg0254877	cg0254877	44637449	RCCTAAAAACCTAAACTTAAC			II	

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0.139241	cg0255073	cg0255073	31707440	TAACACTCTAATACTACTAACT			II	
0.2147764	cg0256417	cg0256417	13637463	TCCTAAA	48691441	TCCTAAA	I	C
0.1037125	cg0256425	cg0256425	66654397	CCCTTCRTCTCTAATAATAACA			II	
-0.103713	cg0256625	cg0256625	72648474	TAAAAATTAAAAACRCTAAAA			II	
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0.1249054	cg0256787	cg0256787	44632442	TTACCACTTACCAATTATACCA			II	
-0.153254	cg0257484	cg0257484	38756423	CAACTAA	17704375	CAACTAA	I	A
-0.152279	cg0257738	cg0257738	31618469	ATTACAA	37668450	ATTACAA	I	C
0.1134661	cg0257870	cg0257870	62603494	RTAAAAAACCCTAATCCAACT			II	
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0.1478904	cg0258449	cg0258449	29652303	AAAATTTTTAAAAACTATTAC			II	
0.1310359	cg0258544	cg0258544	56782510	CTCCCTACATTCTTCTCTAAAA			II	
0.1038032	cg0259008	cg0259008	44686465	ATTTTCTCTCCTCACCAAAAAT			II	
0.1311516	cg0259453	cg0259453	73663496	CCRTAACTACRATATTCCTACT			II	
0.1044782	cg0259833	cg0259833	10689459	ACTTTACCAACTAAAAATAAA			II	
0.100876	cg0259880	cg0259880	51673307	CCCTTAA	71733392	CCCTTAA	I	T
0.1347407	cg0259949	cg0259949	27809452	ACAAAAT	55635418	ACAAAAT	I	C
-0.105201	cg0260302	cg0260302	64671423	AACCTAAAAATTTAACACAAA			II	
0.1533235	cg0260473	cg0260473	51751449	TATACTATTCTAAAAAAACAA			II	
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0.1531951	cg0260656	cg0260656	17781341	CRCAATACATCCTAAAATCRA			II	
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0.1306746	cg0261454	cg0261454	32703318	CAATTTAATATCTTTAATAACR			II	
0.1099087	cg0262033	cg0262033	31791443	CAAAAACRTAATATATCAACC			II	
0.104196	cg0262225	cg0262225	38804348	TAAAACTAAAATAAAAACCAA			II	
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0.1935304	cg0262626	cg0262626	50637301	ACTCCAAAAATAAAAACTACC			II	
0.1106111	cg0262801	cg0262801	59615327	AACAACTCTAATCCAAATATTT			II	
0.1684242	cg0263231	cg0263231	27615380	AACACCACTTCCCCAATCTACA			II	
0.1251816	cg0263303	cg0263303	25763469	ACAACCAAAACCACCAACTCT			II	
0.1691466	cg0264014	cg0264014	44716428	CATAAATACATTCATCTCCCAA			II	
0.125729	cg0264211	cg0264211	40687465	TTCCAAAAACATAACAATATA			II	
0.1744621	cg0264358	cg0264358	26774414	TCATACCAAAACCACATAATA			II	
0.1038051	cg0264906	cg0264906	16701425	CRCRAACCAAACTAACTAAAC			II	
0.1182821	cg0265311	cg0265311	71715378	AAAAACA	60658342	AAAAACC	I	A
0.1036263	cg0265921	cg0265921	18801476	ATCTAAAAACACAACTTCRAA			II	
0.1046268	cg0266064	cg0266064	59607315	TAAACACTATAAAATTTAAAA			II	
0.1101008	cg0266710	cg0266710	35784414	AACAACATATTATTTCTACTTA			II	
-0.108436	cg0267876	cg0267876	14641394	CTCAAAT	39634389	CTCAAAT	I	T

0.1059958	cg0268357	cg0268357	16704484	TTTTCTTCCTCTTTACTATTCT			II	
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0.1058403	cg0269211	cg0269211	29670508	CCATTTATAAAACTATCTCCC			II	
0.2121321	cg0269322	cg0269322	27785423	AATTCACCTACTTAATAATATT			II	
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0.1039536	cg0270010	cg0270010	66802462	TAACACAACTCTAATAACAAA			II	
0.1062003	cg0270102	cg0270102	56803304	ACAAAAACTAACACACACAA			II	
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-0.196184	cg0270324	cg0270324	47632385	ATACAAATACTAACRAAAAAC			II	
0.1206197	cg0270448	cg0270448	17772323	ATCTATAATTAAAACCTCTAA			II	
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-0.116577	cg0271630	cg0271630	64765382	AATTCAAATCTTCCCATTTAA			II	
0.1246171	cg0271649	cg0271649	66661469	CTATTCTATAAAACTTTAAAA			II	
0.1481848	cg02719221	cg02719221	61739485	RTAAAAAAACCCAACCTAAAC			II	
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	cg0272339	cg0272339	12798321	AACTAAC	69766403	GACTAAC	I	C
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-0.181964	cg0273030	cg0273030	18609364	AAAAATAAACATATTCACATA			II	
0.1051166	cg0273086	cg0273086	35730376	AAATTTATCCTTAAATCCCATT			II	
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-0.308957	cg0273542	cg0273542	24708417	AAAATAACACTCATACTTATC			II	
0.1227368	cg0273928	cg0273928	22683502	CTAAAATAATCRTATTCTCTCC			II	
-0.467406	cg0274132	cg0274132	66636431	AAAATCTCATCCTACCCATAA			II	
0.1411423	cg0274363	cg0274363	30668416	CAAAACTAAAATAACCTAAAT			II	
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0.2558808	cg0275293	cg0275293	28722350	TATTTAATTACAACACCTACT			II	
-0.105943	cg0275494	cg0275494	28662413	CAAAATCCRCTCCRTTACATT			II	
0.1397633	cg0275668	cg0275668	49771487	TACTAAATAAACCTAAAAACT			II	
-0.158504	cg0275757	cg0275757	74665399	TCTATCCCAATATCCAAAACA			II	
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0.1593354	cg02768671	cg02768671	37621403	ATCTCTAAACACCTACTATTA			II	
-0.101419	cg0277358	cg0277358	48657414	AATAAAC	17667350	AATAAAC	I	A
0.101615	cg0277665	cg0277665	25789310	AAACCCCAAACRTAAATTAAT			II	
0.1011267	cg0278607	cg0278607	25802510	TTATTTCTCTTAAAATCTTCAC			II	
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0.1003142	cg02790691	cg02790691	44660376	CTACATAACCATTAATTTAAA			II	
0.1799498	cg0279332	cg0279332	74753409	TAATTTTATTCRACAATAAAA			II	
-0.155386	cg0279492	cg0279492	41734374	AAACTTCCCTATATCTAAACC			II	
0.1252159	cg0279647	cg0279647	47728452	CCAAACCTCTAACCTCCAAAC			II	
0.208881	cg0280250	cg0280250	54621330	CATTCACRAAACCCAACTCCA			II	

-0.259826	cg0281143	cg0281143	29749452	ATTTTCCTTAAATTTCCTAATT			II	
0.1640079	cg02812891	cg02812891	35743415	CATTCTA	15771381	CGTTCTA	I	A
0.2729375	cg0281413	cg0281413	45768426	ACTTTAAAAAAAAACCTAAAT			II	
0.2235312	cg0281965	cg0281965	57804497	TTAAACAAAAATCCCAACCTT			II	
0.13069	cg0282041	cg0282041	55667427	CRAAAACTCTAAAACTAATAT			II	
0.1032247	cg0282623	cg0282623	10684376	AAACAAAACACTAACTAAAAT			II	
0.1158566	cg02827061	cg02827061	39741477	CTATACTCTCCTACAAAATAA			II	
0.1990569	cg0283251	cg0283251	17780384	AATAAAATCAACCTCATACAA			II	
0.1788912	cg0283623	cg0283623	29694415	CATAATA	29632381	CGTAATA	I	T
-0.117563	cg0283753	cg0283753	23802370	ACTAAAA	41627337	ACTAAAA	I	A
-0.108036	cg0283982	cg0283982	54743405	ATCCACAATAACCAAATTATT			II	
0.1321547	cg0284334	cg0284334	16645310	AAATCACCCCACCTAAAAATA			II	
0.1328758	cg0284722	cg0284722	32642474	TTATAACCATACTAAAACTAA			II	
0.1190069	cg0284883	cg0284883	71766444	AAAATAAACTCCACTCTACTA			II	
0.1013485	cg0284950	cg0284950	51739320	RTCCTAAACTACACTAAAACC			II	
0.1141773	cg0285490	cg0285490	33789400	CAATAACAAAAAATTCTTACC			II	
-0.179084	cg0285955	cg0285955	61635426	CAACTAC	65725476	CGACTAC	I	T
0.1029043	cg0286117	cg0286117	67749342	CAATCTAACCACCTAACTATA			II	
0.1683063	cg0286463	cg0286463	17648329	TAAACCACRACRCCCRACCAA			II	
-0.10091	cg0287131	cg0287131	14607466	RAAAATTCCCTACCCAAAACR			II	
-0.164983	cg0287276	cg0287276	38641425	AAACTAA	28689384	AAACTAA	I	A
-0.267278	cg0287378	cg0287378	31665328	TTCCTTCCTTTTATCCACATTT			II	
-0.267564	cg02877261	cg02877261	15650309	CAACTCATACTCCCRAAAACA			II	
0.135765	cg0288016	cg0288016	62794434	ATTAAAAATACTCTAAATTAC			II	
-0.11603	cg02884661	cg02884661	36660387	CTCTTAAATCCACTAACTCCA			II	
-0.478987	cg0289023	cg0289023	64667483	AAATCTACTTTCTCATAATCTA			II	
0.2062052	cg0289025	cg0289025	67607477	AAAACAAAATTAACAACTTTC			II	
-0.109127	cg0289036	cg0289036	70618332	ATCCTAA	23673423	ATCCTAA	I	A
-0.131732	cg0289766	cg0289766	28808457	AACRAAAACTATACACATCTA			II	
0.1133614	cg0289815	cg0289815	31806316	TAATAAATTCTAAATCTCTTTC			II	
-0.167703	cg0290152	cg0290152	50743364	ATTCACRCCTAAATTCTCTAAC			II	
0.2292239	cg0290957	cg0290957	57637340	TCCTCACTTAAATCCTTATCCC			II	
-0.184267	cg0291049	cg0291049	48751465	AAAATTTTACAAAATATACTA			II	
0.117399	cg0291409	cg0291409	19613479	CTCATCCTATCRAACTACCCA			II	
-0.111509	cg0291825	cg0291825	74716395	TATCCTT	71640376	TATCCTT	I	A
0.1285881	cg0291908	cg0291908	13612435	AAAATACATAATTAATAAAAT			II	
0.1312152	cg0291956	cg0291956	60730314	AATATCA	13641509	AATATCA	I	A
0.168429	cg0292019	cg0292019	33797315	AAATAATCCTAAACAAAACTC			II	
0.1454855	cg0292273	cg0292273	50807418	TATCATCCCCRAAAAAAAACT			II	
-0.21086	cg02929371	cg02929371	27744394	CAAACCA	65657383	CAAACCC	I	A
-0.148411	cg0293160	cg0293160	27668432	AAAAATAACTAAAAACAAAA			II	
0.1023377	cg0293471	cg0293471	64691421	ACTTAATTTTCCTAATAATCTC			II	
0.1975203	cg0293659	cg0293659	33623322	CAAACTAACAACTATTTAATA			II	

-0.109397	cg0293767	cg0293767	38742373	AAAAATAACAATAATAAACRC			II	
0.1386319	cg0293806	cg0293806	50657379	AACCCAA	15635405	AACCCAA	I	C
-0.119976	cg0294400	cg0294400	46759419	CCAAATA	47701300	CCAAATA	I	T
-0.187258	cg0295171	cg0295171	61754442	CACTAAAACCTAAAAAAACCC			II	
0.1049011	cg0295470	cg0295470	44606340	AAACAACTATTTTAATTTTCRA			II	
0.1123996	cg0296179	cg0296179	42782402	AACCATAAATATACRAATTCC			II	
0.100663	cg0296259	cg0296259	17628444	ACACAATAACAATTTCTAAAA			II	
0.1194775	cg0296438	cg0296438	23729497	TCATTACAAACCACACTCRAA			II	
0.1088794	cg0296529	cg0296529	40706498	ATCAATAATAAATCAAACTAT			II	
0.1549542	cg0296647	cg0296647	62807390	AAAATAACATAAACTAAATCC			II	
0.1129023	cg0296809	cg0296809	57674469	TATCTCCCTAAACAACCTATA			II	
0.1141856	cg0296853	cg0296853	10625360	ATAACTTAAAAAAAACTTAAC			II	
0.220771	cg0297820	cg0297820	39717400	ACAAAAATTTAATAAATATAC			II	
0.1184721	cg0297971	cg0297971	62796426	CAAACCCCRAAAACRATATAT			II	
0.158206	cg0298004	cg0298004	65768429	ATTAACCRTACATAAAAATTA			II	
0.1170481	cg0298309	cg0298309	36689346	AAAAATCTACTCCAACAAAAA			II	
0.1025839	cg0298391	cg0298391	73756507	AAACAAAAAAAAATACAACCT			II	
0.1074318	cg0299206	cg0299206	64607371	AAAATCAAAACATTCTCTAAC			II	
-0.13124	cg0299635	cg0299635	19683374	AAACCAT	42635509	AAACCGT	I	A
-0.131848	cg0299939	cg0299939	74772397	ACTTTCC	25804416	ACTTTCC	I	C
0.1632211	cg0300333	cg0300333	29612384	AACAAA	53756368	AACAAA	I	A
0.1455689	cg0300762	cg0300762	25767405	CACAATA	62797494	CGCGATA	I	T
-0.119991	cg0301432	cg0301432	21794330	TTCAAAA	42801352	TTCAAAA	I	A
-0.195927	cg0301482	cg0301482	51660482	AACATAAATTTAATTTCRAAT			II	
0.120584	cg0301893	cg0301893	19795429	AAAAAC	62677307	AAAAAC	I	A
0.277137	cg0301981	cg0301981	47769345	AAATTCCTACCCCRTAAATCT			II	
-0.107071	cg0302000	cg0302000	44797510	AACATAA	16750437	AACGTAA	I	A
-0.181812	cg0302037	cg0302037	14783428	CTAAATACRTCCCRACRCTAA			II	
0.2794567	cg0302068	cg0302068	71641342	CCTACCACATAATTCTCCTAA			II	
-0.168993	cg0302289	cg0302289	74698328	ACAAAA	19758354	ACAAAA	I	A
-0.141276	cg0302448	cg0302448	39704422	TTTATCTCTTCTTTCCCCTATC			II	
0.1003251	cg0302582	cg0302582	49712375	CCCAACTTTTCCAAATTTTACC			II	
-0.104541	cg0302583	cg0302583	28705352	TAATAAA	36682333	TAATAAA	I	A
0.1009065	cg0302611	cg0302611	66747309	ACTTTTCCCTATAAACATATTA			II	
-0.137426	cg0302878	cg0302878	16691439	CCTAATTCAAAATTAAATCAA			II	
0.195408	cg0303026	cg0303026	43711485	AAAATCCACAATAAACTCTAT			II	
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-0.119123	cg0304042	cg0304042	74732478	AATTATCTACCTAATTAATAAT			II	
-0.146787	cg0304312	cg0304312	74784429	TCCTAAAAACAACTATTTAAA			II	
0.1069099	cg0304428	cg0304428	45628426	ATTACCCTTTCCCRAATCTAAA			II	
-0.110517	cg0304837	cg0304837	36677492	AACAAAT	47662333	AACAAAT	I	C
0.1625182	cg0304848	cg0304848	26676361	AATCAACCTAACTCCCTTACC			II	
0.2557728	cg0304892	cg0304892	34718455	TATAAAAACAAAACCAAAAA			II	

0.1250749	cg03049445	cg03049445	69758346	AAATACCTCTCCCAAAAAACCC			II	
0.112533	cg03052004	cg03052004	67625419	TATAACATTACTTAAAACAAA			II	
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0.2627804	cg03053358	cg03053358	71775473	AAAAAAT	31601472	AAAAAAT	I	C
0.1048968	cg03053980	cg03053980	64799492	TAATACTAATCCCAAAAATACT			II	
0.1016483	cg03058412	cg03058412	44779447	CTAAAAAATCTCTTCAAATCAA			II	
0.1248753	cg03059876	cg03059876	19659320	CTCATTC	64653445	CTCATTC	I	A
0.1907889	cg03062944	cg03062944	33708469	ATCCAAA	57620507	ATCCGAA	I	A
0.1001642	cg03065090	cg03065090	31620397	CCTAAAAACAAAATATACTTTA			II	
0.1662816	cg03069731	cg03069731	58731498	AACTCAACCCAAAAAACAAAA			II	
0.1955584	cg03072082	cg03072082	22794385	ACAAACTACTAAATAAACAAA			II	
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0.2028601	cg03084184	cg03084184	52659317	ACCAAAA	67714456	ACCAAAA	I	A
0.1018695	cg03086707	cg03086707	23709502	TACTCAAAATATAACTACTTAC			II	
0.1532076	cg03088958	cg03088958	65682469	CRACTACTCCAAACRTTTCTAT			II	
	cg03089717	cg03089717	54644378	CRATAAAAACAACATCTTTCTC			II	
0.1512312	cg03097134	cg03097134	20764406	CAACCCATTATCCTAAACRACT			II	
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-0.110428	cg03105556	cg03105556	36725473	AAAACAATCTAACCAATACTTC			II	
-0.115804	cg03108070	cg03108070	69757501	AAACCTA	42616429	AAACCTA	I	A
0.1751854	cg03109913	cg03109913	21688303	AATACTTTCTCAACTACATCCT			II	
-0.103807	cg03112518	cg03112518	69725325	CTCTACCTAAAAAAACRACRA			II	
0.1371512	cg03115532	cg03115532	54616458	TTAAAACACAAAAATCTTTCTC			II	
0.1110295	cg03116016	cg03116016	27631430	AAATTTTCCAAACTCRAAAAA			II	
0.129231	cg03117611	cg03117611	46765327	RAAAATTCCATTTAACRCCCCR			II	
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-0.146941	cg03120461	cg03120461	43717452	CAAAATC	72646479	CGAAATC	I	A
-0.237948	cg03122926	cg03122926	52703317	TTCCTACAAAACCTATCTCCCC			II	
0.1914138	cg03123709	cg03123709	27808379	CAAATCTTAAAAACATATTTTC			II	
0.2030264	cg03126739	cg03126739	72746442	CCTAAACAAAACACTAACTCA			II	
0.1499202	cg03127584	cg03127584	51677413	TCAATACATAAAAACCRTATA			II	
0.1116676	cg03128499	cg03128499	50803403	TTTCTAAAAATATCTCCAAAAC			II	
0.2026655	cg03130910	cg03130910	18723328	ATCAATA	71768350	GTCGATA	I	A
-0.103614	cg03133408	cg03133408	67624445	ACRACTTTCACTACTTACCTAA			II	
0.1145753	cg03135948	cg03135948	16702378	AATAACATTATTACCTTCCAAA			II	
0.18333	cg03136151	cg03136151	72796315	CCCCCTATAAAAAATACATTAC			II	
0.1052591	cg03136493	cg03136493	25795438	ATTTAATAACCAATTCAAACCC			II	
0.1191652	cg03142741	cg03142741	53804372	AAACCAACAACTACTCTAAAT			II	
0.1271183	cg03143591	cg03143591	72635510	CAACTATACTATATATACTTCC			II	
0.1028282	cg03147852	cg03147852	61755437	AAAATAAAATAAAACATAAAA			II	

-0.113284	cg0315250(	cg0315250(	20603307	ACACCAC	30748437	ACACCAC	I	C
0.1360974	cg0315654(	cg0315654(	54620402	TTCTACATATCTCAAAATAAAT			II	
-0.109523	cg0316501<	cg0316501<	37801383	AAAACCC	26609473	AAAACCC	I	C
-0.115643	cg0316517(	cg0316517(	25652440	CTACCCTCCCCCCAAATAAAA			II	
0.1593285	cg0316788:	cg0316788:	40793322	CAAAACAAAAAACACAATAAT			II	
0.2424211	cg0318370(	cg0318370(	27689358	AACAATTATTAAACATTCAAA			II	
0.1198641	cg0318477(	cg0318477(	64615357	AAATCAACAATTCTAAAACAA			II	
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-0.160697	cg0318766{	cg0318766{	65795451	CCCCAAAACTAAATACTTTCTT			II	
-0.120808	cg0318839(	cg0318839(	40618341	CRTAAAAAAAAATACAATACT			II	
-0.101563	cg0318902:	cg0318902:	58780320	AAAATAC	40648391	GAAATAC	I	C
0.1296538	cg0320133'	cg0320133'	64645445	AAAACRTTACTATTAAATCAA			II	
-0.170633	cg0320206(	cg0320206(	22773327	CCCTTTC	65733324	CCCTTTC	I	A
-0.166806	cg0321320:	cg0321320:	71778483	TAAAATT	19757345	TAAAATT	I	C
-0.579331	cg0322139(	cg0322139(	23660495	TCTAATAAACATCTTCCCRAA			II	
0.1145448	cg0322148:	cg0322148:	32772437	TAAAAAATATTTTATCTAAAA			II	
0.1253789	cg0322462'	cg0322462'	65721411	ACTTTATTAAACATAACAATA			II	
-0.129014	cg0322544<	cg0322544<	36697398	AAAAACA	38670430	AAAAACC	I	A
	cg0322903:	cg0322903:	61601301	ACTCCAC	12768448	ACTCCAC	I	C
0.1268796	cg03240981	cg03240981	23786387	TAAAAATTTTTCRTTAAATAA			II	
0.1037835	cg0324647{	cg0324647{	74694436	AAAAAAATCTCTATCTCCTCRC			II	
0.1043654	cg0325433(	cg0325433(	14684453	AATATTACTAACTAAATCCTTC			II	
-0.101834	cg0325609(	cg0325609(	35665324	ACTCTCA	46752368	ACTCTCA	I	T
-0.10668	cg0325668<	cg0325668<	48703475	TTAATAT	55689305	TTAATAT	I	A
0.1089261	cg0325742:	cg0325742:	11697450	AAATTCTAAAAAACRTAATCC			II	
0.1245646	cg0325813(	cg0325813(	25724501	CCAAATAATCACAATACACTT			II	
0.1536596	cg03260621	cg03260621	32632363	TTACCCRTTTTATTATACATTC			II	
0.1260422	cg0326269(	cg0326269(	30772379	AAAACRATAAAAACCACTATA			II	
0.1090722	cg0326319'	cg0326319'	36697485	ACAAAATAACATACTAATTAC			II	
-0.31843	cg0326413:	cg0326413:	34617348	CAAAACC	15745431	CGAAACC	I	C
-0.122693	cg0326455(	cg0326455(	20767486	AAATAAA	68790453	GAATAAA	I	C
0.1073329	cg0326526{	cg0326526{	38785503	AACAAACAAATATTCTTATTC			II	
	cg0326936:	cg0326936:	74623352	TAAAATACCCCCAAAAACATA			II	
0.195676	cg0327148'	cg0327148'	29659310	AACTTAAACACAAACTTTCATC			II	
0.1056114	cg0327190'	cg0327190'	49612398	TAATCRTCACAAACCRTCTAA			II	
0.114281	cg0327249(	cg0327249(	45687351	CATATCCACCATTATAAATACT			II	
0.1199921	cg0327293:	cg0327293:	26785499	CTCTATCCCAATCTCCTATTAA			II	
0.1016877	cg0327688:	cg0327688:	24762468	TTCTTTTTAACCTTATATCTCT			II	
0.2402165	cg0327692(	cg0327692(	38610449	CTCTTCTTTCCACAAATTCTCA			II	
-0.142655	cg0327755(	cg0327755(	15760501	AATTCAC	55775356	AATTCAC	I	A
0.107889	cg0328704(	cg0328704(	24810478	TAAATACAACCTCAAACTTTA			II	
-0.187202	cg0329222:	cg0329222:	48643368	CACTTAC	40807439	CACTTAC	I	A
-0.120542	cg0329320(	cg0329320(	71631447	CTATCAA	10656419	CTATCGA	I	C

0.1071932	cg03293507	cg03293507	65794484	ATCACAA	67747316	ATCGCAA	I	C
0.2790326	cg03296304	cg03296304	43767507	CCAAAAA	53655437	CCGAAAA	I	A
0.1074553	cg03302281	cg03302281	17625478	ATAACCACTTCAAATACTACC			II	
-0.120055	cg03307177	cg03307177	36784509	AATCCCAAAACRAAACCCCCT			II	
-0.131572	cg03307659	cg03307659	29779377	CAAAACC	21661421	CAAAACC	I	T
0.1565622	cg0331240	cg0331240	35720308	TTCCAAACCTATCTATATTACT			II	
0.1685655	cg03312587	cg03312587	12722321	AAAAAAACAATTTCCTATAAT			II	
-0.197443	cg03314029	cg03314029	36773421	CCAAAAA	19738374	CCGAAAA	I	A
0.368719	cg03315469	cg03315469	32760433	AAAATAT	15738422	AAAATAT	I	T
-0.125596	cg03327325	cg03327325	56714412	RACATATATTTACACTAACACA			II	
0.1695981	cg03328299	cg03328299	72790425	CTACTTCTCTAAAAAATCCAA			II	
0.1821062	cg03329597	cg03329597	30766334	ACCACATCCATAAATACTTCA			II	
0.1316228	cg03329714	cg03329714	17746301	RCRACCTTTTAAATCTAACTCC			II	
	cg03333149	cg03333149	61768320	CAACATA	73756355	CGACGTA	I	A
-0.156624	cg03335262	cg03335262	61766455	AAAAACC	67632339	AAAAACC	I	C
-0.167038	cg03337057	cg03337057	69804327	AATCCCC	64785367	AATCCCC	I	T
-0.124516	cg03340754	cg03340754	38784345	AACAAATATTAACCTTTATTTT			II	
0.1759402	cg03341641	cg03341641	41716440	AAAAACATTTACCTAAATAAC			II	
0.1081656	cg03342032	cg03342032	24770426	AATAATTCTAAAATAAAACAA			II	
0.2263712	cg03343571	cg03343571	20631385	CCACTAT	65602498	CCACTAT	I	T
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-0.106128	cg03350138	cg03350138	23625367	AAACRCAACTAACAAACTAAA			II	
0.1048747	cg03355554	cg03355554	44712471	ATACATACAAACACRTACTCT			II	
0.2214614	cg0335461	cg0335461	52704320	CCTACCAATTTCCACCTACACC			II	
0.1289171	cg03356172	cg03356172	47793323	TAAAAAACATCCCCRAAAATC			II	
-0.21427	cg03357999	cg03357999	64655397	AATACCA	63787408	AATACCA	I	A
-0.103634	cg03370193	cg03370193	35655452	AAAACAA	43662303	AAAACAA	I	A
0.1002315	cg0337396	cg0337396	61720304	CACTTAAAACCAAAAATATAA			II	
0.1057502	cg03374148	cg03374148	66647422	AAAAAAATAAAACAATCTATA			II	
-0.117141	cg03378197	cg03378197	63667510	CCTAAAT	24806498	CCTAAAT	I	A
0.2271194	cg03386715	cg03386715	21618356	ATCCACTCACCTTAATCTTAAC			II	
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-0.110645	cg0339210	cg0339210	62733384	CATAAATCAAATTCTACAAACA			II	
-0.144307	cg03398919	cg03398919	41748327	TTTTAACRATATAAATAACRCT			II	
-0.43151	cg03398989	cg03398989	26691355	TTAATCTATAAACTCATATCCR			II	
-0.113562	cg03401875	cg03401875	47738484	AAAAAAATTTTATTTTCCTTT			II	
-0.196098	cg03408135	cg03408135	10759351	RAAAAAATAAAAATCTCTTCT			II	
0.1272988	cg03408497	cg03408497	40659498	AAATTAATAAATAATACCTAC			II	
0.1594328	cg03412618	cg03412618	19668486	ACATATAAACAAACAAACAAA			II	
-0.111877	cg0341813	cg0341813	42620358	CCTCCTT	47803332	CCTCCTT	I	C
-0.292985	cg0342097	cg0342097	59754449	ACAACAATATTTTATACCTTAA			II	
0.1444581	cg03422552	cg03422552	17711503	TAAATATCCTCCCTACTCCTTA			II	
0.3003632	cg03422583	cg03422583	33804439	AAAAATCTTAAATCCAAACAC			II	

0.1141062	cg03422749	cg03422749	46741444	ACTCATCAAAACRCRTAAATTC			II	
-0.131899	cg03428619	cg03428619	66699313	CTTCCCAACACTCTTTAAACCA			II	
0.100167	cg03431028	cg03431028	17719341	TAAAATTTCTTCRTAAAAACTT			II	
0.131126	cg03432172	cg03432172	40652429	TTACTCTTTATAACTTTTTAATA			II	
0.1119694	cg03432241	cg03432241	60770382	TTCACTTAATACTATAACCTTA			II	
-0.221566	cg03432589	cg03432589	39795458	TCTTCATAAAAAACCAATATTT			II	
0.1146758	cg03433313	cg03433313	52731440	CTATATCTATACTCAAAACCTA			II	
0.1280657	cg03434907	cg03434907	68617390	AAATAACRTAAAATCCTAAAA			II	
0.1056923	cg03438552	cg03438552	74622436	ATAAAAA	14758435	ATAAAAA	I	C
0.1444326	cg03441493	cg03441493	23789460	AAACAACRTTTCCTCTAACAAC			II	
-0.132519	cg03441844	cg03441844	29779397	ATAATTTACAAACCTATATACA			II	
-0.10553	cg03443143	cg03443143	44675453	CAACACA	11721413	CAACGCA	I	A
0.1009677	cg03455107	cg03455107	28621319	AAAAAACACAAAATTAACTAT			II	
-0.106522	cg03455316	cg03455316	49799466	AACAAAA	27783425	AACGAAA	I	C
-0.111973	cg03464416	cg03464416	62602353	AAAAAAATACCTATAACCRCTA			II	
0.1104687	cg03466587	cg03466587	37758489	ATCCTTCATCAAATATAATATT			II	
-0.354182	cg03466780	cg03466780	29736451	TATAAAACCTTAACCTCAAACA			II	
0.1074532	cg03467235	cg03467235	14657490	TTTAACATTACCCTCTTACTAC			II	
0.1023381	cg03469682	cg03469682	72709302	ACATAATAACCCTATTTTTACC			II	
0.1831765	cg03469766	cg03469766	40613300	TAAAAATACAAATTCCATCATC			II	
0.1186109	cg03485667	cg03485667	52759305	TTTCCTTCRCTAACTCTACAAA			II	
0.1128491	cg03486379	cg03486379	65799476	ATCTACTAAATAACCAATCCRA			II	
0.1428968	cg03487027	cg03487027	61625442	AAAAATA	24710412	AAAAATA	I	A
0.1024629	cg03487983	cg03487983	13617335	ATTTAATATAACATTCAAAATC			II	
0.1033357	cg03491895	cg03491895	62794477	ACACCACCCACACATTCCTTTC			II	
0.2826955	cg03494612	cg03494612	42732495	ATATAAAAACTACATCTAATAA			II	
0.1904547	cg03495084	cg03495084	65757507	TTTCAAAATATTTTCAAACAAC			II	
-0.101682	cg03498886	cg03498886	42799501	AACCAACAACTAATACCCAAC			II	
0.1270568	cg03507593	cg03507593	51754433	ATATACA	13666340	ATATACA	I	T
0.2512942	cg03509467	cg03509467	58778459	TCTAAACCCATTCCACATATTC			II	
-0.101125	cg03514086	cg03514086	28743489	AATACATTTTTCTTAATCTTTCA			II	
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0.1821169	cg03518729	cg03518729	66687328	CTTCACAAAAATACTATCAAAC			II	
0.1077563	cg03529900	cg03529900	51795445	TCCTTAAAAACCTAACAAAATA			II	
0.1511973	cg03532013	cg03532013	34623394	TTACATTC	57743396	TTACATTC	I	A
-0.172435	cg03534453	cg03534453	41700477	AAAATTTACCTAACAAAAAAC			II	
0.1091565	cg03536885	cg03536885	51663335	ATAAATCACAAAAAAATACTA			II	
-0.111019	cg03543861	cg03543861	52790378	CATAAAT	64740380	CATAAAT	I	A
-0.128342	cg03557725	cg03557725	50699401	TCTAAAATACTAAATACAATTC			II	
-0.18146	cg03562350	cg03562350	17636481	ATAAAAC	55688419	ATAAAAC	I	A
0.113126	cg03563842	cg03563842	54607508	TAAACAA	20655340	TAAACAA	I	C
-0.118556	cg03570263	cg03570263	38765376	ATCCCTAAAAATTAAATACCTC			II	
0.1315862	cg03577157	cg03577157	69605321	AAATCTCCTCATAAAAACCACA			II	

-0.165402	cg03582285	cg03582285	21687304	CTCCTCRCRATAAATCTCCTTA			II	
-0.303716	cg03585888	cg03585888	60646402	CTACRAATCCTAAAATTCAAC			II	
-0.133267	cg03586820	cg03586820	72795423	ATCTCTCAAATTAATTACATTT			II	
0.1022071	cg03592824	cg03592824	40639392	ACATAATCCAAAAACTATTAA			II	
0.1071162	cg03594506	cg03594506	20602395	TCTTTCTAACCRATAAAAAATT			II	
-0.108792	cg03594907	cg03594907	59742309	ATCCAAACTCCTCCCCTTTTTC			II	
-0.236543	cg03595348	cg03595348	65622382	ACTTAAAAACACTTTACRTCA			II	
-0.136072	cg03598159	cg03598159	10604387	TAAAACTCTTCRTAAATTTCTA			II	
0.1032637	cg03599197	cg03599197	19632507	AAATACAAATATTTATTATAA			II	
0.1937188	cg03601053	cg03601053	38759429	CCCTCTACAAAATAAACCTAA			II	
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-0.11138	cg03626579	cg03626579	46612344	AAAACTATATCTAAAAACTAA			II	
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0.1045873	cg03635442	cg03635442	42783481	ACCACTA	43778393	ACCGCTA	I	C
0.1229034	cg03637769	cg03637769	31719455	TTCTTAA	24706345	TTCTTAA	I	T
0.1824871	cg03645522	cg03645522	17765492	TCAAAAA	31614469	TCAAAAA	I	C
	cg03648679	cg03648679	13644314	TACCTAAAATATTAATTTCCRT			II	
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0.1444597	cg03658557	cg03658557	30737368	AACCACAATATATTATATAAC			II	
0.1083739	cg03660901	cg03660901	38787488	AAATAAACATTTATACATTAA			II	
0.1057193	cg03661387	cg03661387	20751449	TCTAAATTATAAAAATCTAAA			II	
0.1476188	cg03664443	cg03664443	24714510	TTTTTAAAACTAAAACCAAAC			II	
0.1019821	cg03668763	cg03668763	17638311	CCAAAAATTATATACACAAAA			II	
0.1559109	cg03672997	cg03672997	21735405	ATATATTCCCAATTCTATATTT			II	
-0.125549	cg03679269	cg03679269	10777355	AATCTAT	18679416	AATCTAT	I	C
-0.101442	cg03682112	cg03682112	69640406	AAAAAAC	46602385	GAAAAAC	I	C
0.132206	cg03682581	cg03682581	10616328	AATACACAAATTATTTCACAA			II	
-0.159415	cg03682719	cg03682719	49754473	AAAACCA	58606305	AAAACCA	I	A
-0.105144	cg03683899	cg03683899	30785408	CCCAAAT	48621402	CCCAAAT	I	C
-0.119971	cg03686964	cg03686964	49768495	AAAAATCCCTAACAACTCCTC			II	
-0.111191	cg03699074	cg03699074	23641470	CRTCCCRTTCACACTAATCRTT			II	
0.2031397	cg03699765	cg03699765	35785392	ACCAAAAAAAAATTAAATCAT			II	
0.1263912	cg03705784	cg03705784	39696395	TATTTACCCAATCATAAACAT			II	
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-0.101738	cg03719428	cg03719428	50610459	RAAAAAAACATTTATACRAAC			II	
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0.1270278	cg03723481	cg03723481	74699400	AAATAAAAAATCAAAAAACTA			II	
0.1380615	cg03725115	cg03725115	63676473	CCACAAT	69618420	CCGCGAT	I	T
0.1068236	cg03736235	cg03736235	36778506	RAAAATAAAATTAAAACTCCA			II	

0.1098846	cg03737424	cg03737424	31720431	ACTATTTCRCTAATCTTTCTCA			II	
-0.150819	cg03739955	cg03739955	62631370	AAACTAACCCAAATAAAAATA			II	
0.163157	cg03743861	cg03743861	47696316	TTCTAAA	18739419	TTCTAAA	I	A
0.1034174	cg03744383	cg03744383	39625318	AAAAAAACTTTTCTAATCTCTC			II	
0.1209428	cg03745491	cg03745491	21769466	CAAAACRACTCTCTAATCCTCA			II	
0.2113697	cg03748376	cg03748376	23756382	AAAACAA	36759456	AAAACAA	I	A
-0.130687	cg03749207	cg03749207	32766445	ACCTAAA	20798314	ACCTAAA	I	T
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0.2425912	cg03754882	cg03754882	45731391	CTCCAATTTCTTTCTTTTATAA			II	
0.1191233	cg03761216	cg03761216	26675439	TCTAAATTATTCTAATATAACC			II	
0.273129	cg03767353	cg03767353	65697342	ACCAAAA	43604403	GCCAAAA	I	A
0.1153349	cg03773862	cg03773862	16713429	CAACTTACTACTTTTTTTCTAC			II	
-0.111473	cg03774803	cg03774803	58629324	CACCCCC	58727362	CGCCCCC	I	A
0.1194589	cg03777875	cg03777875	59709412	ACTTTCTA	27678374	ACTTTCTA	I	T
0.1242207	cg03778207	cg03778207	59698354	TTCCCTTCCTACCAAAAAATAT			II	
0.1616184	cg03781748	cg03781748	23616336	CAACCATAATTTAATCCTCCAT			II	
0.1508775	cg03784363	cg03784363	63810344	TAAAAAA	11686466	TAAAAAA	I	A
0.1006303	cg03784886	cg03784886	72630371	AACACCAAAATAAACCAATTT			II	
-0.124179	cg03790740	cg03790740	38691422	TACRAACACTTATACTACTAAT			II	
0.1303581	cg03796943	cg03796943	60733357	CAACATTTTACTACATTAACAA			II	
-0.100472	cg03798915	cg03798915	12611322	AAAAATC	65706440	AAAAATC	I	C
-0.116246	cg03805357	cg03805357	48606424	AAAAACATATATATATTAACA			II	
0.1592759	cg03808001	cg03808001	51627426	AATAATAAATAATCRACATAC			II	
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0.104859	cg03823901	cg03823901	18676319	TACTTTTCATCCTCCTTACAAA			II	
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0.1085305	cg03834116	cg03834116	73629419	TAAAAAATATATCRTAACATC			II	
0.1057149	cg03836586	cg03836586	25758330	ATCACAACCATCAACTATAAT			II	
0.179414	cg03837313	cg03837313	29653407	AACTTTTAACAAAAAAACRAC			II	
-0.131382	cg03837909	cg03837909	52677414	AAAATTCATCACAAATTAAAA			II	
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0.1469472	cg03847896	cg03847896	47666370	ATCCTACTTCTTACCAACTATA			II	
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0.1589287	cg03861065	cg03861065	37747316	TACTAATATAACAAACTTTTC			II	
0.1428951	cg03867465	cg03867465	20600339	ATAACTT	24667343	ATAACTT	I	A
0.10939	cg03868770	cg03868770	45755499	AAAAAAAATATAACTTAACCC			II	
0.2975057	cg03871140	cg03871140	62706422	ACTCCTC	36772431	ACTCCTC	I	A
-0.179593	cg03873153	cg03873153	20701450	TACCTAAAAAAACTACAACTC			II	
0.1332392	cg03875819	cg03875819	24674469	ACACAACCCCAAAATATAAAA			II	
0.1304347	cg03876548	cg03876548	54735462	AAAAAAAACTTATCTCTATAC			II	
0.1396295	cg03880506	cg03880506	37672364	TACCTTA	17649329	TACCTTA	I	A
0.167325	cg03885343	cg03885343	20804380	TTCCCCAAACAACACAAAATT			II	
0.1056728	cg03886436	cg03886436	44773505	AAACAACTTAACACCAAAAAA			II	
0.1059901	cg03887438	cg03887438	32679333	TTAACTTCCATATTAATACRAA			II	
0.1733462	cg03887721	cg03887721	38655438	TATTTCTATCCCAATAAAAACC			II	
0.1256937	cg03887906	cg03887906	46708323	ATTTACAAAAATTAAAAAACT			II	
0.108072	cg03888553	cg03888553	17680413	TTTCCAAACACCCCTAAAATTT			II	
0.1822681	cg03896685	cg03896685	28760490	AAACTCCTCCTTATATTATTCA			II	
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0.3204426	cg03900028	cg03900028	73681507	CCTCATTATCAAAAATATCCA			II	
-0.225838	cg03905819	cg03905819	35676433	TCCAACTTCCCCCAAAACCAA			II	
0.1098598	cg03910557	cg03910557	41728473	AATTAAAAAAATATTCTTTAA			II	
0.2400472	cg03913278	cg03913278	55660410	AAATTTCCAATAATCTAAAAT			II	
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0.1966367	cg03930097	cg03930097	64626443	TTATTACTTTACTTATTTCAAA			II	
-0.117009	cg03936031	cg03936031	19732471	ACATCTACTAAACTAATATAT			II	
-0.261062	cg03940883	cg03940883	47771340	AAAAACTATATCAATCTAAAA			II	
0.1106792	cg03944375	cg03944375	55626364	AAATAACTCAATAAAACCTAA			II	
-0.103555	cg03945122	cg03945122	34680310	ATTTAAAAAACAACAACAATA			II	
0.1189255	cg03947384	cg03947384	41640303	TTTCCAATAATCATCACAATA			II	
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0.1425952	cg03952520	cg03952520	30712464	ATCTATCAACTCTTCAAAAATT			II	
0.1041095	cg03953626	cg03953626	73703331	ACAAAAA	52738498	GCAAAAA	I	A
0.1439429	cg03957898	cg03957898	65681454	TTCCTCTCTTCCTAACAACACT			II	
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-0.37532	cg03964373	cg03964373	12623394	TAAAATTCTCCTATTAACTTTA			II	
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0.1047816	cg03967448	cg03967448	17763502	CATACAACTCCTAATACAAAA			II	
0.2000227	cg03970567	cg03970567	30702313	CTTTCAAATAAAACTTCAATTA			II	
0.1313922	cg03970900	cg03970900	29755467	CAAACTAAAAAAATCCCTAAA			II	
0.1499503	cg03977174	cg03977174	60708333	TTAACTCATTTACATAATTCAT			II	
0.1901558	cg03977831	cg03977831	65797345	TCTAAAA	71688451	TCTAAAA	I	C
-0.132176	cg03978067	cg03978067	49650305	AAAACACCCTAACCCAATAAC			II	
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0.1054346	cg03982831	cg03982831	47650436	CTTTAAA	40804378	CTTTAAA	I	A
0.1163319	cg03987818	cg03987818	51643436	TCTTAAAATACATATCTAACCA			II	
0.2227079	cg03988092	cg03988092	13710427	ACACTTTACTACTTAAAAATTC			II	
0.101092	cg03989520	cg03989520	49681350	ATAAAAATTATATTTAACCTCT			II	
0.2658098	cg03989711	cg03989711	33807483	TAAACTA	71810430	TAAACTA	I	A
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0.1981881	cg03999583	cg03999583	28696355	CTATACT	30670361	CTATACT	I	C
0.1203315	cg04001071	cg04001071	19737355	TCAAACTCCTATCATTACACA			II	
0.1472143	cg04004561	cg04004561	11720499	ATTCTATAATATTACCTTCAAT			II	
0.1071909	cg04010296	cg04010296	12795452	CACAACAATAAACAAATATAA			II	
0.2311059	cg04026937	cg04026937	41732346	AAAAAATCAAAAAACTACTCA			II	
0.1273535	cg04028570	cg04028570	24670475	ACCCAAA	10773329	ACCCGAA	I	C
0.1599874	cg04028695	cg04028695	31763342	CTCCCTATTATCAAAAATTTA			II	
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0.1969257	cg04045544	cg04045544	41600309	CTAACCAATAATACACAATAA			II	
0.5076566	cg04049719	cg04049719	47707333	TTTAAACCACCTCTTAACTATC			II	
-0.142072	cg04050824	cg04050824	65726481	ATAAACA	42808445	ATAAACA	I	C
-0.130601	cg04052466	cg04052466	15726311	TTCCACA	30744315	TTCCGCG	I	A
0.1707245	cg04054303	cg04054303	50614476	CCTTCCTTCCTTCCTTCCTCRCT			II	
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0.2210455	cg04061372	cg04061372	42790393	CRAACCAAAAACTTCTCAAAA			II	
0.1435453	cg04064998	cg04064998	44739322	ATTACAACAATAACTAAACTA			II	
	cg04071689	cg04071689	13644319	AACAACT	44696344	AACGACT	I	C
-0.317611	cg04072301	cg04072301	34790439	AAACACC	17704395	AAACGCC	I	C
-0.149213	cg04074536	cg04074536	22685497	ACAACCA	26702345	ACAACCA	I	C
0.1021407	cg04076044	cg04076044	25793345	TAAATATTTCRTTTAACATAAA			II	
0.112826	cg04077979	cg04077979	22760414	TTAAAATACCCAATTAATCTCT			II	
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0.129665	cg04084354	cg04084354	19803510	TCACTTCCCTCTAAATCTTACA			II	
0.100532	cg04088474	cg04088474	55790411	TATATAATAATACTTAACACAT			II	
-0.133122	cg04089743	cg04089743	63791383	CTACACAAAAAAACCATTATA			II	
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0.1185429	cg04093633	cg04093633	50690440	TTCTCCTAACCAAATCTATCCT			II	
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0.1199492	cg04102894	cg04102894	65796411	AAAAACT	51770392	AAAAACT	I	A
0.1033683	cg04103251	cg04103251	70694425	CCATTCCTAATTCTCTAAACCR			II	
0.1189518	cg04105416	cg04105416	62734499	CAAATAA	36735379	CAAATAA	I	C
0.1022803	cg04116469	cg04116469	16629405	TAACTTAATACAAAAACCCAA			II	
0.4050458	cg04118610	cg04118610	24633384	CTAAAAATTATTAATCRCTACC			II	
0.1320177	cg04130557	cg04130557	60630321	TCCAAACCAACRACTAAAATTA			II	
-0.71073	cg04131969	cg04131969	65713421	CACTCCCCCAAACACACACAA			II	
-0.149763	cg04132418	cg04132418	10725414	TCATAAAAAAACTCCCTAACTA			II	
0.1090492	cg04137323	cg04137323	38671432	ATAAAAAATCRTATATATATAA			II	
0.1155843	cg04138046	cg04138046	28701482	CTATAAACCACAATTATTATCT			II	
0.2004181	cg04141080	cg04141080	48617498	AAAATAA	10741347	AAAATAA	I	A
0.1277693	cg04143348	cg04143348	20794319	TTATAATACTTCACTTAAAAAT			II	
0.1064088	cg04143592	cg04143592	62748360	CCCTCCAAACATTTAAAATCTA			II	
-0.236443	cg04145539	cg04145539	29613448	AAAACTAAAATAAATTCCCRTA			II	
-0.471971	cg04145681	cg04145681	64786405	CAAAATCAAACAAATTATTAA			II	
0.1140835	cg04148163	cg04148163	72691505	CATTTAATTTAAAACACTCACT			II	
-0.13657	cg04152793	cg04152793	69793334	AACTCAACTTCACTAACCCCAC			II	
0.2265601	cg04154653	cg04154653	26748302	TATAAAT	31658404	TATAAAT	I	C
-0.10485	cg04155289	cg04155289	66691464	AAAACTAATAATTCCTAAAAA			II	
0.2093343	cg04157272	cg04157272	37726509	CAAACTA	40626453	CAAACTA	I	A
0.1313851	cg04163391	cg04163391	32771384	AATATAA	44700368	AATATAA	I	A
0.2513441	cg04168479	cg04168479	67712315	TACCCACCCAATTAATCAATAT			II	
0.1877331	cg04169747	cg04169747	29742458	CRAAACTTATTTTACTATCCAA			II	
0.1896449	cg04172345	cg04172345	19607404	ACCAACATAATAAAAACTCCA			II	
0.312974	cg04176452	cg04176452	28673491	CAAAAAA	69744457	CGAAAAA	I	T
-0.237679	cg04178011	cg04178011	73754376	ATCCTCCTCTATATACAAATAA			II	
0.1011594	cg04180046	cg04180046	54600475	TAAATCCRACTAAACTAAAATA			II	
	cg04180623	cg04180623	55606429	CCATCAAACATAAAAAAACCA			II	
0.1121325	cg04187039	cg04187039	20735354	TAATAAAAATTTAATAAAACC			II	
0.1213368	cg04188920	cg04188920	22781319	CAACCTC	14717364	CGACCTC	I	A
0.2136872	cg04189187	cg04189187	55635408	CCAACAA	34753355	CCGACAA	I	A
0.1056374	cg04192412	cg04192412	49720372	CTCCAAAAACATATTACAAAA			II	
0.1507027	cg04193779	cg04193779	29756474	AACTACCCCATATATTTACTAA			II	
0.1043339	cg04195941	cg04195941	33747415	CTTCATATCCCTCCTCATCCCT			II	
0.1090618	cg04200010	cg04200010	11606507	ACTTTAATTTATAATCTACCAA			II	
0.1215195	cg04205653	cg04205653	23688303	TAATACATAAATTCAATACCTA			II	
-0.108865	cg04206342	cg04206342	10679419	AAACCTA	52733447	AAACCTA	I	A

-0.156916	cg0420991	cg0420991	14635360	TAACCTA	48705467	TAACCTA	I	A
0.2375593	cg0421493	cg0421493	58754429	ATAAATA	17690433	ATAAATA	I	C
0.1067098	cg0421528	cg0421528	29723399	CTAAAAAAACCTTCTTAAATC			II	
0.1170361	cg0421717	cg0421717	48747345	ACCTCCRACAATTTACTTTAA			II	
-0.130819	cg0422578	cg0422578	63641301	CAAACTC	36627303	CGAACTC	I	C
0.1177901	cg0422611	cg0422611	21633351	TCCTTTAACCTCTTAACAAAA			II	
0.1037952	cg0423104	cg0423104	42740411	CRAATTCAACTTAAAAACTAC			II	
0.1328654	cg0423167	cg0423167	26740419	TTATTTTATTTCATCAATAAAC			II	
0.1026894	cg0423362	cg0423362	54649330	TTCRTAATAAATCACATAACC			II	
0.1181438	cg0423791	cg0423791	54624473	TCCTAACATTCCTATCTAAAA			II	
0.1007476	cg0424265	cg0424265	43759422	TCTCCTACCACAAACTATAAT			II	
0.1066114	cg0424554	cg0424554	41682325	TCAAATTAAATTATTTCTAAA			II	
-0.192484	cg0424587	cg0424587	55739300	CATATAAAAAACACRTTCCCR			II	
0.1033209	cg0424670	cg0424670	15809316	TTTACTCTAACACTAAACACA			II	
0.1644681	cg0425120	cg0425120	12723403	TAACCATAAAAAACCCAAATC			II	
-0.128993	cg0425686	cg0425686	49672435	AAACTCC	57665313	AAACTCC	I	C
0.1010769	cg0425813	cg0425813	29610361	AACTAACTCAAATAATACAAA			II	
0.1045238	cg0425867	cg0425867	64664362	ATAAAACTCTTACCATACRAT			II	
-0.12172	cg0426443	cg0426443	55714325	TTTATAATACTTCTTTACACCR			II	
-0.142344	cg0426777	cg0426777	19708438	CCCAATAACCCCAATAAAAAC			II	
0.1341313	cg0427569	cg0427569	25630462	ACTACCCTCACRAAAAATTTA			II	
0.133251	cg0427662	cg0427662	65695394	AAAACAAAAACAAACCAAAA			II	
-0.104984	cg0427705	cg0427705	63702454	AAATCACAAACTCCCAACTAT			II	
-0.102513	cg0427816	cg0427816	65795333	ACCACTAAAACATCAAAAACR			II	
0.1242334	cg0427941	cg0427941	10740331	TTTACTCAAAAAAAACCCCAT			II	
-0.103917	cg0428414	cg0428414	66658300	AACTTAAAAAACAAACCCAAA			II	
	cg0428547	cg0428547	63703394	TACAATT	54606510	TACGATT	I	A
0.1365514	cg0428673	cg0428673	54677371	ACAATCC	57724403	ACAATCC	I	C
0.1056836	cg0429140	cg0429140	54610397	TTTAAAATTTCTTTCCCAAAAC			II	
0.1022505	cg0429297	cg0429297	57794473	TAAAAAACAAAACTATATAAT			II	
0.1048584	cg0429740	cg0429740	22686369	TTAACACRCCTATTTAAACAA			II	
-0.158624	cg0429766	cg0429766	53709380	CCAAAATATTCCTTCRCTAAA			II	
0.1045879	cg0429799	cg0429799	36722316	CACAACAATATACCACAAACC			II	
-0.131495	cg0430134	cg0430134	31784487	AACAACT	18629332	AACAACT	I	C
0.1250767	cg0430648	cg0430648	20604407	RAATTAACTTAACCTTACCCA			II	
0.1021877	cg0430808	cg0430808	23717416	CTTTACAATATCRCCTATAATT			II	
0.1430028	cg0431436	cg0431436	48680374	TCCACTTCATAACCTTCATCCA			II	
-0.181894	cg0431653	cg0431653	27713329	TTTAAACACCTATCAAATAAC			II	
0.1154459	cg0431832	cg0431832	48628377	TTCTTTTATTCAAATAACCCTA			II	
0.1246469	cg0432938	cg0432938	59712409	ACTAAAAAAAACTCTAACTAA			II	
0.3622797	cg0433156	cg0433156	34804418	ACCCAAAACTTAAAAAATATA			II	
0.1297101	cg0433292	cg0433292	31677454	AATTCTTATATCTACTTTTATA			II	
-0.119298	cg0434248	cg0434248	51793470	TACTTCCCACAATCAAACATA			II	

0.1275096	cg0434419	cg0434419	24707481	AAATTAAAAATATTAAACAAC			II	
0.1466271	cg0434533	cg0434533	62676500	CAAATCAATTTCCCCTCCTTTC			II	
0.1757641	cg0434628	cg0434628	57650456	AATACCAACTTTAACAATTAC			II	
0.1511904	cg0434998	cg0434998	14680348	CAAAAAAACTAACTAACCAAC			II	
0.1100021	cg0435021	cg0435021	20649484	AACCTCACTATAAAATCCTAT			II	
-0.154963	cg0435467	cg0435467	50762343	CTTATAC	12708313	CTTATAC	I	A
0.1071963	cg0436607	cg0436607	64714487	CAAATTCAATCTACRACRCCC			II	
-0.114675	cg0438264	cg0438264	63775343	CTACTAA	41620489	CTACTAA	I	A
0.1005361	cg0438468	cg0438468	58699305	ACCCTAAATCATAAAAACTCA			II	
0.119967	cg0438675	cg0438675	30780483	ATCCCAA	12632309	ATCCCAA	I	A
0.112162	cg0438739	cg0438739	74728348	CAACAAAACCAAACAACCATT			II	
0.1460888	cg0439229	cg0439229	29727438	AAAAAC	31669319	AAAAAC	I	T
-0.109673	cg0439845	cg0439845	31692348	AAAAAC	53722489	AAAAAC	I	A
0.1844553	cg0440678	cg0440678	23738383	CACTATCAAAACCRTAACTTT			II	
0.1258611	cg0441611	cg0441611	47656320	TCTACTCCCTAAAAACTAACT			II	
0.114294	cg0442086	cg0442086	39624466	ATAAAACTTTCATACCCAATA			II	
0.121749	cg0443699	cg0443699	50606366	TTAAAAT	10676470	TTAAAAT	I	A
0.1235943	cg0444736	cg0444736	37705438	ATTTCAAAACTAAATAACAAA			II	
-0.119828	cg0445312	cg0445312	70784496	ATATATA	64778315	GTATATA	I	A
-0.489164	cg0445649	cg0445649	42668379	ATATACTCATTACTACTCCTAA			II	
0.1054588	cg0445892	cg0445892	46692322	ATATCAA	31679409	ATATCAA	I	T
0.1061156	cg0446114	cg0446114	74779469	TCCRAAATCACAACAAAAACT			II	
0.2466198	cg0446452	cg0446452	17674305	AAACCATTCTAACTTCAACAT			II	
-0.131619	cg0446763	cg0446763	63703470	TAAACCTCCCTATTCTATTCCC			II	
0.1233454	cg0446874	cg0446874	24733338	TAAACRCTCACAAAACCCAAA			II	
0.1170868	cg0447005	cg0447005	46713489	CCTAAAT	71707481	CCTAAAT	I	T
0.1290224	cg0447340	cg0447340	37756496	TTTATAACCCCCAAATTATCCC			II	
0.1251318	cg0447365	cg0447365	34713510	AACTATTATTACATATCCTATA			II	
-0.100423	cg0447498	cg0447498	21737403	AACATCA	67710393	AACGTCG	I	A
-0.118548	cg0447818	cg0447818	67706389	TCTAAAATAACAAACRAAATA			II	
-0.172628	cg0448107	cg0448107	24728365	ACAAAA	73620326	ACAAAA	I	A
-0.160744	cg0448192	cg0448192	52700462	AAATAACAAATTATACCRAAT			II	
0.1021487	cg0448398	cg0448398	51717475	TTCTCTAAACCTCTATAAAAA			II	
0.3423056	cg0448683	cg0448683	61780346	ATATTTCTAAACCTCAACTAA			II	
0.2125331	cg0449761	cg0449761	64633508	ATAACCCTTAAAAAATATAAA			II	
-0.223075	cg0449782	cg0449782	17807329	ATTCAATAAACAAAAATTTAA			II	
0.100446	cg0449970	cg0449970	50767325	TATTATTAACTTAAATATATAA			II	
0.1015942	cg0450090	cg0450090	59763439	TTCTACTAACTTCTAAATTAAC			II	
0.1029728	cg0450611	cg0450611	60742376	ACTACAACCCACATTTTTAAA			II	
-0.145431	cg0450846	cg0450846	12601343	CRCCCTTTTTCTTCCAAAAAAA			II	
-0.242568	cg0450860	cg0450860	60779380	TTTCCTATAAAAACAACAATC			II	
0.1481144	cg0450887	cg0450887	13685312	CAAAACCACATATCTACTCCA			II	
0.105321	cg0450954	cg0450954	20802351	TTCAATCTAATAACTCAACAC			II	

-0.101068	cg04518186	cg04518186	24810402	ACCTCTTCCATCTACTTTAAAA			II	
0.1090662	cg04520251	cg04520251	25723405	AACACAATCCACCTATAAACA			II	
-0.108598	cg04527018	cg04527018	59694500	ACCACTA	61646402	GCCGCTA	I	C
0.1094011	cg04540882	cg04540882	55660423	AAACCACAACTAACTCTACCA			II	
-0.135045	cg04546413	cg04546413	27692361	AAACAAA	48797310	AAACAAA	I	T
0.1186059	cg04547675	cg04547675	56639317	CCTTAAC	60731417	CCTTAAC	I	A
0.1112536	cg04551500	cg04551500	35639474	CTATATACTTATACRTAACTAA			II	
0.1783472	cg04556550	cg04556550	30700461	AACAACTTAAATAACTAAACA			II	
0.200849	cg04559508	cg04559508	67748477	TAAAAACTACACTACAAAACA			II	
0.1166713	cg04565201	cg04565201	26796328	CAATCCAACTTTATTTATTTTT			II	
-0.15425	cg04565337	cg04565337	16658336	CCTACCTCCTCTTCTAAACTAC			II	
0.2799587	cg04566473	cg04566473	27702400	AAAATCAAATCRTCCTATTACT			II	
-0.112646	cg04570208	cg04570208	20621488	CTCTATAAATTAACRCTACTAC			II	
-0.128393	cg04571847	cg04571847	47714450	TAAACAA	67730454	TAAACAA	I	C
0.1348925	cg04573316	cg04573316	43739323	CTTTCTATTTATTTTCTCTTAA			II	
0.1361971	cg04576607	cg04576607	51641403	TAAAAATCACAATAACACAAA			II	
0.1323446	cg04577451	cg04577451	72658302	AATTTTAAAAAACAACTCAAC			II	
-0.108759	cg04579398	cg04579398	69669504	CCATCAA	19709324	CCGTCAA	I	T
-0.176432	cg04580344	cg04580344	25651423	ATATTAAACATAAACACRCRA			II	
-0.12956	cg04581018	cg04581018	13632488	AACTAAACRAAATCCCAATTA			II	
0.108402	cg04587220	cg04587220	28773426	ACACATA	49617473	ACGCGTA	I	A
	cg04600795	cg04600795	12768416	TTAATACRACCRAAAATAATA			II	
0.2088451	cg04609971	cg04609971	51746418	AAATTTTTAATAAATTATAATC			II	
0.1765318	cg04610742	cg04610742	73737474	TACTCCTTTAAATCCAAATACA			II	
0.1120927	cg04610897	cg04610897	33741308	TATCCRAATCACTTAAAAAAC			II	
0.1942991	cg04613452	cg04613452	46669321	CTCTAATATTCCCCATCTCACC			II	
0.4747696	cg04613734	cg04613734	53697417	ACCACACATAAACAAAAACAC			II	
0.1152922	cg04614339	cg04614339	58717451	ATTTTTAACCTTTATTCCCTCA			II	
0.1244565	cg04619882	cg04619882	26668420	ACTTAAACTTTAACCTAACACA			II	
-0.208264	cg04628741	cg04628741	36639383	CTTAATATCCCCAACACCACC			II	
0.1258791	cg04628742	cg04628742	62642490	TAAACAAACCCACTTAAAATA			II	
0.1722574	cg04633676	cg04633676	32794308	AAAAAAATCTAAAACACAACT			II	
0.1612622	cg04637727	cg04637727	26709488	CCAAACTATCCCTCTTAAATA			II	
0.1174977	cg04638710	cg04638710	51654333	ATATAAATCATACCATATAAA			II	
0.1920328	cg04645070	cg04645070	31737440	ATTTACTAAAACAACCATAAC			II	
-0.206753	cg04645150	cg04645150	66707449	AACCAAA	64668343	AACCGAA	I	A
-0.106246	cg04645914	cg04645914	26762316	AATTTACRCAATAACTAAAAT			II	
0.1300156	cg04646674	cg04646674	17674322	AAACTAACAAACCTCTATAAA			II	
0.15958	cg04646987	cg04646987	38752364	CTTATCA	20800510	CTTATCG	I	T
-0.117278	cg04647918	cg04647918	34703440	ATAAAATAAAAAAACATCRCT			II	
0.1455866	cg04649587	cg04649587	28701345	AACAACTCTAATTTACTCTCAA			II	
0.1153109	cg04650676	cg04650676	19801302	CCACACA	12656422	CCACACA	I	A
0.173261	cg04654299	cg04654299	26694475	AAAACATCAAACTTAAAAAAT			II	

0.1113288	cg04656015	cg04656015	48755337	AAAACAAAAAATTAAAACCCA			II	
0.1924902	cg04657470	cg04657470	40674393	TACAAAT	71674460	TACGAAT	I	A
0.1094049	cg04674421	cg04674421	29671443	ATTCCAAAATCATAAAAATTCA			II	
0.1308595	cg04680738	cg04680738	32758383	TCCRCATACTAACATCTATAAA			II	
-0.11316	cg04683035	cg04683035	38634378	ACRAAAACCACATACTATAAT			II	
0.1875597	cg04683516	cg04683516	51686418	AAAAAAACTTAAATTTTACRTA			II	
0.1167014	cg04686117	cg04686117	58738369	TACCATACACCTTCATTCTAAA			II	
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0.107507	cg04689178	cg04689178	65787344	AAACATTTAAAAATAACCAAA			II	
0.1780032	cg04689606	cg04689606	53746496	AACAAAC	74787350	GACAAAC	I	A
-0.110049	cg04689676	cg04689676	52679475	ACTAAAT	38638386	ACTAAAT	I	C
0.1170023	cg04690342	cg04690342	22674468	TCTTTTAACAAAACTAAAAACT			II	
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-0.159669	cg04717802	cg04717802	70612470	TAATAAA	43628375	TAATAAA	I	C
0.1098564	cg04721775	cg04721775	71733492	TTTTAACT	40773328	TTTTAACT	I	A
0.1123685	cg04722610	cg04722610	69631444	CAAATATAATACTACAACACA			II	
0.1140116	cg04723343	cg04723343	56759391	ACCAACT	73789489	ACCGACT	I	C
0.2161292	cg04724556	cg04724556	51798439	CATACCAAATAACAAAAAACT			II	
-0.147038	cg04727458	cg04727458	15647330	ACTCTAAACCACTTCATTTAAT			II	
0.1017349	cg04738028	cg04738028	50687365	CCTATAATCTAACTCTCACTAT			II	
0.1472693	cg04741094	cg04741094	34664418	AAATTCCCTCTAACTATATAAT			II	
0.1384249	cg04741728	cg04741728	29673307	AAAAAAT	55646402	AAAAAAT	I	A
-0.112251	cg04742556	cg04742556	38787419	RACATAATAAACAAATCCCRC			II	
-0.215367	cg04748098	cg04748098	67770356	AACTCAT	59728417	AACTCAT	I	C
0.1400592	cg04750517	cg04750517	12704357	AATCCTATAAAAAACTACAAT			II	
-0.104178	cg04755386	cg04755386	67777468	AAAAATCACATAAACCAATAA			II	
0.126453	cg04762129	cg04762129	59633472	TACATCCAAAACCCAAACCAA			II	
0.1443034	cg04762351	cg04762351	33726399	AAATACAATTATTCCAAACCTT			II	
-0.140483	cg04764476	cg04764476	23729413	TATTTCA	48630353	TATTTCG	I	A
0.1153069	cg04768488	cg04768488	11726510	TAAAACRCTAATCACTCTACAA			II	
0.1100194	cg04775631	cg04775631	63713495	CATTTAATTATCTAATATAAAA			II	
0.2263358	cg04777551	cg04777551	51795368	AATAATAAAAATACCCTAAAA			II	
0.1064841	cg04785902	cg04785902	13637343	TCTTATCTTACTAATATTATCCT			II	
0.1086075	cg04786142	cg04786142	21802497	ACTAAAA	69752328	ACTAAAA	I	A
0.3759203	cg04787784	cg04787784	17610381	CCACAAACRACCCCTCAAACT			II	
-0.101518	cg04789475	cg04789475	59774428	AATTAAA	65809342	AATTAAA	I	A
-0.14994	cg04791718	cg04791718	43680426	ATCTATTAAACRAAAATTCTAA			II	
-0.176894	cg04798314	cg04798314	22669441	AATAAATATCTTAAATTAACTA			II	
-0.117843	cg04799210	cg04799210	33704489	CAAACTA	58709466	CGAACTA	I	C
0.2156831	cg04801779	cg04801779	70767489	AATAACT	28790376	AATAACT	I	T

0.1436272	cg0481074	cg0481074	71757363	TAAAAAAAATAAATTCCTAAT			II	
-0.359802	cg0481478	cg0481478	23715415	AACCACTACACCCRACCATAA			II	
-0.109218	cg0481617	cg0481617	52656395	CTTTACCTACAAACCATTATTA			II	
0.1042491	cg0481859	cg0481859	10772349	AACCAACTAACATTTAATACA			II	
0.3177392	cg0481949	cg0481949	65742498	CAAAATA	50659359	CGAAATA	I	C
0.1312549	cg0482329	cg0482329	27605338	CAACAAATTAATAAAATACAC			II	
0.1199241	cg0482446	cg0482446	60670408	CCCCTCTACCTTATTTCATACT			II	
0.1084559	cg0482455	cg0482455	35717372	ACCAACTATAACAACTTAACC			II	
-0.216784	cg0483095	cg0483095	62753323	CACCCCCAACTCAATAAACCT			II	
0.201708	cg0483224	cg0483224	74756468	AAAATAACCTAATACTCCTAA			II	
0.1175054	cg0483565	cg0483565	11793330	AACACTCTAAAACTCCTTCCT			II	
-0.21241	cg0483685	cg0483685	42810329	AAACTACTCAAACTCAAAAAC			II	
0.1381626	cg0484016	cg0484016	21717353	TATACCC	40702418	TATACCC	I	A
-0.122836	cg0484306	cg0484306	14661409	ACTAAAA	53617378	GCTAAAA	I	A
0.1521847	cg0484355	cg0484355	11792390	TTTCTAAATAACTTACATCRAA			II	
0.1584561	cg0484356	cg0484356	20664453	TCRAATACACAAATCACTCCA			II	
-0.172708	cg0484382	cg0484382	65737502	AACAATTACAATTTTTACCAT			II	
0.1049843	cg0484403	cg0484403	71684466	TACCCTCTTATATATAACCTAA			II	
0.2529703	cg0485014	cg0485014	49780437	TACCTAACCATAATCCATATA			II	
0.1290499	cg0485028	cg0485028	40677367	ACACCCTAAATAATAACCATA			II	
-0.120543	cg0485239	cg0485239	66716355	AATCTAAACTAAATTTCATAT			II	
-0.101041	cg0486043	cg0486043	47788359	AATCTAAATATAATTCTCTCCT			II	
-0.209451	cg0486419	cg0486419	64737453	CTAAAATAACCRCCATCTAAA			II	
0.3512255	cg0487570	cg0487570	64738345	AAACCRTTTTTAAATCCCATCC			II	
0.1251799	cg0487815	cg0487815	11640487	CAATCTCAAAATAATTAAACC			II	
-0.186162	cg0488009	cg0488009	72782399	AAATAAC	30807398	AAATAAC	I	A
-0.14126	cg0488506	cg0488506	37672455	CAAACTA	19804385	CGAACTA	I	T
0.1144918	cg0488534	cg0488534	33675510	CAATCTATAAATAATTAACAT			II	
0.1733555	cg0489060	cg0489060	31650394	AAACCCA	33631300	AAACCCC	I	A
0.2286561	cg0489157	cg0489157	71749414	ATCTAATATTTTTCCRTAAATT			II	
0.1555071	cg0489264	cg0489264	44686303	AACCACACTAATAATTTCCCA			II	
0.1589648	cg0489276	cg0489276	32609356	AAATAAACAAATTAAAATTAA			II	
-0.211237	cg0490018	cg0490018	51623431	CAACATAAATATTCAATCAAC			II	
-0.132756	cg0490456	cg0490456	46702384	CATTAAT	28655481	CGTTAAT	I	T
0.1203514	cg0490784	cg0490784	38628462	AAACCAAACCAACAATAATAC			II	
0.1138681	cg0490807	cg0490807	59694326	CTCCCTTTACAATTTTTCTCAA			II	
-0.106567	cg0490862	cg0490862	39653503	CTCAATA	65636462	CTCGATA	I	A
0.1052226	cg0491422	cg0491422	39603336	AAAACTATAATCCTAACCTTT			II	
0.1503927	cg0492638	cg0492638	55636431	AAAATTAAATAATAATAATAT			II	
0.1298669	cg0493069	cg0493069	57798484	CCCAAATATAAAACTAAACTA			II	
0.1288934	cg0493510	cg0493510	52753423	AATATCACCAAAACCTCCATC			II	
0.1221807	cg0494485	cg0494485	11722332	CTCAACRCTACAACCCAAAAA			II	
0.1257482	cg0494755	cg0494755	58797382	AAAATACATAAAAAATACTTA			II	

-0.147968	cg0494768	cg0494768	52674493	TCAAAAT	40797436	TCGAAAT	I		T
	cg0495511	cg0495511	55807479	AAAAAA	32768451	AAAAAA	I		A
0.1113398	cg0495790	cg0495790	23701353	ACCAACAAAAAAACCTAACTA			II		
0.1345447	cg0496166	cg0496166	43701398	CRTAAAACAAATAATACCCCT			II		
0.1103942	cg0496369	cg0496369	39699304	TTACCTATCATAACAAACAAA			II		
0.1683867	cg0496980	cg0496980	31745472	AAATTAAACAACCTCCTCTAA			II		
0.1055207	cg0497028	cg0497028	42628435	ACAACRAAAATATTTATAACC			II		
0.1215911	cg0498632	cg0498632	10608343	ATATATCTATACRTATCCRTAT			II		
-0.166239	cg0499037	cg0499037	57701483	AAACAACCCCAAATATACAAC			II		
0.1172676	cg0499327	cg0499327	49795447	TAACCAAAACCAATAAATCTA			II		
0.1568935	cg0499360	cg0499360	40755441	ACTATAAAACTATTCTATATA			II		
-0.108765	cg0499531	cg0499531	61765307	TACAATC	60715439	TACAATC	I		A
0.1494396	cg0499832	cg0499832	66624499	TATAAACCTCATAACTCCCTC			II		
-0.123346	cg0500193	cg0500193	58718381	ACCTAAAACCTCTTATTAAAT			II		
0.176515	cg0500507	cg0500507	68653306	TAATCCCACTAACTTACTTTAC			II		
0.1345117	cg0500538	cg0500538	43602318	TTAACAT	35604442	TTAACGT	I		T
-0.152566	cg0500623	cg0500623	29722314	AAAAACT	32626329	AAAAACT	I		A
0.1249706	cg0500882	cg0500882	29686412	CTTCCAATAAAACCAATAAAA			II		
0.1239067	cg0501064	cg0501064	62808422	CTATCATTTTATTCTCACCTCT			II		
-0.159243	cg0501472	cg0501472	35803400	AAATATA	11650317	AAATATA	I		A
0.2833083	cg0502319	cg0502319	73670346	TTTTAACAAAAAACAATTCTT			II		
0.1212705	cg0503284	cg0503284	40772427	TTAAAACAATCAATAAACTAC			II		
0.1131561	cg0503323	cg0503323	56793502	CTTTTTCTTTCATATTTCTAAA			II		
0.1005955	cg0503336	cg0503336	13689323	TCTAACTATCCAAAACCCACA			II		
0.1299331	cg0503506	cg0503506	31708457	TCACTCTTCTACCCTAATAACC			II		
0.1602242	cg0504034	cg0504034	17788344	AATCCTAATATTTAAAATTCA			II		
-0.103455	cg0504050	cg0504050	56744475	ACTAAAAAATAATATAAACRT			II		
0.1036565	cg0504371	cg0504371	44750351	CCAAAAATTACRATAAAAACC			II		
0.1296899	cg0504658	cg0504658	10713425	AATATCTCTAATTACATTAAC			II		
0.1242753	cg0504672	cg0504672	73735407	AACCTAATCAAACRTAATATC			II		
0.131389	cg0505005	cg0505005	57704510	AATACTT	69704315	AATACTT	I		T
-0.124149	cg0505126	cg0505126	27733467	AAAAACAAAAAATACACRTAC			II		
-0.110862	cg0505468	cg0505468	47799466	AAAACAA	29804509	AAAACAA	I		A
0.1422479	cg0505500	cg0505500	53600355	AAAATAAACCAAAACCACAAA			II		
0.1027131	cg0505735	cg0505735	48676426	CCCAAAACTCCCAATAAATAA			II		
0.1451842	cg0506248	cg0506248	55672506	ACTATAAATCCAACTCCTATA			II		
0.1014925	cg0506584	cg0506584	36760325	ACTCRACTAAAATAATTCTAT			II		
0.1031162	cg0507027	cg0507027	74735361	ATATATACAACCAATATAAAC			II		
0.1206561	cg0507530	cg0507530	53659444	TAATATTCACCRTACTATCCAC			II		
-0.140913	cg0507904	cg0507904	37750481	ACAAAAT	20718489	GCGAAAT	I		C
-0.111791	cg0508644	cg0508644	40631330	CTTACTCATTCAACAAATATTT			II		
-0.157891	cg0508762	cg0508762	65796378	TAAACTACAAATCTCTATATCT			II		
-0.125947	cg0508815	cg0508815	70699479	CCAAACC	11603418	CCGAACC	I		A

-0.113782	cg05092371	cg05092371	44765425	TACAAACAAACAATTATAACA			II	
-0.199012	cg0509641	cg0509641	16639308	ACTATATAACTTACATCATCA			II	
0.1013669	cg0509663	cg0509663	23740403	ACAACCCCRAACCTACATCAT			II	
-0.102611	cg0510006	cg0510006	74770356	CTCTACTATCCTCAAATACAA			II	
0.1038341	cg0510846	cg0510846	49607442	CRAATATTTTTAAAATCTCRTC			II	
0.1271619	cg0510956	cg0510956	63659395	TTCTCAAAATAACRACTAAAA			II	
0.1787525	cg0511164	cg0511164	35658390	TATACTCAAAAAACCCTCAAT			II	
0.1428963	cg0511189	cg0511189	60744436	AAATACCCTCTAAACCTCCAA			II	
0.2171689	cg0512651	cg0512651	31756325	AACATACAATCTACATATATC			II	
0.1236487	cg0513148	cg0513148	22610307	ATAAACTAACACTCTCAAACR			II	
-0.107053	cg0513169	cg0513169	26788413	AATTAAAACACTTACTTCAAT			II	
-0.200623	cg0513473	cg0513473	21667314	CATTATCCACCTAACAAAACT			II	
0.1228428	cg0513889	cg0513889	23627462	CATTATATATATCTATATACRT			II	
-0.125149	cg0513902	cg0513902	44804476	TAATCTAATCTCCACAAACTC			II	
0.1004843	cg0514481	cg0514481	43802320	CTACCAACATATAAACCCTCA			II	
0.1215612	cg0515504	cg0515504	74711312	CAAACAAATTCCCAAACTTCC			II	
0.1017769	cg0515762	cg0515762	67795434	ACACCTACCRAACTTTACCTTT			II	
0.1045678	cg0516056	cg0516056	37643374	TACTCCTCTTACTCTAACATAA			II	
-0.265401	cg0516177	cg0516177	17630455	AATAACAAAAAAAACTAACC			II	
0.1317914	cg0516454	cg0516454	27745334	TAAATCCAAAAAAATCACTAT			II	
-0.10681	cg0516493	cg0516493	60782338	AAAACA	35771437	AAAACG	I	T
-0.11581	cg0516525	cg0516525	11635354	AAAAATTAAACTACAATAATA			II	
0.2777572	cg0517388	cg0517388	46787473	CAATAACAAACTACCTAACCC			II	
0.1403801	cg0517580	cg0517580	48646417	AATACCCAAAATATAATCCAA			II	
0.1517784	cg05176551	cg05176551	36699356	AACACCTACCTCTAAACTCCA			II	
0.1332507	cg0517949	cg0517949	30707435	CCCTTTTACCTACCCTTAACAA			II	
-0.109506	cg05181941	cg05181941	23806365	TATCAAC	74751351	TATCAAC	I	A
0.1497556	cg0518221	cg0518221	61755450	ACTTACAATAATACAAATTCR			II	
0.1317675	cg0518715	cg0518715	30652418	AATAAAAACCCCRAACATTTA			II	
0.1635193	cg0519442	cg0519442	29773460	AAATAAACTAATAAAAAACRC			II	
0.1388138	cg0519463	cg0519463	50704485	ACCCAAAAACRCAACCRAAAA			II	
0.1200731	cg0519531	cg0519531	64698331	AATTTCTATTTACACCTATA			II	
0.1668587	cg0519706	cg0519706	15746499	AAATCTA	57747438	AAATCTA	I	A
0.1050373	cg0519766	cg0519766	30610409	AATTTCTTTTCCAACAACATAC			II	
0.1372126	cg0520860	cg0520860	35706389	ATCACATCAAAATTCTTCAAA			II	
0.1021207	cg0521068	cg0521068	50646447	AAAATAAAAATTTATAACCCA			II	
0.2172234	cg0521289	cg0521289	20718326	RCTACTATATACCTAAACCTC			II	
0.1041952	cg05223441	cg05223441	19777426	ATTTCCTCTATCCTAATTAACC			II	
	cg05226061	cg05226061	13644381	CTTCCCT	49734466	CTTCCCT	I	C
0.4795203	cg0523294	cg0523294	55732352	RCAAAATAATAACATAAACRA			II	
-0.140502	cg0523456	cg0523456	22664389	CAACTAC	63716334	CAACTAC	I	C
0.1494007	cg0523726	cg0523726	38699421	TTATCCCAACCRTACAAATAA			II	
0.1379437	cg0524182	cg0524182	69780466	AAACCTA	22600367	AAACCTA	I	A

0.1098703	cg0524401	cg0524401	60716387	AATATACTCTTTTACCATATTA			II	
0.1067112	cg0524423	cg0524423	63742314	AAAAAA	55731365	AAAAAA	I	A
0.1502319	cg0524468	cg0524468	61615347	AACTTAATTTCATCCTATAAC			II	
0.1439517	cg0524551	cg0524551	46695455	TTTCCTATTTTAAATTAAACCA			II	
-0.18562	cg0524823	cg0524823	35685425	TTCATCA	33667479	TTCGTCG	I	C
0.101046	cg0525093	cg0525093	16606320	ATCAAAA	24728332	ATCAAA	I	A
0.1429833	cg0525800	cg0525800	22771355	TTAAACA	74616339	TTAAACA	I	T
-0.107865	cg0526588	cg0526588	44763466	ACACAA	18750386	ACGCGA	I	A
0.1137545	cg0526678	cg0526678	17733366	CAAACCACATAAACAACAAA			II	
-0.324088	cg0526739	cg0526739	24754470	AAAAAC	74622419	AAAAAC	I	C
0.1231239	cg0526932	cg0526932	56681340	CTAAAAAACAAATCTTTAAAC			II	
-0.11427	cg0527075	cg0527075	60810486	AAAAATAAAACRCRATAAATA			II	
0.1116974	cg0527431	cg0527431	30668497	CTCCCAAACAATACAAATATT			II	
0.1169264	cg0527615	cg0527615	55614329	TTACTAAAAAACRAAATCAAA			II	
-0.137768	cg0527646	cg0527646	56713435	CCAAAAACCAATAACRAAAA			II	
0.2815802	cg0527697	cg0527697	48800415	RACCCTAAATACTCCTAACTT			II	
0.1855587	cg0527750	cg0527750	14769334	AAAAAA	22620442	AAAAAA	I	A
0.1941355	cg0527933	cg0527933	65802421	ACTTAACAATCTAACCAAAAT			II	
0.1485584	cg0527973	cg0527973	10734455	CTATTCTTTATTTAACTTTTTC			II	
0.1077269	cg0528033	cg0528033	46730385	TAATAACCTAAAAAACCTACA			II	
0.1013643	cg0528226	cg0528226	54763316	AACCAC	74643422	AACCACC	I	C
0.1347631	cg0528472	cg0528472	26726429	TAAACCAAACCTAAACTTTAT			II	
0.1187361	cg0528737	cg0528737	26636348	TAATACTCACAACATTCCAAA			II	
0.1394243	cg0528817	cg0528817	43740492	AACRTACACCAAACTAAACAA			II	
-0.103978	cg0530147	cg0530147	34644326	TCCTTTC	16671467	TCCTTTC	I	A
0.1189604	cg0530210	cg0530210	63795474	TTTTTTTTTCTAAACTATTTAA			II	
0.1033098	cg0530602	cg0530602	57645327	TATAAATAACTAAACTTCCTA			II	
0.2004601	cg0530824	cg0530824	24788496	CCTAAATATATCCCTAAACCA			II	
0.1420778	cg0530998	cg0530998	43799373	AAATAACTAAAATTTCACTTA			II	
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0.1212933	cg0531391	cg0531391	66616450	TAACTACAATTTCCCTCTCTTC			II	
-0.128258	cg0531720	cg0531720	55733446	CRATAACTTAAAAACTCCRAC			II	
0.1296286	cg0531827	cg0531827	29749314	CTTAATAACATACTAACCTCC			II	
-0.121085	cg0532122	cg0532122	18708411	CCCACAC	26771434	CCCACGC	I	C
-0.190238	cg0532805	cg0532805	12687466	AAACATA	40657444	AAACGTA	I	A
0.5680553	cg0533176	cg0533176	73723426	CCAAAACTAAACCTAACACRC			II	
-0.108111	cg0533605	cg0533605	61607478	AACCTATACAACATTTATTAT			II	
-0.385771	cg05337761	cg05337761	29669478	TCTCTAC	52623471	TCTCTAC	I	A
-0.170434	cg05338731	cg05338731	63790402	TTTACCTTAAAAAACTAAAAA			II	
0.1237965	cg0534246	cg0534246	33611312	AAACTAACATATTACTTATTC			II	
0.1192163	cg05343811	cg05343811	37807421	TCTCATT	22788356	TCTCATT	I	A
-0.209993	cg0534449	cg0534449	41766314	ACTAAAC	59774305	ACTAAAC	I	A
-0.210824	cg0534515	cg0534515	71714446	TCAAACC	74795345	TCGAACC	I	A

0.1585917	cg05348852	cg05348852	47681322	TTCCATACCCAAAACAAATTC			II	
0.1080503	cg05349016	cg05349016	48603467	CATCCCAAAAACCAAAATTCA			II	
-0.105689	cg05354195	cg05354195	43785387	AAAAATCTCCCAAATTAATAC			II	
0.1410312	cg05357039	cg05357039	73681375	CTAAAAACAAATAATAATATT			II	
	cg05360176	cg05360176	13644444	ATTCTCC	57798408	GTTCTCC	I	C
-0.126915	cg05362314	cg05362314	51624441	ACCCCCCAATCRCAAAAAATA			II	
0.1227667	cg05363955	cg05363955	48629338	CAACCAAACTATCTTCCAAAC			II	
-0.106848	cg05364567	cg05364567	35650419	AAACACTTCTAACCCATATAA			II	
-0.17692	cg05365033	cg05365033	50628338	AAAAAA	50656399	AAAAAA	I	T
0.104484	cg05366050	cg05366050	36747348	TATTTCAAAATATCCTAAATT			II	
0.167404	cg05366160	cg05366160	46809478	CAAAAAACCTTCCCTAATATA			II	
-0.117575	cg05370638	cg05370638	62802309	AAAAAA	14641348	AAAAAA	I	T
0.1564118	cg05372444	cg05372444	68766487	AAAACA	12685351	AAAACG	I	A
0.1162392	cg05374809	cg05374809	18625342	AAAAAAACAACCATCAATTCC			II	
0.1001878	cg05377120	cg05377120	43729306	AACAAACAAATAAACATATAA			II	
-0.179402	cg05378695	cg05378695	58773343	AAATTACCTACATAACCCTAA			II	
0.144327	cg05383619	cg05383619	34752490	ATTTTACATAAATAATCACCA			II	
-0.149899	cg05385718	cg05385718	24681459	CACAACA	20709500	CGCAACA	I	C
	cg05387399	cg05387399	55706492	AAACCCC	67765452	AAACCCC	I	A
-0.22011	cg05392448	cg05392448	18694399	CAAAAA	53806343	CGAAAA	I	C
-0.107243	cg05392989	cg05392989	48634406	AAACAACCAAAAATCTCACCC			II	
0.114861	cg05393086	cg05393086	60695447	AAAATACCATCAACTAAAAAA			II	
0.1004261	cg05400732	cg05400732	22781377	CAAAATTATTTATACAAACAC			II	
0.2782376	cg05401575	cg05401575	16750363	ATTTATTTAACAAACATAACA			II	
0.3741565	cg05407200	cg05407200	36709476	AAACCATTCTAAACCATAAAA			II	
0.162138	cg05408674	cg05408674	25687314	ATAATTCAACTTTACTTCTCAA			II	
0.1075279	cg05411594	cg05411594	29600456	TCRTACAACTCTAAAACAAAA			II	
-0.148124	cg05412137	cg05412137	27777372	AATATTTAAAACATCCRTACT			II	
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0.1172507	cg05413061	cg05413061	47649504	AAAAAAATAAATCACAACATT			II	
-0.166956	cg05416337	cg05416337	23758313	AAATTTCCCTAATAATAATTTT			II	
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-0.151924	cg05424366	cg05424366	62680335	AACTCRAAATCACTAAAATAC			II	
0.1338157	cg05428452	cg05428452	45790381	TAAAACTCCTCRTCTCCATCA			II	
0.1041546	cg05432034	cg05432034	65788499	CTAATACAACTTCTTACAAAT			II	
0.103694	cg05435390	cg05435390	54763400	ACTACCTCAACAAAATACAAA			II	
0.2603966	cg05440824	cg05440824	31727406	ATACTTAAAACATATTAATAA			II	
0.1352552	cg05450336	cg05450336	18797427	AACAAAAATATAAAACTAACA			II	
0.2218158	cg05453001	cg05453001	28709352	AAAAAC	48752321	AAAAAC	I	A
-0.100401	cg05453358	cg05453358	26780499	ACAACA	39755368	ACGACG	I	A
0.1402938	cg05455372	cg05455372	25618490	ATCTCCAAAAATAACACTCCT			II	
-0.187119	cg05457730	cg05457730	20682433	ATCAAA	46804394	ATCAAA	I	A
-0.229815	cg05463589	cg05463589	74757478	CTAAACA	42741510	CTAAACG	I	A

0.1610511	cg05469819	cg05469819	27641340	AATCACAAAAAAATTAATTAA			II	
0.1469649	cg05471169	cg05471169	66715450	AAAAAAA	58792400	AAAAAAA	I	A
0.1712424	cg05471495	cg05471495	35724480	TCCTATTCTCAAAAACTTATCA			II	
0.1544971	cg05472468	cg05472468	38742324	TAACTCC	51726304	TAACTCC	I	A
-0.134758	cg05475524	cg05475524	11770420	ACTACAA	54677365	ACTACAA	I	A
0.2005414	cg05477582	cg05477582	72609395	ACACCAA	29778323	ACGCCAA	I	A
0.1164855	cg05479627	cg05479627	41672359	TACTTATCTAACRTATATATAT			II	
0.1170493	cg05481961	cg05481961	20808492	TCCTTTAATCAAAAACATAAAA			II	
-0.100096	cg05483388	cg05483388	64758315	TTAAAAACAATTACAAAAACT			II	
0.1025054	cg05483731	cg05483731	33804472	AAAAAAA	66666305	GAAAAAA	I	C
0.1631417	cg05484949	cg05484949	74646447	AAAACAA	32655314	AAAACAA	I	C
0.1128594	cg05486191	cg05486191	13749432	ATAAAAACCACRTATTCATTCC			II	
-0.448981	cg05502360	cg05502360	29714300	AAATAAAAAACCAACTCATTC			II	
0.2380519	cg05509228	cg05509228	16658506	CCRATTCAAAAAAACCCAAAA			II	
0.1202888	cg05513157	cg05513157	59733359	CCCTTAACTTCRTCAATAAACR			II	
0.1240068	cg05514299	cg05514299	19661387	TTCAAAACTACAACTATTAATA			II	
0.2003614	cg05515244	cg05515244	48649474	ACRAATAATTAACATTATTATT			II	
0.1358333	cg05524038	cg05524038	13743318	TCCCTTCAACTCTAAATCTCAT			II	
0.1045081	cg05526364	cg05526364	47799399	CATCATATACTCAACTATAATA			II	
0.1586787	cg05526809	cg05526809	44650361	RAAAAACATACCACAAAACRA			II	
0.1396535	cg05528899	cg05528899	54661458	ATAAAAATCCTCTAACCCRCTA			II	
0.389017	cg05531409	cg05531409	13799421	CAATTCAATTTAAATCCCTTAA			II	
-0.109041	cg05548393	cg05548393	70714466	AAACAACCAAAATTAAAACTA			II	
0.1409407	cg05548425	cg05548425	50692329	ACAAATAATCACTTAAATAAA			II	
0.1509393	cg05563515	cg05563515	33659451	TAAAAAA	37700348	TAAAAAA	I	A
-0.162678	cg05574272	cg05574272	67759423	ACCTACA	31698311	ACCTACG	I	C
0.2734885	cg05575505	cg05575505	44635308	AACTCTATCCACATAAAACTCA			II	
-0.107583	cg05575614	cg05575614	64745329	ACACAAC	21727313	ACACAAC	I	A
0.2687097	cg05579598	cg05579598	25738399	RACTACAAACTAAAACCCRAC			II	
-0.191477	cg05580809	cg05580809	64802438	CRATCCTTCRACTATAAACAAT			II	
0.1690214	cg05581878	cg05581878	30628482	AAATAACAATAATAAAACCCA			II	
0.1204754	cg05583636	cg05583636	46659302	AACAAAACAAAAACCCTATCT			II	
-0.105188	cg05589784	cg05589784	11736345	AAATCCA	69604436	AAATCCG	I	A
-0.123888	cg05590257	cg05590257	30699439	ATCCCAA	69690416	ATCCCGA	I	C
0.1003525	cg05597181	cg05597181	32754347	CCTACCA	62789334	CCTACCG	I	T
-0.111254	cg05601623	cg05601623	24741423	ATCTTACCTACTCCRAAAACCT			II	
-0.185963	cg05606115	cg05606115	19715310	ACTTTTCCTTACTAAATCAATT			II	
0.1439319	cg05606455	cg05606455	19706326	ATATTAA	12671388	ATATTAA	I	C
-0.114523	cg05612744	cg05612744	18642335	TAACRATAAAAACTATCACCAC			II	
0.3043037	cg05621349	cg05621349	31682310	AACAAAC	67795408	AACAAAC	I	A
0.1138893	cg05622577	cg05622577	27694449	CATTCCCAACCAAAACTTCACA			II	
0.1189468	cg05628506	cg05628506	41697390	ATATTACAAAAATATTCCCTAA			II	
-0.133628	cg05630111	cg05630111	44650460	TTTTATAA	45650392	TTTTATAA	I	A

-0.10503	cg0563027	cg0563027	63604429	ACCTATAAATCTATTACACAA			II	
0.1078616	cg0563463	cg0563463	71771403	AATTACCTTATACTTCTTACTT			II	
-0.109749	cg0563617	cg0563617	29763331	ATACTTAAAAATAACTACTAC			II	
0.1863303	cg0563864	cg0563864	29643404	TCCTTCT	46795366	TCCTTCT	I	A
0.1016888	cg0564053	cg0564053	28683489	CAACTAC	22722453	CGACTAC	I	T
0.2152731	cg0564907	cg0564907	57772441	CTTACCAAAAATAACACATTA			II	
0.1239316	cg0565348	cg0565348	59616435	CTTAACTAATAACCRATACTT			II	
-0.397383	cg0565621	cg0565621	17758490	TCCACAA	64650421	TCCACAA	I	T
0.153934	cg0565765	cg0565765	20687501	ATAAATTACACAACAAAAATT			II	
-0.139522	cg0566682	cg0566682	51636353	AATCAAA	49620410	AATCGAA	I	C
0.125814	cg0568212	cg0568212	54772377	CAAATCAACTATATAAAACTA			II	
-0.180482	cg0568363	cg0568363	11611477	AAAAAC	63673338	AAAAAC	I	A
0.1214208	cg0568941	cg0568941	43736462	ATCACAAAACRTTCTCAAATA			II	
0.1117509	cg0569064	cg0569064	61628317	TCAACTC	41624466	TCAACTC	I	A
0.1143194	cg0569569	cg0569569	55753504	TCCACCT	70682427	TCCACCT	I	A
0.1012287	cg0569587	cg0569587	51767359	CTCTACTTTTAACTACAACTAA			II	
0.1174988	cg0570147	cg0570147	15736509	AACTAAAATCACAACACTAAA			II	
-0.139273	cg0570494	cg0570494	54720467	CAACACCAACAAAAACTTCCA			II	
0.1090108	cg0570533	cg0570533	57763359	AAATTCA	24659427	AAATTCA	I	T
-0.115299	cg0571006	cg0571006	58692328	TTACTTAATTATCAACCTCATC			II	
0.1000165	cg0571385	cg0571385	24654401	AAACAACACCAATATCAATAA			II	
-0.13146	cg0571395	cg0571395	15619486	TAAACTACTCCTAACTAAACR			II	
0.1196154	cg0572203	cg0572203	37645504	ACCCTATTAACCTTCAAACTA			II	
0.1098046	cg0572317	cg0572317	19643461	ACAAACTTTCTCTCCAAACTC			II	
-0.1285	cg0572477	cg0572477	42650320	ATCACCA	17720392	ATCGCCA	I	C
0.3021189	cg0572816	cg0572816	38761400	TACCTAAAATCAAAATAAAAA			II	
0.2222957	cg0573097	cg0573097	57661493	TCATTAAATATCACCCAAACA			II	
0.102447	cg0573346	cg0573346	12626393	AAAATATTAATCATTTCAAAA			II	
0.1049355	cg0573874	cg0573874	26798357	TTCATTTTCAATTTAAACCAAA			II	
-0.116608	cg0574046	cg0574046	26607306	ACAACAT	68601390	ACAACGT	I	T
-0.116828	cg0574371	cg0574371	10754333	AATATAT	21656445	GATATAT	I	A
0.5204028	cg0575105	cg0575105	71632416	AAACAACRAAAACTATACTCT			II	
0.1237844	cg0575118	cg0575118	62667342	AATCAAATCAAAACAAATAAT			II	
-0.115674	cg0575897	cg0575897	15708458	ACACACA	48696497	ACACAC	I	T
-0.119166	cg0576660	cg0576660	57620314	TTAAAAT	40810434	TTAAAAT	I	A
0.1071362	cg0576741	cg0576741	31782365	ACTACTT	34773427	ACTACTT	I	A
-0.132488	cg0577215	cg0577215	60764301	TACAAAC	51746329	TACGAAC	I	C
0.1295854	cg0577586	cg0577586	21695381	TCTCTAAAAAACTTTACATAT			II	
0.1103008	cg0577959	cg0577959	65709488	AACAAAACRAACTATACTTCT			II	
-0.128521	cg0578141	cg0578141	29648301	CAATCCC	64671432	CAATCCC	I	A
0.1126289	cg0578542	cg0578542	14634377	ACTACCA	37653502	ACTACCA	I	A
0.1286567	cg0578614	cg0578614	34710350	ACTTTATTAACATCTTAAAAC			II	
-0.253525	cg0579082	cg0579082	57639389	TCCAATAATCTAACCCAACTA			II	

0.1079503	cg05797854	cg05797854	34754487	TCAAATAAAAAATACTACTTA			II	
0.1077369	cg05799169	cg05799169	45648303	AACCTTC	49757422	AACCTTC	I	C
-0.105085	cg05806645	cg05806645	42653354	CRCTCTATACCACRAATATCA			II	
0.1028816	cg05809586	cg05809586	47748455	AAAACTAAAAAACACAAACC			II	
0.1023344	cg05819221	cg05819221	19633331	AAAACCRTATCTATACRAAAA			II	
-0.104666	cg05820861	cg05820861	61761478	CAAAATA	42702498	CGAAATA	I	C
0.1063693	cg05828605	cg05828605	17657409	TATAACCAAAACTCAAAATTT			II	
-0.103375	cg05831083	cg05831083	60732331	ACATAACTTAATATAATAATT			II	
-0.102889	cg05833351	cg05833351	43687316	AACATCT	60660364	AACGTCT	I	T
-0.176465	cg05837990	cg05837990	67797503	TAATTCC	63734392	TAATTCC	I	C
-0.142381	cg05839741	cg05839741	31774410	AAAAACC	27712404	GAAAACC	I	A
0.1539037	cg05839762	cg05839762	60790473	TCTCACA	42737448	TCTCACA	I	C
0.167635	cg05845592	cg05845592	15645506	ATTACTC	58733352	GTTACTC	I	A
0.1202675	cg05847075	cg05847075	71762411	CTATTCCTCCCACTCCTCTTAA			II	
-0.267051	cg05852276	cg05852276	24780491	AACAAAC	33620417	AACGAAC	I	A
-0.187676	cg05857999	cg05857999	35725469	TTTACAA	53770372	TTTACGA	I	A
-0.292814	cg05860956	cg05860956	46756506	CTAAAAAATCAATACTAACTA			II	
0.13427	cg05865243	cg05865243	60680491	ACCACCC	45667398	ACCGCCC	I	A
-0.115862	cg05867245	cg05867245	72691431	AACCAACTCTAAAAAAAACCT			II	
-0.119895	cg05867884	cg05867884	70766497	ACRTCAAAAAAACAATAACCA			II	
-0.12392	cg05868531	cg05868531	23655430	AAAAAAC	16636475	AAAAAAC	I	C
0.1825105	cg05876883	cg05876883	62609471	AAAATAAAACTCATAACTAAA			II	
0.12635	cg05879075	cg05879075	19630488	ATAATATAAACAAAAAAACCA			II	
0.1045134	cg05888894	cg05888894	36646450	AAACCCTTATATATAACCTCT			II	
0.1826608	cg05890457	cg05890457	73789453	TCATCTCTAAACCAAAATAAC			II	
0.1043198	cg05890956	cg05890956	28736421	AAACATTAAAACCCAAATATC			II	
0.2063798	cg05893845	cg05893845	47708472	TAAATCAAAAAATAAACTTTA			II	
-0.124635	cg05896682	cg05896682	43787408	ATAAAATAATTAAAACRACRA			II	
-0.211279	cg05900567	cg05900567	64696429	TAACCTCAATTTCTTATAACCT			II	
0.2875285	cg05901462	cg05901462	61780480	TATCTAA	59786389	TATCTAA	I	A
0.103522	cg05903720	cg05903720	15673451	TACACTTATAAATCTACRAAC			II	
0.1163308	cg05914894	cg05914894	34617449	TTATCTCTATATATCTATCAAC			II	
0.1645596	cg05918715	cg05918715	47716437	CCTTTAAAATCAACTCTATAA			II	
-0.183127	cg05921762	cg05921762	68642362	TTTTAATCTTATTCTTTCAAAA			II	
-0.117598	cg05922210	cg05922210	55756442	ACTATAAATCCACCCAAACAT			II	
-0.125757	cg05922253	cg05922253	29795415	AAAAAAC	18626373	AAAAAAC	I	A
-0.221542	cg05925927	cg05925927	19725472	CTAAATAACTATAATCCATCC			II	
0.1276935	cg05929272	cg05929272	68636326	TTCACCRTCCTAAAAAAACRA			II	
0.1117074	cg05929864	cg05929864	57686485	TTACTACTCTATTAATTTATTA			II	
-0.262526	cg05931366	cg05931366	61691305	AATATCTAAAATATTCTCTCCT			II	
0.1001805	cg05935904	cg05935904	19706355	TCTACRATCTAAACCTAAACT			II	
-0.10661	cg05936219	cg05936219	73743360	ACTAATT	65633311	ACTAATT	I	A
-0.154755	cg05938207	cg05938207	13669487	ACCTAACRCTAAATACTAAAA			II	

	cg05940452	cg05940452	42729309	TAAAAAC	54606483	TAAAAAC	I	C
0.154151	cg05942349	cg05942349	66605322	AAAAAATAAAATAAATAACCC			II	
-0.207101	cg05942459	cg05942459	33666445	ACTAACA	24706418	ACTAACA	I	T
-0.13514	cg05945782	cg05945782	11806482	AACTCCC	41603461	AACTCCC	I	A
-0.100856	cg05948955	cg05948955	69613476	TAACTCTACTCCRTTTTATATA			II	
0.1134995	cg05948962	cg05948962	65710411	ATTTATATTCACCATCTATAAT			II	
0.1361882	cg05950572	cg05950572	57658365	TTACCTACACAAACATTTCRTA			II	
0.1219976	cg05953243	cg05953243	19760425	CCACCAAATTCTTCTTTAAAAT			II	
0.255165	cg05956518	cg05956518	14636450	CACAATTTATTCACTAACCCCT			II	
0.113433	cg05957544	cg05957544	21789302	TATCACA	21635341	TATCACA	I	C
0.1665938	cg05959430	cg05959430	73612424	AATTATTACTACCTCRAAAACA			II	
-0.114896	cg05966431	cg05966431	59724427	TAACCCTTTCCCATTATTAAAA			II	
-0.487064	cg05971102	cg05971102	74626404	AATATTACTCTTTCCCCTTACT			II	
0.1229206	cg05971911	cg05971911	22669432	AACAACA	35631500	AACGACA	I	A
-0.106744	cg05977333	cg05977333	32673456	AACCAAACAATTAAAACCAAT			II	
0.1190154	cg05981038	cg05981038	66692405	TAAAATCCTTCAACATAATCCT			II	
-0.135875	cg05994819	cg05994819	30625300	CTAACAA	30682303	CTAACGA	I	C
0.1277404	cg05994974	cg05994974	24671300	CTATACCCCTCAACACATAACT			II	
0.1356093	cg05999364	cg05999364	65737401	AAATTTCTCCTCTTAAATACAA			II	
0.1018711	cg05999628	cg05999628	74634432	TAAAATCTAAAATCTAATCAA			II	
0.1194566	cg06000878	cg06000878	57671398	ACTACCCCTTAACTAATACTAA			II	
-0.177669	cg06002203	cg06002203	56698398	TCRACCTACCTAAATTTCAACC			II	
-0.132919	cg06002687	cg06002687	24632477	AACTATT	52784353	GACTATT	I	A
0.1292222	cg06013395	cg06013395	47646471	ATTATTTATAATTTACCRAACR			II	
-0.12818	cg06013769	cg06013769	64700324	TACTAAA	57768426	TACTAAA	I	C
-0.179508	cg06016684	cg06016684	35736339	AATATATTTAAAATAAAAATA			II	
0.1182234	cg06021990	cg06021990	49639420	ACACAAATCCACAAATTACAT			II	
-0.283512	cg06023351	cg06023351	36691480	TTAACAACRCTAATTTACAAA			II	
0.1100895	cg06023791	cg06023791	53738457	AAAAAACRCRAAAATTAAAAA			II	
0.4077285	cg06032337	cg06032337	48708300	AACACATAAACRCATTCAATA			II	
0.1025201	cg06044945	cg06044945	71687311	ATAAAAAACATACAAACCTCT			II	
-0.106359	cg06051662	cg06051662	33803347	TTTCTTTCCTCCCTTTCTCTCTT			II	
0.1019863	cg06052090	cg06052090	21676383	TTCTAAAAACTTTAAACACTTA			II	
0.1013522	cg06052372	cg06052372	47624464	CAAAAACCACAATCTAAACTT			II	
-0.108104	cg06061081	cg06061081	71649437	CTCTTCCATCTACTTTAAAAAC			II	
0.1272795	cg06065495	cg06065495	26611336	TTTATCCACCTCAAAAACTAAC			II	
-0.260646	cg06075393	cg06075393	49713492	TCCTAACACTAAAAAAAATCT			II	
-0.108907	cg06077305	cg06077305	66671508	AAAAACA	25699377	AAAAACC	I	A
0.1075909	cg06085726	cg06085726	47672424	ATTTAAATTCTTCCRAAACCCT			II	
0.1358684	cg06090818	cg06090818	58734382	AAACAAA	66670400	AAACAAA	I	A
-0.13253	cg06093861	cg06093861	67783467	ATTAATCAATCTAATCTCCAAC			II	
-0.107102	cg06106763	cg06106763	29736310	RTAAATCCACTTTTATAAACCA			II	
0.1457823	cg06108661	cg06108661	20803430	TCTATCTAACTTATTAACACTC			II	

0.1801357	cg06112171	cg06112171	16684338	TTTTTCCTTTCAAATAATAACC			II	
0.1214873	cg06112204	cg06112204	64656387	CAACAATCRCATTCCTAAATAT			II	
0.1077102	cg06118302	cg06118302	40647492	TCTAAAACCCCTAAACCAAAA			II	
-0.203878	cg06120313	cg06120313	47767466	AAAAATAAAAAACCCTCTAAA			II	
0.2532889	cg06129455	cg06129455	58661340	CCACCCCTACAAACTAAAATA			II	
-0.162668	cg06130360	cg06130360	19774377	ACAAAAT	53699496	ACGAAAT	I	T
-0.114371	cg06132727	cg06132727	67672504	AAAATAA	63621429	AAAATAA	I	A
0.162446	cg06134678	cg06134678	43631399	TAAAACTCTAATATATCATTTC			II	
-0.112949	cg06135529	cg06135529	33738316	AAAAAAC	65637472	AAAAAAC	I	A
0.1130183	cg06136702	cg06136702	48627478	TAACATTCCTCACCTTCTAAAT			II	
0.1732873	cg06139006	cg06139006	24717442	AACCAAC	41733314	AACCAAC	I	T
-0.148707	cg06143315	cg06143315	73685375	CCAACTC	56706412	CCAACTC	I	T
0.1353974	cg06147194	cg06147194	51660422	CTTAATCTTATCCTAAAACCC			II	
-0.132438	cg06148736	cg06148736	73691439	AACAAAA	49675416	AACAAAA	I	A
0.1274357	cg06150148	cg06150148	12697439	TCCTATC	55755303	TCCTATC	I	A
0.1074965	cg06150772	cg06150772	24683399	ACRCACTAAAATATAAACTAT			II	
-0.105119	cg06152856	cg06152856	10766356	AAAATAACTAACTTTAACCTA			II	
0.1271304	cg06157924	cg06157924	56734322	TATACTC	28736442	TATACTC	I	A
-0.240768	cg06159404	cg06159404	30625391	AAATAAA	28698390	AAATAAA	I	A
0.1439676	cg06173319	cg06173319	35726343	AAAAAAA	60720359	AAAAAAA	I	T
0.1343144	cg06176650	cg06176650	43701306	AAAAAATACCAACAAACCTTA			II	
0.1155971	cg06179228	cg06179228	58688505	CCCAAAAAACCAAAAACCCTA			II	
0.1033288	cg06190732	cg06190732	21644359	ATCTAACAAACCCRTATTACCA			II	
-0.208984	cg06193597	cg06193597	54605425	CTACCCA	40778416	CTACCCA	I	C
-0.101831	cg06193958	cg06193958	66632377	AAAAAATTAACCAAAAAAAAT			II	
-0.209738	cg06202470	cg06202470	56672358	TAAAACT	50807436	TAAAACT	I	A
0.1295019	cg06202802	cg06202802	59743377	ATACAAATAAATAATAAATAC			II	
0.1296405	cg06206801	cg06206801	20679486	CAACAATTTTAAATACTACTTA			II	
0.1050833	cg06211550	cg06211550	55734452	TAACAAA	52660431	TAACGAA	I	C
0.1433441	cg06213900	cg06213900	18623376	AACAACAACTAACTTTTAAAA			II	
0.2061768	cg06225639	cg06225639	29665383	AAAAATCCATAACRAACRCAA			II	
-0.118079	cg06230664	cg06230664	34757465	TAAAATACRATAAACACTATC			II	
-0.115174	cg06231362	cg06231362	54718487	CTATCCTTACACCAATACCACA			II	
-0.125699	cg06238316	cg06238316	64747498	AAAATCCAAAACTACCCTAAA			II	
0.1603068	cg06241208	cg06241208	32773363	TCTATTCTAAAAAAATTTACAA			II	
0.1051638	cg06245711	cg06245711	53646379	AATCTAAATATTCACTTAATAA			II	
-0.151501	cg06247406	cg06247406	48713397	CCTAACAAAACCTTTACTAACA			II	
0.1115254	cg06248701	cg06248701	39711332	CTTAATAACTAAAACCRCCCAA			II	
0.175019	cg06249604	cg06249604	59671348	CTTCTAA	41668405	CTTCTAA	I	A
-0.108948	cg06250751	cg06250751	20661503	ATCCTCTAAAACCAATCACAA			II	
-0.13238	cg06252276	cg06252276	71777325	CATAACT	74715399	CATAACT	I	A
-0.110705	cg06255006	cg06255006	12730365	ATCAATA	42684362	ATCAATA	I	A
-0.329292	cg06264882	cg06264882	13672375	CTAATAAATCAAAACTTCTATC			II	

-0.12184	cg06266227	cg06266227	73642449	CAACATATCAAAAAAATACAA			II	
-0.105861	cg06268875	cg06268875	60793361	TTTTCCA	25655400	TTTTCCG	I	A
0.1251661	cg06271046	cg06271046	52771317	CAAACTACCTTAAATCCAAAA			II	
0.1435675	cg06271387	cg06271387	16652309	CAACCTCTATCTTTCATCAACA			II	
	cg06271696	cg06271696	55809408	ATACAAA	32768487	ATACAAA	I	T
-0.122851	cg06282524	cg06282524	26626360	CTCCATA	44734401	CTCCATA	I	T
0.1180278	cg06285575	cg06285575	52656335	AACCCCTCCTAAAAACAAACT			II	
0.1006202	cg06287548	cg06287548	10792391	CRTATAAACTCCCTTCACATTT			II	
0.1291139	cg06288089	cg06288089	66766464	CAAAATATAAACTTCTAAAAA			II	
-0.254721	cg06293782	cg06293782	28697451	TTAAAATTCATAATAAAACAA			II	
-0.107335	cg06297958	cg06297958	46733479	CACATAA	29713394	CGCGTAA	I	A
0.10494	cg06298480	cg06298480	56632370	AAAACAAATACAAAAACTACT			II	
0.2035785	cg06300880	cg06300880	17736396	TATTTACACAAATAAAACCTA			II	
-0.101009	cg06302025	cg06302025	32682378	ATAACAA	56655426	ATAACAA	I	A
-0.17655	cg06305758	cg06305758	33684488	AATTTCACCATATTAACCAAA			II	
-0.436402	cg06306564	cg06306564	34681342	TAATATCAAACTACTTTTAAA			II	
0.1132001	cg06312469	cg06312469	31807475	TCTAAAATCAAATCTTAAATA			II	
0.1227171	cg06314883	cg06314883	31801434	AAAACCCAAATCCAAAACACT			II	
-0.114169	cg06315390	cg06315390	12656471	CCTTATA	71690449	CCTTATA	I	A
0.2351006	cg06316104	cg06316104	32645422	CCTATTC	59657486	CCTATTC	I	A
-0.108755	cg06322277	cg06322277	28786458	AACAACA	65607459	AACAACC	I	A
-0.148573	cg06330593	cg06330593	45767371	ACATATA	34810417	ACGTATA	I	T
0.1378359	cg06333233	cg06333233	68734430	CTCACCCTAAAAACAATATTA			II	
0.1177881	cg06334238	cg06334238	63754370	AACCATA	37773495	AACCGTA	I	C
0.1586913	cg06342072	cg06342072	39699315	CCATTCTTTTATAAATATTAT			II	
0.1151609	cg06348773	cg06348773	21770427	AAACTAT	34717427	AAACTAT	I	A
0.1196298	cg06349762	cg06349762	43635502	AAAACCA	69640364	AAAACCA	I	A
-0.174466	cg06350542	cg06350542	36770426	CTAAACT	46765377	CTAAACT	I	A
-0.110488	cg06352616	cg06352616	58777301	ACTAAAA	47654342	ACTAAAA	I	T
0.1618819	cg06354695	cg06354695	25729301	CAACACACAAAACCTCTATTA			II	
0.1058921	cg06358191	cg06358191	63797319	RAACCTCCTTAAAACCCACCC			II	
0.1013157	cg06359884	cg06359884	38799348	ATATAATTATAATTAAACATT			II	
-0.182412	cg06360820	cg06360820	31759367	AAACAATAAACRCAAATCCCA			II	
0.1366052	cg06363034	cg06363034	39683376	TAAATATAAAAAAAACCAATA			II	
-0.134556	cg06366791	cg06366791	47605483	CTCATTTTCCATATTCAAATTA			II	
0.15101	cg06374430	cg06374430	53655465	AAAAAACRAAAACTATACACC			II	
0.1123834	cg06380401	cg06380401	16791420	AATAATAAACTCCTAATTCTA			II	
	cg06390368	cg06390368	12768371	TAACCAA	71778401	TAACCGA	I	A
0.1278291	cg06394820	cg06394820	64600507	CTAAACAAAAAAATATCCCRA			II	
	cg06397523	cg06397523	13644325	ACAACTC	70688368	ACAACTC	I	A
-0.118995	cg06398242	cg06398242	62623438	ACTAAAA	62629443	ACTAAAA	I	A
-0.181966	cg06407043	cg06407043	50810438	TATATATAAAATCATCTAATA			II	
-0.103309	cg06416685	cg06416685	29808391	TTACCCTCTACAAAATTATAC			II	

0.1085643	cg0642203	cg0642203	49645414	AAAACA	28720374	AAAACG	I	A
0.1800885	cg0642275	cg0642275	16691453	AATTTAATCTTAAAAACCTAA			II	
0.1144699	cg0642919	cg0642919	10616505	TAACATATACACTTTCTAAAC			II	
-0.127977	cg0643068	cg0643068	65688320	CTAATCATCTATCACCACAAA			II	
0.1230891	cg06431681	cg06431681	14667388	AAAAAAACTCCAACCTAAAAA			II	
0.1252624	cg06433801	cg06433801	15792435	ATTCCTTTTCCTCAATAAAAA			II	
-0.116926	cg0643720	cg0643720	60686369	CCAAACCTATAAAAAACCTCC			II	
-0.148999	cg06437931	cg06437931	70650364	CTCTATAAATCCAAATTTCCC			II	
0.1141392	cg0643855	cg0643855	27606375	AAACAATAAAAAACTAACATA			II	
0.121103	cg0645037	cg0645037	51739444	TTCTTACTCTTCTCTCAATAAC			II	
0.2013787	cg0645773	cg0645773	67621496	RAATTAAACAATAACTTATCA			II	
-0.106602	cg0645910	cg0645910	35778480	CTTCTCACTAAACTAAACCCA			II	
0.1238686	cg0646018	cg0646018	51774338	CRACCAATTTAACTACAAATA			II	
-0.124191	cg0646047	cg0646047	36624324	CACACC	55735341	CGCGCC	I	C
0.3717501	cg0646158	cg0646158	71687503	TAAATAAAAATACAAAACCCA			II	
0.416702	cg0646407	cg0646407	49764417	CTAAAAACACACTCAAATTCC			II	
-0.100135	cg0646838	cg0646838	70632375	AAAAAAATCRCAAAACCTACA			II	
0.1016733	cg0646944	cg0646944	73698361	TCTTTATTTATTACAATCTCTT			II	
-0.187157	cg0647085	cg0647085	57681456	CCAAAA	66764464	CCAAAA	I	C
-0.12117	cg0647242	cg0647242	26623439	TTACCTTCTAATCACCCTTAAT			II	
0.1200341	cg0647669	cg0647669	48787484	AATTCACTTCTTTACCCTACTC			II	
-0.102662	cg0647850	cg0647850	67604416	AACAAA	42625372	AACGAA	I	T
0.1470259	cg0648412	cg0648412	69796300	CCATTTCCCTATTTACTACTCC			II	
0.2428651	cg0648416	cg0648416	56663455	AAAATTTCTCCATATTAATCA			II	
-0.215037	cg0649159	cg0649159	35796438	CTACAAAACTCAAAAACACTA			II	
0.1028378	cg0649237	cg0649237	65606397	AAAATAACCCCATAACTTCTA			II	
0.1299965	cg0649380	cg0649380	35687442	AAAAAAACTATACCRAATACT			II	
-0.188688	cg0650325	cg0650325	39702400	AAATAA	23802427	AAATAA	I	A
0.2144342	cg06503981	cg06503981	38736460	CCTACTCCTCAATTCTTACATT			II	
-0.137413	cg0650763	cg0650763	70618405	ACTTCACACCTTTATTATATCC			II	
-0.117627	cg0651118	cg0651118	53644305	CCAAAA	31626381	CCAAAA	I	C
0.1202405	cg0651133	cg0651133	14741422	CACTCCCRACACCRCATTTCTA			II	
	cg0651386	cg0651386	73790437	CACCACA	56733367	CGCCGCA	I	A
-0.110009	cg0652147	cg0652147	29670416	ACACCAA	38737311	ACACCGA	I	A
0.1976867	cg06523151	cg06523151	20745504	AATCTTTAATTTTCCTACACAT			II	
-0.127275	cg0652426	cg0652426	16628418	CTAAATAATCTCRATCAACTC			II	
0.138929	cg0652545	cg0652545	49601316	TCTACTTAACCAATTATAAAA			II	
-0.150714	cg0653157	cg0653157	15760498	CRAATCCCTTTACCATCCCCCT			II	
-0.350937	cg0653615	cg0653615	72678327	ATAAACRCCACCTAATAACCA			II	
-0.104256	cg0654520	cg0654520	29750446	CTCAAAA	66809442	CTCAAAA	I	C
-0.102001	cg0654923	cg0654923	10808332	CCCTAAA	37751507	CCCTAAA	I	A
0.198039	cg0654987	cg0654987	32756434	ATTCACCCCTAAAAAATCCTA			II	
-0.100013	cg0654992	cg0654992	51784479	CTCCTAT	16726332	CTCCTAT	I	A

-0.279944	cg06550274	cg06550274	44615360	AACRAAAACCCAACACTAACC			II	
0.1270134	cg06559575	cg06559575	11755457	TCCCTCTTCCTCTCTCTTATAAA			II	
-0.147692	cg06562718	cg06562718	51790496	AAAAACACCCRATATAAATCC			II	
-0.105609	cg06566034	cg06566034	36644315	ACAACAA	30733327	ACGACAA	I	A
0.1080141	cg06568346	cg06568346	44629445	AAACTTAAAATAAAACRTAAA			II	
-0.111328	cg06570432	cg06570432	32654390	RATACTAAATTCCTTTCTATAT			II	
-0.112128	cg06573096	cg06573096	26705468	TTTAATCATATCTTATTCTCAA			II	
0.1137182	cg06578276	cg06578276	16637439	TTAAAACCCACAAAATACTCC			II	
-0.162789	cg06583549	cg06583549	34632461	ATTCCAA	67678312	ATTCCGA	I	A
0.1381559	cg06584218	cg06584218	10757344	ACRTTCCCAAAACAAATATAT			II	
0.1548431	cg06586265	cg06586265	45613487	AAATAACAATAAACACAAAA			II	
0.1628414	cg06587249	cg06587249	21769327	TACTTCA	21685348	TACTTCG	I	A
0.1264344	cg06587955	cg06587955	36701322	RATCTATTTTTCCTTTAATTCC			II	
-0.129826	cg06588556	cg06588556	53606434	AAATAAA	63683508	GAATAAA	I	A
0.1006772	cg06589191	cg06589191	27753383	ACTATAA	13726352	ACTATAA	I	C
0.1001306	cg06589199	cg06589199	35615321	TCCAAACAAACCCRATAACTTA			II	
-0.163178	cg06593753	cg06593753	36733361	CCCTAAACTAACAAACTTTAC			II	
0.1240645	cg06595154	cg06595154	23641489	CTACTAAATATTTTCTAAATAA			II	
0.126712	cg06596943	cg06596943	71618389	CAACRTATTAAAAACACRCAA			II	
-0.239153	cg06617490	cg06617490	32784332	CAAAAAACTAAATACCAACAA			II	
-0.106111	cg06618134	cg06618134	49798311	TAAATCACTTTCCTCAAATCA			II	
-0.120699	cg06619621	cg06619621	23669487	ACTATAC	68801420	ACTATAC	I	T
-0.10436	cg06619938	cg06619938	66703337	AACCTCA	55610394	AACCTCG	I	C
0.1022609	cg06620117	cg06620117	10731450	CAAAACTAAACTATACCACAA			II	
0.1173673	cg06621027	cg06621027	43726361	CCACAAAAACTACCAATCCTCA			II	
-0.105918	cg06624527	cg06624527	25798433	AAAACAA	10630451	AAAACAA	I	A
-0.141854	cg06628792	cg06628792	19665466	AAACTTCACCCAATACTTCTA			II	
-0.104887	cg06630839	cg06630839	52715317	AACAAA	32741367	AACGAA	I	A
0.2083445	cg06631775	cg06631775	24644310	AATATTT	56680385	AATATTT	I	A
0.5070584	cg06634367	cg06634367	16610505	AATTCTA	11714504	AATTCTA	I	C
-0.32193	cg06634576	cg06634576	33763414	TCTTTTTA	35721391	TCTTTTTA	I	T
0.1250085	cg06634717	cg06634717	14804417	ACAAAA	35630510	ACGAAA	I	T
0.1289884	cg06635764	cg06635764	50764414	TATCCTTA	53675436	TATCCTTA	I	C
-0.110451	cg06645921	cg06645921	61626420	ACAAAA	38633476	ACGAAA	I	C
0.1521166	cg06647930	cg06647930	43653440	ATTTACTATTCTATCTTCCACA			II	
-0.103284	cg06649034	cg06649034	54780312	AAAATCA	22711458	AAAATCC	I	C
0.1756823	cg06650246	cg06650246	51790402	TTCTCTTA	33744484	TTCTCTTA	I	C
0.1646034	cg06650786	cg06650786	41798378	AAACTTACATTTATACRTCCRT			II	
-0.111662	cg06657917	cg06657917	49756328	AAAAACA	30766450	AAAAACA	I	A
-0.109196	cg06665333	cg06665333	11641398	ACAAATA	43666501	ACGAATA	I	A
0.1306144	cg06665622	cg06665622	27804429	AACATAAACACTCRACTACAA			II	
0.1421248	cg06674117	cg06674117	25647452	AATTCAAAACTTCCTACTACC			II	
0.164876	cg06675417	cg06675417	36780493	TATATAAAATAAAATAAACRC			II	

-0.227959	cg06686422	cg06686422	43760371	TTAAAAAACACTAATTCATTCA			II	
-0.177722	cg06688803	cg06688803	54745316	TCTATATTTAAACCTCAATTTC			II	
0.1021149	cg06689619	cg06689619	67729462	CTAAAACTCTTATTATACTTCT			II	
0.1523764	cg06690085	cg06690085	36632421	AAAACCCCTCCCTCTAAAATCA			II	
0.140682	cg06691616	cg06691616	52766478	TCCATAAAACTACATCTTTTTT			II	
0.1292993	cg06698332	cg06698332	67659489	AAATTTAAAAAAAACCTAAAT			II	
-0.199503	cg06699489	cg06699489	29618468	TAAAAACCACAAAAACAAAA			II	
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-0.258656	cg06706443	cg06706443	74749383	CTCTACTCCTAAAAACCATTAA			II	
-0.137125	cg06707236	cg06707236	59657317	ACCCAAA	55660419	ACCCAAA	I	C
0.1346024	cg06709297	cg06709297	23667375	ATCRATTCTCTCAATCAATCAA			II	
0.1207606	cg06711418	cg06711418	59719305	TAAAAAACRCRACTTCCACAA			II	
0.161664	cg06713116	cg06713116	15697445	CAAAACCCCAACTACTAATAA			II	
0.2271218	cg06718159	cg06718159	36768332	ACCAAACTATTAAAAAACCAA			II	
0.1168816	cg06718920	cg06718920	19726359	CTATAAAAAACCCCTAACTAA			II	
-0.177115	cg06721546	cg06721546	71751418	CAAAAAACCACCCACRAAACT			II	
0.110676	cg06726231	cg06726231	11759300	CTAAAAATCCCCACACRCAAA			II	
0.1071161	cg06727338	cg06727338	52647447	CRACTATATAATCTCCTAACTA			II	
-0.130221	cg06728252	cg06728252	17687483	TACATAA	53744414	TACATAA	I	T
0.1876193	cg06736229	cg06736229	35758367	CAAAAACTTCACTACAAACTC			II	
-0.136776	cg06737308	cg06737308	27715457	TTATCTTCTCAAAAACATACAA			II	
0.1520143	cg06738063	cg06738063	27652434	CTTTATCCTATATATATAACCR			II	
0.1007078	cg06741336	cg06741336	37611325	AAAAAA	50676357	AAAAAA	I	A
0.2452028	cg06743454	cg06743454	20769409	CCCCACCAACAAAATACAAAA			II	
-0.149573	cg06747330	cg06747330	50797362	CAAAACCCTTCTAAATCCTCRA			II	
0.1106536	cg06755258	cg06755258	12697311	AACRACTACATCTTCCTATCAA			II	
0.1654817	cg06758191	cg06758191	30630472	TAAAAAAAAATCCTTAACTCT			II	
0.1177325	cg06760904	cg06760904	36602415	ATATTAA	16749429	ATATTAA	I	C
0.2788438	cg06761912	cg06761912	63615329	TATCTATATTTCTTAACCTAAA			II	
0.1409986	cg06763776	cg06763776	49682499	TATTTCTATCTTATAAAAATAC			II	
-0.103828	cg06763829	cg06763829	31694485	AAAAACA	27758434	AAAAAC	I	T
0.157831	cg06769820	cg06769820	11806416	TTACAACCAAAAAAAAACTAC			II	
0.1170107	cg06778662	cg06778662	26715408	CCTACTC	26609404	CCTACTC	I	C
0.1805662	cg06781948	cg06781948	26739477	TATTTCTCATTTATAAACTCCA			II	
-0.150059	cg06789824	cg06789824	73669314	ACTTACAACCAAAAATATAAA			II	
-0.143856	cg06792262	cg06792262	54757347	AAAAAAA	18617354	AAAAAAA	I	A
-0.400761	cg06792428	cg06792428	17787407	CAAAAACTATAAATACCCRAT			II	
0.1215725	cg06794141	cg06794141	30800394	TATACATAAAAATCACTCTAAA			II	
-0.151033	cg06796435	cg06796435	60704500	AAACAC	63750357	AAACAC	I	C
0.1016354	cg06796713	cg06796713	55650417	RTAAAAAAAATACCTACTCCA			II	
0.1464808	cg06798115	cg06798115	30656349	CTCAAAAAATACTTTCCAAAC			II	
0.1433868	cg06798887	cg06798887	43788459	CTATAAAAACCTTCCCACCAAA			II	
0.1472094	cg06799747	cg06799747	61602392	CCTACTACTCTAAATATTATAA			II	

0.1296765	cg0680022	cg0680022	69728463	CCRAATCCCAACCATATCCAA			II	
0.1262676	cg06804411	cg06804411	43684436	CTAAAATCATTAAAACCAATC			II	
0.1105759	cg0680686	cg0680686	35635464	ACAAAAACTTACTAATTCTCT			II	
-0.112597	cg0680928	cg0680928	44783365	TCATATCCCAACTCAACTAAT			II	
-0.104869	cg0681206	cg0681206	47611437	CCCCATC	50686435	CCCCGTC	I	C
0.2052432	cg0681279	cg0681279	49703384	TAACCAAAAAACCRATATTTC			II	
0.113474	cg0681283	cg0681283	70635328	CCRATATTTACTAACCRTATA			II	
0.1134881	cg0681655	cg0681655	29782437	AAACACAATAAAACCAAATCC			II	
0.1217424	cg0681815	cg0681815	51757488	TCATAATATATATCTCACTACC			II	
0.1196045	cg0681886	cg0681886	24810505	CCTTTCAATTCCTTAAATATAT			II	
0.1088299	cg0682107	cg0682107	72731423	ACAACCTAAATAACTTTTAAC			II	
-0.127364	cg0682182	cg0682182	17685494	AAAATCTAAATTACRTACTCC			II	
0.1197544	cg0682219	cg0682219	59677439	TTTAAAATTCCTACTTTACAAA			II	
-0.126982	cg0682303	cg0682303	74683424	TAAAAAA	66622482	TAAAAAA	I	T
-0.141029	cg0682612	cg0682612	41603422	AACACAT	42687466	AACACGT	I	T
0.1058714	cg0682814	cg0682814	52714396	CTAATTCTTCTAATAAAAAAA			II	
-0.104383	cg0683106	cg0683106	47715326	AACAAAC	23803388	AACGAAC	I	A
-0.270011	cg06833981	cg06833981	30630339	AATACCAAACATATACCCTTC			II	
	cg0683581	cg0683581	54768320	AACRTATAAAAAATAAACCTA			II	
0.1825294	cg0683821	cg0683821	18744339	TAACCTCTACTTACACCTTAAC			II	
0.1013014	cg06839111	cg06839111	24758505	ATCCAAACAATAAATATACAA			II	
-0.109325	cg0684471	cg0684471	72651489	TCATTTATTCTCACAATAAAA			II	
-0.268528	cg0684484	cg0684484	19796492	CCATCCTAAAAATAACAAATA			II	
0.1145258	cg0684848	cg0684848	21716407	ATTCCCTAAATTCTCTCCTCCA			II	
0.1118641	cg0685808	cg0685808	53796358	TAATTAAAAACCTAAAAACTA			II	
-0.173256	cg0686564	cg0686564	73713481	TAAACATTCAATAAATACRCR			II	
0.1023777	cg0686748	cg0686748	27650399	CCAAACA	24604317	CCAAACA	I	T
-0.117585	cg0687011	cg0687011	38774451	TCCCAAAATCCAAATTCCCTA			II	
0.2003369	cg0687134	cg0687134	41643338	CAAAAAACTCTAAAAACACRA			II	
-0.108917	cg0687607	cg0687607	28674327	CTAATAACACCTATAACCTAA			II	
-0.104595	cg0688449	cg0688449	46682499	CAAACTTCCCCTAAAATCCTA			II	
0.1226335	cg0688673	cg0688673	61790357	ACACACA	42731362	ACGCACC	I	T
-0.134634	cg0688846	cg0688846	43681321	ATACAAA	32771453	GTACGAA	I	C
-0.151263	cg0689576	cg0689576	37722354	AACTTTAAAAAACCAACAAAC			II	
-0.11733	cg0689744	cg0689744	31666360	TACAAATATCAAAAAACAACC			II	
0.1100523	cg06900571	cg06900571	11749329	RTACCATCTCCCCRAAATCTA			II	
	cg0690576	cg0690576	30674312	AAATAAA	29675455	AAATAAA	I	C
0.1084983	cg0690925	cg0690925	19690510	TACTCTATTACTAAACCAAAC			II	
-0.127726	cg0691351	cg0691351	62658445	AAACATC	69802376	AAACGTC	I	A
-0.310951	cg0692490	cg0692490	13759383	TTTTTCATCATCCCATAAAAA			II	
0.1098329	cg0692530	cg0692530	19801472	AACCAAAAAACCTTTCCAAAA			II	
0.1086651	cg0693253	cg0693253	31652477	CATAATAAAAACTTCCAAACC			II	
0.1517849	cg0693543	cg0693543	28700404	CCTAAAACTCTCTCTATTTCTT			II	

0.1780057	cg0693629	cg0693629	23804420	TCTCTAAACTTAACAAAAAAC			II	
0.1364722	cg0693792	cg0693792	36675346	AAAATAACTAAACAAATCTAT			II	
-0.149562	cg0693826	cg0693826	35664356	CCAAAA	40687337	CCGAAA	I	C
0.1222973	cg0694115	cg0694115	46659489	ACAAAATAAAACCAACRTAAA			II	
0.1733964	cg0694211	cg0694211	15602396	AAATCCAACCTTACTTATCTTA			II	
-0.112257	cg0694898	cg0694898	20774355	CACCACC	58714333	CACCACC	I	C
-0.124826	cg0695112	cg0695112	14612478	AAACCTC	44784383	AAACCTC	I	A
-0.292093	cg0695595	cg0695595	16625306	ACCTACCTTATATCRCAATATA			II	
0.1638317	cg0695876	cg0695876	24600374	AACTATA	60790506	AACTATA	I	A
0.1219632	cg0695944	cg0695944	23708426	AAATTCTACTCTCCAAATCTA			II	
-0.189759	cg0696071	cg0696071	65763472	TTATCAAACCCATTCACACAT			II	
0.1177855	cg0696142	cg0696142	69617424	ATATTATTTTAACTAATATCAT			II	
-0.112319	cg0696871	cg0696871	14737440	ATCRCCTCTAAAAAACAAAAT			II	
0.1974752	cg0697122	cg0697122	39602432	ATATTAAAAAAACCCRAAACA			II	
-0.100222	cg0697597	cg0697597	22680370	AAAAAC	58647446	AAAAAC	I	A
-0.102248	cg0697622	cg0697622	32734337	ATACAAAACAAAAATATCCAT			II	
0.116546	cg0697902	cg0697902	11702434	AATTACCTCCATCTAAAAAAA			II	
-0.139594	cg0697938	cg0697938	27693451	ATCTTCTCAACCAAAAACTAT			II	
-0.114405	cg0698216	cg0698216	50801467	ACCACCCRAATAATACAAAAT			II	
0.1082518	cg0698282	cg0698282	50657301	TTTATTTATCTCTCCCCTAATC			II	
-0.10219	cg0698420	cg0698420	15792440	TAAACACACTATCATCTCRCA			II	
0.2183425	cg0699550	cg0699550	72669423	TCTACTCATATACACATCTAA			II	
0.1008264	cg0700712	cg0700712	48715323	CTACATTTTCATTTCTAACCTA			II	
0.1475047	cg0701153	cg0701153	24806349	TACCTCTTAACAAAAACTAAC			II	
-0.175339	cg0701574	cg0701574	14780443	CAATATA	28697376	CAATATA	I	A
-0.104674	cg0701843	cg0701843	69725465	TAATTTCCAAAAAAAACAACA			II	
0.1713272	cg0702153	cg0702153	23767478	TAAAATTACAAACCTAACCAA			II	
0.1510144	cg0702349	cg0702349	16735430	ATCAAATATTTATACCTCAAT			II	
0.1044733	cg0702598	cg0702598	61761330	TCCTCAA	60706463	TCCTCGA	I	C
0.1229748	cg0702895	cg0702895	16757359	AAAAACAAAAAACCRAACRT			II	
0.1026001	cg0702977	cg0702977	36775473	TAATTCCTAACRTCAATCRAA			II	
-0.126654	cg0703140	cg0703140	19606305	AAAAAC	30614363	AAAAAC	I	A
0.1037028	cg0703329	cg0703329	55606483	TCTATCTAAAATACTTCCRATA			II	
-0.104719	cg0703596	cg0703596	32670378	AACATTT	50677405	AACATTT	I	A
-0.101245	cg0703796	cg0703796	34643500	AAAACTAATCTTTAACAATTT			II	
-0.101434	cg0704148	cg0704148	57693376	ATTTCTATAAACTATTTCTAAT			II	
0.1059828	cg0704821	cg0704821	11754467	CTACAAAAAACCTCTATTTAA			II	
-0.138936	cg0705116	cg0705116	37752468	CAAAAA	24601384	CAAAAA	I	A
0.1037191	cg0705311	cg0705311	69632377	CCCAACA	18728350	CCCAACA	I	T
0.1505633	cg0705468	cg0705468	27678345	CAATAAA	12778447	CGATAAA	I	T
-0.166425	cg0706178	cg0706178	17644464	AACAACT	65610316	AACAACT	I	C
0.1038321	cg0706355	cg0706355	13760348	ACATTCA	30774479	ACGTTCG	I	C
-0.147835	cg0706449	cg0706449	58683483	TACCCTA	13674339	TACCCTA	I	T

-0.1137	cg07068181	cg07068181	28608460	TTAAAAAAATTTCCTCRTCTTA			II	
-0.109109	cg07075347	cg07075347	59760319	ACAAACC	26780402	ACGAACC	I	A
-0.122229	cg07075387	cg07075387	49604440	ACTATCA	42704427	ACTATCG	I	A
0.1868958	cg07078958	cg07078958	64671370	ACRCCACTCAAAAAATATAAA			II	
-0.110652	cg07082452	cg07082452	47687428	TAACATC	35795412	TAACGTC	I	C
0.12168	cg07083818	cg07083818	16708468	CRAACCAATCAAAATTCTCACT			II	
0.1321563	cg07092880	cg07092880	17741334	CTTTTAAAAAAAACTTTTAATA			II	
-0.1182	cg07093060	cg07093060	24677315	ACTTCACTAAAACATATAAACC			II	
0.1055903	cg07101208	cg07101208	16671320	RAAACTCATAACTCRTAACAAA			II	
0.1036602	cg07101841	cg07101841	23606375	AAAAAAA	67630445	AAAAAAA	I	C
0.1804444	cg07103846	cg07103846	31649399	ACAATTC	60701397	ACAATTC	I	A
-0.112274	cg07105947	cg07105947	28654322	AATCCAA	29639424	AATCCGA	I	C
-0.105265	cg07106927	cg07106927	30800449	TACTACCTAAATTCTAACACAA			II	
-0.105656	cg07113199	cg07113199	56696398	CAAACAA	18634480	CAAACAA	I	A
-0.142433	cg07114310	cg07114310	16646394	AAACRTTTCTTCCTTTTCTTCTT			II	
0.1121279	cg07114810	cg07114810	63676506	AAAATAACCRTAAATAAAACT			II	
-0.102635	cg07116631	cg07116631	69808469	AAACAAT	36794428	GAACGAT	I	C
0.1221692	cg07116712	cg07116712	20799343	CAACCCT	72652348	CGACCCT	I	T
0.1430759	cg07119157	cg07119157	37708397	AAACRTAAACRTAAATATAATT			II	
0.2438986	cg07124183	cg07124183	18742431	TCTCCATAAATAACAACCAATA			II	
0.130363	cg07128503	cg07128503	47802391	AAACCAAAAAACTTCCCTCCTA			II	
0.1252008	cg07134368	cg07134368	31604480	ACRAAAACATATATACACCCA			II	
0.1051308	cg07136254	cg07136254	18664440	CCTAAACAACTCACAACTCAA			II	
0.1715668	cg07136920	cg07136920	11658305	CAAAACC	10709499	CAAAACC	I	A
-0.135865	cg07137336	cg07137336	25632370	TAAAATAAACCCTTCCCCAAAC			II	
0.1157826	cg07139527	cg07139527	17733357	TATAATAACATCCCTAAACTTC			II	
0.137822	cg07143158	cg07143158	32685420	AAAATCA	35752322	AAAATCA	I	A
-0.10857	cg07161993	cg07161993	15623461	AATATACCAAAATTAAATTAAC			II	
0.1103269	cg07167933	cg07167933	69741325	TAAAAAAAACCTACTAATCCTC			II	
-0.111239	cg07173547	cg07173547	13618386	AAAAACTAAAAATAACCRAAT			II	
0.1365528	cg07179033	cg07179033	38633370	CTTTTAAACTATTATATAATCA			II	
0.1197351	cg07181702	cg07181702	61745374	ATAACTTATCAAACTAATATTA			II	
-0.227208	cg07182616	cg07182616	60691506	TCCTTTATCTTCTTTTCAAATTC			II	
0.1686386	cg07187202	cg07187202	60725377	TCAAACAATAATATATCCAAA			II	
-0.107223	cg07188591	cg07188591	73779374	TCAAAAC	32785438	TCAAAAC	I	C
-0.105009	cg07200874	cg07200874	62797430	ACCCAAA	40779370	ACCCGAA	I	C
0.177291	cg07200939	cg07200939	66618309	ATTCTTCAAACRACTTAAAAAC			II	
0.1514328	cg07201475	cg07201475	51673397	CAATTTACTAACAACATACCTA			II	
0.1213442	cg07204662	cg07204662	35802327	ATCTCCA	63636368	GTCTCCG	I	A
0.1004141	cg07205796	cg07205796	40763390	ACATAAC	29665340	ACATAAC	I	A
0.1268863	cg07213181	cg07213181	31748390	ACACAACTATCCAAAACTAAA			II	
0.1222849	cg07213780	cg07213780	13608319	AAAAAACTCCCAAACCTACTTC			II	
-0.204333	cg07215504	cg07215504	63601400	TATTCTTC	69745364	TATTCTTC	I	C

-0.11934	cg0721569	cg0721569	25803509	TTAACAC	69798377	TTAACGC	I	A
0.1103117	cg0721652	cg0721652	44631403	ACAATTATTCTAAAAACTTAA			II	
-0.452999	cg0721661	cg0721661	16609425	TATAAATTTACTTCTAAAATCR			II	
0.1014203	cg0722065	cg0722065	24778345	TCAAACTAAAATACAAATTTC			II	
0.109435	cg0722125	cg0722125	20797361	CTCCTTAACAACAAAATATTA			II	
-0.170922	cg0722320	cg0722320	65740494	AAATTCA	49653476	AAATTCA	I	C
0.1308138	cg0722718	cg0722718	68679473	AACCCTC	13794443	AACCCTC	I	C
0.1025972	cg07228241	cg07228241	56749353	AATTACA	60751355	AATTACG	I	A
0.1101831	cg0722976	cg0722976	26611405	TAACTCATCCTAAATAAAAAC			II	
0.1110163	cg0723035	cg0723035	72645482	AAAAAA	46695468	AAAAAA	I	A
0.1782406	cg0723200	cg0723200	46717453	ACTCAAAAAACCTTCAAACTA			II	
0.1459285	cg0724084	cg0724084	35619467	CAACAACTATTACTAATTCAA			II	
0.1038873	cg0724108	cg0724108	48806509	CAAAAA	37709383	CGAAAA	I	A
0.2426672	cg0724948	cg0724948	24611488	TAAACCCTACAAAAATTTCCA			II	
0.1884856	cg07254421	cg07254421	19650479	RTATACTTCCTCAATAAAAAT			II	
0.1191223	cg0725782	cg0725782	28751331	ACCACAA	39657373	ACCGCAA	I	C
-0.510695	cg0725840	cg0725840	41739423	ACCAACT	37800497	ACCGACT	I	T
-0.293593	cg0725898	cg0725898	61749335	AATTAAAATCAAACAATATAA			II	
-0.110518	cg0726059	cg0726059	60648498	CACCTACCTAAAAATCAATCC			II	
0.1027006	cg0726580	cg0726580	13716447	ATATCTAAAATAAAATATTTC			II	
0.1202848	cg0726760	cg0726760	14746373	AAAAACTAAAATCRTACAAAC			II	
0.1351286	cg0726824	cg0726824	30758428	CACATATTTTATATTAATTCAC			II	
-0.209355	cg0726872	cg0726872	12744392	RAAAACRAACTACRAATCTCC			II	
0.1417065	cg0727322	cg0727322	35708382	ACTCCCAAAACTTATATTTCAT			II	
0.1735193	cg07284261	cg07284261	13671359	CCATATACTTTAACTTTAACTA			II	
0.1909759	cg0728523	cg0728523	64612381	TACAACTATATTCAACTAAAA			II	
0.1238365	cg0728567	cg0728567	27652378	AACCTATCTAAAAACATACCT			II	
-0.105189	cg0729411	cg0729411	58629344	ACTAAAAACAAAAACAAATTA			II	
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-0.111318	cg0729524	cg0729524	57635507	AAACCCTAAAAACTTAAAAAA			II	
	cg0730150	cg0730150	71714478	CTAAAAT	67810399	CTAAAAT	I	A
0.100335	cg0731050	cg0731050	58778310	AAAAAAAAACCTAACTCAAAA			II	
-0.118184	cg0731102	cg0731102	59645339	AAAAAACRTAAACTTTATCAA			II	
0.1286579	cg0731673	cg0731673	53683400	CTAATCTATAACTAACCACCT			II	
-0.108257	cg0732214	cg0732214	48755323	AATCTAAAAACCCRACCTTAA			II	
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	cg0735116	cg0735116	15625403	TTCTAAA	13644383	TTCTAAA	I	C
0.1012793	cg0735568	cg0735568	39768474	CRAAAAAATCACCCTCRTTTA			II	
-0.121989	cg0735592	cg0735592	25621344	TATCACT	61624473	TATCACT	I	A
0.153902	cg0735771	cg0735771	33649493	TACTACTACCAAAAACCACTA			II	
-0.140084	cg0736512	cg0736512	45618394	AAATCTAAACAAAACRTAAAA			II	
-0.171302	cg07365741	cg07365741	61780399	AAAACCACCRACTAATACTAC			II	
0.1359021	cg0737141	cg0737141	51725339	CTCCAAAACAATAATAAAAAT			II	

0.1065148	cg0737174	cg0737174	40673411	RACRAATTTATAAACACCCAA			II	
-0.10377	cg07376381	cg07376381	10710408	TCACTAC	19680443	TCACTAC	I	T
0.1552933	cg0738020	cg0738020	11717415	AAAACTACAAACATCCATTCA			II	
-0.142374	cg0738150	cg0738150	33659300	AACATAA	30603504	GACGTAA	I	A
0.2811573	cg0738234	cg0738234	18809480	AAACCAT	52801344	AAACCGT	I	A
0.1564745	cg0738452	cg0738452	35693419	TCTAACATAAAAAACCCRAAT			II	
0.1257988	cg0740293	cg0740293	29764440	TCTCTCCTTCTAATAATAAACC			II	
-0.105415	cg0740448	cg0740448	14653354	CTACTTATAAATATTCTATTAA			II	
0.1458015	cg0740773	cg0740773	64794458	ACRAAAATTCCAACTACTAAA			II	
0.1309362	cg0740823	cg0740823	10764503	ATTCTAAACATCTATCTATCCC			II	
0.1652496	cg0741395	cg0741395	24651408	CAAATTAAAACTTAACTATCA			II	
0.1810151	cg0741442	cg0741442	17763405	ACAACCAAATCATATCAAATA			II	
	cg0741970	cg0741970	13644507	AAATCAA	12806455	AAATCGA	I	A
0.1066759	cg0741979	cg0741979	53683423	AAAAATCTACAAAACAAACTC			II	
0.1172225	cg0742132	cg0742132	14643465	AAAAAATACAAAATTTATCTC			II	
0.1768061	cg0743792	cg0743792	41664365	ATAAATAATAATCCTTATCAA			II	
0.1115763	cg0743824	cg0743824	58738403	AACCCCATAAAACTTTAATCA			II	
0.1089521	cg0744127	cg0744127	32783348	TCCAAACACCACACTAAAACC			II	
0.1254566	cg0745180	cg0745180	29693347	TCTCCATTTAAAAACAACTCA			II	
-0.339884	cg0745344	cg0745344	22631335	TAAATTTTAAACCAAACTTCCT			II	
0.1118733	cg0745385	cg0745385	63781398	AACCACTATAACAAAATAAAT			II	
-0.239945	cg0745579	cg0745579	47702338	AACAAAA	44613324	AACGAAA	I	A
0.2402348	cg0745658	cg0745658	68672490	ATACAAAAAATATCTAAAAAA			II	
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-0.154871	cg0746616	cg0746616	66752401	TCTCCAC	36759444	TCTCCGC	I	C
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-0.126246	cg0747467	cg0747467	68614381	CRATAATAAACAACTAAATAA			II	
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-0.108293	cg0747961	cg0747961	71612425	AACTTCT	25622453	AACTTCT	I	A
0.1054952	cg07488141	cg07488141	69607345	CCTACCTCTAAATTCTACTCCT			II	
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-0.154288	cg0749204	cg0749204	65743337	ACAAATA	57795458	GCAAATA	I	A
0.1075839	cg0749304	cg0749304	39621398	ATATCTC	32729495	ATATCTC	I	A
0.174662	cg0749319	cg0749319	52717438	AATCTCATACTTTCTATATCTC			II	
0.2054449	cg0749540	cg0749540	53603450	TATCCAACAAACAAAAATCAA			II	
0.1617897	cg0749808	cg0749808	32632486	ACACCTAACRAAAAAACRATT			II	
0.1327495	cg0749918	cg0749918	19642415	ACTCTAAACCATTTTTAAACTA			II	
-0.162041	cg0750102	cg0750102	48646448	TTTAATCTATCTTCCTAAATAA			II	
-0.114589	cg0750615	cg0750615	30804471	CCTCRATAACAAATTTTAAAC			II	
-0.191901	cg0750993	cg0750993	35669497	TAAACAA	40808423	TAAACAA	I	T
0.1044493	cg0751773	cg0751773	41655378	AAATAAAATACCTCRTTCAAA			II	

0.1145344	cg0751942	cg0751942	40786373	ATCAAAT	54737359	GTCGAAT	I	T
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0.1299052	cg0752297	cg0752297	19647471	CTTATACACACTACRTACAAA			II	
-0.304825	cg0752371	cg0752371	15798465	TTTATTAAAATTTTCCTTAACC			II	
0.1070175	cg07525471	cg07525471	59768415	ACCCCCA	45696375	ACCCCCA	I	A
0.1111786	cg0752912	cg0752912	51782346	CAAAAA	55734325	CAAAAA	I	A
-0.127281	cg0753208	cg0753208	66676374	TCCATTC	52766421	TCCATTC	I	C
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-0.16782	cg0753756	cg0753756	34743307	RACTTAAAAATTCTATAAAAC			II	
0.118324	cg07537821	cg07537821	60767362	ATACTAAAAAACAAACTTACT			II	
0.1328436	cg07563611	cg07563611	57705400	AAAACA	69681379	AAAACG	I	A
-0.153052	cg0756497	cg0756497	69750510	TATAATTCATAATTTTCCCTA			II	
0.1104211	cg0757468	cg0757468	65680381	AAAAAATTCACCCCCRCAACC			II	
0.1029293	cg0758409	cg0758409	20662320	AAAAATATCTACCTTTATCTTA			II	
0.2767876	cg0758462	cg0758462	33708372	RTCTTCTAAATACRAAAACCC			II	
0.1459396	cg0758485	cg0758485	18629366	CTACAAA	26751504	CTACAAA	I	T
0.1159888	cg0758542	cg0758542	50730344	AACAAATCAATTTCAAAAAAT			II	
0.1061618	cg0758698	cg0758698	38602306	ATACCATTACTAACTTCCAAA			II	
-0.113556	cg0759272	cg0759272	36761355	CAAAAATATCAACAAACACTT			II	
-0.224485	cg0759277	cg0759277	12673368	AATAAAACCTAATAAACCCTC			II	
0.1201659	cg0759797	cg0759797	32649400	ATTCATTTCTATTTTCTACACA			II	
-0.111592	cg0759895	cg0759895	44802330	AAAAAA	54623508	AAAAAA	I	A
0.2426614	cg0759913	cg0759913	30633361	AACCTAAAAACTATACAAAAC			II	
0.2370452	cg0760062	cg0760062	71672475	CAACACC	12755445	CAACGCC	I	C
-0.123734	cg0760752	cg0760752	39677319	AAAATACTATATATTCTAAAA			II	
-0.126354	cg07611121	cg07611121	29737489	AAACCRAAAAAAAATTCCTAA			II	
-0.14511	cg0761580	cg0761580	60627488	TATACRCATCAAACCTAACAT			II	
0.1107133	cg0761968	cg0761968	27762364	TTTTAAA	39611482	TTTTAAA	I	A
0.233622	cg0762085	cg0762085	70743481	TTTCACAATCAAACCTAATAA			II	
0.1638928	cg0762169	cg0762169	53769468	CTAACTTCTCCTAAACACTTAC			II	
0.1193129	cg0762577	cg0762577	59768425	ACAAAAT	70628390	ACAAAAT	I	A
0.3304715	cg0762962	cg0762962	50723326	ACAAAAA	15760401	ACAAAAA	I	T
-0.107029	cg0763366	cg0763366	37800461	TATTCCTAACRTCTAAAATTTA			II	
-0.341844	cg0763919	cg0763919	19621471	CTACATAAAACCTCAAATCCT			II	
-0.11444	cg0764157	cg0764157	58611359	ATCATAAAATATCATATAAAT			II	
0.1804428	cg0764276	cg0764276	12687381	TTTACTTATTCCCACRACCTAA			II	
	cg0764961	cg0764961	45763323	CCAAACT	73790462	CCAAACT	I	C
0.1276408	cg0765218	cg0765218	49739311	CTCATCAAAATAACCTTTATTA			II	
-0.193929	cg07655261	cg07655261	68715408	AACTTAAACCAACTAAAACAA			II	
-0.10967	cg0766083	cg0766083	70620322	TAAAAACCTACTCAAACTCRC			II	
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-0.142082	cg0766457	cg0766457	35709459	TTTCCAACRATACCCCAAAAA			II	
0.1115856	cg0766522	cg0766522	40601507	TAAAATCAAAAAAACAATTAA			II	

-0.114206	cg0767051	cg0767051	47794342	AAAAAAAAACCAATACCTATC			II	
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-0.113583	cg0767302	cg0767302	10645390	ATTTTTACCCCTTAAACTATAC			II	
-0.112818	cg0767413	cg0767413	66667457	ACAAAA	22611489	ACGAAA	I	T
-0.14431	cg07676361	cg07676361	48778458	CCAAACT	46705324	CCGAACT	I	T
0.1194801	cg0767715	cg0767715	18621333	TAATAAATAAATCATCACCTA			II	
-0.146471	cg0768694	cg0768694	62687300	CACAAA	70644435	CGCGAA	I	T
0.1037025	cg07689731	cg07689731	47623328	TAACTCTAACTATAACATCAA			II	
0.1138563	cg0769627	cg0769627	11720369	TAAAATTCTTTTCTATTACTAA			II	
	cg0769722	cg0769722	26785447	AATAAAC	13644463	AATAAA	I	C
0.1132448	cg0769819	cg0769819	22657484	ATTTAACACCAACRAAATTCC			II	
0.123244	cg0770039	cg0770039	59645308	CTTCCCATAACTCTATAAAAA			II	
0.1042991	cg0770130	cg0770130	54789502	TATACCAATAACTAATCTCCA			II	
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0.11729	cg0771108	cg0771108	22672493	CTAAATT	66748471	CTAAATT	I	A
0.2080329	cg0771216	cg0771216	36762442	CAAAAA	63613473	CAAAAA	I	C
-0.113395	cg0772462	cg0772462	62627470	AAAAATACAAAATCCRAAAAA			II	
0.1278539	cg0774030	cg0774030	60667476	TTCTCTA	32658314	TTCTCTA	I	A
-0.139923	cg0774570	cg0774570	28677340	CATAAAA	68655410	CATAAAA	I	T
-0.138871	cg07747251	cg07747251	64713395	ATTAAAA	39679370	ATTAAAA	I	A
0.1818912	cg0774796	cg0774796	30725447	AAAAAC	24621454	AAAAAC	I	C
0.1364633	cg0774959	cg0774959	52632437	ACCAAACCCACRAATCTAAAC			II	
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0.1391922	cg0775336	cg0775336	65787348	CAAAATACTAAACATTAAAAC			II	
0.1010506	cg0776405	cg0776405	27785330	AACTACACATAAATATATTTA			II	
0.1371812	cg0776598	cg0776598	58716480	CTACAAATCTTTTAACTACCA			II	
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0.2185503	cg0777704	cg0777704	71750361	TCCRTATCTAATATAACCACTT			II	
-0.112865	cg0778034	cg0778034	20804304	CRAATTAAATTAACTTAACRA			II	
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0.1165398	cg0778754	cg0778754	21627306	ACACRATCTAACAAAACATAA			II	
-0.417255	cg07792871	cg07792871	37774469	AATTCTCTAATCCATTTATAAA			II	
0.2340067	cg0779516	cg0779516	41604509	AAACAAC	41702418	AAACGAC	I	C
0.1111146	cg0780447	cg0780447	29663367	ATACTTCTATCTTAATCAACTC			II	
0.1122965	cg0780506	cg0780506	48751392	AAAATCAAAAAACTTAACTTA			II	
0.1748158	cg0780554	cg0780554	11719474	ATATCAT	33743421	ATATCAT	I	T
0.182264	cg07807111	cg07807111	28755369	CTTTACTAAAAACACACACAC			II	
0.2846488	cg0780737	cg0780737	56788301	TAAAAACAAATCATTCTAATA			II	
-0.106583	cg0782078	cg0782078	37641313	TAAAATA	69718340	TAAAATA	I	A
-0.128551	cg0782137	cg0782137	36780352	ACRATAATAACAAAAAAACCT			II	
0.1938998	cg0783131	cg0783131	61647402	AAATTTAAATATATTCCAAAA			II	

-0.158066	cg0783200	cg0783200	45781488	AACCTAA	70708348	AACCTAA	I	A
-0.122917	cg0783992	cg0783992	62620439	AACTCCA	52777432	AACTCCG	I	C
	cg0784513	cg0784513	13644465	TCCTACCAAAAAACTACRATA			II	
0.1429958	cg0784687	cg0784687	12763311	TAAAAATATATTTCCTCAAC			II	
-0.247996	cg0784848	cg0784848	28767464	CCTCTAAAATCTATCTCATCC			II	
0.1918575	cg0785032	cg0785032	53702395	TAAATATTATCAACATAACCT			II	
-0.174416	cg0785126	cg0785126	56711481	ATAACACAACCTATAAACAAA			II	
0.1186125	cg0785411	cg0785411	10734336	AAATAAAATAAATCAAAAAA			II	
0.1832101	cg0785557	cg0785557	14780479	TCTATAAAAATAACATTAAAA			II	
0.1472152	cg0786246	cg0786246	34704447	CACAAAAAAAACCCTCCAAAA			II	
0.1004099	cg0786302	cg0786302	57771331	CTATCTT	68707371	CTATCTT	I	A
-0.292845	cg0786672	cg0786672	28615375	TAACTAAAAAATCAATACTAA			II	
0.1492693	cg0786690	cg0786690	41604333	ATATTTTCTAATCCTTCTTCAT			II	
-0.10029	cg0787054	cg0787054	55751327	CCAACTACTTAAAACRATAAA			II	
-0.216296	cg0787092	cg0787092	17666406	CAAACTATTAAACCTATTAAT			II	
-0.104612	cg0787401	cg0787401	16673473	ACTACTAAAATCATCRCCCAT			II	
0.1187772	cg0787506	cg0787506	46632507	AACTTCTACAAACACCTCTAA			II	
0.1186846	cg0787632	cg0787632	17621427	AAAACAAACTACAAACTCAAA			II	
-0.11348	cg0787683	cg0787683	50661376	CCTTCTATATCTAAAATATACR			II	
-0.297579	cg0787862	cg0787862	18757475	AACTATAAAAACCCAAATCAA			II	
-0.168422	cg0788283	cg0788283	55609344	AATTTACTACTAAACCTCCTA			II	
0.153387	cg0788486	cg0788486	20720372	AAAAAAATTTAACCTCATAA			II	
-0.101768	cg0788900	cg0788900	49677481	CTCATCT	55756510	CTCATCT	I	T
0.105166	cg0789600	cg0789600	35729356	TCAATACTCTCCTATAATAAA			II	
0.1533995	cg0790151	cg0790151	28689449	AAATCTAATTCACTCACTATTA			II	
0.1086414	cg0790429	cg0790429	58651475	AAACCTC	39795354	AAACCTC	I	T
-0.1312	cg0790626	cg0790626	13766454	AATAACA	53717395	GATAACA	I	A
0.1012136	cg0790917	cg0790917	30800340	AACRTTCRATAAAATCRATTA			II	
0.1180405	cg0791597	cg0791597	42781406	CAAACTCATATTTCCTTAATAA			II	
-0.129832	cg0791760	cg0791760	69634403	CCCTAAACCTAAAACCTACRT			II	
0.1151134	cg0792506	cg0792506	41794502	ACAAAA	24744335	ACGAAA	I	A
-0.130853	cg0792976	cg0792976	27741510	TACCCAATAACCTAACACTTA			II	
-0.180628	cg0793058	cg0793058	63750350	TTACTCTATATTAAATCTACAC			II	
-0.107847	cg0793289	cg0793289	25694489	TCAAAATCACCCAAAACCCCC			II	
-0.122734	cg0793307	cg0793307	54680309	AAAAACA	28641391	AAAAACC	I	T
-0.100569	cg0793695	cg0793695	73760356	CCAAACC	74623336	CCAAACC	I	A
0.1425642	cg0794383	cg0794383	28624394	ACATTTTAAATCAATATTAAT			II	
-0.114411	cg0795097	cg0795097	33721323	CAATAAAATAAACTTTAACAT			II	
-0.113651	cg0795242	cg0795242	11676351	AAATTAATTTAATCCCTAAAA			II	
0.4522102	cg0795510	cg0795510	72695488	ACCAAAAACAACRAAACACA			II	
0.1457539	cg0796062	cg0796062	62713349	AAACAATACTTATATATCTAA			II	
-0.17885	cg0796293	cg0796293	60709444	AAACAAA	30743500	AAACGAA	I	A
0.1172881	cg0796421	cg0796421	48640371	TTCCCTACTTATTCTATCCTAA			II	

0.1512706	cg0796475	cg0796475	67661509	TTCCCCA	23759375	TTCCCCA	I	C
0.1271624	cg0797079	cg0797079	46613418	AATAAAC	31718497	AATAAAC	I	C
0.1012443	cg0797159	cg0797159	30638432	AATTCATTATATCTAAACTACR			II	
-0.198178	cg0797316	cg0797316	72765306	CAACTCATTCCTACCTAACAC			II	
0.1270259	cg0797330	cg0797330	71741400	ATAAACCCTTAACACACAACT			II	
0.1158289	cg0797678	cg0797678	44746439	TCTACCRTACATCTTTACTTAT			II	
0.115746	cg0797934	cg0797934	53691440	TCACATAACAACCACAAATCT			II	
0.1323496	cg0798126	cg0798126	67766331	CCCTAACTTAATTCTAAATCAC			II	
0.1386829	cg0798438	cg0798438	69795483	ACAATTTACACCAAAATTCCT			II	
0.1001793	cg0799683	cg0799683	28746438	ATAAAACCCCTTCACAAAAAA			II	
0.113793	cg08000731	cg08000731	52628380	AAAAAAAACAAAACCAAACA			II	
0.1227784	cg0800340	cg0800340	55749387	CTACRCTTAATACRAAACCAA			II	
-0.220164	cg0800823	cg0800823	50707487	CCCRATTCTCAAAACATAATA			II	
0.1814135	cg08010331	cg08010331	64762362	AACACTTACTTATACCAAACA			II	
0.1200455	cg0801763	cg0801763	39801427	TCCTAATAATACAACTACTAA			II	
0.1028074	cg0801814	cg0801814	71767433	TCCTTCCRATCCCACTTCCAAA			II	
0.3285781	cg0802426	cg0802426	66713451	TAAACTTTTCAAAAAATATCC			II	
0.1318196	cg0802929	cg0802929	48617371	AATCAAATATACCCCCCRACC			II	
0.1113562	cg0802996	cg0802996	61672364	TAAAAA	73645392	TAAAAA	I	A
0.1443585	cg0803092	cg0803092	36730347	AACTTTATTTAACACAACCA			II	
0.1103452	cg08035351	cg08035351	43606408	TTAATTAAATAACTATATAAT			II	
0.1179264	cg0803803	cg0803803	10739488	ACACACTCTTCTATTAAAAAA			II	
0.139995	cg0803958	cg0803958	10696356	CTTATAAAAAACCAACCCRAA			II	
0.125322	cg0804144	cg0804144	36801357	AAACCAC	14739409	AAACCGC	I	C
-0.334711	cg0804826	cg0804826	49647508	CATCCAA	41755442	CGTCCAA	I	A
-0.254431	cg0805313	cg0805313	35684432	ACCCAACAACCCAAAATCTAC			II	
0.1838312	cg0806220	cg0806220	39733387	AAAAAA	35620477	AAAAAA	I	C
0.124105	cg0806429	cg0806429	58725450	AAAAACCRAACAACACCTAAT			II	
0.1144995	cg0806522	cg0806522	56800391	CTCTTTATAACCATAAAACTTA			II	
-0.174301	cg0807643	cg0807643	38678341	CCCAATT	17774500	CCCAATT	I	C
0.1011966	cg0808178	cg0808178	53621420	CTTTCCRATTTAAAATATTATT			II	
-0.111927	cg0808415	cg0808415	46694365	AAACTAA	21755423	GAACTAA	I	A
0.1620789	cg0809166	cg0809166	65671470	AAAAAATATAAAATTTCCCCT			II	
0.1337979	cg0809781	cg0809781	37758335	TATCTAAAAATCATACTATTA			II	
-0.115861	cg0810130	cg0810130	20654307	AACAAA	28717434	AACGAA	I	A
-0.232518	cg0810256	cg0810256	29676374	AAACAAAACAACCTAACTAAA			II	
0.1162637	cg0810347	cg0810347	27698360	CACCTCCCACCCTTAAAAAAA			II	
0.1210296	cg0810637	cg0810637	57799424	TCAAAAAATAAAAACAATACT			II	
-0.101535	cg0810980	cg0810980	54645374	ACTACTCTACCATTACATTCCA			II	
-0.148686	cg0811828	cg0811828	33687506	AATATAT	63705377	AATATAT	I	C
0.2213495	cg0811952	cg0811952	29757498	TCACATTCTAATACTCTAAAA			II	
0.2472957	cg0812140	cg0812140	50683352	CCCCTTATCTTTCACACTAACC			II	
-0.126469	cg0812145	cg0812145	29648478	AAAAAA	69782310	AAAAAA	I	A

0.1035403	cg0812168	cg0812168	67779397	CCCAAAAAAACCCRTTAATAA			II	
0.1852252	cg0812341	cg0812341	47778399	AAAAATCCAATATCTTCAAAA			II	
0.1144629	cg0812582	cg0812582	74679390	CTCAAATACTCACTAAAACAT			II	
0.2217754	cg0812826	cg0812826	12676359	ATAAACATCRTATAAAAAAAC			II	
0.1285927	cg0813366	cg0813366	65716403	AAAACATTATAACCACTCTTC			II	
0.1902505	cg0813369	cg0813369	66746321	CCTACATTAAACATTAACCAT			II	
0.1121895	cg0814011	cg0814011	17754498	TACTAAAATATATTAACCTCT			II	
0.1541265	cg0814304	cg0814304	39734330	AATTATATTAATCCRTTCTCAC			II	
-0.205791	cg0814670	cg0814670	24809380	ACATACA	58767470	ACGTACA	I	C
-0.331645	cg0814686	cg0814686	26716431	CTCTTTACTAAAAACTATTCAT			II	
-0.111951	cg0815162	cg0815162	67731429	CTCACAC	47650332	CTCGCGC	I	C
0.1268312	cg0815731	cg0815731	34648300	ACTACTTCATTTTTAAATTTTA			II	
0.2850244	cg0815810	cg0815810	26747343	ACCAACTCAACTATCCAATTC			II	
0.1383789	cg0816094	cg0816094	31700426	TATCACTACCAATACTCAAAT			II	
-0.176596	cg08166631	cg08166631	15660481	CTTAAAAACAAAAAATCTCAC			II	
-0.102788	cg0817029	cg0817029	38600397	CACCCAA	32703303	CACCCAA	I	A
0.1280339	cg0817210	cg0817210	29651467	TAAACCTAAATTCCATATCTTT			II	
-0.180323	cg0817247	cg0817247	43682494	ATCAATAATAAATAAAACTTA			II	
-0.128841	cg0817478	cg0817478	29778377	TAATAAA	66723452	TAATAAA	I	T
-0.202327	cg0817641	cg0817641	41780301	ATAACTCCCTTTCCTTTCCACA			II	
0.1067869	cg0817701	cg0817701	10682320	CTTAAAACCRAAAATTTAAAA			II	
0.1044523	cg08191781	cg08191781	53774317	TCCAAACTAAACATTTAAACA			II	
-0.112685	cg0819432	cg0819432	26713357	AAAATCCAAAAAAACCCTACA			II	
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-0.29123	cg0820054	cg0820054	49726317	AAAATCCCATAAAAAAACTTA			II	
0.1149466	cg08200621	cg08200621	13714477	AAACTCC	49744305	AAACTCC	I	T
0.2485292	cg0820346	cg0820346	15742320	TCACAAATAACTATAAATTAA			II	
0.1308624	cg0820609	cg0820609	64636505	TTCATCCATAACTTAAAAATA			II	
-0.114741	cg0821286	cg0821286	13607487	AACRATCCTACATCTAAATCT			II	
0.2959591	cg0821735	cg0821735	21657325	TATTCACTCAACAACCCTTTAA			II	
0.1328193	cg0821917	cg0821917	23631406	AATATCTATCTCCTCCTCTAAA			II	
0.1046992	cg0821921	cg0821921	10722412	TAACACC	37623347	TAACGCC	I	T
-0.17244	cg0822251	cg0822251	65721447	TAAACAA	29784479	TAAACAA	I	C
-0.154286	cg0822261	cg0822261	38686484	CAAAACC	44694343	CAAAACC	I	C
-0.283437	cg0823169	cg0823169	38645482	AACACTA	71666438	AACACTA	I	A
-0.165362	cg0823314	cg0823314	35780324	CTTTATAAAACTCAAAATCAA			II	
0.1353603	cg0823756	cg0823756	55635419	RCCTTCCAAAACTCATAATAA			II	
-0.193351	cg0823831	cg0823831	35661439	TTACTAACTCAACCAAAAAAA			II	
-0.490015	cg0823837	cg0823837	47615483	CTTCACCRAATTTTATCTTACT			II	
-0.113397	cg0823969	cg0823969	56785368	AAAAATC	50644420	AAAAATC	I	A
0.1671234	cg0824223	cg0824223	61655384	CTAATAT	16797406	CTAATAT	I	T
0.10553	cg0824285	cg0824285	16673423	AACCTAAATCAAAAACTCAAA			II	
-0.125782	cg0824372	cg0824372	43786494	TACTATA	33657422	TACTATA	I	A

-0.412715	cg08250118	cg08250118	44675342	TCCAATTTCATACCCCCTCTCC			II	
0.4214152	cg08253809	cg08253809	62661502	TAAAATAATCTTTCTACCTCAA			II	
0.1548395	cg08258654	cg08258654	11782430	TCATTCCACTCCAATTAAATAA			II	
0.1149902	cg08263140	cg08263140	54700302	TCACTCTACTCCAAACACATTA			II	
0.1343079	cg08265392	cg08265392	51662354	TCCAATAAATATCACTTCCRTA			II	
0.1002246	cg08268692	cg08268692	68794349	ATATCTAAATCACTTATTAATC			II	
-0.223056	cg08269974	cg08269974	27605303	ATCAACC	16682363	ATCGACC	I	C
0.2672935	cg08272429	cg08272429	24608456	AACCAAATAAAATAATAAAAA			II	
0.1134489	cg08272591	cg08272591	70605446	AAATAATTCAAATAAATTAAC			II	
-0.141815	cg08274589	cg08274589	28666467	TAACCAA	37803421	TAACCGA	I	C
0.1158624	cg08282819	cg08282819	42753354	AATACACRAATTTCCTACCATT			II	
0.1659979	cg08285768	cg08285768	34793433	ACTCCAAAATAACTAACTCTA			II	
0.3769266	cg08289272	cg08289272	23652432	TTCCTAACAAACTTTAACAAAT			II	
0.1752833	cg08292959	cg08292959	70754447	ACAAAA	36781418	ACAAAA	I	C
0.1376459	cg08293002	cg08293002	20705346	RCRAAATAAACTAAACTTAAA			II	
-0.148726	cg08293242	cg08293242	47695457	TAAACCC	43706315	TAAACCC	I	A
0.2431689	cg08293392	cg08293392	58736354	CACRAAAACCCAACTCCACCT			II	
0.1042964	cg08296868	cg08296868	37627429	TCACAAA	27764490	TCACGAA	I	A
0.2414083	cg08299859	cg08299859	52694424	TTCTACRTATTCCTTTCTATTCT			II	
-0.228682	cg08300475	cg08300475	10660302	AAAAACACACACAAACACAAA			II	
0.178906	cg08305942	cg08305942	20600451	AATAATACRAACACAACTAAT			II	
-0.10316	cg08308214	cg08308214	44803398	TACTTCATCTCTCTCTCTTTA			II	
0.1261563	cg08309687	cg08309687	50726380	ACTCTACAAACCACACTCAAA			II	
0.1352236	cg08312765	cg08312765	63701438	TTTTATCACAACAAAAATCTTA			II	
0.1002296	cg08316699	cg08316699	12625334	AAATATAACTACTACTAAAAC			II	
-0.100957	cg08317694	cg08317694	40661481	ACTCATA	58673376	ACTCGTA	I	A
0.1086729	cg08319103	cg08319103	33739454	TACTATT	52676471	TACTATT	I	A
-0.131433	cg08333400	cg08333400	22642441	CTATCTACTTAAAATACATACA			II	
-0.110216	cg08335008	cg08335008	54613424	CAAAATC	69684370	CAAAATC	I	A
-0.100484	cg08348121	cg08348121	70650432	AATAAAC	41667361	AATAAAC	I	A
0.1443407	cg08355045	cg08355045	52778306	AACATATAAACACAAAACTTA			II	
-0.156958	cg08355157	cg08355157	52777483	ACAAATCAAAAAATCCTTAAA			II	
-0.15133	cg08355456	cg08355456	49704335	ATAAAAC	42675320	ATAAAAC	I	A
-0.132641	cg08357436	cg08357436	14790391	AAAAACA	62719414	GAAAACC	I	A
0.1125311	cg08360511	cg08360511	36755457	AAAAACT	30758505	AAAAACT	I	A
0.1751365	cg08367801	cg08367801	35601365	TTCTTTAACAAAATTAATCRCT			II	
0.1016095	cg08368875	cg08368875	46750400	TATAAATTCATACTTAAAATAA			II	
0.1008298	cg08373528	cg08373528	57676503	CAACCTC	38676483	CAACCTC	I	A
0.1732172	cg08373622	cg08373622	71729412	AAATACCTAAACTTAAAAAAA			II	
0.1275376	cg08373989	cg08373989	65751422	CCCCATCTATACACAAAATTAA			II	
0.1548124	cg08378932	cg08378932	65704464	AACAAAAAAACAACAAATATT			II	
0.1058357	cg08381046	cg08381046	64661310	ATACACAAAAAAAACCTAAAA			II	
-0.168043	cg08381537	cg08381537	45777500	AAAAAA	32712359	AAAAAA	I	C

-0.148792	cg0839020	cg0839020	16629508	AACCTAAATTATAAATTCACC			II	
0.1626788	cg0839274	cg0839274	41786390	AATAATTTTCTTAAACAATAA			II	
0.1124759	cg0839574	cg0839574	63799460	AACAAAAATTACAAACTAAAT			II	
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-0.131724	cg0839579	cg0839579	70795332	AACCAA	34745451	AACCAA	I	A
0.2531378	cg0839799	cg0839799	71613387	AAAACRCCACAAACCATAAAA			II	
0.1315473	cg0840172	cg0840172	14735409	CAACCAACTCTCATCCTCAAA			II	
0.1277377	cg0840193	cg0840193	24802413	AACACTA	60775315	AACACTA	I	A
-0.107645	cg0840400	cg0840400	43785333	AATTAATCTCCAAAACTAACA			II	
0.1277192	cg0840451	cg0840451	10750439	AAATATTTATACATAATTATC			II	
0.1021813	cg0841221	cg0841221	41660507	ACAAATAATAACAAATTAAAC			II	
0.1062266	cg0841945	cg0841945	65690351	TAATCATAAATAAAAACAAAA			II	
0.1595522	cg08421351	cg08421351	30674480	ATAAACCAACTAAACTAACAA			II	
-0.22496	cg0842242	cg0842242	47792331	ACACAA	14673478	GCACGA	I	C
0.1065222	cg0842615	cg0842615	32668320	ATAAATT	55698420	ATAAATT	I	C
0.1085569	cg0842970	cg0842970	51699499	AATACTTACATATACACCTCT			II	
0.2088843	cg0843027	cg0843027	70781380	AAAATATACATTTATTTCCAC			II	
-0.124947	cg08431931	cg08431931	62738320	AAAAAA	38635408	AAAAAA	I	A
-0.138168	cg0843311	cg0843311	15624481	TACTATATAAACATCCRCTAA			II	
-0.193242	cg0843988	cg0843988	23712406	CCTAAAA	17785323	CCTAAAA	I	T
0.1073277	cg0844205	cg0844205	52701303	CCTATTCTATTTAAAATATCCT			II	
0.116593	cg0844356	cg0844356	54652399	TCTCCACRTATAAATCAAAAA			II	
0.1036612	cg0844704	cg0844704	55731332	AACTTACAACTCCCACTCRAT			II	
-0.105271	cg0844913	cg0844913	33641400	TATCTCTTAACTACCRTACCTA			II	
-0.137298	cg0844955	cg0844955	39708435	CAAATACTACTTCATTTTATAT			II	
0.1430532	cg0845401	cg0845401	10677480	CATACCCTTTACTTACAAAAC			II	
0.2197807	cg0846007	cg0846007	54647413	TTTTACRTCTCTATATCTTTTC			II	
-0.177994	cg0846177	cg0846177	65755313	ATACTACCCAAACRAACTTAT			II	
-0.100111	cg0846512	cg0846512	54709363	TTCTTATAATCRAATAACRTCC			II	
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0.2373981	cg0847648	cg0847648	66810458	CTATCCAAAAATTTCTTAAAC			II	
0.1039985	cg0847698	cg0847698	12689487	AATAACTCTAACTAATAACCC			II	
0.1920692	cg0848100	cg0848100	13800314	AATAATCTTTAAACAAAATTA			II	
0.1785951	cg0848499	cg0848499	56696315	AAACAATAAATATCCCCCCAA			II	
0.1042475	cg0849148	cg0849148	35789426	CTACATA	50652323	CTACGTA	I	A
0.1493719	cg0849484	cg0849484	49659388	TATCTCAATAAACTACTTTCCA			II	
-0.130838	cg0849523	cg0849523	12625354	TAAAACT	24649304	TAAAACT	I	A
0.1245939	cg0849871	cg0849871	12646452	AATTAAAATTAATATTTTAAC			II	
0.1080869	cg08499861	cg08499861	71658448	CCCCCCATTTAATTTTCCTTTA			II	
0.1086856	cg0850013	cg0850013	22635426	ACAAACAACTACCCTAAAAAA			II	
-0.214189	cg0850466	cg0850466	47748432	CAAATACTCRACCAAATTAAA			II	
-0.143032	cg0850660	cg0850660	25649385	CCATAAAAAAACACTCAAATA			II	
0.1084335	cg0850667	cg0850667	22731330	ACTCAAAATCCTAAAAAACAA			II	

0.1172377	cg0851023	cg0851023	26625348	AACRCTTCTACAATAACCAAC			II	
-0.268577	cg0851419	cg0851419	72705460	ATACCAAACTATAATTATCTC			II	
0.1019353	cg0851459	cg0851459	26704441	AAATTCTCRAACCAACAATAA			II	
-0.111815	cg0851650	cg0851650	74769420	AAAAACT	31620311	GAAAACT	I	C
0.1478333	cg0851938	cg0851938	40635303	AAATTTTAAACAAAAAAATAA			II	
0.185554	cg0852247	cg0852247	53649408	TCTAATCACCTACAACCTTCTA			II	
-0.330454	cg0852851	cg0852851	50744305	ATTTCATTATTTCTTCATCCTA			II	
0.1088546	cg0853401	cg0853401	31770413	AAATTCTATTAAAACCTTAAT			II	
0.1064101	cg0853483	cg0853483	72715472	CRATTAACAAACCCTACAACT			II	
0.1143776	cg08544331	cg08544331	36602436	AAACRTATAAAAAATCTTCCA			II	
-0.120667	cg0854512	cg0854512	49601481	AACAAA	35603438	AACGAA	I	A
0.1190709	cg0854804	cg0854804	70708459	AACATCC	57646326	AACATCC	I	C
0.182145	cg0854933	cg0854933	25671469	TCATTAACTCTTCACTTATTAC			II	
0.1326653	cg0855455	cg0855455	30790360	ATCAAAATAAAAATAACRCAA			II	
-0.131455	cg0855586	cg0855586	41732344	AAAACC	67769494	AAAACC	I	C
0.1114679	cg08556511	cg08556511	73691397	CTAATCTCRTATATTTATAATA			II	
-0.122766	cg0856814	cg0856814	46628382	RAACACAAACCCACRTAAAAA			II	
-0.120144	cg0857007	cg0857007	41775416	ATAACATCTATTACAACCATA			II	
0.1066889	cg0857024	cg0857024	44686396	AAAAACCRACCATAACAAACR			II	
0.1185171	cg0857368	cg0857368	50731446	CATAATA	73728429	CGTAATA	I	T
-0.115114	cg08575621	cg08575621	17797489	TAATAAA	42789326	TAATAAA	I	A
-0.133398	cg0857957	cg0857957	36793409	AACTCAA	64755341	AACTCAA	I	A
0.1700161	cg0858022	cg0858022	21671300	AATATTT	73718316	AATATTT	I	T
-0.112162	cg0858094	cg0858094	46631351	TAAAAAAATTTCCAAACTACC			II	
-0.162092	cg0859093	cg0859093	22698447	AATTCTAAACCTCTAAAAATT			II	
-0.11285	cg08593141	cg08593141	34654499	AAACTTCTTATAACCCAACCT			II	
0.1326931	cg0859424	cg0859424	23637373	CTAAAACCAATAAAATTACRA			II	
-0.159769	cg0859714	cg0859714	12766306	CTACCCCTACTCTATCAAAAA			II	
-0.100378	cg0859979	cg0859979	56784382	ATATACT	10679329	ATATACT	I	A
0.1124714	cg0860037	cg0860037	27601382	RATTATATCTACTAAACACAA			II	
-0.132711	cg0860162	cg0860162	40606444	TCCTAAA	64681421	TCCTAAA	I	T
-0.11535	cg0860234	cg0860234	59802479	TTACACTAAAATTAACTTAAT			II	
-0.371724	cg0860367	cg0860367	74712324	TCCTAACAACATCTACATTTA			II	
-0.412688	cg0860589	cg0860589	73641389	AAAAACTAATTATCTTACCAT			II	
-0.194252	cg0861042	cg0861042	44703481	TTTAAAA	34722474	TTTAAAA	I	A
0.1013988	cg0861181	cg0861181	14733362	AAACCC	65701446	AAACCC	I	A
-0.119779	cg0861357	cg0861357	38600454	CRATATTTCCTCAACCCCCTT			II	
0.1248278	cg08616111	cg08616111	28786359	CCAACTAACCAAACTAAAACR			II	
-0.19056	cg0861716	cg0861716	16688382	AATAAA	27638409	AATAAA	I	C
0.122699	cg0861929	cg0861929	58688430	ATAAATTATCTATTAACATATT			II	
-0.113036	cg0862192	cg0862192	17740470	CTTAATCRCTAAACTTTAAAC			II	
0.1109802	cg0862195	cg0862195	31758403	ACRAAACTACCAAACACTAAT			II	
0.1227906	cg0862219	cg0862219	36738381	TAAATCAACCTCATAAAAAAA			II	

0.1077507	cg0862491	cg0862491	55739509	CACATTTTACAAATAAACCAC			II	
-0.142836	cg0862664	cg0862664	26754487	ACAACA	20803365	ACGACG	I	A
-0.182155	cg0862939	cg0862939	27702369	ATCATCTTAAAAATTTCCTTAA			II	
-0.155109	cg0863216	cg0863216	30708378	CAAATAC	47671432	CGAATAC	I	A
-0.177958	cg0863347	cg0863347	67714503	TCCCCAA	57641490	TCCCCGA	I	C
-0.192523	cg0863422	cg0863422	56607509	CACAAAC	74768387	CACAAAC	I	C
0.1010218	cg0863540	cg0863540	52656319	CRAAACCCAACTCCAAATAAA			II	
0.1278734	cg0863863	cg0863863	56799350	CTATACCTTCTAATACTCTAAC			II	
-0.106715	cg08640901	cg08640901	44605456	TACAAAACCCTAATTCAACTC			II	
-0.107385	cg0864399	cg0864399	15644504	CACAAAC	38770333	CGCGAAC	I	A
0.1114974	cg0865595	cg0865595	34747398	TTAAAAA	53704486	TTAAAAA	I	T
-0.105303	cg0865677	cg0865677	52684461	TATAAAC	49781466	TATAAAC	I	A
-0.100925	cg0865722	cg0865722	67723380	AATTATATAAAATAATCCTAT			II	
0.136812	cg08660971	cg08660971	45613376	TCCTAAATCTATTCTTTCTTTC			II	
0.1411823	cg0866167	cg0866167	73644489	TCAATATCTAAATCAAAATCT			II	
-0.197684	cg0866916	cg0866916	33740361	CAACCCTACAACTTACTAATT			II	
-0.186671	cg0867322	cg0867322	10730369	TATACTACRCAAACRTATATA			II	
-0.136723	cg0867511	cg0867511	65772402	TTAATATCTCAAATTCAAAAC			II	
-0.112968	cg08679971	cg08679971	33602320	CCCTTAA	31609499	CCCTTAA	I	T
0.1122788	cg0868147	cg0868147	36789373	CCCAAAAAATACTCCTAATAC			II	
-0.106177	cg08682981	cg08682981	35702373	AACTAAACCAAAACRAAATAC			II	
0.1507926	cg0869267	cg0869267	73808406	TAACTTACCCAAATTCTAATA			II	
0.1294	cg0869314	cg0869314	63669365	ATCATAAAACCTTTTACAACC			II	
-0.158391	cg0869317	cg0869317	40800304	TAAAACAAAACTTTCCRAACC			II	
0.1318876	cg0869716	cg0869716	11621437	CTAAACCRTACCTAACCRAAT			II	
0.1134639	cg0869773	cg0869773	33712307	ACCATAACACCCCCATAATAA			II	
	cg0869801	cg0869801	58624364	AACCTACTTATTAAAACAACA			II	
0.2354706	cg0869894	cg0869894	23600491	CAACCCTATAATATAATTTAT			II	
0.1534717	cg0869899	cg0869899	28655508	TACTACC	44682395	TACTACC	I	C
0.1460714	cg0870352	cg0870352	69614440	AATATAT	66759488	AATATAT	I	T
0.1647442	cg0870415	cg0870415	41716415	TATACATAATATAATATTTAC			II	
-0.106525	cg0870456	cg0870456	26630392	TAAACCC	14673368	TAAACCC	I	T
0.137065	cg08708231	cg08708231	26660462	TCACATTCCAACACATACACA			II	
-0.243041	cg0871443	cg0871443	62790489	CTCTATC	69754401	CTCTATC	I	C
0.1090403	cg0871625	cg0871625	20732476	TAACTAATACAATTAAATTTA			II	
0.2031852	cg0872002	cg0872002	69803482	AATACTA	44618480	AATACTA	I	C
	cg08723131	cg08723131	54643455	AAAATCAAAACCAACAACAA			II	
0.105781	cg0872397	cg0872397	72721356	CAATCTCCCAAATCCTAACCT			II	
0.1085217	cg0872536	cg0872536	64717485	CAACTATAATAACTATCTTTA			II	
-0.118984	cg08726801	cg08726801	26735476	AAAAATC	62677324	AAAAATC	I	T
-0.103642	cg08743751	cg08743751	19709509	ACCTTCCTATAATCCCTATTAC			II	
-0.138545	cg0874596	cg0874596	36726498	AAAATACTCCTCAACAACCTA			II	
-0.121936	cg0875043	cg0875043	31749440	ACCCTACTTACTATTACAACT			II	

0.2404078	cg0875184	cg0875184	37652351	TCRATATCATAAAATAAACAA			II	
0.2082422	cg0875187	cg0875187	66702311	CCATACAACATATACTTAACA			II	
0.1982883	cg0875472	cg0875472	53774390	AACCAA	57711316	AACCGA	I	T
0.104081	cg0875659	cg0875659	11755499	CCCCCTCCTCCTATTCTACRTA			II	
-0.152531	cg0876242	cg0876242	72782327	ACATCTA	44675452	ACATCTA	I	A
-0.109778	cg0876260	cg0876260	64718325	TCAAACT	57715309	TCAAACT	I	C
0.1020696	cg0876676	cg0876676	41769319	AAAAATAAATCACACAAACAC			II	
-0.145468	cg0876768	cg0876768	26708436	AATAAA	54725351	AATAAA	I	T
-0.155159	cg0876782	cg0876782	64622436	TAAACAC	17761482	TAAACGC	I	C
	cg0877513	cg0877513	13644397	AAACCTA	10761385	AAACCTA	I	A
-0.273043	cg0877859	cg0877859	20629338	TAATACA	18760384	TAATACG	I	A
-0.10786	cg0878762	cg0878762	68644470	AAACCAT	20784419	AAACCAT	I	A
0.1010168	cg0878798	cg0878798	69718393	ACRATAAATACTCAATATATA			II	
0.108743	cg08789101	cg08789101	60601499	AATCTCA	47658449	AATCTCA	I	A
-0.123371	cg0880003	cg0880003	55608402	CTAAATTTAAAAACCRAATAC			II	
0.1064481	cg08805241	cg08805241	36619474	AAAAATAAAATAACACTAACA			II	
-0.213468	cg08806681	cg08806681	72794300	AACAAC	58644482	AACAAC	I	A
-0.206844	cg0880804	cg0880804	57720364	AAATCAC	19705326	AAATCAC	I	A
0.1222917	cg0881210	cg0881210	49736318	ATAAAAC	70704466	ATAAAAC	I	T
0.1435689	cg0881402	cg0881402	10723353	AATTTAAAAAAAATCCAAAAT			II	
-0.144427	cg0881748	cg0881748	32807411	ACTAAAA	31629403	ACTAAAA	I	A
0.1289669	cg0881882	cg0881882	12738459	ATTCATA	62639458	ATTCGTA	I	A
-0.140105	cg0881902	cg0881902	64789365	ACAAAA	34786465	ACGAAA	I	T
-0.156422	cg0882078	cg0882078	37658307	ACATATACCTATTCTAAAAAA			II	
-0.264219	cg0882335	cg0882335	50670510	AAAAAA	63789405	AAAAAA	I	C
0.1596132	cg0883107	cg0883107	43701438	ACTCCCA	50623425	ACTCCCA	I	A
-0.116033	cg0883260	cg0883260	22730507	ATACTCA	24800396	ATACTCA	I	A
0.1138977	cg08837481	cg08837481	46643471	CCCTTCCCTAAACTCAAAACT			II	
0.2351668	cg0883980	cg0883980	50807329	TTCAAAT	42772412	TTCAAAT	I	A
-0.148587	cg08840441	cg08840441	53646483	AAACCTA	46678500	AAACCTA	I	T
0.1364833	cg08842441	cg08842441	73622480	CACCAAACAAATTTTACTATA			II	
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0.1158443	cg0885483	cg0885483	32621455	AAAAATAAACACACCACACAT			II	
0.1867018	cg0885631	cg0885631	28731361	CTTCCCAACAACTATCAATCA			II	
0.1234091	cg0885771	cg0885771	66670482	AACTCAATTTAACTCCCTAAA			II	
0.1123181	cg0885829	cg0885829	54657471	AATTAACTTATCCAAAATCAC			II	
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0.1007907	cg0885921	cg0885921	24711352	AATCTCCCTTTCTACAAAACTA			II	
0.215509	cg0886143	cg0886143	43725335	AATAAA	30676486	AATAAA	I	C
-0.142614	cg0886434	cg0886434	47644483	AAAAAATACCTAAAACRCTTC			II	
0.1118246	cg0886666	cg0886666	29655384	CCCACAA	52639411	CCCGCGA	I	T
0.1341706	cg0886669	cg0886669	30707379	TAAAACTATAAACATAAACCA			II	
0.1263978	cg08866991	cg08866991	25793447	AATCCTA	61788475	AATCCTA	I	T

0.172286	cg0887003	cg0887003	13778435	TATACTTTATATATATATACCA			II	
0.1295656	cg0887009	cg0887009	44761460	TACTACTAATAAAATTTTTTCA			II	
-0.105398	cg0887064	cg0887064	66725454	ACCAACA	51730363	ACCAACC	I	C
0.1317891	cg0887123	cg0887123	15681417	AAAATAACCTACTCAAATACA			II	
-0.105561	cg0887394	cg0887394	33689432	ATAACCT	70689423	GTAACCT	I	C
-0.239677	cg0887984	cg0887984	19624427	ATTTACTATTTATTTATATCT			II	
-0.106657	cg0888820	cg0888820	16725414	CTAAACT	55726318	CTAAACT	I	C
0.1231115	cg0888891	cg0888891	24794482	AACTCCAAACACCTTACCCAA			II	
0.1129554	cg0888911	cg0888911	12723366	AAACACAATTATTACAAAATA			II	
-0.106995	cg0889289	cg0889289	44664353	TACTCACCTACAAAAATATCC			II	
0.1220433	cg0889303	cg0889303	34672391	ATAAAAATAATATTATATCTC			II	
0.1348257	cg0889381	cg0889381	32715460	CAAAAACTCAATTTCCAAAAT			II	
0.1184617	cg0889886	cg0889886	31694463	TTCAATAAATCCTCATATACT			II	
0.1114935	cg0890630	cg0890630	45651328	ATTAACTAACTCCTTACTCAA			II	
0.1414193	cg0891185	cg0891185	23691310	ATAAACTAAAAAAATTAAACT			II	
0.1114263	cg0891352	cg0891352	23809314	RACATTCTCACAAACTCTTAT			II	
0.2540009	cg0891683	cg0891683	34624375	AAAAAC	13683355	AAAAAC	I	A
-0.309842	cg0892045	cg0892045	34635319	TAATCTT	43616387	TAATCTT	I	A
0.1557393	cg0892359	cg0892359	37730375	AAATAACTAAAACAACAAAA			II	
0.1257729	cg0892366	cg0892366	53698352	ACTTCCA	16617450	GCTTCCA	I	A
0.2145935	cg0892402	cg0892402	58652340	CCTTAACCTTCATACCAAAAA			II	
0.1729476	cg0893090	cg0893090	32738498	AACACA	66800498	AACACG	I	A
0.1088693	cg0893328	cg0893328	74759488	ATACTATCCTAACATTACATA			II	
-0.255871	cg0893879	cg0893879	40803324	TACCCAACCTAAAACAAACCT			II	
0.1145408	cg0894252	cg0894252	72750374	TTTAATACCTACACCTTTAACA			II	
0.1657138	cg0894417	cg0894417	61667441	ACTACCCTTCCRCAAAAAACA			II	
0.1166509	cg0894580	cg0894580	30799426	TAAAATTCTAAACCAAAATTA			II	
0.1176092	cg0895918	cg0895918	49644505	ACTTTATCTAATTCTCCATTAA			II	
0.1076787	cg0896054	cg0896054	30662428	CTCCTTAAACCCAAATAAAAT			II	
-0.387564	cg0896301	cg0896301	43682431	ATAAACCACACCAAAATAAAC			II	
0.2525921	cg0896473	cg0896473	40751468	TAAAAAAATTCATATCTTCAA			II	
-0.328837	cg0896758	cg0896758	38708324	CTATAAACTCRCCACCCATTA			II	
0.1460199	cg0897321	cg0897321	53746316	TTATTATTACTTTCCACTACAA			II	
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0.5562427	cg08977311	cg08977311	31717420	CCAAACAAATTTCTACAATAT			II	
0.1429918	cg08977931	cg08977931	50694496	CTTTAAAAACACTAAAAACCA			II	
-0.163419	cg0898557	cg0898557	29724312	ACCAACACRATTATATTATAC			II	
0.1096339	cg0898597	cg0898597	11618323	TTTAAAACCRTTAAAAAAAC			II	
0.1249108	cg0899222	cg0899222	64715381	CTCACATCATTTCATAACTATA			II	
0.1100431	cg0899408	cg0899408	62731396	CACTATATCCTAAAATAAAAA			II	
-0.11162	cg08994891	cg08994891	60713466	AACAAA	19662452	GACAAA	I	A
0.2349647	cg0899659	cg0899659	14613307	CRCCCACTAAAATAACTCATA			II	
0.1394327	cg0899680	cg0899680	29671410	ACTTTCATATCTATAATCACA			II	

-0.101829	cg0900681	cg0900681	68781379	CCTACTAAATAACAAACACTC			II	
-0.102668	cg0901241	cg0901241	47722454	TTACTATTTCTTCAATTTCATA			II	
-0.18862	cg0901480	cg0901480	46749397	ATATCATTTCCTACCTTATTAA			II	
-0.10277	cg0901523	cg0901523	65740305	AAAATTCCAAAAAACTCTCTC			II	
0.127443	cg0901792	cg0901792	40738312	CAAAAA	63803425	CAAAAA	I	C
-0.139267	cg0902517	cg0902517	52707318	TAACTACATAAACTCCACCTA			II	
0.1056518	cg0902990	cg0902990	43605483	ATATCACTAATTCTTTCCACAA			II	
0.1006087	cg0903956	cg0903956	31788448	TCCTACCAACACRATTCAATA			II	
0.1855282	cg0904099	cg0904099	16652505	AATATTCTATAATTCTTTTAAA			II	
-0.102937	cg0904773	cg0904773	18789360	ACTATCC	20681432	ACTATCC	I	A
-0.161599	cg0905083	cg0905083	39669307	TCAATACRACTATAACATTAA			II	
0.2063588	cg0905134	cg0905134	70723444	ACCTCTATAATTCATTTTACAA			II	
0.370756	cg0905218	cg0905218	30675395	AATAATACTAAATCATTTAAC			II	
-0.102405	cg0905324	cg0905324	48664509	TATTTATTTTTAATTAACAAAA			II	
0.1043721	cg0905353	cg0905353	13687487	CCCAAAAAATACTCCAAAAAA			II	
0.1066536	cg0906562	cg0906562	56721316	ACAACA	48793480	ACGACA	I	C
0.144288	cg0906944	cg0906944	23607486	ACAAAA	61723462	ACAAAA	I	C
0.1077915	cg0907019	cg0907019	69715359	AACAAAAAATCCTCACAATAA			II	
-0.231272	cg0907334	cg0907334	62617399	AAAAAACATCCCCRCAATAAA			II	
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-0.117508	cg0907584	cg0907584	15775384	ATCCAAATCCRAATAAACAAA			II	
0.1151825	cg0907988	cg0907988	29693349	AATTTTTCTTTTTTCCTACAAA			II	
0.3147087	cg0908078	cg0908078	25733472	ATTACCAAAATTCTAAATTCT			II	
0.2229514	cg0908251	cg0908251	65781502	CCCTAAATTAACCTACCTATT			II	
0.171411	cg0908424	cg0908424	53720344	CAAACTAACCACRTTTCAACR			II	
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0.1285828	cg0908815	cg0908815	18651434	ATCCAAAACCCTAATTAAAAA			II	
-0.152467	cg0909118	cg0909118	45778436	CTTCTTA	58766345	CTTCTTA	I	A
-0.123889	cg0910027	cg0910027	65753302	ATAACAACAAATTATAACCCA			II	
-0.17846	cg0910033	cg0910033	34641304	AACCCA	16627472	AACCCA	I	C
0.1878902	cg0910106	cg0910106	50699371	AAACACTACACAAATTCCTTA			II	
0.1558045	cg0910203	cg0910203	50621483	ATAAAACTATCATAACCTAAT			II	
-0.125603	cg0910402	cg0910402	44752306	AAACCCCRTCTCCACCAAAAA			II	
0.106927	cg0910743	cg0910743	71729464	CAAAAT	43641419	CAAAAT	I	C
0.1522961	cg0911500	cg0911500	43694400	TTTATCTTATCTCCACTTTCAA			II	
-0.142534	cg0911744	cg0911744	10664468	AATACA	25779417	AATACG	I	A
0.1017227	cg0911968	cg0911968	14679432	TTCCCTCTCCTCCTTTCCAAAT			II	
0.1915237	cg0912627	cg0912627	46810317	TAAAAATATAATTAAAACAAA			II	
0.1302243	cg0912906	cg0912906	63697332	AAAAAA	24746334	AAAAAA	I	A
-0.238686	cg0913565	cg0913565	31614324	CCTACAC	10734365	CCTACAC	I	T
0.1718723	cg0913820	cg0913820	34645343	ATATAAACATTAAAAACACTA			II	
0.1056964	cg0914027	cg0914027	72623414	ATAATAAAATACAAAACCAAA			II	
0.119539	cg0914706	cg0914706	14689356	AAACCCTTCTCCTCCTAATTTT			II	

0.1897153	cg0914885	cg0914885	49790464	TCTCCAAAACCTAAAAACTAA			II	
-0.291457	cg0915801	cg0915801	33693506	TTTATAATTACTCTTTTCTATT			II	
-0.10274	cg0916300	cg0916300	61695508	ATAATACRATATATTATATAA			II	
0.1425447	cg0916641	cg0916641	46645488	TTCCTATAACATCTAATATCA			II	
-0.106381	cg0916653	cg0916653	23692396	CRCCAAATCCCCCAAAACCCC			II	
0.2342328	cg0916872	cg0916872	39751484	TTAAAAAATCCCTTCACCATT			II	
0.1007187	cg0917481	cg0917481	34733453	ACCRAAAAACTTTATTTAAAA			II	
0.1912537	cg0918208	cg0918208	37645409	CRTAAATCACACTAAATAAAT			II	
-0.113946	cg0918750	cg0918750	18689460	AAAAACC	24679402	AAAAACC	I	A
0.1449839	cg0920874	cg0920874	38683434	TAATAAT	42741493	TAATAAT	I	T
-0.227203	cg0921417	cg0921417	21745343	ATACCCRTAAAAACTACTACR			II	
0.1083154	cg0922236	cg0922236	29764455	ACCATAAACTTAAAAAAATCT			II	
0.23688	cg0922289	cg0922289	35723454	TTATTTTATTCAAACCTCTAAA			II	
0.1769235	cg0922537	cg0922537	29799387	TATTTCACTCAACCTACCAATT			II	
-0.148582	cg0922766	cg0922766	14777384	AATCAAAACATAATTAAAAAC			II	
-0.102688	cg09231171	cg09231171	55751311	CRCCCTTCAATAATTAATAAC			II	
0.1041372	cg0923445	cg0923445	34761355	CACAAAT	47705509	CGCAAAT	I	C
-0.12519	cg0923556	cg0923556	57682351	TAACAAC	15675506	TAACAAC	I	A
0.1029178	cg0923970	cg0923970	50684442	TATTTCCCRAATCCTACAAAA			II	
-0.115011	cg0924500	cg0924500	53729338	CRAACCTATTCTTTCTAAAAA			II	
0.1418293	cg0924797	cg0924797	28668413	TCAAATTTTTAAAATTATAAA			II	
0.1112967	cg0925887	cg0925887	14635367	TCTTAACCCTCRTTTTAACAAT			II	
0.2149233	cg09261791	cg09261791	39749313	ACAACACAAAACTCTCTTAAC			II	
0.1422382	cg0926614	cg0926614	54763332	ACAACCATAAAAACACTAATA			II	
0.1323276	cg0926871	cg0926871	66806458	ACAAACA	13759348	ACGAACA	I	A
	cg0927086	cg0927086	67639301	TACTTACRACTATAAAACAAC			II	
0.1407489	cg0927869	cg0927869	52623414	AAACATTCATTCAAAAAACAT			II	
0.2925184	cg0927973	cg0927973	20706454	ACTTAAA	15790347	GCTTAAA	I	C
-0.169038	cg0928420	cg0928420	49729377	CCTCCRTAACCAACRACTTCT			II	
-0.14169	cg0928494	cg0928494	32618445	AACCTAT	50615413	GACCTAT	I	A
0.1013712	cg0928688	cg0928688	73669337	AACCTACTCCTAAATATAATA			II	
0.1035592	cg0929266	cg0929266	47722311	CRCTAAACTAAAATATTCTAC			II	
-0.105116	cg0929415	cg0929415	14668374	TCACAAA	35739312	TCGCGAA	I	T
0.1030203	cg0929424	cg0929424	21626310	ATAACTACAAAAAAATCACTA			II	
0.1512091	cg0929645	cg0929645	49654360	CCACAAT	35808326	CCGCGAT	I	T
0.1003786	cg0930149	cg0930149	49688431	CCAAAAAACCTTCCAATACCT			II	
-0.127356	cg0930719	cg0930719	26614375	AAACTCATCTTTATAATACTA			II	
-0.102492	cg0930926	cg0930926	14719371	AATAATATTTCACTTCATCACR			II	
0.2464393	cg0931289	cg0931289	52654394	CAAATACCAAACATACAATAA			II	
0.1554443	cg0931767	cg0931767	46637510	ATACATACATAAAATACAAAC			II	
-0.106427	cg0932225	cg0932225	56681355	CTAAACC	27673401	CTAAACC	I	T
	cg0932340	cg0932340	54606301	AATAAAAACCCCCAAATAACT			II	
-0.173946	cg0932372	cg0932372	42679433	TTTAACA	10738438	TTTAACA	I	A

-0.111323	cg0932411	cg0932411	55750413	AAAAAATTAAAAACTAAAAAC			II	
0.1024269	cg0934961	cg0934961	47637471	AACTAAAAACCCTAAAACTTC			II	
-0.124629	cg0935089	cg0935089	67715351	AACAAA	54602303	AACAAA	I	A
0.1433424	cg0935233	cg0935233	36766335	CCCAACTTAAAAACRACACAT			II	
-0.200535	cg0935251	cg0935251	49644447	CTAAACCCTAACCTAAAATCC			II	
0.1768826	cg0935455	cg0935455	24636339	ATTCACC	62621337	ATTCGCC	I	T
0.1218201	cg09357761	cg09357761	61605474	AAACCTAAAATACRACCTAAT			II	
-0.125447	cg0935911	cg0935911	46760494	CTAATAA	24619494	CTAATAA	I	A
0.1361258	cg09360041	cg09360041	50648414	AAATTTAAATAACTCACTTAT			II	
-0.192582	cg0936149	cg0936149	64613328	CAAAAA	49665304	CGAAAA	I	A
-0.1443	cg0936196	cg0936196	16705402	ACCAAA	23736493	ACCGAA	I	C
0.1731533	cg0936651	cg0936651	38653371	ATAACCAAACTCATAACTATA			II	
0.1047068	cg09373511	cg09373511	45691334	ATAAAACTACAATCTCAATAT			II	
-0.113614	cg0937506	cg0937506	51652388	ACACTTTTCTACAACTACAAA			II	
0.1918885	cg0937828	cg0937828	47684491	TCCTTACAACTCTAACAACCA			II	
0.1050507	cg0938006	cg0938006	55661463	TACTAAAATAACTAACTACRA			II	
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0.1258323	cg0939519	cg0939519	68777485	AAATAAATTATAAAAATAATT			II	
0.1113785	cg0939943	cg0939943	37793317	CAAAACAACTACCAATATACT			II	
	cg0940621	cg0940621	73790463	ACACCTACTATTTAATTAAAT			II	
0.1121449	cg0940819	cg0940819	20795464	CCTTTAAAAACTTTCRTATTAC			II	
0.1848133	cg0941051	cg0941051	48782467	TACACCATCTTATAACTCATTT			II	
0.2123933	cg0941191	cg0941191	53774381	RAAACTCACATATCAAAATAC			II	
0.1400401	cg0941325	cg0941325	20802377	TATTTTTATTTTTACACCATAC			II	
-0.112517	cg0941394	cg0941394	35711450	ATTACATAAAAAATATCTTCT			II	
0.1136482	cg0941494	cg0941494	63742393	AAACTA	46678324	AAACTA	I	A
0.2355631	cg0941618	cg0941618	13620337	TAAAACATAAAAAACCAACAC			II	
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0.1056146	cg09419251	cg09419251	61797307	ACAACACAAACTACAATTTTA			II	
-0.122827	cg0941967	cg0941967	15624446	CCTTCRTCAAACTCCTAAAAA			II	
-0.112466	cg0942516	cg0942516	70661382	ATACCTAAAAAACCTCACAAA			II	
0.1489477	cg0942701	cg0942701	14785328	ACRTACCTAACTAAATACTAA			II	
-0.131201	cg0943064	cg0943064	69676349	CCAACAACCAAATAAATAAAA			II	
0.1258297	cg0943460	cg0943460	38809442	ATAAATCTATAAAACAAACCC			II	
0.1105408	cg0943517	cg0943517	59669343	ATAAATCATAATACCAAAAAT			II	
0.1079409	cg0943747	cg0943747	22650352	AAACAA	45648320	AAACAA	I	A
-0.166979	cg0943806	cg0943806	12618375	TTTCTATCCCCTATTAAAACTC			II	
0.3637553	cg0944245	cg0944245	27751347	CTCATCT	69745434	CTCGTCT	I	A
0.1110397	cg0944279	cg0944279	22708472	AACTCCCACAATATTTCCACT			II	
0.1278058	cg0945121	cg0945121	17618421	ATAAATATTCAAAAAACCCAA			II	
0.145706	cg09455881	cg09455881	50789347	TAACTTTAATACACATAAAAA			II	
0.2738467	cg09462281	cg09462281	35725439	ACAACTC	46723333	ACAACTC	I	T

0.1681129	cg09467607	cg09467607	22690379	TACCAACCAAAATAACAACCA			II	
0.1252302	cg09478002	cg09478002	17627420	AACTATATTTAACCAACTATAT			II	
0.1279322	cg09487575	cg09487575	43673449	AAAAACCCAAATATTAAACCT			II	
-0.105943	cg09491897	cg09491897	52670370	AACCTAA	62692490	AACCTAA	I	T
0.1055395	cg09496634	cg09496634	23706474	AAAAATCTACAAATAAAATTC			II	
0.1855773	cg09501687	cg09501687	31735424	CACTCATTCTAACTTTAATATT			II	
-0.143244	cg09508496	cg09508496	10692335	TAAAATC	13645385	TAAAATC	I	C
0.1050662	cg09510698	cg09510698	21692351	TCTATACTCACCACTCCRATAT			II	
0.1060594	cg09516200	cg09516200	19782308	TAAAATAAAACAAACACTACA			II	
0.117517	cg09524613	cg09524613	48745352	AAACATTATTTCTAAAATCTAA			II	
0.1353014	cg09532840	cg09532840	50750421	TATATTTTTCTCTTTAAAAATC			II	
-0.132484	cg09533869	cg09533869	19733415	TAACTCTATTTATCTACTACTC			II	
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0.1267743	cg09535226	cg09535226	32765492	AATCCATAAAACATCTTCTCTA			II	
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-0.120502	cg09581911	cg09581911	74718307	CTACTACTTACTAACTACAAA			II	
0.112415	cg09583302	cg09583302	46605357	ATCATACTTACCTCTAAACCTA			II	
0.1052741	cg09584711	cg09584711	41796336	AACATTACCCCTATTAAAAATT			II	
0.1269924	cg09592244	cg09592244	53629317	TAAATAAAAAATACAAACRAC			II	
0.1238832	cg09597022	cg09597022	10787338	TCTTCCCA	42678415	TCTTCCCA	I	A
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0.2341724	cg09603707	cg09603707	68689333	TAATACTACTAAAAAAAACTT			II	
0.1684289	cg09603919	cg09603919	51701470	AAAATTAACCAACTCRTACCA			II	
0.1502718	cg09611620	cg09611620	29737300	CATAACTAATCTTTACTATTAA			II	
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0.1096784	cg09630706	cg09630706	20687478	AATAAA	18721434	AATAAA	I	A
0.1461623	cg09632136	cg09632136	35642329	AATTAACACAAAACCAATAAT			II	
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0.3095427	cg09644806	cg09644806	51682447	TATATTAAAATTCACCATATAT			II	
0.1480746	cg09648454	cg09648454	12751316	AAAAAAATAACTAAACCATTT			II	
0.1381975	cg09650180	cg09650180	74722344	CTTCAAAAAAACTAAACCTCA			II	
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0.3811402	cg09672255	cg09672255	62646475	AAAAATAAACATAACATTTTC			II		
0.1468589	cg09680007	cg09680007	59639463	TAAATCACTAAACTAACATAA			II		
0.1075003	cg09714852	cg09714852	52742438	TTCACATTAAAACRACAAAAC			II		
0.1136999	cg09715009	cg09715009	49694411	TAAAACCRATTTTATCCAAAT			II		
0.1000873	cg09715545	cg09715545	66620425	AAAACCTATCCTAAAATTAAC			II		
0.1047387	cg09717927	cg09717927	48701360	AAAAAAACTAAAAACCTAAA			II		
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-0.199146	cg09727206	cg09727206	37740333	CCAACTA	52756471	CCAACTA	I		C
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0.1002712	cg09729274	cg09729274	57748486	AAAAAATTATCTATATAACAT			II		
0.1047001	cg09729624	cg09729624	12741436	AAACTCACRACAAATACAAAA			II		
-0.103183	cg09731946	cg09731946	64723470	TTTAAATAAAATCTATTACTTC			II		
0.1242436	cg09740450	cg09740450	64711383	TTCATACCTAAACAACCTCTC			II		
0.1042643	cg09755784	cg09755784	69641461	TACTACATTCCCTATATATACT			II		
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0.2520639	cg09768983	cg09768983	34706422	AACAAAACTAAAAACATTTAA			II		
0.1024966	cg09773458	cg09773458	29730503	TATACAAACCATAACTTCCTC			II		
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0.1062591	cg09782560	cg09782560	32622429	ATAAACCCCAATAAATACTCT			II		
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0.1857376	cg09790226	cg09790226	62741461	CTAAATCATCCACAACCCTCA			II		
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-0.117625	cg09797202	cg09797202	70668390	TTCACTAACAACTTAAAAAAT			II		
0.1227471	cg09802066	cg09802066	33648424	AAATAAAAAAAATCCCTAAAC			II		
0.1048242	cg09804649	cg09804649	21670387	CACTATATAAAACTCTATTTAT			II		
0.1450757	cg09807817	cg09807817	21771379	AACTACTCCTTCAAAAAAACT			II		
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0.1175562	cg09811510	cg09811510	18684453	TATAATCTCATTATTAACCATC			II		
0.1156345	cg09814029	cg09814029	45712411	ACCRTAACAAAAAAACCTTTA			II		
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0.1203421	cg09829904	cg09829904	70657476	AAAAAAATATATTAACCTCTT			II		
0.1063926	cg09830083	cg09830083	20631334	CTTAAAAAAATCTAAAACTAA			II		
0.116988	cg09831875	cg09831875	38750445	AAAAAT	57622344	AAAAAT	I		A
0.1166693	cg09832276	cg09832276	21697348	TATATAAATATTTTCTCATACT			II		
0.1224561	cg09834172	cg09834172	61602344	AACATAACAACACCAAATAAC			II		
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0.1036366	cg0984047	cg0984047	58662317	TTAAAATCCCCAAACCAAATC			II	
0.2698671	cg0984736	cg0984736	14607396	RAATAACATCCAAAACTTACR			II	
0.1201304	cg0985291	cg0985291	44761470	CCACAACATAAAACCCCACCC			II	
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0.2440719	cg0986341	cg0986341	70614430	ATTAACCTAATTTTTCATCTAA			II	
0.2423653	cg0986614	cg0986614	29794391	RTAACATCTCCRAAAAACTCA			II	
0.1068005	cg0986732	cg0986732	73678369	CTCAAAACAATAACTTCAAAT			II	
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0.1280246	cg0990345	cg0990345	12791479	AAAACATCCTCTCTATCTTTAA			II	
0.1434277	cg0990692	cg0990692	40799410	ACTAACCAAAACAATAAACAC			II	
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0.1052369	cg0991665	cg0991665	63625400	CTCAAAACCATTAACCCCCAC			II	
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0.1114243	cg0992725	cg0992725	36675362	ACTAACT	65676467	ACTAACT	I	C
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-0.229176	cg0996308	cg0996308	64809446	CCAAACACTTACTAAAAATAT			II	
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0.1162596	cg0998143	cg0998143	25773436	TAAACAAAAAATTTATTCACT			II	
-0.168452	cg0998192	cg0998192	29649484	AACCAAC	74797315	AACCGAC	I	T
-0.10054	cg0998294	cg0998294	49748412	ACCTATA	18605351	GCCTATA	I	A
-0.133833	cg0998526	cg0998526	32797451	AAAAACRATAAAATCTACAAA			II	
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0.1413697	cg0999815	cg0999815	66795482	TAACRCTAACATCCTAATAAA			II	
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0.1272727	cg1001762	cg1001762	46734487	ATCAAAAATCCAACATTACCA			II	
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0.1104871	cg10028823	cg10028823	67770391	TACAAAC	12704501	TACAAAC	I	A
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0.1331112	cg10051588	cg10051588	36644327	ATAAATCATATTTAACTCCTCA			II	
-0.104157	cg10056482	cg10056482	42642363	AAACCCA	44755425	AAACCCA	I	A
-0.200788	cg10058204	cg10058204	46658359	ATCAAAATCTTCATTTTTAACT			II	
0.1232483	cg10063575	cg10063575	36606308	TCCTTCATAAATCACCTTATCT			II	
0.2161173	cg10064922	cg10064922	53768307	CACTAAACTTACTAATTTCATA			II	
-0.144492	cg10067510	cg10067510	64604404	AACATAC	21764398	AACGTAC	I	T
0.102703	cg10067523	cg10067523	74698434	CTAATCTTTACACTTTAACTCC			II	
0.1163941	cg10068464	cg10068464	41718349	AAAAAAAAACTTCTATTTTATA			II	
-0.21313	cg10070328	cg10070328	25698303	AAAATAAAAACTTAAAAACAT			II	
0.1034131	cg10072319	cg10072319	74723489	ATTTAAATCATTTCTCTCAATC			II	
0.1294481	cg10076068	cg10076068	10770329	CCRAAACCCTTAATATAAAAC			II	
0.1725504	cg10076560	cg10076560	19623402	CCAATCA	67797490	CCAATCG	I	C
0.1122279	cg10081994	cg10081994	39717404	TACTAATTACTAAAACATTCAA			II	
-0.135771	cg10082647	cg10082647	42713510	AAATAAC	12690452	AAATAAC	I	A
0.1459139	cg10085138	cg10085138	51671322	TCTTCTTTAACRTACTTAAAAA			II	
-0.121469	cg10087780	cg10087780	18679499	RTTCTCCATTTACATATATATT			II	
-0.105198	cg10088890	cg10088890	60701395	CAATTATATTAAATCAAACAC			II	
0.1037779	cg10090591	cg10090591	26699355	TCCAATATAATACCTAAAATA			II	
0.1041588	cg10091686	cg10091686	65664331	AATCTCAATAACCRACCCCRA			II	
0.1556825	cg10091792	cg10091792	46644403	RAATAAATACTAATCACCATC			II	
0.1030583	cg10097313	cg10097313	35801339	ACAACTAAACAAACAATAAAT			II	
0.1319336	cg10098373	cg10098373	26730410	ATAACTCCCATAAATAAAATA			II	
-0.266739	cg10099275	cg10099275	36626469	CCTTTTTATTTCTATCTATATC			II	
-0.383151	cg10100585	cg10100585	10701414	AAAAAAAACCCTCCTATAAAA			II	
0.2498184	cg10104252	cg10104252	49750464	AATAAAC	62603505	AATAAAC	I	C
0.1025287	cg10104336	cg10104336	48667441	CTAATACATTAACACTAATAA			II	
0.1079321	cg10104420	cg10104420	65770434	RCRTTCATCCTATAAACACTTC			II	
0.1029766	cg10104674	cg10104674	63686350	AACACAAATTAAAATTTCAAC			II	
0.131926	cg10109635	cg10109635	66763415	CTCCTAAACCAAAACCCCTATA			II	
0.1285222	cg10109731	cg10109731	26610493	AAACAAT	57771424	AAACGAT	I	A
0.1366947	cg10110335	cg10110335	56642304	AACATAACAATAACTAAATAA			II	
0.1140518	cg10111629	cg10111629	17632460	TCCCRTATTTCATTTCTACACC			II	
-0.15875	cg10115321	cg10115321	59657306	ACTTATTCTCATATTTTCTAAA			II	
-0.164876	cg10117077	cg10117077	38767335	TAATTATATTAAAAACCAAAA			II	
0.1201427	cg10117599	cg10117599	58659388	TAACTAAATAAAAAACTCTAC			II	
0.10173	cg10127375	cg10127375	33693488	TCTACCTTCAATTAAATCTATA			II	
-0.144892	cg10130374	cg10130374	62620348	AACAAAA	35738443	AACAAAA	I	C
-0.14103	cg10140536	cg10140536	63698418	ATCTTAA	26738315	ATCTTAA	I	C
-0.134988	cg10141715	cg10141715	68626466	AAATACCCAAAACAATAACRA			II	
0.1296206	cg10143883	cg10143883	20708490	ATATAAAACCACAAACCTATA			II	

0.2345867	cg1014447	cg1014447	65705415	AATAACCCTTAAAAAAACCRA			II	
0.1508658	cg1014486	cg1014486	23692465	CAAAAAAACAAAACTCAATAT			II	
0.3637597	cg1014633	cg1014633	74684498	TCCATAC	33624416	TCCATAC	I	T
-0.123377	cg1015090	cg1015090	71758432	AAAACTTCATCTCTACAAAAA			II	
0.1452649	cg1015299	cg1015299	46736327	AAAACATAACTTAAATCATTC			II	
0.3932671	cg1016698	cg1016698	67703338	TACTTAATCCACATCCTAAAA			II	
0.1227044	cg1016723	cg1016723	62695354	TACTATATACCAACAAACCTA			II	
0.1894067	cg1016737	cg1016737	13650306	AAACTAA	66699494	AAACTAA	I	A
-0.237407	cg1016797	cg1016797	65742433	TAAAATAACAAACTTTCCCAC			II	
0.2035786	cg1017798	cg1017798	71804313	TATACCTAAAAAATCCCCATA			II	
0.1097399	cg1018009	cg1018009	18728379	TCCATTAAAAATACATCATAT			II	
-0.117583	cg1018432	cg1018432	37717325	AATTAAACRCCCRCCTACTAA			II	
-0.110748	cg10193721	cg10193721	28779428	AAAAACA	15772359	AAAAACC	I	T
-0.147244	cg1019733	cg1019733	24672333	AAAATTAACACCAAAAAACTA			II	
-0.13875	cg10200291	cg10200291	43600311	ACCACAT	32739338	ACCGCGT	I	A
-0.129603	cg1020037	cg1020037	33809357	CCAAAAACCTCRTATCTCTTAC			II	
-0.14494	cg1020254	cg1020254	64646353	AAAAATTAACCTAACATACTA			II	
0.2167687	cg1020283	cg1020283	41624389	AAACATA	21791419	AAACGTA	I	C
-0.186633	cg10205431	cg10205431	14745467	ACAATCT	57800340	GCGATCT	I	C
0.1004167	cg1020877	cg1020877	40616479	CTATTTAATAATTACTTCTTCT			II	
-0.113237	cg1021330	cg1021330	58784432	CCTACAA	72762391	CCTACAA	I	A
0.1383818	cg1021365	cg1021365	68644458	TTATCTCCATTTCATATAATCT			II	
-0.137836	cg1021387	cg1021387	36762446	AATCACC	71698444	AATCACC	I	A
0.3996179	cg1021705	cg1021705	62734347	RAAAACCAAAATCAATCATAA			II	
0.1030939	cg1022054	cg1022054	68744315	TCRACCACTATAAAAAATTTC			II	
0.1101362	cg1022101	cg1022101	48768314	AAAAATATAAACCAAATATAC			II	
0.2113787	cg1022453	cg1022453	48788306	TTATAACAACTACCCACATTT			II	
0.1817957	cg10225951	cg10225951	63694309	RAACCAAACRAAAAACTAACC			II	
0.1151281	cg1023447	cg1023447	34641380	CCTTTTTTCTCCCTCTCCCTCA			II	
-0.131968	cg1023545	cg1023545	72747457	AAAAATAAAACTAACCCAAAA			II	
0.1383975	cg1024035	cg1024035	61792426	AACCAAAACCTTTTCTATCRA			II	
0.1113501	cg1024118	cg1024118	58737492	AATAATACAAATCTAATTTCA			II	
-0.111123	cg1024334	cg1024334	44789485	CTCCTAA	58730396	CTCCTAA	I	A
0.1240368	cg1024385	cg1024385	18793443	CCAATATTTACRTTCTAAACAC			II	
0.1837347	cg1024907	cg1024907	54753406	CRTAATACTAATCTATAAAAC			II	
0.156692	cg1025224	cg1025224	51767492	AACCCTT	47795418	AACCCTT	I	A
0.1161131	cg1026205	cg1026205	73673357	TTACTCACACRAACTATTTCTC			II	
-0.576526	cg1026300	cg1026300	16672373	CTCACAAACCTAAAATAAACA			II	
-0.138352	cg1026538	cg1026538	20622426	AATCCCA	14759462	AATCCCG	I	A
0.1495948	cg10266681	cg10266681	48690416	CAAAATTTCTAACATTCCTAT			II	
0.1008951	cg1028852	cg1028852	36721481	ATAACTAAACCATACRCRAAC			II	
0.143867	cg1028974	cg1028974	39617333	AATACAAACAACAACCTAACA			II	
-0.143621	cg1029199	cg1029199	69803510	ACCTCAA	47734337	GCCTCGA	I	C

-0.227292	cg10292584	cg10292584	16687334	TTAAAAA	39646344	TTAAAAA	I	T
0.1195452	cg10293824	cg10293824	58769488	AACTTAAAACTCRCTCAACCTA			II	
-0.147577	cg10295955	cg10295955	55774489	TCCTCAACACTCRTATATCRCC			II	
-0.113893	cg10297211	cg10297211	31682503	AATCCCA	57660444	AATCCCG	I	A
0.2102591	cg10306192	cg10306192	19754448	TCATTTATTAAAACAATACCTA			II	
0.1173892	cg10308629	cg10308629	37725360	TTTCATTCTCTATAATTAACAT			II	
0.1234359	cg10310917	cg10310917	32759433	CACTAAAACAATTACAACCAA			II	
0.1653567	cg10311048	cg10311048	12710436	CCRCCAAACCCACACCCAAAT			II	
0.1333914	cg10312513	cg10312513	48627497	CTATCAC	62620306	CTATCAC	I	T
-0.193192	cg10317314	cg10317314	11754397	ACCTCTA	46702490	ACCTCTA	I	A
0.104106	cg10318368	cg10318368	54669481	TCCAATCACAATTTAAATTTAA			II	
-0.100402	cg10319942	cg10319942	49746468	CAAAAAACCTCAACATACCCA			II	
0.1242	cg10328089	cg10328089	74799317	AAATCCCACAATATTAACTATA			II	
-0.278647	cg10328548	cg10328548	42739345	CCACCAT	42793430	CCACCGT	I	A
-0.162983	cg10329418	cg10329418	17781495	AACTCATCTTCTCCAAAATTTA			II	
0.1089876	cg10333144	cg10333144	72648369	CACTCTTAACTCTAAACACAAT			II	
-0.106651	cg10334741	cg10334741	62616428	ACACAAA	41794445	ACGCGAA	I	A
0.1037076	cg10336025	cg10336025	59765370	TAAAAATAATATAAACRAACA			II	
0.1136383	cg10336193	cg10336193	66689473	ATAACCACACTTCTTCATAATA			II	
0.1392902	cg10338539	cg10338539	32639331	RAATTTAACTTAATCRCCAATT			II	
-0.208797	cg10340904	cg10340904	67667448	TCTATTA	68789383	TCTATTA	I	A
0.1060922	cg10342016	cg10342016	73764451	CAACTCAACCCAATAATAAAC			II	
-0.10866	cg10347293	cg10347293	31743462	TACATCC	36775445	TACGTCC	I	A
-0.118032	cg10350492	cg10350492	28641376	AACAATTCTAACTAAACCTCTA			II	
0.1003797	cg10351284	cg10351284	59704379	CCCATAATATAAACRTATCCRT			II	
0.1309833	cg10352237	cg10352237	31715407	AATAAAAACCRTTTTTATCACR			II	
0.1156596	cg10370305	cg10370305	23744363	AAAACTCACATATATTTACTTT			II	
-0.15888	cg10372770	cg10372770	17666483	TCTCRACTTCTCTAAAAATACT			II	
-0.163347	cg10375597	cg10375597	16737369	TACACCTAAAATAAAAACTAT			II	
0.1483068	cg10384133	cg10384133	38628314	TCCAAACCTATTTCTCTCTCCA			II	
0.3346064	cg10385522	cg10385522	25755461	AACTTATTACAAACATCTCTAC			II	
0.1133963	cg10392572	cg10392572	12774369	TTTTCCCTATAAAACAACATAA			II	
0.1134418	cg10407894	cg10407894	65651440	AATAAAAACTTATAATATCTTA			II	
0.1456971	cg10409680	cg10409680	57807397	ATCCACCTTAAAATAAATCTCA			II	
0.1429234	cg10413089	cg10413089	26784326	AATCTATAACTTCCCAAAATAC			II	
0.1045401	cg10413861	cg10413861	18762412	TAAATTTACCCCTATATAATAA			II	
0.1763147	cg10415021	cg10415021	27769303	CTATACTATCTATATTTAACCT			II	
0.1510989	cg10423607	cg10423607	11618340	TCTATAAATTTAACATTCTTAA			II	
0.130736	cg10423842	cg10423842	61754407	TATCTATTATCCTCATTATTAT			II	
-0.129117	cg10424681	cg10424681	43636484	ATAAAAA	56690452	ATAAAAA	I	A
0.1127488	cg10436792	cg10436792	59662421	CCAAAATAAAAAAACCCTCAA			II	
-0.131583	cg10440578	cg10440578	70725460	AAAAAAA	29631307	AAAAAAA	I	A
-0.108682	cg10449329	cg10449329	28685469	AATAACTATTCCATTTTACTTA			II	

0.1087631	cg10466421	cg10466421	37620417	CATAAACTATTATTAAATCTAT			II	
0.1066413	cg10475690	cg10475690	69766330	TTTAATAATACACATATTACTT			II	
-0.118876	cg10481072	cg10481072	27771430	TAATAACTTAAAATTCTTACTT			II	
0.221998	cg10482512	cg10482512	72767486	AAAATAAAAACCCCAAAAAAC			II	
0.2195411	cg10483660	cg10483660	52770325	AAAAAAAAATATCCTCATAAT			II	
-0.10442	cg10484673	cg10484673	70756443	TACTTAATAATCCTTATCACAT			II	
-0.184535	cg10486069	cg10486069	26671487	AATACAA	74620448	AATACGA	I	T
0.1931662	cg10488050	cg10488050	73621324	AACTCAAAACRAAATCTACTTA			II	
0.124121	cg10493436	cg10493436	16743503	TAAACCACTCAACTAAACTCTA			II	
0.1202402	cg10497894	cg10497894	27600436	ACCTAACTACTTATTCTTTTAA			II	
-0.172928	cg10500026	cg10500026	42755347	AAATCCC	56698327	AAATCCC	I	A
0.1347331	cg10500702	cg10500702	52679452	ACCTATATCTCATAAAAAAATC			II	
0.1066144	cg10501093	cg10501093	58622410	AAACAAA	29711507	AAACAAA	I	T
0.1305093	cg10501210	cg10501210	43774458	CAAAACT	66775341	CGAAACT	I	A
-0.164041	cg10507759	cg10507759	43648365	ACCACTACAAATAAAACCTAA			II	
-0.123221	cg10507965	cg10507965	33752434	CTAAAAAACTCACATCRTCCTA			II	
-0.103063	cg10511429	cg10511429	51782318	CCTTCACCTTATCRCTCAAACA			II	
0.1230623	cg10513323	cg10513323	69603337	TAAATCTACCCAAAAAACTCA			II	
0.149954	cg10513992	cg10513992	44786356	ATTAAAAATTATACTATCTAAA			II	
0.1001308	cg10518155	cg10518155	24682375	CTACCTATACTAAACAATATAT			II	
-0.18134	cg10528424	cg10528424	27765350	TACAAAA	41611371	TACAAAA	I	C
-0.131298	cg10539898	cg10539898	35729325	CAAATCT	38628452	CAAATCT	I	A
0.1028004	cg10541843	cg10541843	13613324	CTACACTCTCCCATCACAAAAA			II	
-0.158732	cg10544018	cg10544018	16767305	AAAAAAA	42611322	AAAAAAA	I	C
0.1401655	cg10546210	cg10546210	74613345	ATTATACCACAAATCCCAACTC			II	
0.1088899	cg10549071	cg10549071	59810379	CAAAATCCCAACTAAACACCC			II	
-0.111675	cg10553103	cg10553103	33767380	AAAATAAAACAAATACTACTT			II	
0.1004191	cg10553204	cg10553204	61671309	TACAAAA	19659376	TACGAAA	I	A
-0.325008	cg10553219	cg10553219	15624313	TTCAATACTCTAAATAAACTCC			II	
-0.153148	cg10557683	cg10557683	47625505	AATACCTCTAAAAAAACCTCTA			II	
0.1046342	cg10557907	cg10557907	15629450	ACAATATTATCTTTAAATACCC			II	
0.1305445	cg10559151	cg10559151	48602325	CACAAACCAAACTACTCTTAA			II	
0.1422875	cg10560561	cg10560561	65732339	TTACTTATTTACCACTAAAAAA			II	
0.1023259	cg10564001	cg10564001	41624467	ACTTCTAAAATACAATAAATTC			II	
0.3795986	cg10568066	cg10568066	39730413	CCAATTA	41722336	CCAATTA	I	A
0.1007373	cg10574499	cg10574499	39690462	CTAACTAAAAACCTAATACAA			II	
0.1584056	cg10576245	cg10576245	37667504	CCTACATCCAAACTAAAATTT			II	
-0.112606	cg10578777	cg10578777	72761345	CCTAAAA	11607503	CCTAAAA	I	C
0.1091034	cg10586672	cg10586672	73667307	ATCTAACTATAAAATAACCAA			II	
0.1141389	cg10587183	cg10587183	16804357	ATCACCAAAATTACTATAATCC			II	
-0.113401	cg10593416	cg10593416	19741306	AAAAACTAAATTTCTAAAACA			II	
-0.124253	cg10599384	cg10599384	17680427	CTCCTCCTAACCTATATATACT			II	
0.1025883	cg10601171	cg10601171	16611329	ACCTAACTCAAAATAAACCCTA			II	

-0.179511	cg1060612	cg1060612	54774472	AACCACA	52617432	AACCAC	I	T
0.1310906	cg1060986	cg1060986	20806344	CTCCATCCATCTATAAACTATC			II	
-0.199783	cg1061480	cg1061480	44746361	ATACTAC	45807398	ATACTAC	I	C
-0.113702	cg1061621	cg1061621	28810412	AAACCAACCCCATACAATAAT			II	
0.1087049	cg1062088	cg1062088	53719509	CAAAAC	39727434	CGAAAC	I	A
-0.100727	cg1062255	cg1062255	28629497	CACCCAC	70809301	CGCCCAC	I	C
0.2095342	cg1062616	cg1062616	26755468	TTAACTTCAACATAAAACAAT			II	
0.1141356	cg1063128	cg1063128	49739470	TCTCCTT	12756462	TCTCCTT	I	C
0.1033565	cg1063214	cg1063214	73771431	AAAAAA	16606388	AAAAAA	I	A
-0.124267	cg1063265	cg1063265	45693300	TTAATCCCTAAAAACATACCA			II	
-0.444445	cg1063277	cg1063277	49764464	TAATCAAAACCTCTAAAACAA			II	
-0.112566	cg1063289	cg1063289	49752455	AAAACA	45646503	AAAACA	I	A
-0.186097	cg1063589	cg1063589	47783382	AACACAT	19651386	AACGCGT	I	T
0.1030821	cg1064696	cg1064696	21727497	AAACACACAATACAAAACTTC			II	
0.1041579	cg1065165	cg1065165	67683365	CTCCACTCAAAATTAACCACC			II	
-0.118296	cg1065555	cg1065555	74623332	AAAATA	35659384	AAAATA	I	A
-0.104748	cg1065820	cg1065820	19749453	TCCCTCCCTATTATACTCTCCR			II	
-0.190665	cg1066231	cg1066231	27686326	ATTCTTC	47643473	ATTCTTC	I	A
0.1305032	cg1066430	cg1066430	60733432	CTCCCACTAAAACCTAAAATT			II	
0.1501645	cg1066634	cg1066634	71792334	AACTTTCCCATACATACTTAA			II	
-0.105909	cg1067039	cg1067039	42685325	AAAAAAACCRATAACCTAAAC			II	
-0.199962	cg1067256	cg1067256	28763342	ACCTCCT	42751473	ACCTCCT	I	A
0.1258816	cg1067480	cg1067480	20619509	AATATAA	60731404	AATATAA	I	C
-0.114487	cg1068022	cg1068022	18770414	TTCAAAA	41604395	TTCAAAA	I	C
0.1849265	cg1068139	cg1068139	40676346	AACCAAAACCCCAAAAAATCT			II	
-0.161518	cg1068708	cg1068708	68731469	CACAAA	64679387	CGCAAA	I	C
0.1131422	cg1068713	cg1068713	55799382	AATACCATAAAATTAAACAAC			II	
0.1110565	cg1068940	cg1068940	62688381	AAATCCA	20720486	AAATCCA	I	A
0.156495	cg1069015	cg1069015	37773346	AAACAAT	49711327	AAACGAT	I	A
0.1396754	cg1069214	cg1069214	24663433	CAACCACRTAAAAAATTAAAT			II	
0.1441974	cg1069472	cg1069472	10773446	AAAAATCAAAAATAAACACA			II	
-0.100497	cg1069554	cg1069554	33611395	ATAAATCCCTATATAATATTA			II	
0.1007263	cg1069635	cg1069635	56781474	CCAATACTTACAAAAACAATA			II	
0.1072986	cg1069917	cg1069917	26650456	ACTCAAAAAAATATATATTTA			II	
0.1665246	cg1070103	cg1070103	65615318	TAACCACTAAAATAATCAACA			II	
0.1398813	cg1071247	cg1071247	43792404	AAAATTCTTCCCAACTTTTAA			II	
0.107953	cg1071358	cg1071358	33739367	AAATCTATAACTTCTCAAATT			II	
-0.117291	cg1071527	cg1071527	51719344	TAAAAACTTCCCCCCAAAAAA			II	
0.1806626	cg1071979	cg1071979	70612465	TTACCATATCTACTAATCCTCA			II	
0.1261123	cg1072244	cg1072244	53683501	TAAATTTAATATCCTATCAAA			II	
-0.123147	cg1072463	cg1072463	51626331	TTCATACCCAACATCRTTATA			II	
0.1242212	cg1072534	cg1072534	26603501	AACACATCTAAAATAACTCAC			II	
0.1265697	cg1072584	cg1072584	54602367	ATCATTAAACTTACTCATATA			II	

-0.118891	cg1072766	cg1072766	21678464	AAAATATATCTACACATAACC			II	
-0.130084	cg1072949	cg1072949	56800480	ACCCAAA	63799480	ACCCGAA	I	A
-0.11872	cg1073547	cg1073547	54683477	AAACTTCTAATTAAAACCTCT			II	
0.1336279	cg1073560	cg1073560	16760467	ATATTCTTTTAACTCTATCRTC			II	
0.1602075	cg1073630	cg1073630	64642498	ACCCAAACTAAACRAAATAAA			II	
-0.125166	cg1073864	cg1073864	44601351	AATACATTAAATTCATTCATTC			II	
0.1921972	cg1074141	cg1074141	63646479	TTACTTCACATATTATAAAATA			II	
0.1435328	cg1074407	cg1074407	37605414	AAAAAAAACCAAAATCTAAA			II	
0.2355773	cg1074748	cg1074748	53606504	TCACAAA	65610464	TCGCGAA	I	A
-0.243986	cg1075026	cg1075026	57779501	TATTTATCAATATAAAAAATTC			II	
0.2800673	cg1075030	cg1075030	47659388	AATATACTACTTAAAATAAAA			II	
0.1272792	cg1075361	cg1075361	19627345	CCTAAAAAAAACCRTTAAAAA			II	
0.1664058	cg1075439	cg1075439	26699375	ATACTCC	46663315	GTACTCC	I	T
-0.106297	cg1075981	cg1075981	14739477	ATAAAAACCAAAAAAACATCC			II	
-0.179104	cg1076163	cg1076163	48664460	TATAAAAAAACCCTACCCAAA			II	
-0.107853	cg1076323	cg1076323	64765384	TAAACCA	33699316	TAAACCG	I	A
0.2895731	cg1077253	cg1077253	66671425	ACCTCCTATCATTTCTTCATAA			II	
0.1345747	cg1077734	cg1077734	74689428	TCAACAAAAAATCTTATAATC			II	
0.1208898	cg1078077	cg1078077	24632369	AAAAAAAAATCATCTACCTAA			II	
0.1345381	cg1078220	cg1078220	18809487	TATATCTAAAAACCTACCRTCC			II	
0.1926167	cg1078515	cg1078515	28625444	ATTCTAACCTCCTTTCCAATAC			II	
-0.219997	cg1079230	cg1079230	51612373	AACAAA	31716425	AACAAA	I	A
0.1655704	cg1079291	cg1079291	14625395	TAACTCTAACTCCTTCCTCATA			II	
0.1017136	cg1079511	cg1079511	22779306	CCTCCCA	39773476	CCTCCCA	I	C
0.1029451	cg1080034	cg1080034	60620379	CTATTTTCTATTAAAATAACCA			II	
-0.103392	cg1080357	cg1080357	57726430	AATTCRAATAAAACTAAAATC			II	
	cg1080497	cg1080497	54606328	AATCAACAAATCAAAATACAA			II	
-0.14915	cg1080919	cg1080919	30762401	AACACA	38713319	AACGCG	I	T
0.1186809	cg1080928	cg1080928	17670482	CAAAAACTTCCCCTCTTACAT			II	
0.1076824	cg1081142	cg1081142	47696321	AAACCCCTTAAACCAATCTAA			II	
-0.215825	cg1081263	cg1081263	67759420	AACAAC	70703360	AACGAC	I	C
0.1065843	cg1081288	cg1081288	45734474	CTCTTTAAAACTATCTTCTACA			II	
-0.290958	cg1081565	cg1081565	53795414	AAAACA	51795457	AAAACG	I	A
0.1248022	cg1081567	cg1081567	17802397	ATCATTTCCTAACTTATAAATA			II	
-0.11405	cg1082004	cg1082004	59617490	AACAAC	60758463	AACAAC	I	A
0.212857	cg1082073	cg1082073	54723450	RTAACAACCACAAATACRTAT			II	
-0.400033	cg1082196	cg1082196	48742463	ATATTAAAAAACATTCRCTAA			II	
0.1082559	cg1082351	cg1082351	39601303	ATATTATTTCCTAAAATATTCC			II	
0.1072266	cg1082765	cg1082765	41715408	AAACAACACRTACAAAAATCC			II	
-0.123111	cg1083124	cg1083124	19744411	ACTAAAT	48735439	ACTAAAT	I	A
-0.178413	cg1083209	cg1083209	50693368	TAAATCT	52631312	TAAATCT	I	C
-0.15411	cg1083778	cg1083778	26715316	AATAAAT	36715368	AATAAAT	I	C
-0.112762	cg1083972	cg1083972	28804403	TTAATAAAAACRCTAATCCCC			II	

0.1707647	cg1084427	cg1084427	53653457	TATCTAAATTACCACAATCAT			II	
-0.122898	cg1084438	cg1084438	29765465	ATATAACCCCAAACTATCCTA			II	
	cg1084661	cg1084661	67669371	ACTTCAT	10643503	ACTTCGT	I	A
0.1729279	cg1085542	cg1085542	37707303	CCTTTACCCACRTATAATCTCA			II	
0.2930345	cg1085864	cg1085864	61677417	TCRCAAAACTAAATAACTCAA			II	
0.1177042	cg1086246	cg1086246	52672494	CRAATACTATTACTATAATAT			II	
-0.127642	cg1086253	cg1086253	23757363	TTCTCTAACTAAACCAAAACR			II	
0.1974615	cg1086296	cg1086296	59766311	AATAAAAACAACTAACCCTAA			II	
0.1803011	cg1086373	cg1086373	74759421	TTATTCCTACCTCCCACRCTCC			II	
0.1189755	cg1087409	cg1087409	47607347	TTTATCATCATATTTTACATA			II	
0.1232178	cg1087823	cg1087823	55679444	TTTACATCCTCTAAAACCTAA			II	
	cg1088362	cg1088362	13644317	TTAATCCAATTCTTTAATCCTC			II	
0.1351589	cg1088881	cg1088881	56793416	TACTAAATAATAACAAACACA			II	
-0.184886	cg1089064	cg1089064	66636357	TTAAATAAACTCTCAATAATT			II	
-0.135468	cg1089157	cg1089157	20679318	AAATTTTCCAAAACTTATATA			II	
-0.141632	cg1089327	cg1089327	41806353	ATTATCCAAAACAAAATTAAA			II	
-0.133698	cg1089587	cg1089587	18781332	CTAAAAATATTAATACTCCTA			II	
0.1202654	cg1090031	cg1090031	20670427	RTAAACTTTTATACCTATCCTT			II	
0.1845283	cg1090285	cg1090285	42604354	AAATTAATCAAAAAATTCATA			II	
0.1277139	cg1090918	cg1090918	69618411	AATAATA	69736444	AATAATA	I	A
-0.112607	cg1091128	cg1091128	63683505	CAAAACCATATAATCRTATCC			II	
-0.124539	cg1091297	cg1091297	12672439	CAAAATA	53693413	CAAAATA	I	C
-0.121181	cg1092075	cg1092075	66645436	AAATAACTACCCCCCRAAACT			II	
0.1093745	cg1092685	cg1092685	59711416	AAATTAAAAAATCCCTAAAAA			II	
0.2114435	cg1093030	cg1093030	73636451	CAAACAA	49750505	CAAACGA	I	A
0.1230889	cg1093740	cg1093740	40607452	ATAAAAC	37633345	ATAAAAC	I	A
0.1478886	cg1094020	cg1094020	51614481	AAAAATT	58624406	AAAAATT	I	A
0.1170653	cg1094626	cg1094626	21687351	TATACATTAACATCTCAATTA			II	
0.1078365	cg1095315	cg1095315	22773335	CTCACCTCATAATCTACCTTTA			II	
0.1281908	cg1095433	cg1095433	25645386	ACCACCTTAAAAAATTTCCTA			II	
0.3838305	cg1095700	cg1095700	62702473	TTATTCATTTATTAAAACATTT			II	
-0.134426	cg1096702	cg1096702	13720352	ATAAAAA	28601475	ATAAAAA	I	A
0.1177076	cg1096946	cg1096946	74632373	AACACAA	25717329	AACGCGA	I	C
-0.106323	cg1097034	cg1097034	48671357	ATCRAAAAAATCACCAACAAA			II	
-0.159472	cg1097362	cg1097362	17606321	ATAAAAAATCAATACAAAAAC			II	
-0.206174	cg1097441	cg1097441	44729430	CTAACTCATCAATTCTAACAA			II	
-0.129408	cg1097535	cg1097535	39806406	TAATAAAAAAAAATACTCCCT			II	
-0.104242	cg1097858	cg1097858	71789303	TACACCC	59608377	TACGCCC	I	C
0.1179894	cg1097984	cg1097984	62606363	ATAAAATCAACCTTCACTACA			II	
-0.100567	cg1098204	cg1098204	10766315	TTAAAACTTCTACAAAAACCA			II	
0.1295922	cg1098348	cg1098348	56735443	ACAAACCCATAACAAAATCAT			II	
0.1069726	cg1098784	cg1098784	27796427	TATATATTTTCCCCATCAAAAC			II	
0.1184282	cg1098921	cg1098921	70728324	AAAACCA	53740485	GAAACCC	I	A

-0.274561	cg10989317	cg10989317	24719408	CTAAAATACAACAACTATACA			II	
-0.119398	cg10989981	cg10989981	66708439	CCTACTAATCTACTCRATAACA			II	
-0.105678	cg10990188	cg10990188	18656427	AAAATATATCCRCACCTAATA			II	
-0.226099	cg10990737	cg10990737	42615324	TACCCCTCCCCTTCTTAAAAAA			II	
0.1002041	cg10991855	cg10991855	69672418	CAAAAAAACTAACTAAAAACT			II	
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-0.143351	cg10995081	cg10995081	25735316	CACAAAC	13767374	CGCAAAC	I	A
0.1767006	cg10995422	cg10995422	23622307	TAAATCCACACTATCACRATTA			II	
0.1132427	cg10995873	cg10995873	36602457	TATAAACTACAAAAATAAAAT			II	
0.106256	cg10997190	cg10997190	20780397	CAAATACTAAACATAAAATAA			II	
-0.110123	cg11002686	cg11002686	70796444	TACCTAACCTCRTAAAAATAT			II	
-0.109737	cg11002923	cg11002923	28620325	TTCCCTACTCATAATCAAAAA			II	
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-0.103699	cg11005845	cg11005845	30791422	AAACCTC	39669490	AAACCTC	I	A
0.1204076	cg11008123	cg11008123	46645482	ACCAAAA	54708500	ACCGAAA	I	T
0.1793214	cg11010744	cg11010744	21757438	CAACTCTCTCCAATATAACCAC			II	
-0.161261	cg11011512	cg11011512	10722313	AAAATAA	43809366	AAAATAA	I	C
0.217876	cg11012153	cg11012153	72808343	TAAAAAC	33661308	TAAAAAC	I	A
0.1189691	cg11015768	cg11015768	73789466	ACACCTCTCTCTATATATCTTA			II	
0.1009326	cg11016151	cg11016151	72708381	TAAAATTCTAAACTTACATTA			II	
-0.124159	cg11019791	cg11019791	68715414	ACACTAAAAAACTAACTAACA			II	
-0.156622	cg11024449	cg11024449	51660345	CAACTCT	58651460	CAACTCT	I	A
0.1176878	cg11026604	cg11026604	17765356	TTTCTCCTATTTACATACAATT			II	
0.1152308	cg11031567	cg11031567	21750367	ACTCTAACCCAAACCAAAACA			II	
-0.15524	cg11035303	cg11035303	11654432	AATATTACRATACCATTTTATC			II	
-0.250693	cg11036359	cg11036359	58702337	AATACAAAATAACCACTATAT			II	
0.114228	cg11038231	cg11038231	68803380	CCCCTACCTTAAAAATCATAA			II	
0.1355621	cg11043993	cg11043993	40798374	CCCAACAAATACAACCACACC			II	
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0.1452152	cg11046772	cg11046772	29796509	ACCCTAAATACTTCTATTCAA			II	
0.1367173	cg11047442	cg11047442	36635354	CACAACA	44677485	CACGACC	I	T
0.1604477	cg11048797	cg11048797	33699510	TACCAACTCTTTATAACRAATT			II	
	cg11053062	cg11053062	11802432	ATATAATCTCACTCCACCCAA			II	
-0.160723	cg11053632	cg11053632	38637330	TAAACTCTAAAAAATCACCTC			II	
-0.133304	cg11059159	cg11059159	12606302	AAATAAAAAACRCAATTAACA			II	
-0.110462	cg11060532	cg11060532	27709499	AAAAAAATTCCATAAAACTAA			II	
0.1192884	cg11063088	cg11063088	17792508	TTTTAATTAACRCAAAACATTC			II	
0.1401693	cg11066244	cg11066244	42649325	TTTTTACATACATTATCTCATT			II	
0.1441264	cg11066601	cg11066601	57787312	AAAATTC	34636361	AAAATTC	I	A
0.1070406	cg11068881	cg11068881	34643333	ACTTTACAACTTTAAATAATA			II	
0.1252909	cg11073579	cg11073579	60741458	AACAAAATCTAAAAACCTAAT			II	
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0.1214039	cg11081272	cg11081272	66631343	RAATCCCCTACCACRTACTTAA			II	
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0.1028112	cg11092836	cg11092836	13748326	AAAAACACAAATCCTACAACA			II	
0.1000921	cg11104088	cg11104088	31681490	AACCAAA	62791345	AACCAAA	I	A
-0.150354	cg11108474	cg11108474	10605372	TCTAAAA	42766351	TCTAAAA	I	C
0.1337218	cg11111460	cg11111460	25733438	ACCCAAACTTTAAATAAACTA			II	
0.1049508	cg11116274	cg11116274	71647392	CCTTTTCCRAAATTAAAAACRA			II	
0.1684201	cg11119767	cg11119767	11633490	ATACTAAAAAATCTCCTATTAC			II	
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0.1056508	cg11128021	cg11128021	56652322	AAAATAATAATACCAACCTCA			II	
0.1177914	cg11128212	cg11128212	30791331	TTTAAAATATAAATATAATCAT			II	
0.1020517	cg11128956	cg11128956	52764301	ATTAAAACCRTAAATAACCCC			II	
0.101386	cg11132534	cg11132534	34739436	AAAAACCTCACTATCAACCCTA			II	
-0.133628	cg11133658	cg11133658	35656319	CATCAAAAAAAACCRTAAATA			II	
0.1241814	cg11139248	cg11139248	65602468	AAAACACAATAATTACCCAAC			II	
0.290427	cg11144103	cg11144103	33619359	AAAATCTAAAAACTCTAACCCC			II	
0.1052511	cg11147866	cg11147866	21731367	AAACTTTACATAACCAAATATC			II	
0.117977	cg11155432	cg11155432	23722457	AACTCTCTATCTAATTAATTTC			II	
0.1084652	cg11156873	cg11156873	24770432	TTTCAAA	34671340	TTTCAAA	I	T
-0.163977	cg11166453	cg11166453	71682363	AAAATAA	20729361	AAAATAA	I	C
-0.119743	cg11168104	cg11168104	66770303	ACAACCC	39654448	ACGACCC	I	C
0.1467473	cg11169848	cg11169848	48640443	AAACTTCTTAAATAACTCAAC			II	
0.1123199	cg11173609	cg11173609	30675437	ACTTTAAAACAAAACTATAAA			II	
0.1458334	cg11173822	cg11173822	12663331	ATTAAAACCATATTTTCCCTTA			II	
-0.130355	cg11181693	cg11181693	17786435	AAAATAC	54779449	AAAATAC	I	C
0.1281864	cg11188666	cg11188666	68683459	AACTTTAAAAACTTTAAAAATC			II	
0.1032458	cg11198851	cg11198851	26635475	RAAACCAAAAACCAACACACC			II	
-0.110693	cg11199639	cg11199639	35723384	AACAATA	44733367	AACGATA	I	C
0.103714	cg11200743	cg11200743	15605331	TAATATCTACTAAAATCCAACC			II	
0.1065162	cg11201654	cg11201654	31712468	CATTATCTAACACCAAACTCCT			II	
-0.189715	cg11204974	cg11204974	74804386	CCTAAAATCCCAACCTTACCTA			II	
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0.1330224	cg11214507	cg11214507	61632480	AATTTCCTATTTCTACATTTCCC			II	
0.1190989	cg11214962	cg11214962	17728452	ACCAAAT	10767414	ACCAAAT	I	A
0.1237011	cg11216176	cg11216176	50717467	AAAAACAACRAAAACACTCRA			II	
0.2605044	cg11219411	cg11219411	51645476	ATCCTCTCATCTCCTATTAACA			II	
0.117305	cg11223933	cg11223933	45608323	AAAAAATTTAAATTATAAACTC			II	
-0.183621	cg11225091	cg11225091	21723504	AAATACRCRTCAACAATTTATT			II	
0.1440884	cg11229273	cg11229273	37646416	TACTAACCCCTACAAACRTCTA			II	
0.1438487	cg11231735	cg11231735	29646482	AAAAACCTTATCCCCTAAACTA			II	
0.1239249	cg11235594	cg11235594	33659459	ACCATTCCAATCTTAACAATAT			II	
-0.117698	cg11236452	cg11236452	23667335	ACCCACCAATATTTACTCAACC			II	

-0.122212	cg11238952	cg11238952	10745507	AAATACC	55675345	AAATACC	I	A
0.1049671	cg11244648	cg11244648	35662458	AAACAAC	53636494	AAACAAC	I	A
-0.104289	cg11245569	cg11245569	73703494	CAAACTA	63631386	CGAACTA	I	T
0.1655175	cg11256764	cg11256764	74600393	CATTAAA	27676391	CATTAAA	I	A
0.1316157	cg11257300	cg11257300	34664436	TACTAATTCTCCTTTCTCTCTTA			II	
0.1310783	cg11261412	cg11261412	56712505	CAAACTAACCATATACATTTTC			II	
-0.114896	cg11273655	cg11273655	61728324	AAACRAATACCCTTCTCTTTCC			II	
0.1260024	cg11276189	cg11276189	13703378	AAAACAAACTAAATCAACAAT			II	
0.1656764	cg11282828	cg11282828	71675337	ACACAAA	46766498	ACGCAAA	I	C
-0.104702	cg11290168	cg11290168	19810503	ATTACTAAAACAAAATCTTTCA			II	
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0.2151856	cg11294750	cg11294750	45729316	AAACACATTACACATCTTATAA			II	
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0.2489807	cg11307715	cg11307715	46738432	CCTTACTAACTTCTTCRAAATA			II	
0.1129959	cg11313468	cg11313468	45809489	TACATACCTATAATCAAAAACC			II	
-0.120746	cg11314617	cg11314617	20789330	ATCACTAAATATTATAACTAAT			II	
-0.122415	cg11315989	cg11315989	67658342	TAAAACRCRATAAACACTATCA			II	
-0.120716	cg11322406	cg11322406	43709503	TAAAACC	64619450	TAAAACC	I	A
0.1300247	cg11328149	cg11328149	20625410	AAAAATCTACTCTATCAACTAC			II	
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0.1186622	cg11331837	cg11331837	11745317	TAACAATACACTTAAAAAAAA			II	
-0.132709	cg11333230	cg11333230	43751304	CTTAACAAAAATTTACTAACRC			II	
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0.1341342	cg11344614	cg11344614	14770336	AAAAACAACCCCTTATCATAA			II	
-0.163436	cg11347582	cg11347582	66606414	AACCCCT	66679395	GACCCCT	I	A
0.1175687	cg11348583	cg11348583	70762458	ATAATTT	29807455	ATAATTT	I	A
-0.114401	cg11356767	cg11356767	10795372	CAACCAA	11779447	CGACCGA	I	C
-0.142622	cg11361344	cg11361344	23608346	CATTTAA	46604473	CGTTTAA	I	C
-0.107299	cg11367354	cg11367354	65625460	TCTCCTTA	38750478	TCTCCTTA	I	A
-0.11172	cg11376198	cg11376198	36695359	TACTCAA	39793413	TACTCGA	I	C
0.1279335	cg11381655	cg11381655	40714400	ATATTCATCTATCTTCAATTCTT			II	
-0.13206	cg11382082	cg11382082	33670461	ATTAAAAAAACTACTTATTCAT			II	
-0.164863	cg11382666	cg11382666	54618301	ACAATTA	61739303	ACGATTA	I	A
0.1213752	cg11383134	cg11383134	12727427	CTAAAAA	48709346	CTAAAAA	I	A
-0.121231	cg11383474	cg11383474	46689417	TAACTATAATATATACRTCTAT			II	
0.1108473	cg11387985	cg11387985	10603474	TCCTCCACTAACCCATAAATCT			II	
0.1543142	cg11391732	cg11391732	49616463	TATCRAATAAAACTTCTTAAAA			II	
-0.160235	cg11395062	cg11395062	59607487	ATTAAAACACAAACACTTAAT			II	
-0.496492	cg11399582	cg11399582	35765460	CTCCAAC	69623425	CTCCGAC	I	T
-0.21682	cg11400162	cg11400162	65791488	TCAATCAAACCACATATATAAC			II	

0.1030546	cg1140129	cg1140129	74707387	AACACAC	18753308	AACGCGC	I	C
0.1014298	cg1140182	cg1140182	57610366	AAAATAAAAAAACTCATTCCA			II	
0.106505	cg1140373	cg1140373	71720352	TAAAAAACACRTTCCCATCTT			II	
0.1181899	cg1140697	cg1140697	23807351	ATAAAACCTATAATAAACACT			II	
0.1055606	cg1141064	cg1141064	41707436	ACTACTAACCAAATCTTTAAA			II	
0.3107132	cg1141860	cg1141860	28663477	AACCTACCTAATTCCAAAACA			II	
-0.123502	cg1142014	cg1142014	40618306	ACRATCTTCATAAATTATTTAC			II	
0.1136298	cg1142231	cg1142231	15807379	TCTATATAAAATCCACACCAC			II	
0.1267234	cg1142437	cg1142437	15684506	AATACAACTAAAATCTATTCA			II	
0.1731393	cg1142477	cg1142477	12730499	CCCAAAACAAATATATCTTAA			II	
-0.137776	cg1143470	cg1143470	48736392	AAAACCT	60678355	AAAACCT	I	C
-0.132828	cg1143550	cg1143550	47788310	TCCAATT	12673349	TCCAATT	I	A
0.5106072	cg1143746	cg1143746	63779342	CATTAAC	40684324	CATTAAC	I	A
0.1786116	cg1143828	cg1143828	53729382	ATTTCCTATACRTCTAAAATAA			II	
0.1028571	cg1144510	cg1144510	30735412	AAAACAA	38697402	AAAACAA	I	A
-0.157791	cg1144907	cg1144907	31795338	AAAAAAC	10773428	GAAAAAC	I	A
0.1125709	cg1145371	cg1145371	39675490	ATAAACAAAACAAAATTCRAA			II	
0.1094906	cg1145689	cg1145689	12760376	AACTCCTCTTTCATAACTTTAA			II	
-0.157035	cg1145964	cg1145964	61650494	AATATTA	61741509	AATATTA	I	C
0.2005206	cg1146342	cg1146342	54630353	ACCTCATCATCATCCCAATAA			II	
-0.172384	cg1146763	cg1146763	49685357	AAACAATTACTACTTTTATCTA			II	
0.1183338	cg1146814	cg1146814	52715444	AACTACA	31789306	AACTACG	I	A
0.1358615	cg1147140	cg1147140	36806374	AAAATACTAACTCAACRTCTA			II	
0.2022153	cg1149560	cg1149560	45775369	TCTACAT	34713473	TCTACGT	I	T
-0.156765	cg1151058	cg1151058	29790445	AATCCCA	29707302	AATCCCG	I	A
-0.152298	cg1151746	cg1151746	17608352	CCCTCCC	57733485	CCCTCCC	I	C
0.1963443	cg1151970	cg1151970	66764502	ACCTCACACTATAACTCCRAA			II	
-0.115129	cg1152832	cg1152832	41789306	CCCTTAA	59802488	CCCTTAA	I	A
0.1427399	cg1152923	cg1152923	58607316	RATAATAATTATCRAAATTTAT			II	
0.1735656	cg1153040	cg1153040	29795504	TAAAAAAATCTAAAAATTATT			II	
0.1020963	cg1153371	cg1153371	60750330	ACTAAAACCCAATATAAACAT			II	
0.1121202	cg1153429	cg1153429	70761405	CCTTCRCCTCCRTAATACCCTA			II	
-0.123602	cg1153967	cg1153967	24742430	AAAAAAATATCCRATAACTAA			II	
-0.143503	cg1154070	cg1154070	71744395	AAAACCCRTCTCTACAAAAAA			II	
0.1126128	cg1154720	cg1154720	64696506	CCACAACCCTCAAAAACATAA			II	
0.1074324	cg1155207	cg1155207	42614480	ACAACCA	65626337	ACGACCC	I	T
-0.129796	cg1155506	cg1155506	18610442	TACAATAACRAACTCTATACT			II	
-0.13056	cg1155865	cg1155865	62620354	AATAACRAATAATTAACCTAA			II	
0.1154602	cg1156231	cg1156231	42736499	CACTCCTAACTTTAAAACTTAT			II	
0.1035383	cg1156423	cg1156423	46721362	TAAAAAACCTCTACACACCCA			II	
-0.102561	cg1156591	cg1156591	24744444	TAACTTCCAATATAATATTCRT			II	
-0.102412	cg1156831	cg1156831	11631401	CAAAAAAACAAATAATTCCAC			II	
0.1338205	cg1157112	cg1157112	50647374	AAAAAAAAAATACTAATTCTA			II	

-0.100536	cg1157474	cg1157474	66802480	CTATTCTAACRCAAACTAAAA			II	
0.1109704	cg1158079	cg1158079	25751411	AATAATAACTAAATCAATAAC			II	
0.1174277	cg1158335	cg1158335	19794335	AATCCAACTATTAAAATTCTT			II	
-0.102691	cg1158376	cg1158376	34739476	RTATCAATACTAAAACRCTTC			II	
-0.142227	cg1158618	cg1158618	55749302	TTATATTCTAAAAATAAAAAC			II	
0.1867119	cg1158706	cg1158706	36628408	CTTCCCA	11720427	CTTCCCG	I	A
0.1004175	cg1160073	cg1160073	47754482	AAAAAAAACCAAATTTAAAAA			II	
0.111643	cg1160418	cg1160418	55609355	TAAACRCTAACRCTCTAACCC			II	
-0.12593	cg1160815	cg1160815	10777317	TTAAAAC	61659390	TTAAAAC	I	A
0.133836	cg1161158	cg1161158	64602334	TTACCCAATATTTTCATTATAC			II	
0.2071889	cg1161374	cg1161374	59635467	TTAAAACAACTAACCATCCAC			II	
0.1541541	cg1161502	cg1161502	59612379	TACAACC	60706338	TACAACC	I	C
0.1015643	cg1161809	cg1161809	39746495	ACCTACAAAAATAAAACTAAA			II	
0.2088363	cg1162013	cg1162013	63721382	CTAAAAAATCRATCCACTCTA			II	
0.1055044	cg1162649	cg1162649	39632421	ACCTCTCTAATCTCAACCRAA			II	
0.1169755	cg1162796	cg1162796	65699398	AAAACCCTTAATAATTCCAAT			II	
0.1309506	cg1163093	cg1163093	34709464	CTAAACA	15666478	CTAAACG	I	T
-0.138507	cg1163519	cg1163519	58689347	CACACAT	58611358	CACACGT	I	T
0.1663271	cg1163796	cg1163796	65748382	AACTTCTAAAACCTTTTTCCT			II	
0.1007431	cg1163961	cg1163961	56766398	ACRCTTATAATCAATACACTA			II	
0.1040449	cg1164545	cg1164545	70678460	ATATAAATAAAACAACAAACA			II	
0.1218222	cg1164553	cg1164553	36627324	AATTCCCAAAAACTAACCAAC			II	
-0.113138	cg1165193	cg1165193	11709328	AAATATTTAATCTCCCTACCC			II	
0.1066901	cg1165549	cg1165549	72635435	ATAAATCACTAAAAAAAATCC			II	
0.1025639	cg1165732	cg1165732	45643453	AAATAACCTATAACCTTTAAC			II	
-0.147019	cg1166081	cg1166081	22797392	AAATCCTTCRTACTAAAATCT			II	
0.1013534	cg1166206	cg1166206	39723430	AATAATAAACCRCAATAAAAA			II	
-0.105513	cg1166339	cg1166339	67761493	TATAACA	15688477	TATAACG	I	A
0.1154724	cg1166369	cg1166369	17615336	TACTTTCTTTCCCTTTTAAAT			II	
-0.182083	cg1166653	cg1166653	18631405	CAACAAAACAATTAACAAATA			II	
-0.209806	cg1166738	cg1166738	56612305	TAACTTA	14770408	TAACTTA	I	T
0.116732	cg1166841	cg1166841	74728327	TTAAACTCAATTAATAATATC			II	
-0.239948	cg1168584	cg1168584	13703448	ATTCCAA	22787371	ATTCCGA	I	A
0.1261314	cg1168975	cg1168975	29610312	ATACTAAAAATACAAACCTAA			II	
0.1203964	cg1169240	cg1169240	58733431	TTCTAAACCATAACTATAATA			II	
0.101835	cg1169504	cg1169504	74647411	CAACTTT	43604473	CGACTTT	I	A
0.1102794	cg1171250	cg1171250	54694405	TTTAAATCATTCATAAACAAC			II	
0.1195122	cg1171950	cg1171950	52666370	CCTAACA	10666383	CCTAACG	I	T
-0.105708	cg1172110	cg1172110	36771440	CCAAAA	15759409	CCAAAA	I	A
-0.201523	cg1172392	cg1172392	34635449	TAACTACACTATATAATCCAC			II	
-0.11319	cg1172414	cg1172414	50745468	AACAAAAAAATAACTAAATAT			II	
0.1037499	cg1172541	cg1172541	13727428	CTAACCAACTCTTACTAACCA			II	
0.1134717	cg1172874	cg1172874	26802426	TAACAAAACCCAACTACTTCA			II	

0.2185671	cg1173313	cg1173313	52698501	AACCCCTACTAAATTTAACAA			II	
-0.155012	cg1173775	cg1173775	73704494	AAAACATACCTAATCCRTAAC			II	
0.103571	cg1174034	cg1174034	44639397	CACCTAA	37643418	CGCCTAA	I	A
0.1037145	cg1175073	cg1175073	59636326	ATAAAAACCCATAAAAATAAA			II	
0.177115	cg1175269	cg1175269	65627450	CTAAAAATATACCTCCCRTTT			II	
0.1103278	cg1175828	cg1175828	23682302	CTAAACCTAAACCACTAAAAT			II	
-0.132851	cg1176474	cg1176474	39628357	AAATAAAAAAAAACCCRAATA			II	
0.112469	cg1176531	cg1176531	68621315	TATCTAAATACCTCAAATCCA			II	
0.1595337	cg1176934	cg1176934	36795500	CCCACAA	38669411	CCCACGA	I	A
0.1684297	cg1177871	cg1177871	50746371	TTTTCRTATTTATTAAAAACTA			II	
-0.10245	cg1178130	cg1178130	26694315	TATTTAT	41715429	TATTTAT	I	A
-0.100945	cg1178352	cg1178352	71794496	ATAAAACCACRAACCCCCRCR			II	
0.239755	cg1178429	cg1178429	38799338	TTTCTTTTCTCAAATATTACCT			II	
-0.115465	cg1178658	cg1178658	20739373	ATACTCACTCAACATAACATC			II	
0.3916615	cg1179107	cg1179107	19636496	TAAAACTATAACTCAATTCTT			II	
-0.1208	cg1179128	cg1179128	10745380	ACATCCTACTATATACAATTA			II	
0.1305271	cg1179840	cg1179840	64656334	TATATATACAACACTCAACTT			II	
-0.105637	cg1180172	cg1180172	13714508	AAACAA	58789321	AAACGA	I	A
-0.102485	cg1180229	cg1180229	35756476	CAATAAAAATCAAAAAAACA			II	
0.1280844	cg1180715	cg1180715	64719320	AACTCACTTTATAACRTAAAT			II	
0.1005921	cg1180810	cg1180810	30622386	ATATTAAAACCAAAAAACACR			II	
-0.137888	cg1181858	cg1181858	62638468	TACTTAATAACACTTTAAAAC			II	
0.1300474	cg1182065	cg1182065	25615372	TCATTACTCACCATCCTTAATC			II	
0.1525269	cg1182456	cg1182456	27806415	AAATCAATTTCTAAAAATTTA			II	
-0.118594	cg1182573	cg1182573	18661402	TAAAAA	62632378	TAAAAA	I	C
-0.205064	cg1182672	cg1182672	52788439	ATAAAC	16650359	ATAAAC	I	A
0.1068047	cg1183463	cg1183463	39775431	TAATCTAATCCRTCRCAAAAT			II	
-0.218676	cg1183554	cg1183554	52804376	CTCACTTCCTCTTCAAAACTAC			II	
0.1421595	cg1183956	cg1183956	17742472	AACRAAAAAAAACCCAAAAAA			II	
-0.102033	cg1183968	cg1183968	69605379	TAACCTA	59741403	TAACCTA	I	T
-0.110603	cg1184177	cg1184177	72702348	TCAATCA	19639374	TCGATCA	I	C
-0.215654	cg1184186	cg1184186	29652450	CAATACTTAACTCAATCAAAT			II	
-0.115937	cg1184957	cg1184957	48660405	AAAACTT	27635396	AAAACTT	I	A
-0.309061	cg1185780	cg1185780	30613358	ACTAACCAATACAAATCTCCA			II	
0.1270913	cg1185992	cg1185992	34662471	TAATCATCTCAAAACTAAAAC			II	
-0.186988	cg1186138	cg1186138	19803414	ACTCCCC	63613441	ACTCCCC	I	C
-0.108818	cg1186190	cg1186190	67809443	AAAACC	30721352	AAAACC	I	C
0.1049152	cg1187106	cg1187106	30688439	CCAAATCCTCTTTCAACTCAA			II	
	cg1187154	cg1187154	13644500	CAAATTCCCAAACAAATTAAC			II	
0.1566539	cg1187497	cg1187497	48786440	CATTCCT	45700445	CGTTCCT	I	T
0.1569063	cg1187781	cg1187781	26647449	TCCAAAATCTCTAATATAACC			II	
0.1039407	cg1187909	cg1187909	30655510	TTATTTCTTATTAATTAAAAAC			II	
-0.114562	cg1188103	cg1188103	24635354	CRAATTAAATCCATTTTCAAA			II	

0.3369749	cg11882358	cg11882358	66678315	CCTTACTTTTCTATTCTATTAA			II	
	cg11883141	cg11883141	22757330	ATAAAAAACTATCTAACATAC			II	
0.1702293	cg11884832	cg11884832	35693488	AAACTAATTTTAACATTATAAA			II	
0.1359209	cg11885357	cg11885357	13736432	AAACAAA	71638330	AAACGAA	I	A
-0.140173	cg11891395	cg11891395	51682484	AAAAAAACAATTTACTTATAA			II	
0.1263906	cg11897628	cg11897628	51606301	AAATATAAAAACCATAACTCA			II	
-0.116422	cg11897887	cg11897887	41757509	AAACCTATATCCTAATTAACAA			II	
0.154685	cg11898347	cg11898347	24804430	ATACCCTAACAATATATTCAT			II	
-0.155755	cg11900328	cg11900328	63649415	AAACCATCATCATTCCTACTT			II	
-0.220177	cg11900447	cg11900447	23645312	TTACCAA	30728493	TTACCGA	I	A
0.1967297	cg11903206	cg11903206	37679389	AATTAAAAAATTCTCCCTACC			II	
0.1412692	cg11907323	cg11907323	56729493	ACCATCCTTTCACAAAACACAA			II	
-0.162606	cg11909574	cg11909574	70734487	CAAAAAC	69691433	CAAAAAC	I	A
-0.109916	cg11917288	cg11917288	28715494	CTATACTCAACTTCTAATAAAA			II	
0.1051977	cg11918822	cg11918822	44775332	AAAACACTAACTAAAAAACAA			II	
0.2340713	cg11923920	cg11923920	16652322	AACRACCTATATAACTATCAC			II	
-0.132662	cg11934170	cg11934170	51707449	TAACAAA	21754348	TAACAAA	I	T
-0.119687	cg11941060	cg11941060	59797491	CTCCAAA	41669341	CTCCGAA	I	C
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-0.287758	cg11942206	cg11942206	70765391	TCCTTCTATTTCTCCTTTTATCT			II	
0.1040324	cg11942594	cg11942594	32810500	TAAATAAAAACCAATTTTAAA			II	
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0.113852	cg11949175	cg11949175	55763401	AAAAATCCAAAACCCAAAATT			II	
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-0.386451	cg11956442	cg11956442	51600385	AAAAATCAATAAAAAATTAAA			II	
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0.1992412	cg11969526	cg11969526	45736441	AACTCTTTAAAAATTCRAAAC			II	
0.1831126	cg11973981	cg11973981	49644409	ATTTAAAACAATAAAAACTAT			II	
-0.102402	cg11975397	cg11975397	61717500	CAACCAAAACCTCTTTAAAATA			II	
0.1082197	cg11976736	cg11976736	56765422	AAACAAAACATAAATATACAA			II	
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0.1048631	cg11983196	cg11983196	11806442	AAATAATCCTTTACTTCTACRA			II	
0.1397672	cg11984971	cg11984971	37634448	AAAAAAATAATACTAACTTCC			II	
-0.195624	cg11986643	cg11986643	25709418	TACACTTACCRAAAAAATCTC			II	
0.1195126	cg11986743	cg11986743	44644324	TCTCTTCRAAAAAAACTCTCTT			II	
0.1532804	cg11987751	cg11987751	11733380	ACTTCCT	65689343	ACTTCCT	I	C
0.4160441	cg11993350	cg11993350	62621397	AACTCCC	50713487	AACTCCC	I	A
0.1010199	cg12002455	cg12002455	55794335	TTTCCTTAAAAACTATAACAA			II	
0.1052703	cg12005412	cg12005412	47709311	CTCTCCTTTTTTTATTCTCCACA			II	
0.1067102	cg12010476	cg12010476	35705472	CAACAAAACCAATATAAACTA			II	
0.3684176	cg12012426	cg12012426	66781467	AAAACAAACRAAAATCAACTT			II	
0.1578395	cg12014181	cg12014181	17657505	AAACATT	15640378	GAACATT	I	A

-0.154857	cg12024822	cg12024822	38736307	ACTAAAA	72718469	ACTAAAA	I	C
0.1128795	cg12025137	cg12025137	23680449	ATCCCAAATAACAACAACTCTA			II	
-0.245253	cg12036633	cg12036633	34610328	ACCTTAAAATACCAAACTCTAA			II	
0.11089	cg12044531	cg12044531	73684393	CTATACCTTAAAAACCTATAAC			II	
0.1001026	cg12051819	cg12051819	59730440	TTAACTAAACATTAAAATTACA			II	
-0.150173	cg12058262	cg12058262	30635302	TTAATTA	56774418	TTAATTA	I	A
-0.1264	cg12070022	cg12070022	48721390	ATTCCAA	27615377	ATTCCAA	I	C
0.1381571	cg12072024	cg12072024	71732385	TAAACCRATTCTAACCAATATA			II	
-0.210446	cg12074485	cg12074485	39644373	TATTCCAACCCCTAAATCTACA			II	
-0.137009	cg12076350	cg12076350	71604490	TACAAATACTACTATCTAACTA			II	
-0.222203	cg12078775	cg12078775	51701343	TCTAAAA	39654350	TCTAAAA	I	A
0.1222708	cg12082015	cg12082015	69749311	ATAACATAATATTAAATACTTC			II	
0.1003426	cg12089079	cg12089079	39701347	AATAATTATAAAACTTTTCTTC			II	
	cg12094863	cg12094863	13752450	CACTTCCRCTTACCTCTCATTA			II	
0.1240412	cg12096487	cg12096487	69672368	CATAAAAACTACRCRTCTAAA			II	
0.1224758	cg12097550	cg12097550	74670410	TACAACTTAAACAAAAACACT			II	
0.1183644	cg12097671	cg12097671	42757396	CTATTCTTCAATATCTCTTTTA			II	
-0.115538	cg12102973	cg12102973	59743375	AAAAAAACAAACCRATAAACT			II	
-0.133679	cg12105899	cg12105899	13790458	CAAAAAA	24602442	CGAAAAA	I	T
-0.110468	cg12109260	cg12109260	74638358	TACTAAA	51763428	TACTAAA	I	T
0.1257378	cg12111149	cg12111149	36794431	TAAAACTCTTTTACCACCCCCA			II	
0.1053723	cg12119988	cg12119988	38752400	TACTAAAACCCTACTCCCTCAA			II	
-0.13603	cg12121446	cg12121446	66659507	ACACATA	20782356	ACACATA	I	A
-0.106175	cg12121660	cg12121660	45689375	ATAAAAA	52608417	ATAAAAA	I	T
-0.156798	cg12123879	cg12123879	64640419	AACAATTATCAAAATTACTAAC			II	
0.1476087	cg12127811	cg12127811	51740387	ATATATAATATTAAATCTCTAT			II	
0.1741853	cg12128445	cg12128445	15615502	AAAAACTACTTTATTTAAAAAC			II	
-0.125168	cg12130015	cg12130015	11796352	TAAACAC	72630412	TAAACAC	I	T
0.1267521	cg12146763	cg12146763	20676448	CATATCTTATTCATCTTTATATC			II	
-0.147375	cg12159023	cg12159023	19779377	ATAAACA	57795385	ATAAACA	I	A
-0.108462	cg12160424	cg12160424	74764369	TAAAAAT	61763322	TAAAAAT	I	C
-0.120893	cg12161971	cg12161971	14739431	CAAACAC	73762406	CGAACGC	I	A
0.3507917	cg12167002	cg12167002	63634497	TACTACA	57679423	TACTACG	I	A
0.1282933	cg12168509	cg12168509	25749369	TACTCAACRTCACRTAACTATA			II	
-0.1579	cg12173150	cg12173150	14667323	AAAAATA	12605439	AAAAATA	I	C
-0.12789	cg12177182	cg12177182	32796360	AAAAACA	28663432	AAAAACA	I	T
0.1661988	cg12179658	cg12179658	10600406	ATAAACACCAAAACAAACCTA			II	
0.1194378	cg12198140	cg12198140	17740335	AATTTAAAAACACTAACRTCA			II	
-0.249759	cg12208638	cg12208638	27767440	TTCAAAACCTAAAAAACRATA			II	
-0.217445	cg12209881	cg12209881	44636452	CCCTAATAAACACTAACCCCA			II	
0.225235	cg12213037	cg12213037	23751502	CTAAACRACAAAACAAAAACT			II	
0.1764701	cg12217954	cg12217954	29749437	ACCAATAACTCTATATAATCTC			II	
0.1281553	cg12219469	cg12219469	24798379	ACCTAAAATCACCTCRTAACTC			II	

-0.111967	cg1221970	cg1221970	51713307	AAAACCTTAACCCAATAATAT			II	
-0.131241	cg1222602	cg1222602	21727322	AATATTA	44763391	AATATTA	I	T
0.1498241	cg1222694	cg1222694	15672418	ACTACAATTAAATCRTAACAC			II	
0.1436125	cg1223246	cg1223246	48788346	AAAATCTAACTTCCAACCTTT			II	
0.1286	cg12232731	cg12232731	71697384	ATAACAA	42681335	ATAACAA	I	T
0.175789	cg1224133	cg1224133	32689477	TCACAAATCACCACAAAAATA			II	
-0.149048	cg1224326	cg1224326	65639315	CAAATAA	48785495	CGAATAA	I	C
0.1157418	cg1225064	cg1225064	40669385	ATTAACAAAAATCCCACCCCA			II	
0.1839934	cg12253071	cg12253071	71659403	CTATAAAAAACTAAATATATA			II	
-0.116288	cg1225589	cg1225589	74711503	AATCAAAAAACCCTACRTTCA			II	
-0.13098	cg1225817	cg1225817	15655389	ACTACTA	20620474	ACTACTA	I	C
0.1164765	cg1225989	cg1225989	53781503	TTAATTATTCTAAATATTCCTA			II	
-0.151354	cg1226997	cg1226997	43644410	CAATAAAAAATCAAAATAATA			II	
0.1600513	cg1227131	cg1227131	10739502	TAATTACTAACTTTAATTACRC			II	
0.3481065	cg1227973	cg1227973	32767338	AAATCAAATTCACACATCATA			II	
0.110742	cg1229655	cg1229655	28660318	CAATAATTAAAACACTCTCAC			II	
-0.112968	cg1229759	cg1229759	50692476	AAAACAA	66741323	AAAACGA	I	A
0.1563049	cg1230331	cg1230331	36649384	CRAACACAAAAATCAAACCTT			II	
0.1164808	cg1230381	cg1230381	51607504	CCRAACCAAAACATTATAAAC			II	
0.1199041	cg1230737	cg1230737	49606365	ACAATTTAAACTCCACAACAT			II	
-0.466653	cg1231002	cg1231002	72708489	CATCTAT	39781349	CATCTAT	I	T
-0.132341	cg1231245	cg1231245	30631400	CTTTCAC	39730423	CTTTCGC	I	A
-0.22024	cg1232166	cg1232166	29698322	RAACAATACTAAAACRCTAAT			II	
0.2223081	cg1234142	cg1234142	16642311	ACTCATCCCCTTACACTTTAAA			II	
0.206247	cg12342501	cg12342501	18752444	CCAATAAAACAACAATCRCTA			II	
0.1123271	cg1236004	cg1236004	70788465	AAAATAA	42634485	GAAATAA	I	C
0.1110103	cg1236198	cg1236198	14683391	TATCATAACCTACTACRACTAC			II	
0.180174	cg1237017	cg1237017	58620371	TCATCAATATATACTCTAAAA			II	
0.1416509	cg1237781	cg1237781	55643407	TATCTCTAATTCCCTATTAATT			II	
-0.112338	cg1238369	cg1238369	64618426	ACCATCC	60658391	GCCGTCC	I	A
0.4894441	cg1238661	cg1238661	42678409	AAACTAATAACCTTATTAAAT			II	
-0.191249	cg1238852	cg1238852	15780459	CATTTTACAACCTATATTAAAA			II	
0.4238711	cg1239137	cg1239137	17745430	TACTATCTAAAAACCCAAATA			II	
0.1008284	cg1239157	cg1239157	47783490	CTATTAATCTATACRTCTATAC			II	
-0.100524	cg1239247	cg1239247	67717362	TCTACCT	45613312	TCTACCT	I	A
0.1094521	cg1239582	cg1239582	42695344	ACCATCA	11610410	ACCGTCG	I	T
-0.124754	cg1240086	cg1240086	67609391	CCCAAAAAACCRAAACCAAAA			II	
0.1063498	cg1240195	cg1240195	23721353	TAACTTAAATAAAATTTACAA			II	
0.1112951	cg1240316	cg1240316	37764433	CTAATTACTAAATAATAATCA			II	
0.156376	cg1240668	cg1240668	39642444	ACTTTCAATAAAAACAACAAA			II	
0.1145756	cg1241098	cg1241098	63628360	ATTAATA	74804390	ATTAATA	I	C
0.1731881	cg1241277	cg1241277	64764403	RTCATACTAATTATACCCTACA			II	
-0.151489	cg1241770	cg1241770	50725348	AAAACAC	50627440	AAAACGC	I	A

0.1006397	cg1241804	cg1241804	15670433	CTTACCCTTAATAATAATTTTC			II	
-0.100615	cg1241938	cg1241938	38641411	AAACCCT	13767478	AAACCCT	I	A
-0.138199	cg1242010	cg1242010	64652348	ATAATAA	45732372	ATAATAA	I	T
0.147016	cg1242108	cg1242108	74634484	TACCCTATAAATAAATAATAC			II	
0.1453294	cg1242253	cg1242253	12612468	ACACACT	29704333	ACACGCT	I	A
0.1167544	cg12425861	cg12425861	52664318	AAAACAAAAAATCAACAAAA			II	
0.1147842	cg1242716	cg1242716	57684372	TTTTAAT	27774501	TTTTAAT	I	C
-0.142097	cg1243077	cg1243077	11781506	ACCTACACRAAACACTACTTT			II	
0.1996354	cg1243280	cg1243280	10741417	TTCRCATATACAATATAATTA			II	
0.111805	cg1243488	cg1243488	20673311	CTCACRAAATTTTCCRAAACC			II	
-0.242838	cg1243489	cg1243489	20616326	AAAAATTCRAAATCTATAAAA			II	
-0.255628	cg1244224	cg1244224	17757417	TCAACAT	65807459	TCAACGT	I	T
	cg1244484	cg1244484	39719478	AACCTAC	59656491	AACCTAC	I	A
0.1620967	cg1245001	cg1245001	26697303	ACAAATAAATACTAACTACTT			II	
0.138295	cg1245362	cg1245362	64643493	AACCCCCAACACCAACATCTT			II	
-0.320258	cg1245416	cg1245416	55636429	TTCCTCCCAATTCCCATAACAA			II	
-0.110504	cg1246013	cg1246013	47668470	CACACAA	56640492	CGCGCAA	I	A
-0.151251	cg1246877	cg1246877	65744355	AATTACC	33762399	AATTACC	I	A
-0.194017	cg12469471	cg12469471	44602352	CCTACAA	24782322	CCTACGA	I	T
0.1194328	cg1247818	cg1247818	24720423	AAAATTCTAATCCAACCRCRA			II	
-0.236664	cg1247844	cg1247844	51764498	AATCACT	72769417	AATCGCT	I	T
0.1198309	cg1248300	cg1248300	53609398	AAAAAAACAATCTTCAAAAAT			II	
-0.126494	cg1248518	cg1248518	37798323	AATAACA	33742393	AATAACC	I	A
0.105372	cg12493761	cg12493761	15634478	ATAATAAAATAAACCCTAAAT			II	
0.1533902	cg1249420	cg1249420	61705307	TCTAAAAATCCTTTACAAACR			II	
0.1982616	cg1250030	cg1250030	19792426	CATAACTATATCTCCTCTCTTT			II	
-0.229889	cg1250128	cg1250128	16765481	AATCTAAAACCTACCCAAAAA			II	
-0.101242	cg12501761	cg12501761	15663356	AAAATAC	10749417	AAAATAC	I	A
-0.124509	cg1250508	cg1250508	33715503	AATTTTCTTTTCTCTCCTTTAA			II	
0.1375784	cg1251099	cg1251099	50637410	CRCTATAACTATTAAAATCCC			II	
0.3817115	cg1251565	cg1251565	21610491	AAAAAAAAAACTATATCTAAA			II	
-0.120947	cg1252397	cg1252397	10612336	CCTCTCT	69641414	CCTCTCT	I	C
	cg1252629	cg1252629	62624444	CCRAATCCAAATTAAACCTCA			II	
0.1177448	cg1253209	cg1253209	51755472	ACATACTTCTATACTAACATA			II	
0.1061064	cg1253700	cg1253700	60713304	CCTCACAAAAACACACAATAT			II	
-0.100443	cg1253941	cg1253941	58609470	ATATCTAACAAAAACTCTCAA			II	
-0.140075	cg1254635	cg1254635	61744370	TTTCACA	67790412	TTTCGCA	I	C
0.1300593	cg1254817	cg1254817	37622434	CATACCTATAAATAAATCAAT			II	
-0.161342	cg1255656	cg1255656	63705396	TAACTCATCCTAACTCATTTCC			II	
-0.207945	cg1256282	cg1256282	25616402	AATCACA	66711311	AATCACA	I	A
0.1026454	cg1256352	cg1256352	59700446	ATAACAACAAACATACCATAA			II	
0.1032152	cg1256578	cg1256578	36716357	CAATCAAATAAATACCCCACA			II	
-0.267931	cg1256988	cg1256988	11794464	AAATTAATTTTAAAAACTCA			II	

0.1116675	cg1257266	cg1257266	21613381	TTCCCTAAAAATCTATAATAA			II	
-0.135617	cg1258089	cg1258089	61808327	AACCTTAAAAAAAACTAAACA			II	
0.101812	cg1258129	cg1258129	29693368	CCTACACRACAAAATAATAAC			II	
-0.124846	cg1258496	cg1258496	55799317	AATCTATCCCCTAATCCTCATA			II	
-0.101634	cg1258638	cg1258638	21646472	CAAAAC	10807359	CAAAAC	I	C
0.1449285	cg1259166	cg1259166	67703325	ACATCTAATATAAAAAAAATC			II	
0.1137184	cg1259236	cg1259236	57675375	AAAATTCTTCCATACTACCTA			II	
0.1128238	cg1259322	cg1259322	33788324	AACCCTTCTACTCACRTAAAT			II	
-0.117449	cg1259761	cg1259761	30728473	CRTAAACCCATATATACRAAA			II	
0.1128085	cg1260053	cg1260053	13627485	ACAAACCACCTTTCACAAAAC			II	
0.1399729	cg1260669	cg1260669	62677356	AAATAACCACAAACAAAAAT			II	
0.1040529	cg1261240	cg1261240	42723447	AAAATACCACTAATAAAAACT			II	
0.1039301	cg1261827	cg1261827	44631474	CCTACTTCTTACTAAAAAATA			II	
0.1190513	cg1261858	cg1261858	12792490	CACTAATCCTAACATTCAAAT			II	
0.3671333	cg1261974	cg1261974	24654347	CAACATCRCTTTAAAATACTC			II	
-0.311804	cg1262265	cg1262265	12675381	CTAACCTATACTACATTACCT			II	
-0.105113	cg1262314	cg1262314	27656419	AATACAA	73632474	AATACGA	I	C
0.308625	cg1263315	cg1263315	50649400	AATAAA	56766334	AATAAA	I	A
0.140761	cg1263512	cg1263512	15798509	ACTTAACTTTAACTTCTATAAC			II	
0.1013287	cg1263649	cg1263649	66659489	AAACTTCCCTAAACCACTTCT			II	
0.1050226	cg1263744	cg1263744	60623484	CRAATTTATCTATTACTACTAA			II	
-0.138396	cg1264271	cg1264271	36748372	CTTAAAA	17689406	CTTAAAA	I	T
0.1351146	cg1265576	cg1265576	18755483	TTTACAATTCTACTTCTCAACA			II	
0.1149531	cg12656291	cg12656291	44615392	CAAATTAAAAAACCTTTACAT			II	
0.1653149	cg1265741	cg1265741	36650391	AAACTTCRATATAATTTCTAA			II	
0.1078849	cg1265892	cg1265892	68601326	CTACAACCCAAACTCTAAACC			II	
0.1053527	cg1266852	cg1266852	10768401	AACAAA	37791311	AACAAA	I	A
0.2735482	cg1267163	cg1267163	66621406	TACCTAAACATTTTAATCATC			II	
-0.130482	cg1267558	cg1267558	45738312	AAAATAAAAAAAACTAATAA			II	
0.1033454	cg1268140	cg1268140	16744343	TCTTTCAAACACCTCCRCTAA			II	
-0.12064	cg1268405	cg1268405	63666330	AAACAC	69645424	AAACAC	I	C
0.1295115	cg1268495	cg1268495	25719432	AATAAATCATAATCCTATTCA			II	
0.1259932	cg1269206	cg1269206	19807430	ATAAAAAATTACTAACACAAA			II	
-0.172606	cg1269733	cg1269733	32605374	AAAAAA	18611433	AAAAAA	I	A
0.1163046	cg1269862	cg1269862	45734417	CCCTATCCCCAATAAACTACC			II	
-0.112803	cg1271528	cg1271528	56624398	ATTTACA	17604473	ATTTACA	I	A
0.1059195	cg1271858	cg1271858	59674465	TTACTCTAAACAAAACTCRAC			II	
0.1233469	cg1271984	cg1271984	69677404	AAATCCCTACACTAATTATAA			II	
0.1199766	cg1271990	cg1271990	20778318	ATACTTTATAACATAATTAAA			II	
-0.376363	cg1272736	cg1272736	60634435	AAACACAAAAAATCTAAAACR			II	
0.1106574	cg1272794	cg1272794	67795441	CAAAAAACATAAACAACCTAC			II	
0.1407546	cg1273687	cg1273687	10770349	CCAAAA	50650477	CCAAAA	I	T
-0.220693	cg1274341	cg1274341	66736391	TTCACATAAAAACTATCAAAA			II	

0.1043063	cg1274889(	cg1274889(	17670473	TAAAAAA	47654449	TAAAAAA	I	A
-0.204811	cg12770425	cg12770425	38801326	AAACCCTACAATATAATATCAT			II	
-0.146589	cg12775223	cg12775223	27621489	AAAAAAATTCTTATTTATTCTC			II	
-0.117786	cg12798157	cg12798157	24768440	AATACAA	62638473	AATACAA	I	T
0.1138106	cg12807764	cg12807764	26801402	CAACTCCATTTTCTACATTTTCT			II	
-0.112655	cg12813768	cg12813768	16676310	CTCCCAAAATCTAAAATTTCA(			II	
0.2173475	cg12814117	cg12814117	53619503	CTCACAC	69695446	CTCGCAC	I	A
0.3512494	cg12819537	cg12819537	19709454	TACTCTCCTTATATAAAATCTT			II	
0.1926998	cg12829045	cg12829045	29706324	CAACACCATCTCCCAATTTTAA			II	
-0.295403	cg12833683	cg12833683	69732368	ACATTAACATAATCATAATTAA			II	
0.1051517	cg12844324	cg12844324	17775456	TCAAACTCCCAAAACTACTTAA			II	
0.1059651	cg1284665(	cg1284665(	31662374	AAAATATTATAATTTCTAACAA			II	
-0.152261	cg12850379	cg12850379	41671327	AACCTAA	30766302	AACCTAA	I	A
-0.121881	cg1285039(	cg1285039(	62624375	TTCCACTCTTTACTATATTATA(			II	
0.1276812	cg12854428	cg12854428	17691497	ATCCAACTCTTAAAATATCAT(			II	
0.1152255	cg12854611	cg12854611	51755382	CAAATTTAAATAAAAAAATAC			II	
0.1764738	cg12856521	cg12856521	38625322	AAAAATCAACRACATATAAAA			II	
0.4127325	cg1285816(	cg1285816(	24803314	ACAACAACACACACAATTATT.			II	
-0.145643	cg12858577	cg12858577	48618427	CCTCACA	35705303	CCTCGCA	I	A
0.206622	cg12865025	cg12865025	19674471	TTTTCTCCTTATCATTTACCTA(			II	
0.1522775	cg12867728	cg12867728	65606362	ATAAACAACTTTCTAACTTCCT			II	
-0.127047	cg12868067	cg12868067	39648318	ACAAAA(	39735482	GCGAAA(	I	A
-0.135581	cg12868173	cg12868173	42635367	CAACATC	30607507	CAACGTC	I	T
-0.100085	cg12869097	cg12869097	41744326	AAAAACACTAAACTTTCACCC(			II	
-0.220744	cg12870217	cg12870217	72752369	TCCTAAAACAAATCAATTTCTA			II	
-0.129424	cg12880095	cg12880095	59650300	ATAATTT	64739460	ATAATTT	I	C
-0.144208	cg1289075(	cg1289075(	49745331	ATAATAA	28793481	ATAATAA	I	T
0.1062618	cg12894371	cg12894371	26658403	ACTAACACAACTACTATTTCC(			II	
-0.129829	cg12906381	cg12906381	62636340	ACAAATT	14765369	ACGAATT	I	A
0.1583416	cg1291658(	cg1291658(	58790404	CACACAC	62624315	CACACAC	I	A
-0.139506	cg12927641	cg12927641	68672507	AAAAAAA	24708479	AAAAAAA	I	A
-0.104309	cg12934884	cg12934884	11642389	TTTCCCA.	68758402	TTTCCCG.	I	A
0.1428649	cg12936992	cg12936992	52695442	CCTTCACTCAACTAATTTTATC			II	
0.1064489	cg12937413	cg12937413	65750346	TATTTACTTATAACATACATAT			II	
-0.113085	cg12939425	cg12939425	61804397	ACACCAA	16640327	GCACCGA	I	C
0.1274002	cg12947138	cg12947138	68707481	TAAAACCTTTACAAACCAAAA'			II	
-0.102816	cg12955305	cg12955305	69802385	ACACTTAAACAATATCTTCCTA			II	
-0.150003	cg12955789	cg12955789	26792344	CATCACC	56703446	CATCGCC	I	C
0.1296864	cg1296442(	cg1296442(	62633339	AAACTTCATTCTATATAACTTC			II	
0.1310313	cg12972705	cg12972705	51653422	ATTCATAACCCACAATTATCA(			II	
0.1146562	cg12980549	cg12980549	66767338	CTATCTAACTTTTAATAAAACT			II	
0.1235387	cg12981577	cg12981577	28711442	CTAATATTCCCAAATTACAAA			II	
0.1126527	cg12995004	cg12995004	21612374	ATTTTTTCCTAATATCTTTTTCT			II	

0.108071	cg12999084	cg12999084	57650306	TATCCTAATCTCRACAAAAAA			II	
0.1003644	cg12999267	cg12999267	39645503	AAAATTAATTCTAACTAATAA			II	
0.1095189	cg13002506	cg13002506	34656427	ACTTATTAATCAACRATAATA			II	
0.1004291	cg13004509	cg13004509	43734355	CAACAA	12744437	CAACGA	I	C
0.1805474	cg13008339	cg13008339	67763423	CRAAAACTCCCTTCCRAATTTC			II	
0.115737	cg13009819	cg13009819	15796314	TAACCAAAAAAACCRTAAAAC			II	
-0.135029	cg13010797	cg13010797	65732385	ACTATTATAAAACACACCCCC			II	
0.1094301	cg13011003	cg13011003	65677367	ATTCCTATCACCACACTACTA			II	
-0.138366	cg13017022	cg13017022	52689403	ACCCAATCAATACCATTTATT			II	
0.2263854	cg13017929	cg13017929	74607403	ATTCAATAAAACTATATTAAA			II	
0.1414913	cg13019553	cg13019553	20649506	CAAATCT	58748301	CAAATCT	I	A
0.1035121	cg13022534	cg13022534	29702360	ATCTATTTAACTCTAAAACAC			II	
-0.107956	cg13022905	cg13022905	74729492	ATAAACT	42717468	ATAAACT	I	A
-0.197739	cg13024511	cg13024511	48753301	AAAAAA	14609420	AAAAAA	I	A
0.1072765	cg13031029	cg13031029	61688421	AAAAAAAACATCACTAAAACA			II	
0.1292071	cg13033858	cg13033858	18605367	TAAAACAATACTTTCCTAACA			II	
0.1369593	cg13037245	cg13037245	43731416	AAACATTCCCRCTAAATCACC			II	
-0.12052	cg13045351	cg13045351	23605470	CRTAACTTATATATCCTTCCRT			II	
0.2002466	cg13046608	cg13046608	18809380	CATCTAATACRCAAAAAACTC			II	
-0.160801	cg13047157	cg13047157	42694384	CRAAAACRCCCTAATCCCTCT			II	
-0.212314	cg13047869	cg13047869	40640376	CCCTATC	68808498	CCCTATC	I	A
0.1136692	cg13052638	cg13052638	49751453	TTAACATTTTTTTAATCTATC			II	
0.1154668	cg13054358	cg13054358	18653470	TCCCTCTAATCTCTTTCCAATA			II	
0.1266958	cg13058453	cg13058453	46747447	AAAAATAAATAACATAATCCC			II	
-0.135259	cg13058819	cg13058819	20716341	CTACAAC	15736324	CTACAAC	I	A
0.114206	cg13061469	cg13061469	31625467	AACAAAACTTATTTTTAAAAA			II	
0.2083466	cg13066461	cg13066461	74730398	TACTACATATTCACTAATTTTC			II	
0.1013381	cg13067635	cg13067635	73615343	CAATAAAATACATACCAAACC			II	
0.2883348	cg13067974	cg13067974	72755340	AATTACTATCRATATCCCAAC			II	
0.2047825	cg13071508	cg13071508	74728372	TAATTAAACCTAAATAAACAA			II	
-0.1008	cg13076785	cg13076785	63802308	AAAATCTAAAAACTTATTTTC			II	
-0.121253	cg13078381	cg13078381	67681305	TCTAATA	10652505	TCTAATA	I	A
-0.162134	cg13078798	cg13078798	67702356	AAATAAAAATTCTACCTAATA			II	
-0.166581	cg13080565	cg13080565	34620490	AAACCTT	68688337	AAACCTT	I	A
-0.116074	cg13081498	cg13081498	62689375	TTCTAAAATACCTTCTAAACA			II	
-0.125108	cg13099429	cg13099429	10639300	AACTAATAAAACACTACACTA			II	
-0.129858	cg13100190	cg13100190	73796403	AACCTTTTAAAACATATACRC			II	
-0.133889	cg13112404	cg13112404	69686420	AACAAAT	49608353	AACGAAT	I	A
-0.15969	cg13127920	cg13127920	14629366	CTAAAACCTCTATTCCCRATAT			II	
0.2233386	cg13134448	cg13134448	35631470	CCAAACTCCRACAAAATAAAA			II	
-0.270276	cg13137809	cg13137809	60688366	CTCTTCA	70753505	CTCTTCA	I	T
0.1217446	cg13138089	cg13138089	10675383	CCTCATT	71751402	CCTCGTT	I	T
-0.19393	cg13142134	cg13142134	40624323	AAAAAATAAAAATCAAAATCA			II	

0.1017179	cg1315370	cg1315370	41729481	ACATTTTAATTATTTCCAAAA			II	
0.3872594	cg1316085	cg1316085	56732304	ATAACCAAAAAACACAACCC			II	
-0.101636	cg1316804	cg1316804	44665366	AAATAA	48645411	AAATAA	I	C
0.1110019	cg1316869	cg1316869	54790415	AAACCTACCTTCTAAAAACTT			II	
-0.166839	cg1316913	cg1316913	28732384	AACCACT	17730383	AACCGCT	I	C
0.1234684	cg1316922	cg1316922	50629351	TACRAATCATTCCAAATAACT			II	
0.1288944	cg1317167	cg1317167	34693303	CTTAATATAATACAAACCACT			II	
0.1008987	cg1317339	cg1317339	72711319	TTTCCAACTTAAAACTATTAC			II	
0.1070763	cg1317859	cg1317859	38711495	TTTAACCACTCTAATCAAAAA			II	
0.2124274	cg1318365	cg1318365	24757360	CACCTTATACTCCCTCTTAAAC			II	
0.1342141	cg1318444	cg1318444	30610477	CTTACTCCTTTACTAACCCTAT			II	
0.2172931	cg1318541	cg1318541	68665427	TAAAAA	33656307	TAAAAA	I	A
0.1120493	cg1318598	cg1318598	11653303	AAAAAAAATCCRTAACCCAAA			II	
-0.124589	cg1320552	cg1320552	18746348	ACATATCCAACACAAACTCRA			II	
-0.119404	cg1320732	cg1320732	65656400	AAAAAA	58709472	AAAAAA	I	C
0.1026338	cg1321100	cg1321100	13615312	AAAACTATTACRTTAATACAA			II	
0.1444882	cg1321353	cg1321353	20774335	AAAAACCCAAAACAAAATAA			II	
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0.1305625	cg1321955	cg1321955	30733342	ATAATTATATAAACAACTAAA			II	
0.1247442	cg1322192	cg1322192	60630370	TACATAATACAACCTAACTTT			II	
0.1025322	cg1322556	cg1322556	53699406	TTCATCA	53630336	TTCGTCG	I	T
-0.111644	cg1323020	cg1323020	39736499	ATATATAAAATATAAACATCA			II	
0.188866	cg1323207	cg1323207	48807345	AATTATACCTTTAATTTTATAT			II	
0.1325462	cg1323509	cg1323509	55804302	AAAATATTCCTTCATAATACC			II	
0.1346889	cg1323847	cg1323847	24692327	AAAAATAACACTCCTTAAACA			II	
0.1014943	cg1325749	cg1325749	39804309	AAACCCTAAAAATACTTTCAA			II	
0.106111	cg1325769	cg1325769	17725308	ACTACAC	48652391	ACTACAC	I	A
0.129644	cg1326332	cg1326332	60798335	AAAACCAAATCTATTAACAAA			II	
0.2434832	cg1326481	cg1326481	66687414	ACAACRAATACCACTCAACAA			II	
-0.15106	cg1327005	cg1327005	61675434	TTCTCCTTCTAAATACAATTAT			II	
-0.14484	cg1327512	cg1327512	67743403	TTTCCTTTCTCTTTCTCRTCTAT			II	
	cg1328052	cg1328052	13644367	RATAAACAAACRACTAAAATA			II	
-0.107088	cg1328395	cg1328395	28728410	CCACTAC	21693303	CCGCTAC	I	A
0.1085211	cg1329348	cg1329348	10679379	CCCATTC	45674507	CCCGTTC	I	C
0.100339	cg1329508	cg1329508	59763340	ACTTTCACCTTAAACCTAACA			II	
0.2271728	cg1330544	cg1330544	22750457	AACTAACATCTATACATAACA			II	
-0.106884	cg1330608	cg1330608	31664352	ACTTTATAACAATCTACTATA			II	
0.1506625	cg1330681	cg1330681	19670468	CATTCATTTAATTCTAACTCAC			II	
0.1357067	cg1331238	cg1331238	71734364	ATTATAAAAATTCCRTCAAAT			II	
0.1201521	cg1331514	cg1331514	44686337	AAACACTAAATAAACCAACAA			II	
0.1146694	cg1331605	cg1331605	34636377	ACCAACAAATATTCAAAAAAT			II	
-0.152842	cg1331681	cg1331681	32773489	AACRTTTAAACCTCAAACCTT			II	
-0.271197	cg1331976	cg1331976	44669307	ATATAACTACCAACTAACATA			II	

0.1049597	cg1332110	cg1332110	71768423	CCATATTCATTAATAAAATTC			II	
-0.10231	cg1332387	cg1332387	43608313	AAACTAA	10720370	AAACTAA	I	C
0.186998	cg13327911	cg13327911	12684348	AAAATACATAATTAACACAAA			II	
0.1190469	cg1332820	cg1332820	57655330	CCCCAAC	42684337	CCCCGAC	I	A
	cg1333086	cg1333086	17795352	CAAAACT	20737304	CGAAACT	I	C
0.1081883	cg1333214	cg1333214	37674436	CACCACTCTCCATCCCCTCTAC			II	
0.1678149	cg1333894	cg1333894	36617380	TCCTCATAAAAAAAAACTTTC			II	
-0.107395	cg1334089	cg1334089	15707495	ATCCATATTATAACRTATATCC			II	
0.1083172	cg1334739	cg1334739	46672501	TAAATACTTAAAAAAAAATAAT			II	
0.1067142	cg1335186	cg1335186	43675447	AATTAATCAAAAAACTAAATC			II	
-0.207272	cg1335371	cg1335371	46781383	TAATACTAACRATACTAAACT			II	
0.1194713	cg1335625	cg1335625	42751506	AACCAAA	57649361	AACCGAA	I	A
-0.127603	cg1335689	cg1335689	63763425	AAATAAC	15707487	GAATAAC	I	A
0.2523034	cg1335999	cg1335999	29763477	TATACAACTATTACACAAAAC			II	
0.1056162	cg1336000	cg1336000	73724421	AACAAATTCATAACCTCCCRC			II	
0.1130767	cg1336540	cg1336540	61745505	TATCCTTAAAATAAATTTTCAT			II	
0.1193485	cg1336677	cg1336677	45710478	CTCCRAAAAACACTTACTTAC			II	
0.1118133	cg1336686	cg1336686	62607382	CAACAATCATATCAAAAAATA			II	
-0.121511	cg1336788	cg1336788	35644510	ATCCACRAATTATCRAAACCT			II	
0.1059225	cg1337546	cg1337546	62719409	TATTATCAAAACCTCTAAACA			II	
-0.332594	cg1337696	cg1337696	31640450	CTATATT	30715301	CTATATT	I	C
-0.110114	cg1337726	cg1337726	17690478	TAAAAACTCATAAAATCTCTA			II	
-0.221865	cg1338089	cg1338089	56660355	AATTCCTTAAAAAAATCATTA			II	
0.1245215	cg1338111	cg1338111	20648364	TCATAATAACRTATCRTAATA			II	
-0.100362	cg1339107	cg1339107	54702388	ATACAAC	63745430	GTACAAC	I	C
0.1202835	cg1340024	cg1340024	41720443	TTTTTCTTTTTACTCTTAATTTT			II	
0.3396693	cg1340189	cg1340189	47792379	CCTAATA	39659478	CCTAATA	I	A
0.1132346	cg1340802	cg1340802	50619367	ACACACAAAAACAACCTAAAA			II	
0.1233443	cg1341128	cg1341128	25692487	AAAAATCCTCATTAAACTCCA			II	
0.1171274	cg1341371	cg1341371	32644368	AATATTTAACCTCCCCATTCAT			II	
0.1162929	cg1341507	cg1341507	12740426	RAAAAACTATACTCACTCCCA			II	
0.1036989	cg1342596	cg1342596	30702347	CCTATAACCATTAAATAACAA			II	
0.1142529	cg1343067	cg1343067	64741438	ACTAAAAAATATACCTCTACT			II	
-0.497157	cg1343168	cg1343168	48649402	TAAAAAAATCAATATAATTAA			II	
-0.206108	cg1343513	cg1343513	39755502	CTTCCCACTTCTCTTAAAACRT			II	
0.1011602	cg1343994	cg1343994	16700406	TACTAAA	15807510	TACTAAA	I	T
0.1077918	cg1344110	cg1344110	25778496	TTAACTCCAAATAAACCCTAA			II	
-0.103671	cg1344729	cg1344729	62628313	AACAAAC	49742397	AACGAAC	I	C
-0.117145	cg1344819	cg1344819	43789481	ATTAAAA	12730440	ATTAAAA	I	T
0.267734	cg1345281	cg1345281	44787453	ATCCTCACAACTAAAAAAATC			II	
0.1121997	cg1345422	cg1345422	19696331	AAAAAAATAAAAATTTATCTA			II	
0.1213982	cg1345752	cg1345752	24638403	CTTTAAAAACATTAAACATAA			II	
-0.101898	cg1345800	cg1345800	27735482	CCAAAAT	36709474	CCAAAAT	I	T

-0.290445	cg1346255	cg1346255	37731366	AATATCAACAAAAAAAAATTC			II	
0.1105103	cg1346691	cg1346691	38778399	CCATAAACTAATTCTAACCCR			II	
0.1212844	cg1346821	cg1346821	41673352	CRTTCCTTTACAAAATCAACT			II	
0.1574985	cg1347118	cg1347118	18756308	AAATTCTATCTCATACTATAA			II	
0.108512	cg1347125	cg1347125	29732479	CATTTTTCAATAATTCAAAATA			II	
0.1031902	cg1347173	cg1347173	39803450	AACCTATATACTCCAATAATC			II	
0.2156147	cg1347426	cg1347426	52638466	TTTAATACTATTCTAAACTCTA			II	
0.1109433	cg1348460	cg1348460	20602304	ATAAATC	57658429	ATAAATC	I	A
0.1560562	cg1349023	cg1349023	64762462	CCTCTACTAACAACACCAACT			II	
-0.107904	cg1349675	cg1349675	61637457	ATATAACTAACACATAAAAAA			II	
-0.240614	cg1349875	cg1349875	39792356	AAAACAC	49742459	GAAACGC	I	A
-0.103428	cg1350190	cg1350190	35694441	RCRAAATATATATAACCCCAC			II	
-0.120007	cg1350628	cg1350628	66615479	AACCAAATATACTAAACTTAA			II	
	cg1350789	cg1350789	13644391	ACATAAATAACRCTTACAATA			II	
-0.154879	cg1351836	cg1351836	12695312	CAAATATATCAAAAAAACCAC			II	
-0.149098	cg1352053	cg1352053	38730337	AAAACA	33620350	AAAACA	I	A
0.1722327	cg1352077	cg1352077	57808455	AATTTAATCTCRAAATACCTA			II	
0.1194794	cg1352194	cg1352194	14787487	AATTACCTATCCCTTCAACTAT			II	
-0.17626	cg1352371	cg1352371	57794434	ACTTAAATCAAACTAAAATAA			II	
0.1434022	cg1352373	cg1352373	66664363	CATCCATTTTAAAATTCCTTAA			II	
0.1180043	cg1353032	cg1353032	66646497	TAAATAAACCAAATACTCTAA			II	
0.1390566	cg1353166	cg1353166	29803329	AAAAAAATAATACAATATTTA			II	
0.248572	cg1353857	cg1353857	57745326	CTTTCATTCCAAAAAACTACC			II	
0.1314838	cg1354135	cg1354135	27690439	CCTCCCA	21763337	CCTCCCA	I	A
-0.101707	cg1354197	cg1354197	25616349	CTCCTCCRAACTCCRACAAAT			II	
0.1210057	cg1354855	cg1354855	46607455	CRTATTATAATTATCTATATAC			II	
0.146414	cg1355107	cg1355107	73747308	TACTCCTCCTATACTAAATAA			II	
0.100659	cg1356445	cg1356445	21762471	ATCTCAAAAATTAATACTCCT			II	
-0.237732	cg1356452	cg1356452	11616419	TCCCTAATAAAATAAAACCRA			II	
-0.176583	cg1356646	cg1356646	63681301	ACCACCTTCTCTACAAAAAAT			II	
0.1454232	cg1357089	cg1357089	72672431	AATAACTACTTAACCTTAACT			II	
-0.221191	cg1357337	cg1357337	46721383	CAACAAAACACAACAATAAA			II	
-0.110948	cg1357816	cg1357816	67712382	TAACATT	70778385	TAACGTT	I	A
0.10026	cg1358028	cg1358028	34644314	TACAATCTTAAATTAAATCTA			II	
0.1488151	cg1358075	cg1358075	74636371	CAAAATTATTATTACTTCACTA			II	
-0.11584	cg1358115	cg1358115	64768399	ATATTACCACCCRCCAAAACT			II	
0.3276251	cg1358245	cg1358245	41775406	AATATAAAAACCRAAAAATTC			II	
0.1033688	cg1358366	cg1358366	73671306	AACATAA	66714354	AACATAA	I	A
-0.331514	cg1358574	cg1358574	49600485	AAAATCA	60740487	AAAATCC	I	T
0.1022698	cg1358645	cg1358645	41752475	AATTAAAAACACRATATTAAC			II	
-0.101372	cg1359339	cg1359339	64652509	TAAACCT	60798489	TAAACCT	I	A
-0.106487	cg1359637	cg1359637	59628448	CTCAATT	62637351	CTCAATT	I	A
0.1207629	cg1360199	cg1360199	39620393	ACAAAAT	36651379	ACGAAAT	I	A

-0.205535	cg1360331	cg1360331	73652478	CAATACTTTTCATATTAAACCT			II	
-0.128517	cg1360387	cg1360387	13715484	AAAAAA	18624335	AAAAAA	I	A
-0.112709	cg1360602	cg1360602	73649470	ACAATATTAACCAAACCTAAT			II	
0.1077104	cg1361013	cg1361013	21652347	AAAAAATACRTTCTCTTTACTT			II	
0.14392	cg1361045	cg1361045	51627488	AAACCCAAAAAAAACTCTATA			II	
-0.190355	cg1361599	cg1361599	23611369	ACATACA	70657374	ACATACG	I	C
0.113174	cg1361760	cg1361760	28731396	AATTAATTATAAATATCCAAC			II	
0.1100656	cg1362003	cg1362003	64629354	AAAATACTAATAAAATCTTAA			II	
-0.105479	cg1362289	cg1362289	18704435	ATCCRCTTCCRATTCCCAAACT			II	
0.1515456	cg1363131	cg1363131	47616465	ACCAAAAACAAAACAAACCTT			II	
0.1748874	cg1364164	cg1364164	49614330	CTCTCATAACATTTATACTCTA			II	
0.1000357	cg1364986	cg1364986	13798483	ACTCTAAAACCTACACCTCTC			II	
-0.177471	cg1365120	cg1365120	20695422	AAACCAACTCCTACCCAATAT			II	
0.1111556	cg1365200	cg1365200	73691307	TTATTAAATCACTATTTACAAC			II	
0.1137869	cg1365598	cg1365598	25619417	CCTTAATCCAATTTACRACATT			II	
0.328109	cg1366164	cg1366164	70649379	TAAAAACTTCCAAAATCCCCC			II	
0.1069779	cg1367028	cg1367028	63774398	TAAACTA	63803416	TAAACTA	I	C
-0.122547	cg1367141	cg1367141	15647332	AACATAAAATACTATAAATAA			II	
-0.216762	cg1367220	cg1367220	45645324	CACAAAACCRTAAATCATAAC			II	
-0.242391	cg1367273	cg1367273	20690433	CATACCA	10609506	CATACCA	I	C
0.1104285	cg1368393	cg1368393	11708424	TACRAATTTAATAACTCCAAT			II	
0.1263687	cg1368437	cg1368437	46808320	ATAAAAACACTACAACTTAAA			II	
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0.1289489	cg1368550	cg1368550	45677454	TCATTAACACAAAACCTATTT			II	
0.106768	cg1368673	cg1368673	15614366	TATATTATATACAAAAATACR			II	
-0.121779	cg1368818	cg1368818	47755386	AATAATTCTATCAAAAACATT			II	
0.1111861	cg1369054	cg1369054	20743482	AAACTAAAAATAACTCRTTCA			II	
0.1001187	cg1369468	cg1369468	73687362	ATATCCTTCCACCTATACTTTA			II	
0.1036807	cg1369816	cg1369816	64769494	AACATAACTCACTCAAACAAC			II	
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0.1129639	cg1370045	cg1370045	27626458	ATATAAACRCCTAACCTAACC			II	
-0.131524	cg1370605	cg1370605	10640380	AACACCA	67719307	AACGCCA	I	T
0.1577004	cg1370756	cg1370756	33610388	TCACTACTTTTATAAATTCCCT			II	
0.1503538	cg1371131	cg1371131	52794450	TTAAAAC	19687301	TTAAAAC	I	A
-0.174839	cg1371321	cg1371321	57666459	ACTTAAC	24714498	ACTTAAC	I	A
0.1179686	cg1371676	cg1371676	12705336	AAAAAA	65645460	AAAAAA	I	A
0.1687208	cg1372411	cg1372411	64661376	AAAAAATAAAACAAATAACTT			II	
0.1206754	cg1372455	cg1372455	73734496	ATAATCTAACTAAATCACACT			II	
-0.193314	cg1372508	cg1372508	46769405	AAACCACTTCTCRCAAAATAC			II	
0.1009365	cg1372794	cg1372794	62699392	CCTCCCATTAATAATATCTAAC			II	
0.1163365	cg1372800	cg1372800	70610397	AACTTCRCAATTATTTCCACTT			II	
-0.155853	cg1372981	cg1372981	60602308	CTAAATA	17792313	CTAAATA	I	A
-0.193853	cg1373546	cg1373546	40754500	AAAAAAC	46743332	AAAAAAC	I	T

0.1183093	cg1373872	cg1373872	20662462	TAAACTCAAAAAAACCTTAAC			II	
-0.418405	cg1374063	cg1374063	37775382	TCTAACATCAATCATTTATCA			II	
-0.291734	cg1374835	cg1374835	14625475	CRTACACTAACTCTCTAAAAA			II	
-0.141205	cg1374911	cg1374911	27651417	TATCTAA	15717451	TATCTAA	I	C
0.4493738	cg1374954	cg1374954	70725351	AAAAAA	59636392	AAAAAA	I	T
-0.272249	cg1375272	cg1375272	14643338	RATTCCCACTTATACRATAAT			II	
0.1054784	cg1375361	cg1375361	41669312	AATTACTTAAAAACATATTAT			II	
0.1081318	cg1375435	cg1375435	66771492	CCTAAATAAAAACTCTAAAAC			II	
	cg1375551	cg1375551	13644358	AAATAA	50618434	AAATAA	I	C
	cg1376991	cg1376991	50803368	TTAAACTCCAAAATCTAAATC			II	
0.109796	cg1377179	cg1377179	67666468	CAAACA	63745415	CGAACG	I	C
0.1138428	cg1377221	cg1377221	48807457	TCCACAT	25694326	TCCGCAT	I	C
0.1837902	cg1377330	cg1377330	32769322	AAAAACRTAACAAAATCCTAA			II	
-0.101623	cg1377771	cg1377771	57708408	CAAAACC	30628336	CAAAACC	I	A
-0.104269	cg1377856	cg1377856	69709303	ATTTCCTCACCACAAAAATTC			II	
0.1336305	cg1378319	cg1378319	21682334	CTAACAAAACTAAAACCTCTA			II	
0.1338842	cg1379440	cg1379440	41639341	CAATAAAATTCCCCAAAAAAA			II	
0.1328291	cg1379746	cg1379746	73751365	ATCTATAAATCTATTTTTATTA			II	
0.1209005	cg1379874	cg1379874	18768427	ATTCCTAATTTCTAATATCTCT			II	
0.1471436	cg1380648	cg1380648	44707417	ATTTTAAACTCTCCAAACRATT			II	
-0.223893	cg1380803	cg1380803	47649309	TATCCTTACAACTATCAATTCR			II	
0.1025663	cg1381703	cg1381703	67727454	AATAAATTTCTTTCATCCTAAC			II	
-0.250866	cg1382105	cg1382105	40694387	AAAAACATTTTACAAAATCCA			II	
0.1078082	cg1382528	cg1382528	31738487	CCAACCTATAAATTTCCATTAC			II	
-0.113705	cg1382593	cg1382593	15798480	ATCTCAA	33600463	ATCTCGA	I	A
0.1655418	cg1382910	cg1382910	60688420	RTTATAAATTTCACAATTCTCR			II	
-0.204828	cg1382962	cg1382962	59605469	CTCRAATACAAATAACTCAAA			II	
0.118173	cg1382984	cg1382984	55793300	ATATATACCAAAAAAAAATAC			II	
0.1818737	cg1383061	cg1383061	56803382	TTTCCCC	37715327	TTTCCCC	I	C
-0.122032	cg1384263	cg1384263	66679384	AAAATTC	27632433	AAAATTC	I	A
-0.130004	cg1384744	cg1384744	17788362	ACCAACAAACATATAAATAAA			II	
0.1473023	cg1385721	cg1385721	19772354	CAACCAAAACACAAAAAACA			II	
-0.214016	cg1385764	cg1385764	47803479	CTCAAACRACTATAACRACAA			II	
0.1077371	cg1385977	cg1385977	57630509	ACAAACATTAATAAATCTAAA			II	
0.1094849	cg1386028	cg1386028	15706467	TTACAAATATAAATACACACA			II	
0.1680824	cg1386626	cg1386626	69686405	ATCTCTT	30663316	ATCTCTT	I	A
0.1001879	cg1387053	cg1387053	25770477	AAAACCTCTATAAAACATAAC			II	
0.1375992	cg1387442	cg1387442	52603344	CCTCTTT	64705354	CCTCTTT	I	A
-0.343148	cg1387475	cg1387475	73714364	CATAATA	10734352	CGTAATA	I	C
0.1642688	cg1387791	cg1387791	73751347	ATCCTTCTAAATAATATAATTT			II	
-0.101817	cg1387864	cg1387864	29736459	CTTTAATTAAAACACCCCTAA			II	
-0.168612	cg1388578	cg1388578	52680473	TTCCAACAAAACTCTACAATA			II	
0.1166318	cg1389485	cg1389485	52642474	AAAATAA	62668499	AAAATAA	I	A

0.1102747	cg13895650	cg13895650	22740391	TATTATCTATTAATATTATAAC			II	
0.2145148	cg13897348	cg13897348	53632377	CTACTTATCTAAAATACTACAA			II	
0.1948507	cg13897388	cg13897388	15654377	ATTACRAAACTAAAATACATC			II	
-0.131357	cg13900773	cg13900773	15714346	TCAACAA	48699432	TCAACGA	I	T
-0.172407	cg13902645	cg13902645	65734370	CTTCTAA	23712404	CTTCTAA	I	C
-0.110636	cg13905298	cg13905298	20689494	TACATACATTTTAAAACCAAA			II	
0.1401321	cg13910785	cg13910785	34779364	ACTACACTCTATACTTTCCAAA			II	
-0.228221	cg13913990	cg13913990	33706467	CAAATTCACCTACAAAAAAAC			II	
-0.151189	cg13915726	cg13915726	52735355	AAAACAAAAACAACTAATATA			II	
-0.106257	cg13916633	cg13916633	18655427	TAACAATAAACAATTACCCTTT			II	
0.1294536	cg13918754	cg13918754	21719430	CACAACT	20681309	CACAACT	I	T
-0.162467	cg13923371	cg13923371	59739471	AACCAAA	61650427	AACCGAA	I	A
-0.133475	cg13924287	cg13924287	58759478	TAAAATAAAACTCCCCCAAAC			II	
-0.138283	cg13924635	cg13924635	48740453	ACTAATT	71705427	ACTAATT	I	T
-0.123679	cg13924715	cg13924715	44757399	TTCCCAT	34704415	TTCCCAT	I	C
0.1137192	cg13925809	cg13925809	54709451	AAAAATAAATCACACCTCCTC			II	
0.1016464	cg13927504	cg13927504	24795399	ACTCTATTCTTATCCCCCATAT			II	
-0.103176	cg13928473	cg13928473	73643338	CCTAAAAAATCCRACAACTCT			II	
0.1508679	cg13931250	cg13931250	43640424	ACTCAAACACTTATTATCCTAT			II	
0.2015792	cg13934990	cg13934990	53634405	TATTAACRCTAATCCTCATATT			II	
-0.118328	cg13937627	cg13937627	67746374	AATATAT	52673303	AATATAT	I	A
0.1249536	cg13941978	cg13941978	27797357	ACTAATT	68657390	ACTAATT	I	T
-0.11841	cg13943333	cg13943333	68725365	ATACATTAAAATAATCCCCTAA			II	
0.1328613	cg13944507	cg13944507	44749313	CCAACCAATCRTAAACTACRA			II	
0.1123897	cg13945576	cg13945576	18780428	TCTCTATTTACCAAACATCAAT			II	
0.1058095	cg13954292	cg13954292	14722349	TCTATATTTTAACTACCRACTA			II	
0.1034998	cg13965612	cg13965612	73643485	TAATATAATAAAATCAAAACA			II	
0.118005	cg13969327	cg13969327	70696502	TATCTTCTCATTATATACCCCT			II	
-0.109082	cg13969662	cg13969662	59724471	AACACCA	67729467	AACGCC	I	C
0.1138344	cg13971504	cg13971504	63642379	AAAAATTTACAACCTACATTCA			II	
0.1162762	cg13972423	cg13972423	15728324	TACTAATATTCATCCTCACCTA			II	
-0.121973	cg13972661	cg13972661	29688442	TAAAAAATATACACCTAATAC			II	
-0.154734	cg13974562	cg13974562	71763399	TCATCCC	56810505	TCATCCC	I	T
0.1416755	cg13979581	cg13979581	62695310	ACTTAAATCAAACTATCAAAA			II	
0.2243201	cg13982037	cg13982037	67788333	AAAATACTTTAAAAACTAAAC			II	
0.1124112	cg13984289	cg13984289	74759420	CAATAATAACCCTAAAAACRA			II	
-0.165676	cg13989295	cg13989295	58727359	AAACCACTTTTAATACTAAAAA			II	
-0.140749	cg13993183	cg13993183	44692337	ATATTTA	66773386	ATATTTA	I	C
0.2983239	cg13994730	cg13994730	32778500	AAAAACTCCAACRAAATTTATA			II	
0.1263556	cg13995427	cg13995427	31735405	ATAAAAA	17760352	ATAAAAA	I	T
-0.121637	cg13996925	cg13996925	58622429	AAAACTAAACAACATCATCRA			II	
-0.150478	cg14001023	cg14001023	47714395	AAAACAT	23603428	GAAACAT	I	A
0.1036409	cg14009900	cg14009900	60778356	CRTAACTAATTAAACCCACTA			II	

-0.134146	cg1401359	cg1401359	15685493	TCCCAAA	14745503	TCCCGAA	I	C
0.1148121	cg1401550	cg1401550	17614455	ATAAACCTTTATACTATACA			II	
0.1142044	cg1401836	cg1401836	55785372	AAACRACCCATAAAACRAAAC			II	
0.1045677	cg1402117	cg1402117	63800497	AAAATAATTTTATTCTCCCRC			II	
-0.126425	cg1402489	cg1402489	14639392	CCCATCA	39722331	CCCGTCG	I	C
0.1320175	cg1402610	cg1402610	56747341	ACAAACTACTTCAAAAAAAAA			II	
0.1486019	cg14032261	cg14032261	16779407	TTATCTCAAACCTACAAAAAC			II	
-0.11527	cg1403524	cg1403524	61732499	TTATAATCCCCAAAACAACCC			II	
-0.109459	cg1404181	cg1404181	66763350	AAAAAACATAAACCTAATATA			II	
-0.146695	cg1404416	cg1404416	13767316	ATAAAAAAATACATATACCTA			II	
-0.541571	cg1404466	cg1404466	49635493	TACTCAATTCCCTTATAAATTA			II	
0.1300275	cg14047561	cg14047561	13705510	AAATATAAAAATTTACTAAT			II	
-0.124477	cg1405223	cg1405223	27659421	AAAAAA	50627420	AAAAAA	I	C
0.1064289	cg1405427	cg1405427	48704449	AATCATTACCCTACCTTTAAA			II	
0.1095803	cg1405500	cg1405500	23702406	ATTAATAAACTACRTAAATCA			II	
0.2402989	cg1405684	cg1405684	70781354	AAACCAAACTAACTATAACCA			II	
0.1068234	cg1405983	cg1405983	34704426	CTTTCTAAAAAACCATTCCRA			II	
-0.254386	cg1406011	cg1406011	10718499	AAAACCC	11806350	AAAACCC	I	A
-0.124837	cg1406552	cg1406552	69708390	AACCACRCAAAATATCTAACA			II	
-0.10052	cg1406559	cg1406559	62675467	AAAATCCTTAAACCACAAAAA			II	
0.1125072	cg1406752	cg1406752	50729438	ATAATTACCACRACAAAAAAT			II	
-0.343376	cg1406818	cg1406818	49793437	TATTTATTTTATTTAATTATTA			II	
0.1132433	cg1406878	cg1406878	35601496	ACTTAACATTCCAAACTCTTA			II	
-0.115075	cg1407545	cg1407545	74698433	ATATTCA	10612313	ATATTCA	I	T
-0.106191	cg1407935	cg1407935	32652312	TAAAAA	66804337	TAAAAA	I	T
-0.2064	cg1407946	cg1407946	47692328	ATACCCAAATACRAAACCAAA			II	
0.1168701	cg1408166	cg1408166	28661448	AAAAACCTAAATACTCCRAAA			II	
-0.132781	cg1408560	cg1408560	28693342	CAAAAC	52792431	CAAAAC	I	T
0.1004266	cg1408741	cg1408741	64747435	ACCCCCACAATACCTCATTCT			II	
0.119489	cg1408904	cg1408904	16772482	AACTAAATTTATCTAACRAAA			II	
0.1776106	cg1408910	cg1408910	36734471	AACATTCAACTTCTAAACAAA			II	
-0.12179	cg1408926	cg1408926	67756328	TAATAAT	26777382	TAATAAT	I	A
-0.113468	cg1409299	cg1409299	42766372	ACTAATTCCTTAAATCCTACA			II	
0.1299348	cg1409618	cg1409618	47710489	CAAACAAAAAACAACAAAAA			II	
-0.183471	cg1410055	cg1410055	42714442	AAATAAACCCTAATATCTATC			II	
-0.358875	cg1410470	cg1410470	24740407	TAACAAATTTCAAATCTACAA			II	
0.1084327	cg1410553	cg1410553	23766507	ATAAAAATCCAAAAAACCCAA			II	
-0.151557	cg14105781	cg14105781	54737451	RAAAACAATTAACRACCTACA			II	
-0.101658	cg1410668	cg1410668	47642418	ACAACA	64766423	GCAACG	I	A
-0.207326	cg1410856	cg1410856	29795429	AACACTT	13648308	AACGCTT	I	T
0.2324384	cg1411016	cg1411016	56687339	TAACCAACATAATAAAACCTT			II	
-0.127288	cg1411633	cg1411633	41652368	CAAAATA	54719324	CAAAATA	I	A
-0.10871	cg1411676	cg1411676	30664401	AAAATAT	39692389	AAAATAT	I	A

0.1018599	cg1412174	cg1412174	40715491	TAATAATTATAATATCCATCA			II	
0.1449318	cg1412240	cg1412240	36711497	CCCAAAAAATAAATAACTCAA			II	
0.1293283	cg1412303	cg1412303	72770339	RCCTCCTCTCCAAAACCCACA			II	
0.1077601	cg1413262	cg1413262	19770390	ACCTCCTAACAACCCTATTAA			II	
0.1133833	cg1413310	cg1413310	27738492	AAAATTACTATTTAACATTTA			II	
0.1144512	cg1414898	cg1414898	52708325	TAACCTACATTAAAAATTAAC			II	
-0.233957	cg1415106	cg1415106	69684374	TCCTTTAAAAACTTTCRTATTA			II	
0.1336976	cg1415246	cg1415246	26803312	ATATAACCATAAAACACAAAA			II	
0.1337196	cg1415297	cg1415297	61620504	AAACCAAACTCTCATAAAATT			II	
-0.131732	cg1415752	cg1415752	32645447	AAAATCTCCTAATTAATTAAT			II	
0.1078842	cg1415855	cg1415855	49786440	AAAAACTCTACACCCCATCAT			II	
0.1193378	cg1416043	cg1416043	22798367	CTACTACTCCTAATAAAAAAT			II	
0.1303345	cg1416670	cg1416670	59676319	AAATATA	27655364	AAATATA	I	T
0.1526033	cg1416703	cg1416703	72735486	ACRAACTCTTAAACCRTACAA			II	
0.1618643	cg1417020	cg1417020	66762308	CCCTTTTCCCTCCTAATATCTT			II	
0.1026493	cg1417422	cg1417422	12618450	CCTCTAAAAACTCACCTCTCA			II	
	cg1417708	cg1417708	13644487	TTAAACTAAATAATCCTTACT			II	
-0.150027	cg1417928	cg1417928	57618362	AACTATAATCTCACAATTTAC			II	
0.1092698	cg1418041	cg1418041	54715503	TAAAATCACACAACATCTATA			II	
0.124089	cg1418495	cg1418495	18710350	AACTTCCTATTCCACCAATAA			II	
-0.108778	cg1418781	cg1418781	38654363	ATAACTAATATTTTCTTTCCAA			II	
-0.108826	cg1418877	cg1418877	21618351	ATTCCCAAAATAATAAATTTT			II	
0.1601783	cg1418911	cg1418911	57754348	TCTAAATCATCAAATCCTACA			II	
0.1019802	cg1418953	cg1418953	16783506	ATTAACTCTATCTCTCAATCCA			II	
0.1267138	cg1418978	cg1418978	48730327	TATAAATCCCCRATTTCCTAAA			II	
-0.102527	cg1419229	cg1419229	66716342	ACTAACC	54642479	ACTAACC	I	A
0.1152477	cg1419517	cg1419517	26730510	CRAAAATTTTAAACTACTTCC			II	
0.1139746	cg1419711	cg1419711	18656448	TATAATTTCCTTCTCAAACTTT			II	
0.143919	cg1419822	cg1419822	55768438	AACCCACTACTTTCCTTCTAAA			II	
0.1677924	cg1420142	cg1420142	33795429	CTAATAA	24648384	CTAATAA	I	C
-0.125573	cg1420408	cg1420408	63639347	AATAAAATCTCCATCCTTATCC			II	
0.1470542	cg1420951	cg1420951	40741482	TAAAAACCTAAATAAAACTTT			II	
0.1383093	cg1421203	cg1421203	33638311	TAAACCTAACAAATTTTAAAC			II	
-0.111679	cg1421339	cg1421339	67685329	CAACTCA	33758460	CGACTCA	I	T
-0.104313	cg1421473	cg1421473	54746417	CAATAAA	31784456	CGATAAA	I	T
0.1278031	cg1421606	cg1421606	38746430	AAAAACT	28745335	AAAAACT	I	A
-0.103536	cg1422367	cg1422367	38743305	ACCATATTAAAATCRAACAAA			II	
0.1401159	cg1422732	cg1422732	42669375	ACTATATCRACRAATTTCTTCC			II	
-0.376759	cg1422810	cg1422810	31747469	TTATTTTCTCAAACACCAATTA			II	
0.1065378	cg1423491	cg1423491	14768483	AAACATCACAAACCACTTAAA			II	
0.3176209	cg1423812	cg1423812	69799509	AAACAAATAATAAAACTCCAA			II	
-0.11048	cg1423965	cg1423965	15745447	CTAAAACTAAAACTAAAACTA			II	
0.1135114	cg1424079	cg1424079	66778462	ACATTAAAAAAATAACRTAAC			II	

0.1282591	cg14241836	cg14241836	55738497	TAAATTTCATAACCCACRAATA			II	
0.1063199	cg14245898	cg14245898	56606470	TTAAAACACAACTACTCACAA			II	
0.1222877	cg14252237	cg14252237	20612393	CCTCCTACRAAAACAAAAACCT			II	
-0.186759	cg14253596	cg14253596	36807492	CCTTCCCTAAAAAATATCAAT			II	
-0.104831	cg14260773	cg14260773	44645465	AATTAACATCATAAACCAAAT			II	
-0.185071	cg14266237	cg14266237	69689428	AAAAAAT	36775365	AAAAAAT	I	T
-0.133144	cg14270002	cg14270002	69655308	AAAACAA	36605363	AAAACAA	I	T
0.1712371	cg14271023	cg14271023	64732448	RAATTACCCAACTATAATAAAT			II	
-0.146912	cg14276083	cg14276083	12607466	ACATTCC	35645443	ACGTTCC	I	C
0.1312933	cg14277298	cg14277298	28755433	TATTACAACTACCTCCCTCTTC			II	
0.1103968	cg14281039	cg14281039	65637437	TTCCTATACCCRAAAATAACTA			II	
0.1095645	cg14283647	cg14283647	50728485	CCTAAAATACAACRATAACCAT			II	
-0.105903	cg14283756	cg14283756	10749446	CCCCAAA	42607466	CCCCAAA	I	A
0.1076598	cg14288049	cg14288049	27600478	ATCAAAATAATATTACAAAAC			II	
0.1501856	cg14290070	cg14290070	13604340	TAAATTCTTTTTTCTTATTAAA			II	
0.378945	cg14293674	cg14293674	29710310	TCATTATCACCCAAAATCCATA			II	
0.200318	cg14294953	cg14294953	42717353	AATACAAATATCAACTCCATA			II	
-0.213943	cg14294971	cg14294971	27708424	ACACAAAACACTATCAAATAT			II	
0.4619071	cg14302130	cg14302130	11677360	ATCTCCCCRCTCTAAAATACTA			II	
-0.131176	cg14307477	cg14307477	14724497	TACAAAC	57715430	TACGAAC	I	C
0.1320259	cg14308311	cg14308311	58623424	TTTATCATCTTAATTATTCTAAT			II	
0.179794	cg14308648	cg14308648	38611396	AAACATCCAATAACTATAAAA			II	
-0.145177	cg14310877	cg14310877	55658463	TTTCCRATTTTCCTACCCTTTT			II	
0.1673117	cg14316629	cg14316629	66809447	TAATCAACRTTACCAATAAAC			II	
0.1602327	cg14316660	cg14316660	45791404	CCCTTTAT	71766344	CCCTTTAT	I	A
-0.105078	cg14317384	cg14317384	74681441	ACCTACA	19676415	ACCTACG	I	A
-0.115644	cg14323204	cg14323204	16761452	CCCTAAATATTACTAAATCAA			II	
0.2460178	cg14323910	cg14323910	22757305	ACTACTACCTATAAACATTTTC			II	
-0.130374	cg14324816	cg14324816	42657509	ATATCACAATCACAAATTAAA			II	
0.1213388	cg14324838	cg14324838	24619461	AACTCTATATTCAAAAACAAA			II	
-0.135906	cg14325153	cg14325153	62672390	TCAATAA	63721444	TCGATAA	I	C
-0.110638	cg14325184	cg14325184	27635449	CACTAAC	25748318	CGCTAAC	I	C
0.1030766	cg14325779	cg14325779	50772323	CCATAATATATTTATCATCTCC			II	
-0.203404	cg14329783	cg14329783	52733448	CAAAACAAATACCTCTAAATAT			II	
0.1295226	cg14329889	cg14329889	38785507	CAATCAA	32800433	CGATCAA	I	C
0.1076887	cg14330868	cg14330868	63688403	TCCTCRAAACTATATCTAAAAA			II	
-0.155056	cg14331206	cg14331206	35601349	AAAAACACAAAACRTTCTAAC			II	
-0.145189	cg14331226	cg14331226	36734408	ATTACTCCCTAAACCACCTAAT			II	
0.1480138	cg14339466	cg14339466	37733330	ACTTTACAAATCTACTTAAAAA			II	
0.1457422	cg14340463	cg14340463	66713386	TTAAATACCCCATTAAATAAAT			II	
-0.148355	cg14340928	cg14340928	43655507	ATCAACATAACTACTCAAAAAT			II	
-0.119367	cg14352508	cg14352508	70794396	AAACRCCTACCACCATACCCR			II	
0.1067192	cg14356919	cg14356919	39662411	CTAAATATAAATAACRCRCTA			II	

-0.160299	cg1436125	cg1436125	20779300	AAAACA	43644329	AAAACG	I	C
	cg1437318	cg1437318	54713385	CCTTAACTTACCCAACTTAAT			II	
-0.132342	cg1437856	cg1437856	49632458	CAATATACCAAACTCCATTCT			II	
0.102601	cg1438441	cg1438441	36707502	AACTAACRAATTTCAAAACCR			II	
-0.111842	cg1438823	cg1438823	21625490	ATAAAAAAAAATCTCCTATAC			II	
-0.126996	cg1439529	cg1439529	46769505	CCTTCCC	22755310	CCTTCCC	I	T
0.104918	cg1440222	cg1440222	60720388	AACTATAACTAACAAATAACA			II	
0.2525862	cg1440883	cg1440883	71685333	AAAAATATCTCRTAATCCAAC			II	
0.1159485	cg1441491	cg1441491	28722498	TAACACAATACCACAAACTTA			II	
-0.14736	cg1441778	cg1441778	18609379	CAACAA	17793438	CGACGA	I	A
0.1107551	cg1442071	cg1442071	40655403	AACTTACCTTAATATACCCAA			II	
0.1575126	cg1442224	cg1442224	28641377	ATCATTTAAATTTTAACATAA			II	
0.2292498	cg1442250	cg1442250	64736341	TTATAATTAAAAAATCCTTTC			II	
0.1285216	cg1442556	cg1442556	65709411	AATTCAA	11727418	AATTCAA	I	A
0.232985	cg1442974	cg1442974	38615468	ATAAAAATACACACACACACA			II	
0.100367	cg1443157	cg1443157	17720381	AATAACTAATACTACAAATAT			II	
0.1200539	cg1443225	cg1443225	73751357	AATTAATTTTAAATAAACACA			II	
0.1082242	cg1443475	cg1443475	67710342	TACRTCTTATCCACTTCTACAA			II	
-0.100843	cg1443555	cg1443555	10673464	CCTTTAA	18684454	CCTTTAA	I	A
0.1061591	cg1443744	cg1443744	27759462	TTATTCACCCTCAAACAACAA			II	
0.1413494	cg1444027	cg1444027	14740455	AACTCCCATAATTAAAAATAT			II	
0.1298694	cg1445409	cg1445409	25606396	CTCCTTATATTATTCTTAAACT			II	
0.1026263	cg1445745	cg1445745	28653324	AACTAAATAAACACCACAATA			II	
0.1161119	cg1446240	cg1446240	22679490	AATTCAATACATAACTAAACC			II	
-0.157722	cg1446373	cg1446373	31733355	ACACTTAACCCAACTTAATTT			II	
0.1058856	cg1446701	cg1446701	53763328	CATTAAAACCTCACAAAATTT			II	
0.112606	cg1446741	cg1446741	17628308	AAACCCCAAATTTATCACACA			II	
0.2225897	cg1447685	cg1447685	36706322	TAAATTCAAACTTCCTAAATA			II	
0.1018388	cg1448564	cg1448564	74770465	CCCTAATCACATAACCAATCR			II	
-0.176993	cg1449309	cg1449309	40603491	ATTTAAAACTCTATAAAAACC			II	
0.1938568	cg1449764	cg1449764	38770382	TAAAAATATAAATAAAAAACT			II	
-0.138267	cg1450048	cg1450048	70643436	ACACAA	26786310	ACGCAA	I	T
-0.16583	cg1450619	cg1450619	53678387	RTCATACTTATACCTCCCAAA			II	
-0.130422	cg1451536	cg1451536	57740498	TCAAATT	21692339	TCGAATT	I	A
0.1001119	cg1451935	cg1451935	71655353	TATATATTATTTATTTCCATAA			II	
	cg1452199	cg1452199	11608485	AAAACA	70606468	AAAACA	I	C
-0.102857	cg1452244	cg1452244	38809464	CACCACA	64726319	CACCACG	I	C
0.1501022	cg1452539	cg1452539	54717343	ATAATAACTCACATATACTAA			II	
-0.147621	cg1453109	cg1453109	48658334	ACCACAT	23714502	ACCGCGT	I	C
-0.143778	cg1453498	cg1453498	67687408	AAAAAC	15645431	GAAAAC	I	A
-0.105987	cg1453533	cg1453533	26651379	CCCAAA	56756319	CCCGAA	I	A
0.1382557	cg1454890	cg1454890	45722301	CCATTTTTAAAAACCAAACA			II	
-0.110894	cg1455006	cg1455006	67643448	AACATCRCTCAAATTCTACCR			II	

0.1147055	cg1455344	cg1455344	68711481	AAACTCCACAAATATCCTCAA			II	
0.122054	cg1455913	cg1455913	59614346	ACTAAAATAACAATAACAAAA			II	
-0.102637	cg1456278	cg1456278	49608347	AAATTAATAAATCTCCTACTTC			II	
0.1556566	cg1456942	cg1456942	25733453	AACCTAATTTTTAATATAAATT			II	
-0.10731	cg1457381	cg1457381	56676465	RACCTTCTAAAATATCTCCTAC			II	
0.1067245	cg1457770	cg1457770	65723423	CAAATTTAATAACAATCTTAT			II	
0.255098	cg1458399	cg1458399	21607472	CCAAAACCCCCTTATAAAACA			II	
0.2266372	cg1459263	cg1459263	33702337	ATACACAACATACTCCCACAT			II	
0.1927962	cg1459786	cg1459786	40691394	AACAACAAAACCACTAACCRT			II	
0.1463231	cg1459833	cg1459833	31791482	CAAAACC	59746308	CGAAACC	I	C
0.162829	cg1459847	cg1459847	54608430	RAATAACAAATAACCAACATT			II	
-0.111214	cg1460447	cg1460447	29608370	TTAAAAAAAACTCTTAATAAT			II	
0.1887338	cg1460452	cg1460452	48802381	AATATCC	62611436	AATATCC	I	A
0.1116987	cg1460535	cg1460535	29713486	TAAAATCTTATACCCTTTCTAT			II	
-0.112425	cg1460877	cg1460877	49753305	ATCACAA	39714411	ATCACAA	I	T
-0.227416	cg1460910	cg1460910	52683440	AAAAAAACTAAAATTCACTTT			II	
0.132916	cg1461145	cg1461145	52757336	ATATATCTACCAAAAATTAAC			II	
-0.184745	cg1461526	cg1461526	69601336	TCTCTCA	40624490	TCTCTCA	I	A
-0.152369	cg1462190	cg1462190	48627421	AAAACCTTAAACCCCCCATAA			II	
-0.116734	cg1462563	cg1462563	10802457	ACRAAAAAACTTAACCACCTA			II	
0.1902223	cg1462901	cg1462901	15711375	AAAATCCTAAAAAAACAATAT			II	
0.1006683	cg1463063	cg1463063	21656316	AAAATAATAATAAATACTTTA			II	
0.124501	cg14636261	cg14636261	25713488	AACAAAAAATATACACAACCR			II	
0.1016078	cg1464233	cg1464233	21795454	CTTCCTATAATCCCCACRATAA			II	
0.1017089	cg1464326	cg1464326	24747360	CCAATTTCCCTACTTCATCAAC			II	
-0.154688	cg1464524	cg1464524	64690436	TATAAAA	36600482	TATAAAA	I	A
	cg14646641	cg14646641	67606429	CATCCTATCTTAAACCACTAA			II	
0.1157508	cg1465143	cg1465143	32620478	CRAACTAAAACATAAATTCAA			II	
0.1223924	cg1465359	cg1465359	60626498	TTCTCAACAATCACTTACTTAA			II	
0.1267193	cg14654171	cg14654171	51679367	ATCACRAATACATTTTACCTA			II	
0.1065799	cg1465912	cg1465912	74709337	ATTCTCRACAAACCAAATCCT			II	
-0.104909	cg1465934	cg1465934	38621481	AACAAC	24713432	AACAAC	I	C
0.1160713	cg1465966	cg1465966	52679362	AAAAAT	47783399	AAAAAT	I	C
	cg1465969	cg1465969	13644387	CATCTAA	66685405	CATCTAA	I	A
-0.165812	cg14661431	cg14661431	51625352	CTACCCAAAACAATCTACAAA			II	
0.1546705	cg1466690	cg1466690	61604365	ACATACCATATAAACAAAAAA			II	
-0.158225	cg1466984	cg1466984	55635406	ATTCTAATTTACAAACAACAA			II	
0.194344	cg1466986	cg1466986	52722450	CAATATT	17619465	CGATATT	I	C
0.1544678	cg1467009	cg1467009	72621416	CTTCATATTTTCACCAATATAA			II	
-0.23156	cg1467925	cg1467925	28650444	AAACTCAATCCCAACAACATA			II	
0.1097367	cg1468594	cg1468594	17609450	TAAAACCTAACTACTTCTAAC			II	
0.4773594	cg1468604	cg1468604	23646341	AAATATCTCTAAAACTCAATT			II	
-0.207794	cg1468729	cg1468729	15679356	TAACTCT	67606421	TAACTCT	I	C

0.119525	cg14688662	cg14688662	27700493	AAATACAACCTACTATAAAAC			II	
0.1095656	cg14691596	cg14691596	70786483	CRAAATTAAACCRCCTAACCC			II	
0.1090549	cg14696601	cg14696601	62721321	CTTAAAATATAAAAACACCTC			II	
0.1001473	cg14698238	cg14698238	33789329	CCACTTTTAAAAATTATAAAT			II	
-0.102338	cg14699257	cg14699257	45651331	ACATAAA	28619402	ACATAAA	I	A
0.1453303	cg14701867	cg14701867	39801313	AAATAAATTCTCTCAAACAAT			II	
0.1335059	cg14704124	cg14704124	11634302	TCTCAAAATAAATACCRATAA			II	
0.1544186	cg14705010	cg14705010	51719320	TAACTTC	39673433	TAACTTC	I	A
-0.120796	cg14708411	cg14708411	48720320	CACTAAA	40616345	CACTAAA	I	C
-0.141925	cg14710850	cg14710850	27638448	TTAAATATAAAAACAAATAAC			II	
-0.158935	cg14711243	cg14711243	18781419	CTCTCTCTCTATTACAATTTCC			II	
0.2697168	cg14715697	cg14715697	46756442	TCACACC	66644400	TCACGCC	I	T
0.4092659	cg14717122	cg14717122	16806408	ACCAAATCTACTTCATCCCTA			II	
0.159142	cg14731462	cg14731462	20687329	AATTCRATCTTACTCAAATAA			II	
-0.107932	cg14736087	cg14736087	48721339	AAATCTTAATAAAATAAACCA			II	
-0.147768	cg14738806	cg14738806	29643446	AAAAATTAAAAATAACTAAAA			II	
0.1348774	cg14740976	cg14740976	28727498	AATAATAAAACRTAAAAACAT			II	
0.1479671	cg14742445	cg14742445	39780473	TACAACACCCCCAAATCCCAA			II	
-0.111583	cg14742615	cg14742615	14627388	CRTTATACCTATTTTTTATCTT			II	
0.2271338	cg14753094	cg14753094	44624466	TCAATTACCTACTATTCTAAAA			II	
0.1674483	cg14758525	cg14758525	73712349	AAAATTCACCAAAACACAATC			II	
-0.121703	cg14759366	cg14759366	41780443	CAAAAACCATATACAAATACR			II	
0.1263691	cg14759494	cg14759494	14686387	TCAAATTCTCAAACTCCRAAC			II	
-0.100787	cg14780132	cg14780132	15659311	TTTCAAACTCCTCAAAACCAA			II	
0.1146658	cg14780466	cg14780466	61629303	AAACAAT	19625435	AAACAAT	I	C
-0.144745	cg14782559	cg14782559	50621445	AAAATCCRTCCTACTAAATTA			II	
-0.143259	cg14793137	cg14793137	46638458	CATTCAT	74760501	CGTTCAT	I	C
-0.103704	cg14795253	cg14795253	25701421	AATTCTA	58790505	AATTCTA	I	T
	cg14795409	cg14795409	13644342	CCCTAACTTCACTTTTACAATT			II	
0.2996336	cg14797147	cg14797147	24788474	TTCCAAATAAAAAACACTATA			II	
0.2767694	cg14799277	cg14799277	74607488	TCTTAACTACCAAAAAAACAA			II	
0.2788808	cg14799809	cg14799809	62630444	ATTTATTCCTTAATAATAAACC			II	
0.1646431	cg14804903	cg14804903	47779475	TCCATAACTATATAAATAAAA			II	
0.1080229	cg14811011	cg14811011	62676339	AAATCTACAACTCTTCAAACA			II	
0.1077294	cg14811014	cg14811014	69627345	ATTTAATTTTATTACTAAAATT			II	
0.1362821	cg14815891	cg14815891	59655461	CAAAAAC	24684340	CAAAAAC	I	A
0.1220356	cg14818277	cg14818277	46681424	ATTCAAAAAACCRAATAAATT			II	
-0.114781	cg14818413	cg14818413	70770367	TTTTATCTCCTCTCCAAATTTT			II	
0.1102012	cg14818621	cg14818621	49708459	ATCATATACTCCCTCTATATAA			II	
	cg14819368	cg14819368	13644372	AACRATAAAAATAACAAATAT			II	
-0.135952	cg14825858	cg14825858	17683414	ATACAATTTCTCTTAACAACA			II	
0.3082348	cg14829303	cg14829303	40753304	TCCATCATTTATCTTTAACRAC			II	
-0.137505	cg14831390	cg14831390	28714477	AAAAACC	25660312	AAAAACC	I	A

0.1491282	cg14832352	cg14832352	73681385	CAAAACAATCCRTACATCAAA			II	
0.1056674	cg14832904	cg14832904	22792504	RAAAACRATAACRATAACRAT			II	
-0.133957	cg14834300	cg14834300	36615392	AAAAAACTAAAAACRCTAAAA			II	
-0.100389	cg14839919	cg14839919	46686446	TTTATAATCCTAAACAATACTA			II	
0.1023025	cg14840848	cg14840848	42796501	CCTCATA	17759429	CCTCGTA	I	A
0.1121665	cg14851460	cg14851460	45778357	CATTCRTTTAAAATAAATAAA			II	
0.1073338	cg14851544	cg14851544	53669497	ACTTTACTAAATTCTAACTTCT			II	
0.1136774	cg14855378	cg14855378	58649403	ATTAAAAACCACAACCTAACT			II	
0.1303185	cg14856563	cg14856563	65740428	ACACATTAACTAAAAATTAAA			II	
0.1019621	cg14858786	cg14858786	33709449	AAACTAC	35701323	AAACTAC	I	T
-0.108309	cg14859874	cg14859874	14694304	TAAACAAAAATAAACCATCTC			II	
0.1559051	cg14873022	cg14873022	39715368	AATTATCCCRAACTAAATATA			II	
-0.102806	cg14877637	cg14877637	70646322	AAAATAATTCTCTCCAATAAA			II	
0.2007279	cg14877834	cg14877834	28804443	TCTACTCATCAAATAACACTA			II	
-0.115611	cg14882966	cg14882966	42626317	CCCACAA	31600403	CCCGCGA	I	T
0.1182527	cg14883605	cg14883605	57691462	CCCAAAAAAACTCTTAAAAAA			II	
-0.107584	cg14891195	cg14891195	74756405	CTTAAAC	18734405	CTTAAAC	I	A
-0.100396	cg14893857	cg14893857	25788482	TAACCRAATATATACCTAATC			II	
0.1207582	cg14894216	cg14894216	47779456	ACTCCCTCATAAATAAATATA			II	
0.1085078	cg14895374	cg14895374	64717338	TTATTAATACCTAAACTAACC			II	
0.1752689	cg14900909	cg14900909	47622405	TTCACCT	73707479	TTCGCCT	I	C
-0.101226	cg14902204	cg14902204	74772470	CCRAAAATCCCAAACTATAAA			II	
0.116994	cg14909614	cg14909614	36667507	CAAACRAAAATACCAAAATAT			II	
-0.1334	cg14915878	cg14915878	47698493	CAAAACC	71778502	CGAAACC	I	A
-0.100621	cg14926196	cg14926196	35619359	AATAAAC	74680402	AATAAAC	I	A
-0.328781	cg14926485	cg14926485	28731492	ATATAAAAACATCTACACAAA			II	
-0.141627	cg14927745	cg14927745	56710417	AAAAAA	64784332	AAAAAA	I	A
0.1562108	cg14931776	cg14931776	40692459	RCAAATACCAAAAACAATAAA			II	
0.1036714	cg14931884	cg14931884	57642487	AAAAAAC	63670403	AAAAAAC	I	T
0.1061105	cg14936938	cg14936938	67655453	AACCATACAAACAAAATCATA			II	
-0.131528	cg14938419	cg14938419	51773359	AAAAAAC	40665371	AAAAAAC	I	C
0.1516106	cg14939821	cg14939821	36751420	AAAAAATTAATAAACTTCCTC			II	
0.1054267	cg14943002	cg14943002	49717489	CCACRACAAAACAATTATTCA			II	
0.1078486	cg14944696	cg14944696	34806455	TAACACTACCCRCAAAAAAAC			II	
-0.139046	cg14949065	cg14949065	38663360	ACAACTC	11652426	ACAACTC	I	A
-0.101129	cg14951292	cg14951292	68654498	CTAACACCTCRATTACCAATCT			II	
0.1221348	cg14953379	cg14953379	73726329	CTACAAAACCACTTCTTATAAT			II	
0.1052287	cg14960373	cg14960373	62676503	TAATACCCTATAACTTAACCTA			II	
-0.100652	cg14970273	cg14970273	18770301	ATCAACTTCTCCCTACCTCTCT			II	
0.1020624	cg14975347	cg14975347	11777315	CTTTTCTATCCCAATAAAATAA			II	
0.1344827	cg14977018	cg14977018	62660356	ACATACTTTTATTTTAATATAA			II	
	cg14981468	cg14981468	30768379	ATTCAAAAAACAACCAACAAA			II	
-0.111854	cg14983135	cg14983135	52602503	CAACCAC	12660507	CGACCGC	I	T

-0.118064	cg1498383	cg1498383	60699371	ATTAAACTACRCCAAAAACTC			II	
-0.114897	cg14984341	cg14984341	43800433	AATATAA	55752431	AATATAA	I	C
0.1924786	cg1498689	cg1498689	48640421	AATTTACTAAATCTCAACTAC			II	
-0.102646	cg1498778	cg1498778	16646398	CACTAAT	66768392	CGCTAAT	I	A
0.1005831	cg1498997	cg1498997	17783337	CTTAAAAATCTCTTATCTAAA			II	
0.1126953	cg1499297	cg1499297	21762414	TACTACAACTATTTATTATCCT			II	
0.1088206	cg1499713	cg1499713	63806388	ATCTACTAAAAACTATAACCT			II	
-0.104683	cg1499759	cg1499759	25771491	CCCAACTACAAAAAAATCTAT			II	
0.1083333	cg1499903	cg1499903	12701332	AATAAAAAAAAAATCCCRAAT			II	
0.1052819	cg1500081	cg1500081	67606447	ATTTCACACCAAAAATTCAAA			II	
0.1139743	cg1500478	cg1500478	28786454	TAACCATTCCACTTACTTTAAT			II	
-0.170445	cg1500795	cg1500795	49757401	TTCTAAT	55726326	TTCTAAT	I	C
0.1043226	cg1500923	cg1500923	64739341	AATCAACCRATAAAAACTACT			II	
0.1605999	cg15014361	cg15014361	14649308	CAATACACCCTACRAATCAAA			II	
-0.128753	cg1502056	cg1502056	70810338	TTCCTTC	64604420	TTCCTTC	I	A
-0.21604	cg1502260	cg1502260	55620414	AAAACA	19793382	AAAACG	I	A
-0.14502	cg1502520	cg1502520	48763405	ACCATAT	22691478	ACCATAT	I	A
0.1097822	cg15027721	cg15027721	22689478	TTACCTAATTACTACATTCTTT			II	
-0.176843	cg1503301	cg1503301	39655305	CTCRTACATAAATTAATTCCRC			II	
0.1365741	cg1503355	cg1503355	74678456	AAAAAAAACCTCAAAACTAAA			II	
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0.1083908	cg1504457	cg1504457	72727466	ACATAACAACATTCTTAAATT			II	
-0.113051	cg1504476	cg1504476	64648420	AAAAACAAATCTCCAATCTAA			II	
-0.102049	cg1504493	cg1504493	49637505	ACTATCAATAACATTTATAAT			II	
0.1124847	cg1505487	cg1505487	33754404	TAACCAAAATACTTACRTAAC			II	
0.1182336	cg1505578	cg1505578	61647408	AATTACTACCCAAACTCTATC			II	
-0.105718	cg1505955	cg1505955	12650335	ACTAAAACACRACCAAATAAC			II	
0.1618482	cg15060081	cg15060081	66673325	AACACTA	30638301	AACACTA	I	A
-0.103167	cg1506059	cg1506059	73696342	AAAAAA	72780487	AAAAAA	I	C
-0.101026	cg1506855	cg1506855	56712415	AAAAAAC	46733418	AAAAAAC	I	A
-0.269746	cg1507470	cg1507470	39607394	TCACAAA	23616423	TCACGAA	I	C
0.1158327	cg1507993	cg1507993	32752434	TACATAT	14738451	TACATAT	I	C
0.1753198	cg1508043	cg1508043	40634450	RTATCTTTCTTTAACCTTAACA			II	
0.2342657	cg1508480	cg1508480	42709321	ATTATATACCTATCCTAAAAA			II	
-0.105188	cg1508790	cg1508790	41711429	CTCCAAC	19799359	CTCCGAC	I	A
-0.101645	cg1509221	cg1509221	41636348	CTAAAACRAAAATCTCCAAAA			II	
-0.115169	cg1509234	cg1509234	24699391	ATAAACA	17737346	ATAAACC	I	A
0.1013749	cg1509864	cg1509864	37710373	AAAAAACCCCRAAAAACAATA			II	
0.1138806	cg1510462	cg1510462	12797491	AATTAAA	31705328	AATTAAA	I	A
-0.171617	cg15105011	cg15105011	18792450	TAACTACATATACAAAACCTT			II	
-0.114975	cg1511609	cg1511609	69657441	TACAAAATACAATTAAACTAC			II	
-0.109867	cg15116481	cg15116481	63633329	TAAAAAC	19609360	TAAAAAC	I	T
-0.168077	cg1511775	cg1511775	27693398	ACCCTCCTAAAAACCAATCC			II	

-0.161184	cg1512299	cg1512299	56723420	ACAACA	53652348	ACAACG	I	A
0.1300034	cg1513229	cg1513229	40628329	ACATTAAAAATCRCCACACAC			II	
0.1223535	cg1513516	cg1513516	56688395	TATAACTTAAAACAAAATCCC			II	
0.1026542	cg1513528	cg1513528	26780484	AATCTCCTAACACTCTCRACT			II	
0.1272505	cg1513576	cg1513576	14697311	CCCCACC	44624470	CCCCACC	I	T
0.2520041	cg1513828	cg1513828	48800482	ATATTTACAAAATATCCTAAA			II	
-0.211049	cg1514269	cg1514269	16736447	AAAACA	23617466	AAAACG	I	C
0.1058511	cg1514517	cg1514517	30645385	AACATA	73619499	AACGTA	I	A
0.134068	cg1514964	cg1514964	68604460	ACRTCCTACATCTCAACRAAA			II	
-0.199939	cg1516603	cg1516603	14662427	TCAATCA	18800399	TCAATCA	I	C
0.1356314	cg15171791	cg15171791	54705472	TAAACCRTAATATAAAACCAA			II	
-0.124495	cg1517429	cg1517429	65800308	AATAACTATAATAAAACTTAA			II	
-0.157283	cg1517761	cg1517761	37632356	AAACCC	48713472	AAACCC	I	A
0.1346321	cg1518766	cg1518766	36727374	ATTACTT	25731376	ATTACTT	I	C
-0.126576	cg1519038	cg1519038	54644436	CTATTTTAACRACTATCTTTTA			II	
-0.123816	cg1519313	cg1519313	25755329	AACAAA	31659427	AACGAA	I	A
0.103781	cg1519321	cg1519321	24717412	ACAATTTAAAACTCACCRAAT			II	
-0.23577	cg1519814	cg1519814	12726408	AAAAAAAATTAAACCCCCCTC			II	
0.1121825	cg1519998	cg1519998	18726423	CTCACTACCCCAAACCAACAA			II	
0.126485	cg1520000	cg1520000	30605453	CTCTTACTACAAACATATCCTT			II	
-0.115004	cg1520542	cg1520542	67685347	CAAAAA	41726414	CGAAAA	I	C
0.1144578	cg1520705	cg1520705	73778471	AAAATTCTCACATTAAAAAAC			II	
-0.128133	cg1521534	cg1521534	72600300	AAATAA	65779478	AAATAA	I	A
	cg1521922	cg1521922	11753320	AAAAAA	16794305	GAAAAA	I	A
-0.281737	cg1522634	cg1522634	58751381	AATACTTCTCCTACTTTCCCAC			II	
-0.152001	cg15236541	cg15236541	56680387	CAAAAA	69765318	CGAAAA	I	A
-0.11193	cg1524385	cg1524385	56716505	ACCAAA	30775414	ACCGAA	I	C
-0.105727	cg15246131	cg15246131	37628397	ATTCACAACRAAATATAAATA			II	
-0.555453	cg1524748	cg1524748	68781455	TACTACTATTAAACTAAAACC			II	
0.1124178	cg15249341	cg15249341	35748431	TATAAACTAAACAAAAATAAC			II	
0.1369164	cg1525063	cg1525063	26733393	ACTAACC	16683386	ACTAACC	I	A
-0.183022	cg1525114	cg1525114	39710464	TATTTCT	50745432	TATTTCT	I	A
-0.129453	cg1525138	cg1525138	43642427	CCCTACT	65714457	CCCTACT	I	A
0.1190722	cg1525464	cg1525464	56711445	TACCCCA	70679503	TACCCCA	I	A
0.1354103	cg1525638	cg1525638	65765430	ACACATTTATCTCAAAATTTA			II	
-0.117102	cg1527810	cg1527810	50758462	ACTACTT	48714335	ACTACTT	I	C
-0.169125	cg15279541	cg15279541	46670416	CACTAATATTCACCTTAACCT			II	
0.1724887	cg1528297	cg1528297	10728416	ACCTCCCAACATCCTTCTATA			II	
0.12835	cg1528603	cg1528603	48760415	CACTATTACTTTAAAAACTAT			II	
0.1165501	cg1528780	cg1528780	47793319	TTATTATCTCAACATCATTCAA			II	
-0.271664	cg1529031	cg1529031	34647475	TCACACA	24790449	TCACACG	I	A
0.1121292	cg1529209	cg1529209	57607317	CCCAATCTAACAAATCTCTTC			II	
-0.181237	cg1529235	cg1529235	21607304	RAATATAAATCCRACCAAATA			II	

-0.10003	cg1529318	cg1529318	46700503	CAAAAATACCTTTATATCTAA			II	
0.1995012	cg1529544	cg1529544	37744473	ACCCTTACATTCTTCTTATCCA			II	
-0.127778	cg1529832	cg1529832	27651418	CTACCTTCTAAAATCAACTCT			II	
0.1508348	cg1530900	cg1530900	44725368	ACCAATAAAATAAACTCCTCT			II	
0.145217	cg1532090	cg1532090	38807401	AAACCTA	45758409	AAACCTA	I	A
-0.100238	cg1532653	cg1532653	39665482	TAATCTAACCCTAATCTCTCAC			II	
	cg1532813	cg1532813	12768428	AAATCATACRTCCTATAATTA			II	
0.2066817	cg1532955	cg1532955	20721361	TACAAACCRACCAACACCTAA			II	
-0.113917	cg1533409	cg1533409	60662308	CAACTACTACTAAACCRCTAT			II	
0.1052945	cg1534052	cg1534052	13611435	CRAACCTCAAAAACAAAACTC			II	
0.1725842	cg1534507	cg1534507	48773449	AAAAAC	29760424	AAAAAC	I	A
-0.112503	cg1534715	cg1534715	27772368	ACCAAAT	48705311	ACCAAAT	I	A
0.1337576	cg1535932	cg1535932	23642399	ACCAACCRAATCTATTAAAAC			II	
0.1044022	cg1536018	cg1536018	48806320	CTTTCATACTAAACAAATCTA			II	
0.1184091	cg1536045	cg1536045	33713458	TAAACAC	69692479	TAAACAC	I	A
-0.166419	cg1536169	cg1536169	68641388	AAAAAA	54794394	GAAAAA	I	A
-0.167119	cg1536461	cg1536461	65807359	TTAACTACRTAATAAAAAACC			II	
0.2562185	cg1536550	cg1536550	35642301	TAATCAATAAACCTCCTTCAT			II	
0.1055004	cg1538132	cg1538132	44630311	TTAACAAAATCAAACAACCAC			II	
-0.100796	cg1538363	cg1538363	21613480	RCTTCTACTATAAACTAACCR			II	
-0.108992	cg1538906	cg1538906	30747383	AAACATT	74746378	AAACGTT	I	A
0.1174581	cg1538919	cg1538919	17749315	TCTTTTCTTCATCAAATAATTA			II	
0.1946931	cg1539214	cg1539214	28645389	CAACATAAAAAAACTCCRTCT			II	
0.1036905	cg1539349	cg1539349	20622482	CCTCACTACCTATCCCCATAA			II	
0.1028286	cg1539425	cg1539425	58728307	TTCTATAAAAAAACTAAATAA			II	
0.1466612	cg1539597	cg1539597	51694313	TATTTCAACCCTTCCACTATAC			II	
0.1042201	cg1540147	cg1540147	10713410	ACTCAAATCAACCTCCCCAAT			II	
0.1583895	cg1540351	cg1540351	31703427	CCRTAAAATTTTCTTCCCRTAT			II	
-0.187933	cg1540466	cg1540466	41703431	AAAAAA	29770308	AAAAAA	I	C
-0.165022	cg1540543	cg1540543	18616329	TTAATTTAACCTTAATTTATAT			II	
-0.339174	cg1540851	cg1540851	34757439	AAACAC	54742333	AAACAC	I	T
-0.204736	cg1541041	cg1541041	39631417	CCCAAAA	32801472	CCCAAA	I	A
-0.15367	cg1541474	cg1541474	72610507	ATAAACT	14768412	ATAAACT	I	A
0.1770211	cg1541849	cg1541849	31742425	CCAACACCATCAAACAAAAAA			II	
0.1775162	cg1542527	cg1542527	35773437	TCCTATAACTACAAAATATAC			II	
0.1357188	cg1542779	cg1542779	60680371	ATTTAAATAAAATAAACTCAT			II	
-0.102109	cg1543165	cg1543165	48761366	CATATTC	24686486	CATATTC	I	T
0.1206066	cg1543576	cg1543576	20696420	AAAACC	31691373	GAAACC	I	A
-0.460625	cg1543695	cg1543695	56792351	CCACCAAAACTCTCRCTACTA			II	
0.1141366	cg1544316	cg1544316	31604507	TATAAACCAAAATAATAAATT			II	
0.1720874	cg1544414	cg1544414	10800311	TCTATAT	46618328	TCTATAT	I	A
0.1120739	cg1545009	cg1545009	23785345	ATCCTTATCCTTTTAAACCTAA			II	
-0.105702	cg1546564	cg1546564	26715498	AAAAAT	51783462	AAAAAT	I	A

0.1508422	cg15466952	cg15466952	21606362	ACAACCTTAATACTCTATTTCT			II	
-0.104573	cg15467834	cg15467834	24807351	ACATCCT	55780486	GCATCCT	I	C
0.1560486	cg15477040	cg15477040	44725479	TTTTTCTAACTTACATACAAAA			II	
0.1028623	cg15491439	cg15491439	57685373	CCTAAAACTCAAAAAATAATC			II	
0.1396282	cg15498409	cg15498409	15694411	TACAATCTCCTTATCTCCCTCT			II	
-0.212547	cg15501526	cg15501526	58784502	ATAAAAC	16797443	ATAAAAC	I	C
-0.102773	cg15505615	cg15505615	35654344	AACTAAC	42775501	AACTAAC	I	C
-0.118833	cg15509177	cg15509177	29713300	RTAACACAAATTTAACCCCRA			II	
0.1200512	cg15512715	cg15512715	67790443	AAAAACATACATTTTCRTAAC			II	
-0.510535	cg15518264	cg15518264	73628441	ATCTAATTTCTCCTTACTAACC			II	
0.1106712	cg15531512	cg15531512	15600489	TAAAACATTTTCCAAATTTCTA			II	
0.1132762	cg15532640	cg15532640	57808427	ACTAAAA	30685341	ACTAAAA	I	A
0.1069363	cg15537850	cg15537850	38629356	ACCTTCATAACCACAAAAAAT			II	
0.1106339	cg15541170	cg15541170	26800467	TCACACAAAAACCTCTTTTCCT			II	
0.1002963	cg15543027	cg15543027	33733322	AATAACAATAAATCCTAAATA			II	
0.1450462	cg15544633	cg15544633	21638446	CACAAAA	11751488	CACGAAA	I	C
-0.115571	cg15548198	cg15548198	68666500	TACCTAAATTTTATTTACATAA			II	
0.1218254	cg15554966	cg15554966	12639475	TTCAAACAAAAAATACTCCCT			II	
0.1270555	cg15561493	cg15561493	45804321	TCTTTATACAAATTCCTCAAAA			II	
0.2835194	cg15567368	cg15567368	45616309	AACTAACATATATTCTACCCTT			II	
-0.242927	cg15568074	cg15568074	21673461	ACRCTAAATACTAAAACAACC			II	
0.1046416	cg15568617	cg15568617	50717475	TTATTATCCRATTCCTATTAAT			II	
-0.117495	cg15570148	cg15570148	51775306	TAAAATTCTAACCTAAACCRA			II	
-0.10613	cg15574437	cg15574437	46744474	CCCACTA	42759335	CCCGCTA	I	C
-0.110273	cg15575880	cg15575880	53732368	AAAAACT	52664438	AAAAACT	I	A
0.1915755	cg15581944	cg15581944	56612410	AAACCAAACCTAAAACAAAAC			II	
-0.155477	cg15584790	cg15584790	15687443	AAAAAAA	40654329	AAAAAAA	I	A
0.1774803	cg15591803	cg15591803	14631428	CCAAAAATTATAAAACTTCTTA			II	
-0.142363	cg15595755	cg15595755	16787451	AACAAAA	67647405	GACGAAA	I	T
0.1097499	cg15599668	cg15599668	26719502	CTAAAAAAAATTTAAATATCA			II	
0.1396115	cg15600437	cg15600437	36605384	AAACTAATTTCTTATTTAATTA			II	
0.1582679	cg15602677	cg15602677	47615484	AAAACATTTCCCTCATCCCAA			II	
0.1083469	cg15609373	cg15609373	18690463	TAATCATAATTCCAAATTTAAA			II	
-0.14966	cg15611600	cg15611600	23664305	AAAAACTAAACCTCCATAAAA			II	
0.1128644	cg15619377	cg15619377	46684424	TCTTCCTATATACTAAATTCAA			II	
	cg15623480	cg15623480	13644384	AAAAAAC	35762463	AAAAAAC	I	A
0.1412095	cg15624335	cg15624335	44808445	ATCCCTACAAAAAACATAATT			II	
-0.101239	cg15626112	cg15626112	42735374	ACATAAATCRTAATCTCTTCAA			II	
0.1437072	cg15633912	cg15633912	46646406	AAAACTAACRCRAAAACTTTC			II	
0.2058812	cg15634083	cg15634083	38800332	TAAAAAC	62793370	TAAAAAC	I	T
-0.260307	cg15642854	cg15642854	39634377	ACCACAA	61726325	ACCGCGA	I	T
-0.104794	cg15648389	cg15648389	31797330	TACRACRATTTTAAAACCAAA			II	
-0.320331	cg15652532	cg15652532	15619492	AACCTAAATTCTATAACTACT			II	

0.1020777	cg1565509	cg1565509	24757507	TATCTATATCTCTACAAAACA			II	
-0.167019	cg1566394	cg1566394	21660393	TTCCACAATATCCTAAAAACC			II	
-0.116202	cg1567145	cg1567145	35775311	CTCCAAATAAACCCTAATCTA			II	
-0.334017	cg15677681	cg15677681	50760476	CTACRATCTCTTCTTTCTATTT			II	
0.3940135	cg1568060	cg1568060	51706372	TAAATAC	48692417	TAAATAC	I	C
-0.137056	cg1568280	cg1568280	60729467	ACCCAAC	58645414	ACCCAAC	I	C
-0.11635	cg1568280	cg1568280	29656395	CACAACC	71664408	CGCAACC	I	C
0.1147933	cg1568349	cg1568349	66639442	AACCCA	56773445	AACCCA	I	A
0.1208519	cg1568395	cg1568395	36756465	ATTTTCAAAAATAATCCCAAA			II	
0.1050481	cg15684661	cg15684661	61802507	ATCCATTCCTCAATATCCAACC			II	
-0.154136	cg1569034	cg1569034	26736445	CACTATC	73634351	CGCTATC	I	A
0.1425704	cg1569259	cg1569259	11651429	ATAAAAAAAAACATTAACAAA			II	
0.2951259	cg1569393	cg1569393	46625496	AACTTAAATCTACCAACACTC			II	
-0.108087	cg1569908	cg1569908	35717465	ATCTACTAAACTCACTTCCTCT			II	
-0.12952	cg1569955	cg1569955	21738485	TACAAAT	70790419	TACGAAT	I	T
-0.115505	cg1570428	cg1570428	65743393	CTAACTAATAAAAATATTATA			II	
0.1627521	cg1570487	cg1570487	66726310	AAAATTTTAAAATCCAAAATA			II	
-0.110777	cg1570615	cg1570615	23704322	ACTACTA	37737444	ACTACTA	I	C
-0.235194	cg1570656	cg1570656	47785393	AATACAACCAACTTCTCTTCA			II	
0.1220206	cg1571468	cg1571468	57675362	CTTCTATAAAATAAAAACACT			II	
-0.11482	cg1571662	cg1571662	39768442	ACRAAATACRATAATATAAAC			II	
0.2000272	cg1571761	cg1571761	60736362	AACRCTAAAATAAATCATACC			II	
0.1068166	cg1572487	cg1572487	62645487	TACTCTAACACATTAATCTATC			II	
0.1023991	cg1572612	cg1572612	31721364	CTAAAAACAAACCCCAACCTA			II	
0.1177712	cg1572869	cg1572869	12782313	ACCTAATAAAAACRAAAAATA			II	
0.1054847	cg1572890	cg1572890	34605452	ATAAACACTAAACCTTTTATA			II	
-0.125536	cg15730931	cg15730931	17635330	TATCCRTCTTAAAATAACTAC			II	
-0.122809	cg1573210	cg1573210	60715449	TATAATCTCTCCACRATAATTT			II	
-0.15665	cg1573717	cg1573717	31610426	AACAACA	20809435	AACAACC	I	A
0.1629413	cg1574050	cg1574050	60703439	CATCAACACCAAAACTTTATC			II	
-0.137936	cg1575275	cg1575275	74780342	CCAATACTAATTAATTCTTTTC			II	
0.1283833	cg1575800	cg1575800	42601307	ATAAAAAAACRAATTTCATAT			II	
-0.137563	cg1576563	cg1576563	43723466	CCTTTATAAAACAACCTAACT			II	
-0.174416	cg1576861	cg1576861	16680480	CTAAAAAAAACTACATTTTTA			II	
0.1945089	cg1577397	cg1577397	44645334	TACTACA	16602440	TACTACA	I	A
0.1430093	cg15779891	cg15779891	50778398	ATTAATCTTCACAATAATCCT			II	
-0.135655	cg1578115	cg1578115	66623406	AATCTAAACCCAAACCTAAAC			II	
0.2624826	cg1578384	cg1578384	30621385	TTTTATTCTATAAAACATACTA			II	
-0.115428	cg1578682	cg1578682	26714352	TATAAAT	50668485	TATAAAT	I	A
-0.106748	cg1578836	cg1578836	40613314	AATCCCA	25712368	AATCCCG	I	A
0.1476371	cg1579018	cg1579018	32663490	CCAACCACAACCTACRTAAAC			II	
0.2363854	cg1579325	cg1579325	63613330	AACTCCCTAAACCCTAACTAC			II	
-0.115649	cg1579886	cg1579886	42764356	CCCTTATCCCTATAATATTCAT			II	

-0.118306	cg1580134	cg1580134	14789485	CTACTTTTCCCAACTTCAACTA			II	
-0.122054	cg1581143	cg1581143	10741416	TTCTCTTAAACTTTTATAACCT			II	
-0.128764	cg1581166	cg1581166	34771443	CAAACTT	39796501	CAAACTT	I	A
-0.107312	cg1581202	cg1581202	19700315	AAAACA	69704377	AAAACG	I	C
-0.120597	cg1581933	cg1581933	15621481	CTCCCCTTAATTAAATATACCT			II	
0.1079686	cg1582443	cg1582443	59628421	TTTAAAAATAATTCACRTTACT			II	
-0.118804	cg1582470	cg1582470	19774392	CCAACCA	25755347	CCAACCA	I	C
0.1585676	cg1582681	cg1582681	22705486	ACTAAAATTTCAACTAACATA			II	
-0.238825	cg1582908	cg1582908	60661444	CTCACAA	58706346	CTCGCAA	I	C
-0.103183	cg1582996	cg1582996	24632422	CCAACCATCTAAATTCRAATC			II	
-0.115621	cg1583794	cg1583794	38745406	CCAACCAACTATAACATTAAC			II	
-0.117636	cg1584055	cg1584055	17633478	CAAATCCCTCATAAATAACTT			II	
0.1086645	cg1584441	cg1584441	24610482	ACCTTTATTTCTAAACAAAAA			II	
0.1012683	cg1584536	cg1584536	68737498	AATCTTCCCAATACAAAACTT			II	
0.1342882	cg1584727	cg1584727	43689412	CCTAAAAATTTCCCAACTTATA			II	
0.1022914	cg1585073	cg1585073	33748413	ACAATTACATAAACRACTTTC			II	
0.1034916	cg1585244	cg1585244	33661343	CRAAACAAACTCCTAAAAAAA			II	
0.3046114	cg15853771	cg15853771	13754467	ATTCTAAATAAATCCAACAAT			II	
0.1034012	cg1585747	cg1585747	56623333	CTACAAAAATCTTAAAACAAA			II	
0.1696611	cg1586608	cg1586608	51799376	TAAATCAAAACATCCACAAAT			II	
-0.172301	cg1587462	cg1587462	58630411	AAATCAA	27706371	AAATCGA	I	A
0.1035675	cg1587470	cg1587470	60799356	AACTCTCAACACCATTTATATT			II	
0.2375034	cg1587752	cg1587752	37656439	CCAACA	23680318	CCAACA	I	A
0.1064741	cg1588179	cg1588179	17795419	ATACCAAATATTTATTTATATA			II	
0.1328417	cg1588309	cg1588309	27730328	AAAACA	22789353	AAAACA	I	A
	cg1589164	cg1589164	12768347	AATAAAATTTCTTTTAAAATA			II	
0.1083472	cg15895121	cg15895121	26673478	AAAAACAAATACCAACAAAC			II	
0.1885768	cg1589533	cg1589533	39716426	TTTATAAATATTTCAAAAAAA			II	
0.1578829	cg1589578	cg1589578	25801508	CTATAAATTCCTAACACATAA			II	
-0.6258	cg1589743	cg1589743	60706393	TCCTCCTAAAAAAATATATCAC			II	
0.2229933	cg1589980	cg1589980	37754400	AATAAATAAAATAACCTCAAA			II	
-0.104935	cg1590897	cg1590897	22676328	TCAAATAAATATTTCATCCAA			II	
0.2253095	cg1590944	cg1590944	64786316	AACCACATATCTTCCTACTAA			II	
0.1014017	cg1591116	cg1591116	66707467	AAATCTCTAAATATATTCATTT			II	
-0.113114	cg1591132	cg1591132	50775463	ATAAATTTATACAAAATCACC			II	
0.1267329	cg1591981	cg1591981	57785429	TAATTTATATATTACRTAATTT			II	
0.1004041	cg1592188	cg1592188	48629388	CTTTCTCAAAACTCCAACCAA			II	
0.152045	cg1592456	cg1592456	34681444	AATAAATAACATCTCTTTCCCT			II	
0.127975	cg1593805	cg1593805	54774355	TTCCTCAAAACACTTCAATTA			II	
0.1001279	cg1594333	cg1594333	64668323	AAATTCCTCATTTTTTCCATAT			II	
-0.161189	cg1594659	cg1594659	11734316	TCCAAAAAAATATAAATTCCR			II	
	cg1594841	cg1594841	13644396	ACACAAAACTATAAACTAAAC			II	
-0.106126	cg1594856	cg1594856	31711352	CAAACTA	26660377	CGAACTA	I	C

0.1253988	cg1594955	cg1594955	61651509	ATATTCTCCTAACCAAAAATA			II	
-0.116703	cg1595146	cg1595146	62699310	AAAAACRCAACTCRACCTTAA			II	
0.1223676	cg1595780	cg1595780	26701411	AATAATTCAATACATTTTAAT			II	
-0.211847	cg1595842	cg1595842	66711467	CCTCTCTTATCAATACAAATA			II	
0.2868934	cg1595946	cg1595946	59777444	TATTTATTTCAACCTCCRTATT			II	
0.1301691	cg1596398	cg1596398	15749386	TCAACCATCCACTCCTTAAAC			II	
0.2153563	cg1596408	cg1596408	66682491	CTTTATAACCTCAACCRTAAA			II	
0.2422457	cg1596459	cg1596459	14786324	TATCACTACTTCAAATCTAAA			II	
0.1104653	cg1596538	cg1596538	64680473	CTTTCTCTAATTAATAATACTA			II	
0.1062114	cg1597849	cg1597849	23618398	ACCACATATTCACATACACAT			II	
-0.293611	cg1597921	cg1597921	53601493	ACCTACRTAAACCAACAATAT			II	
0.1032614	cg1598398	cg1598398	33741381	AAAAATATAATCTACTACAAC			II	
0.1168683	cg1598646	cg1598646	10602301	CAACAACCATATTATCRTAAA			II	
0.107919	cg1598828	cg1598828	22760510	AACACCTATAAATATTCCTAA			II	
0.1519324	cg1598856	cg1598856	68758493	AAACAAAATAAATAAAACACT			II	
-0.235085	cg1599147	cg1599147	59631436	ATATTTC	14688462	ATATTTC	I	T
0.1680778	cg1599812	cg1599812	55707472	CAAAACT	36666312	CAAAACT	I	A
0.1096498	cg1599960	cg1599960	19649402	CTAATTCCCTTACTAAAACAA			II	
0.141508	cg1600279	cg1600279	33698330	AAATAAACRAAAAATAAATTT			II	
0.114593	cg1600696	cg1600696	32687493	TCTATAACTTAACTATTTTAAC			II	
-0.102144	cg1600955	cg1600955	74615493	CAAAAATTTTACCAAACCCTA			II	
0.1001637	cg1601603	cg1601603	34673336	ATTAAACCACAATACCAACAT			II	
0.1043682	cg1603197	cg1603197	63740383	ATAAATAACTTATTTTAACTTC			II	
0.3027641	cg16034991	cg16034991	67689422	TACATATATCCCACAAAACTA			II	
0.103938	cg1603604	cg1603604	20755439	CCTATATTAAACCTACAACTA			II	
0.1146358	cg1603914	cg1603914	51755452	AAAACATAAAAAACATAACTA			II	
0.123456	cg1604179	cg1604179	54771465	ACTAAATATACTATATTTCCTA			II	
0.1035271	cg1604209	cg1604209	73674391	CTTAACATAACTAATAACTAA			II	
0.1158319	cg1604891	cg1604891	74727377	ATAAATTTAAACCTAAAACAT			II	
0.1082883	cg1605032	cg1605032	73642398	AAACCTAACACTCCCRAAACC			II	
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0.1483279	cg1605827	cg1605827	73783407	AACTTACAATAAACATTTAAC			II	
0.1733482	cg16059161	cg16059161	53712386	ACTAAATTATAATCCCCAATA			II	
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0.3946221	cg1606093	cg1606093	38683455	CTATAATTACAACRATAAACT			II	
-0.175066	cg16074271	cg16074271	45695325	CRCACCTTCTACCTAACAAAA			II	
0.2741827	cg1607499	cg1607499	40742491	CRCCCTACAAAATAAAATCAC			II	
0.1032562	cg1607749	cg1607749	13809348	AACCTATTATAAATTTTACAA			II	
0.1292949	cg1607792	cg1607792	39679313	CAAAATCATCTTCTAATTCCA			II	
0.1111376	cg1607941	cg1607941	65692337	AAACAAAAATAACAAAATATT			II	
-0.163378	cg1608185	cg1608185	14675462	AAAAATATCCRTAACRCCAAA			II	
0.1007558	cg1608269	cg1608269	35618508	ACCAACT	61792419	ACCGACT	I	A
0.2368017	cg1608355	cg1608355	58644371	AACTCRAACTCCTAACAAAAA			II	

0.1661486	cg1608419(	cg1608419(	44650375	ACAAAACTCTAAACAACAATA			II	
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-0.122346	cg1609195:	cg1609195:	65657362	AAATACT	49721438	AAATACT	I	T
0.1175961	cg16102739	cg16102739	43808361	TTTTATCACCCAAAAAACATT			II	
0.16038	cg16105569	cg16105569	38611458	AAAAAATCAATATCCACACRA			II	
0.1453311	cg16109381	cg16109381	32601352	AACTAAAATAACTAAATCAAC			II	
0.105403	cg1611222(	cg1611222(	27622453	CCAAATA	32647322	CCAAATA	I	C
0.5510837	cg1611288(	cg1611288(	26722406	ACCCTTCCCCAAAAATTTAAA			II	
0.1297789	cg16118379	cg16118379	21779474	TAAATCACAAAACTTATACCT			II	
-0.332601	cg1612768:	cg1612768:	10784337	CATAAAA	70648368	CATAAAA	I	A
0.1246198	cg16136068	cg16136068	69748499	CAAAAATATTTAATTCACCC(			II	
-0.39168	cg1614290(	cg1614290(	26759327	AATAATA	40629405	AATAATA	I	T
-0.134529	cg16143654	cg16143654	55661306	ACACATA	47767338	ACACGTA	I	C
0.2830378	cg16145187	cg16145187	55618305	CACTACAACTATCTCACAATT			II	
-0.112353	cg16149927	cg16149927	41734416	CAAAAAA	29799492	CAAAAAA	I	A
-0.388345	cg1615611:	cg1615611:	70607365	TTCAAAC	73797430	TTCGAAC	I	T
0.4435889	cg1616293(	cg1616293(	33786330	CTTTATC	68681333	CTTTATC	I	C
-0.194469	cg1616756:	cg1616756:	23663418	CRCCATAAATAAAAACTCTCT			II	
0.1367513	cg16172099	cg16172099	42695463	TAAATAC	57651379	TAAATAC	I	A
0.1036057	cg1617660(	cg1617660(	15652470	CTTTAAAATCAACACCAACTC			II	
-0.110298	cg1617773:	cg1617773:	18663429	CCTAAACTCAATAAAAAATTA			II	
0.1284724	cg1617783(	cg1617783(	26746466	AATAAACTTCRCCTACTTCRTA			II	
-0.125943	cg1618079(	cg1618079(	30757342	ACACAAT	47612460	ACGCAAT	I	A
0.1113022	cg16187528	cg16187528	34809454	AAAAATATATTTCTCCCCAAC(			II	
0.1044898	cg1618964:	cg1618964:	63781485	CCRAATCTATCAACAAAACAT			II	
-0.136312	cg1618995:	cg1618995:	45679329	AAAAACC	45683363	AAAAACC	I	A
-0.125409	cg16191297	cg16191297	59785357	AAAAACRCTAAAATATAACTA			II	
-0.122832	cg1619257:	cg1619257:	56802419	AAAAACCCRCACAAAATAATA			II	
0.1361555	cg16199747	cg16199747	27783418	AAAACTAAAAAACCCATAACR			II	
0.1360726	cg16202259	cg16202259	61760497	TACAAAA	15748418	TACAAAA	I	A
-0.10188	cg16204818	cg16204818	48789442	ACTACTC	68603443	ACTACTC	I	T
-0.228562	cg1620805:	cg1620805:	34695480	TAATTCT	32786455	TAATTCT	I	A
0.1106783	cg1621035:	cg1621035:	44803341	AATCRACTCATTATTAACTCA			II	
0.1665783	cg16210979	cg16210979	27661497	TAATTACTTTTTATAACCTAAT			II	
0.1021302	cg1621415:	cg1621415:	52613413	TAACCAA	17673389	TAACCAA	I	A
0.2193121	cg16233797	cg16233797	19723383	TTTTAACTTTCCCACAAAACA(			II	
-0.10473	cg1623433:	cg1623433:	36711428	CTTCRCTATAAACCACRACCA			II	
-0.178574	cg16235707	cg16235707	60718451	ACAATTTAATTTCCTTAAAAA(			II	
0.2259991	cg1625566:	cg1625566:	63743407	ACTTCAA	63636440	ACTTCGA	I	C
0.1488408	cg1625753:	cg1625753:	12611483	TAACATACACACACATCCTTA			II	
0.1008243	cg16261857	cg16261857	71706473	CTACATACCTAAACAACACAT			II	
-0.152716	cg1626318(	cg1626318(	62685459	ATAAAATACCRCTTTTCRCTCT			II	
0.1136632	cg16273051	cg16273051	23623343	AAAATCTCTACCTCTCTCAAA			II	

-0.112134	cg16284437	cg16284437	53698374	TAACCTT	51644413	TAACCTT	I	A
0.1046756	cg16300553	cg16300553	27665417	CTTCAAAAAATTCATATACAC			II	
0.1018516	cg16306078	cg16306078	24761450	AACTTCATAAAACCAAATTTT			II	
0.1140309	cg16310003	cg16310003	57621323	CAATCTCCAAATACCCCCTCA			II	
-0.225758	cg16310958	cg16310958	59700357	AATACTC	46809418	AATACTC	I	A
-0.15993	cg16316472	cg16316472	64721346	ATTTACA	10688333	ATTTACA	I	A
-0.119394	cg16316624	cg16316624	44670340	TCACATA	45663379	TCGCGTA	I	C
-0.181977	cg16320888	cg16320888	26742496	AAAAAA	49705394	AAAAAA	I	A
-0.113155	cg16330146	cg16330146	30726435	ATACCAA	17606402	GTACCGA	I	T
0.1236013	cg16336556	cg16336556	52782469	CAATTCTAACAAAAATTTTCA			II	
0.1056967	cg16337566	cg16337566	11661353	AAAAAAATTAAATTCCTACCA			II	
0.1731476	cg16342620	cg16342620	46759427	CATAACCCAATCAACTAAAAT			II	
-0.238359	cg16345566	cg16345566	52757468	AATCCCTCTAAATACAAAAAT			II	
0.1038376	cg16354345	cg16354345	37758333	CCCATATTTTATATAAATAATA			II	
0.1565853	cg16355591	cg16355591	27706301	ACAACCRAAATACACAACCTA			II	
-0.106423	cg16359799	cg16359799	63684417	TAAAAACCTATAAAAATATTT			II	
0.1066954	cg16371229	cg16371229	49810458	CAATTACACAATACAACACTA			II	
0.1026957	cg16372632	cg16372632	15747371	TTCCAAA	25733311	TTCCAAA	I	C
0.1390767	cg16375820	cg16375820	56793477	AACTTAAAAACAACCCATAAA			II	
0.1761037	cg16387046	cg16387046	49634405	ACCAATCAAAAACTATCAACC			II	
-0.17203	cg16394018	cg16394018	35675418	AATCCAC	38755351	AATCCGC	I	T
-0.119085	cg16397032	cg16397032	31606396	ATATTAA	68796418	ATATTAA	I	A
0.1086442	cg16397176	cg16397176	25706345	CTTAACCTACTTTATTTATCTT			II	
-0.178143	cg16397968	cg16397968	15795447	TTAAATCTAAACTAAACTCRT			II	
0.1970132	cg16398051	cg16398051	67633365	CCAACTC	34624302	CCGACTC	I	A
0.1009515	cg16398581	cg16398581	54711381	CAATATTAATATATTTCTACCA			II	
-0.174499	cg16400631	cg16400631	15771335	AAAATAC	39755401	AAAATAC	I	A
0.1082422	cg16405432	cg16405432	66643403	ACCATTACCCAAAACACTAAT			II	
0.1978374	cg16406892	cg16406892	43608374	AAAAAATAACRACTTTAAACA			II	
0.1932539	cg16412745	cg16412745	68659506	ACTAAACRTAAACTTCAACRC			II	
-0.103706	cg16414030	cg16414030	58663492	CRAACTCCCCTCACCTTCTAAA			II	
0.1141091	cg16414691	cg16414691	39688492	AAAATTTCTCTATTCTACCTCT			II	
0.1190104	cg16415646	cg16415646	18638488	TATATCTCAATAAATATATCC			II	
	cg16416045	cg16416045	43706325	AAAAAA	55629312	GAAAAA	I	C
0.1245606	cg16418183	cg16418183	63772319	CACACCAAACAACCATCTAAA			II	
-0.16068	cg16419584	cg16419584	46647457	AAATTCC	74795414	AAATTCC	I	T
0.1351475	cg16421411	cg16421411	54701456	ACTATAA	61679335	ACTATAA	I	A
-0.182692	cg16423096	cg16423096	42782411	TAATATAATCTATAACCACAA			II	
-0.179357	cg16426293	cg16426293	63806360	AAAAAA	18607354	GAAAAA	I	A
-0.222785	cg16428357	cg16428357	12763437	AAAAATA	12702443	AAAAATA	I	A
0.1377229	cg16428517	cg16428517	19643510	ATCACTTAACCAACRTCACAC			II	
0.1061256	cg16432908	cg16432908	56670338	CCCTAAACAAAACAACCATAA			II	
-0.204909	cg16435686	cg16435686	63603337	AAATAAATCAATTACATATAA			II	

0.1109237	cg16436762	cg16436762	27747312	ACAAACATAAATCACRACATC			II	
-0.277218	cg16440058	cg16440058	61623436	ACAAACA	42729406	ACAAACC	I	C
0.1120127	cg16449636	cg16449636	11731360	ACAAAACTATTATAACTTTAAT			II	
-0.140504	cg16450309	cg16450309	36715420	CTACCAT	71656455	CTACCAT	I	A
0.1330306	cg16451306	cg16451306	74623409	TCCCAATATAAAACATTCCCCA			II	
-0.194651	cg16453056	cg16453056	59689453	AAAATACAACRAACAAATCAC			II	
0.1040922	cg16455339	cg16455339	57651414	AAATTATACCCAATTTTAAATC			II	
-0.112244	cg16458494	cg16458494	66632451	AAAAAAA	10603352	AAAAAAA	I	A
-0.102115	cg16460383	cg16460383	61602507	TCCAACCCTAAAATATCCTTAT			II	
	cg16467318	cg16467318	13644470	AAAAAACTTCCTCCAAATCCA			II	
-0.123208	cg16476432	cg16476432	53721323	ACAATATCTCAAAATCTCCCAC			II	
0.1911663	cg16477611	cg16477611	39660439	AAATTTATTACTTCTACTAAAC			II	
0.1269258	cg16479633	cg16479633	44641326	AATCACTAATAAATCACAAAA			II	
0.1014134	cg16481280	cg16481280	54714317	TTACAAAATCATTACTTAATCT			II	
-0.138242	cg16484499	cg16484499	32709458	CATCAACAAAAATAAAAAACT			II	
0.2906354	cg16490124	cg16490124	62797474	ACAAACAAAACTATCAACTAA			II	
0.1544791	cg16493238	cg16493238	66732473	ATATATACTACCAATAAATAA			II	
0.3242497	cg16494625	cg16494625	73728435	TATAATCTTTATTCCAACATCC			II	
0.1058856	cg16501561	cg16501561	73623317	AAAACAAAAAACTAATTAAAA			II	
-0.139668	cg16507569	cg16507569	31743395	CACTCTAATAAAATCCACAAA			II	
-0.177523	cg16514085	cg16514085	28678378	CTCCRTCCCATTAAAAAAATAA			II	
0.103291	cg16514513	cg16514513	17773335	ACCCTAC	58738411	ACCCTAC	I	C
0.2594761	cg16515381	cg16515381	35604436	AAAATATAACRCAACTCACAA			II	
0.1038997	cg16516295	cg16516295	64797394	AAACCAAAATAAACTATAACC			II	
-0.148794	cg16527095	cg16527095	61749339	CAAACAAAATCRTTCCTTCCTT			II	
0.1462642	cg16527629	cg16527629	21787337	CCCTTTAAAACTATAAAAAAA			II	
0.1184478	cg16531622	cg16531622	10689391	AAAATAAATAAACCTAAATTT			II	
0.1309639	cg16533146	cg16533146	14607344	AAAAAAAACATCCACAAAAAC			II	
-0.253425	cg16535653	cg16535653	58647457	TAAAATTAAAATTCTCCCCCA			II	
0.1832102	cg16540590	cg16540590	61661377	AACATACTACCCCAAAACATT			II	
0.1150123	cg16549644	cg16549644	69706449	AAATAAA	55803491	AAATAAA	I	A
0.1111948	cg16550264	cg16550264	70779475	AAAACTA	43672350	GAAACTA	I	C
-0.228418	cg16558994	cg16558994	54799486	TAATAACCACCAAAAAAAAAC			II	
0.1142541	cg16564828	cg16564828	11720494	ATCACRAAAAATATTAAAACC			II	
0.1443899	cg16566191	cg16566191	67803420	TTATAAAACAAACACAACCCT			II	
-0.117368	cg16568131	cg16568131	38617479	ACAAATT	16743341	ACAAATT	I	C
-0.106282	cg16570885	cg16570885	40644306	ATATTAACACTACTACATATCC			II	
0.1471606	cg16575544	cg16575544	38718324	AATCCTCCTAAAAACACCCAA			II	
-0.1014	cg16576544	cg16576544	30685373	ACAAAATCCRATAATTCTAAA			II	
0.136839	cg16576930	cg16576930	15746497	TCCTTAAACTCACCTTTACTTA			II	
0.1366734	cg16582419	cg16582419	31791419	AAATACA	56778505	AAATACC	I	A
-0.322963	cg16583552	cg16583552	40659477	ACATTCT	53641413	GCATTCT	I	C
0.1067075	cg16596317	cg16596317	10704506	AAAATAACTCAAACCCAAACA			II	

-0.154173	cg16600991	cg16600991	19676476	AACCAA	72679384	AACCAA	I	T
-0.137678	cg1660231	cg1660231	11806443	TACTAAA	46648400	TACTAAA	I	C
0.1102229	cg1660357	cg1660357	44617361	AACAATA	22607427	AACGAT	I	A
-0.140982	cg1660632	cg1660632	10633509	AACCAC	48719469	GACCGC	I	A
0.1384419	cg1661207	cg1661207	21619432	AATCCAATAAACACRAAAACC			II	
-0.127349	cg1661535	cg1661535	26703479	AAAAATTTTATAAAAACCTT			II	
0.1267298	cg1661725	cg1661725	41734407	ACCTACCACTCACTAAAAAAT			II	
0.1184735	cg1662289	cg1662289	22712323	CCAAATA	39604492	CCGAATA	I	C
-0.1039	cg1662290	cg1662290	32638312	AATTATA	13689444	AATTATA	I	A
0.1193766	cg16623941	cg16623941	43748403	ATTTAAACRAATACAAAATAA			II	
0.1027936	cg1662723	cg1662723	15764432	ATACTAAAATTATATATCCTT			II	
0.1077748	cg16627911	cg16627911	55773343	TCTACTA	51629453	TCTACTA	I	A
0.1263313	cg1663745	cg1663745	33670508	CCTTAACAACTAAAAAAACCT			II	
-0.112787	cg1664163	cg1664163	42786453	AATAATT	54806449	GATAATT	I	A
0.2200589	cg1664972	cg1664972	36757390	CCAACTT	51722444	CCAACTT	I	T
0.1654699	cg1665131	cg1665131	37671494	CCTATTTTCATATTTCTAATCC			II	
-0.191399	cg1665292	cg1665292	40788502	ACTAATCACTAAACAACTACR			II	
-0.477228	cg16655291	cg16655291	74683493	ACACCCAAACTAAAAACAACR			II	
-0.101668	cg1665534	cg1665534	66739312	AATAAAAAAATATTCTTCCTC			II	
0.1005464	cg1665687	cg1665687	10784438	CAATTTTCATTACCCCTCCTCT			II	
0.1221485	cg1665846	cg1665846	20777316	TAATTACAAAAAATACTACCT			II	
0.1620326	cg1665977	cg1665977	41677386	ACAATAACACAAAAATAAATC			II	
0.1257239	cg1666049	cg1666049	57758504	ATAAATAAAATTCAATTTATC			II	
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0.1625218	cg1667352	cg1667352	49780451	CTCCTCATTCCCACAACCCAA			II	
0.1034482	cg1667815	cg1667815	42723496	ACCCTACTATCTACTCTTCACA			II	
0.119266	cg1668164	cg1668164	54754423	CTCCCTCTATAAAAATTAATC			II	
0.1576221	cg1668306	cg1668306	42782316	AAACTCTTTCTATTTTAATCAT			II	
0.1203075	cg1668613	cg1668613	12638432	AAAAAAAAATCTCAAACAACC			II	
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	cg1670002	cg1670002	61810327	CATTAAATAATCATCTCCRACT			II	
0.3327687	cg1670266	cg1670266	16631322	TCACAAAATCAAAACAAAATC			II	
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0.1280525	cg1670447	cg1670447	12688449	TTTAAAACTTCTACTAATATAA			II	
0.263953	cg1670470	cg1670470	15797495	CRAAACAAAACATCTCCCAAA			II	
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0.1260255	cg16711011	cg16711011	48686329	AACAAC	61723395	AACAAC	I	A
0.1030479	cg16713321	cg16713321	50792364	ATCACCTTAAAACTCTTATATC			II	
0.1126983	cg1671362	cg1671362	63809322	TAAATAC	61685313	TAAATAC	I	C
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0.1221179	cg1671951	cg1671951	46679337	TACATAA	32778503	TACATAA	I	T
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-0.10235	cg16722947	cg16722947	30626503	TATTCTAACATTAATCCCATTT			II	
0.1622316	cg16723716	cg16723716	34633487	ACCACAC	57732437	ACCACAC	I	A
0.1472095	cg16724332	cg16724332	72634429	TCTACAAAAACTTCRTAAAAA			II	
0.1055744	cg16724720	cg16724720	14750373	ACTTTCAATAATTCACTTTCAA			II	
0.1095255	cg16727923	cg16727923	26754342	CCATTATACCAATAAAAAAAA			II	
0.102289	cg16728846	cg16728846	66656509	CAAAACAAACATTCTACAAAA			II	
0.1711386	cg16735072	cg16735072	38734362	TATATACCAATAATCTCAATAA			II	
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0.1139198	cg16747885	cg16747885	39769375	AAAAACT	52600460	AAAAACT	I	T
0.1053901	cg16747928	cg16747928	74666366	AAATAATCTACTAACTTAAAA			II	
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0.1012799	cg16748433	cg16748433	62647492	ACRATAAAAAACCAAACCTAA			II	
0.1260486	cg16751493	cg16751493	61726311	CAAAAAAACACTTAAACCCCR			II	
0.1222122	cg16754788	cg16754788	43663360	TAATTACTCCTAAAACCTTCAA			II	
0.1139425	cg16755833	cg16755833	46701389	AATTTCA	11653323	AATTTCG	I	A
0.1346406	cg16765068	cg16765068	22662319	CTAAATCACCTAAACTAAAAC			II	
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0.1017495	cg16768697	cg16768697	63725310	ATCTAAA	11665446	ATCTAAA	I	A
-0.14307	cg16775598	cg16775598	26788369	ATATTTACCTCCTCATTCTTTC			II	
0.1553755	cg16778382	cg16778382	29686413	AAACAAA	57612478	AAACAAA	I	T
0.1168207	cg16780454	cg16780454	17718342	AAAAAATTAACCRAAACRCTC			II	
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0.1104448	cg16785291	cg16785291	11645344	TTACACAACTCAAAATCTAAA			II	
0.1097156	cg16787352	cg16787352	19624446	CTTTAACTCAATTACTACCAAT			II	
0.1199535	cg16788099	cg16788099	10720331	AAACACT	70768333	AAACGCT	I	A
-0.260946	cg16788857	cg16788857	53651382	TAAAAACCAATAAATATAAAA			II	
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0.2898142	cg16791832	cg16791832	37644405	AAATCCATACAAAACCAAAAC			II	
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-0.110704	cg16803846	cg16803846	29616304	TAAAACA	61796314	TAAAACC	I	T
-0.113184	cg16810310	cg16810310	57768347	AACCRAAATCAAAACCACATC			II	
-0.346302	cg16814680	cg16814680	11738460	AATAACTTTATAAAATTCCCCT			II	
-0.117883	cg16822572	cg16822572	73715405	TTTCAAA	21760444	TTTCAAA	I	A
0.1458271	cg16829924	cg16829924	48698301	TAAACTA	64800418	TAAACTA	I	A
0.1289538	cg16835531	cg16835531	10670397	ACCTATTAACTTCTAAAATAAT			II	
0.1797481	cg16836675	cg16836675	50727449	AAATTATTTCCTAATTACTAAA			II	
0.1812911	cg16841014	cg16841014	22679452	ATAAAATATATCCAAAATATA			II	
0.3076231	cg16848221	cg16848221	61804390	TATAAACCACTATACCCRACCT			II	
0.1258844	cg16852369	cg16852369	37748353	CCACTAATAATTTCTACACTAA			II	
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-0.106856	cg16855352	cg16855352	43625305	TCTATCA	72735337	TCTATCA	I	A
0.1069602	cg16860392	cg16860392	17760330	TTCCCAAATACTTCTAAAATA			II	
0.1163412	cg16863522	cg16863522	37648364	AAAAAAACCTCTCCTATTTTA			II	
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0.2813806	cg16871435	cg16871435	21642333	ACCATTCAAACTACTTTTATTC			II	
0.102445	cg16874185	cg16874185	35752411	CTCTCAATTACAAAAAAATTC			II	
-0.128398	cg16877087	cg16877087	61683422	CAAATAT	10674439	CAAATAT	I	A
0.1287643	cg16877681	cg16877681	46660353	AAAAAACTACCATTACCAAAA			II	
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-0.168199	cg16898193	cg16898193	33771462	TCCTTAAACAAAACCTAAAAT			II	
0.14983	cg16904261	cg16904261	15693510	TACCTACCTACCTAAACCCCA			II	
0.1644936	cg16908938	cg16908938	70749340	TCCACCTCTAAAAACTATCCT			II	
-0.150879	cg16914370	cg16914370	20636316	TCACTAA	44607314	TCGCTAA	I	C
0.323177	cg16917903	cg16917903	44682343	AAAAAAATAACCACCATTACA			II	
-0.165847	cg16921727	cg16921727	35751384	AAAATTCAATACCTCTCCCTA			II	
-0.109864	cg16929496	cg16929496	60667430	TAAAACAATAATACTAAATCC			II	
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0.1525443	cg16931770	cg16931770	70737340	TAACCTC	51735392	TAACCTC	I	C
0.1079666	cg16931822	cg16931822	45695381	TATAACTTTTACACCATTATAA			II	
0.106005	cg16932827	cg16932827	42802482	ACAACTTAACTCTAATAAAAA			II	
0.1003477	cg16936421	cg16936421	71731399	AAAAAAC	46620479	AAAAAAC	I	C
-0.113352	cg16967578	cg16967578	35635502	CCCTAAAAAAAATAATTAATT			II	
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0.1545755	cg16988212	cg16988212	48614330	ATAAATCRACCTCTACTTCTAA			II	
-0.134302	cg16989201	cg16989201	37653313	ACCCACCAAAAAAAACACRTA			II	
0.1242365	cg16999994	cg16999994	30712357	TTTTTCAATTCTTTATATTCAT			II	
-0.140238	cg17007628	cg17007628	30775418	AACTTCCRAAAATTTAATAAA			II	
0.10131	cg17009813	cg17009813	36691300	ACRAAAACTAAAATTCCCAAC			II	
0.1802241	cg17013691	cg17013691	14613376	AACAAA	11784376	AACAAA	I	T
	cg17015844	cg17015844	73809492	AACCRAACCCCTCAAAACCAA			II	
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0.4738392	cg17025908	cg17025908	31682354	CTAATACCTAACACTCRATTTA			II	
0.1167865	cg17032848	cg17032848	47601482	TTTAAATATACRTTTACTATCT			II	
-0.118766	cg17033622	cg17033622	20651472	TTTACTAAAATACCCAAACCC			II	
0.1006681	cg17033891	cg17033891	55690443	AATTCAATTCAACCTTACRCA			II	
0.2194172	cg17044529	cg17044529	12616427	CTAAAATCTCTAAAACATATT			II	
0.1059249	cg17047033	cg17047033	32799388	TTACRACTTATATATCCCAATT			II	
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-0.135167	cg17050806	cg17050806	11688438	AATCCTAACCCTATATAATAT			II	
0.1108918	cg17051124	cg17051124	15719372	TTCRTATTAACCTAAAAACAA			II	
-0.111368	cg17055585	cg17055585	19643331	ATCCTAA	56656336	GTCCTAA	I	A
0.1379762	cg17056132	cg17056132	14802443	ATCTCATTTCATTCATCTATAA			II	

0.1273254	cg17058383	cg17058383	70617305	TAATTCTTAAAAAATCAACTC			II	
-0.198775	cg17059388	cg17059388	18662368	AAATCTACACAATACATAATA			II	
0.1114122	cg17066275	cg17066275	12657472	TATCTTAATATTAATAAAACR			II	
-0.108617	cg17070988	cg17070988	27606354	AATTCAC	71630392	AATTCAC	I	C
0.189421	cg17074339	cg17074339	11762494	CTACTCCCAAAACCTAAAAT			II	
0.1391307	cg17080138	cg17080138	25603418	TCCTTTAACTAAAACAACCTC			II	
-0.156146	cg17082366	cg17082366	43632386	CAAACAC	55654463	CGAACAC	I	A
0.1032604	cg17084358	cg17084358	58779333	CACTAAATTCATTCTTACATTT			II	
-0.10232	cg17093485	cg17093485	22676510	ACCTCTT	32753378	ACCTCTT	I	A
0.1501019	cg17096289	cg17096289	33628390	TCAAAAA	46699443	TCAAAAA	I	T
0.1182752	cg17097293	cg17097293	30690393	ATAAAAATAAAAACCRACRAC			II	
-0.154438	cg17098979	cg17098979	46633412	TTAAACAAACTTACTACAAAA			II	
0.1102264	cg17100047	cg17100047	14740471	TAAACTTAACAAAACRCTAAA			II	
0.131082	cg17112812	cg17112812	23659497	ATCACTC	64687370	ATCACTC	I	T
-0.176694	cg17125742	cg17125742	58737438	TTACCAA	50649421	TTACCAA	I	A
0.2201142	cg17126924	cg17126924	44698367	CTCTTTCTAAATATTCCRATTA			II	
0.1058873	cg17133045	cg17133045	54744446	AACACAATAATTATACCATAT			II	
-0.123131	cg17137077	cg17137077	52762384	AAAACTC	70634493	AAAACTC	I	A
0.1012809	cg17143179	cg17143179	61729372	AACTCAAAACACTAAAAATCA			II	
-0.102686	cg17149911	cg17149911	20707449	AAAATTATAAATCTCTCCTTTT			II	
0.1220544	cg17151123	cg17151123	21770331	TCTCAAACCTCACATAATTAA			II	
-0.123265	cg17152375	cg17152375	49763499	CTACATC	74665311	CTACGTC	I	A
-0.204167	cg17155524	cg17155524	21615390	AAACRAAATAAACCRAAACTA			II	
0.10598	cg17162031	cg17162031	50706343	ATAAAAAATTAAACCATTCRA			II	
0.3019905	cg17162911	cg17162911	45807323	CCCTTTACTTCCTATTACTTT			II	
0.1073971	cg17164093	cg17164093	55707310	AAAATTATAAACACAACCTCC			II	
0.1130946	cg17164345	cg17164345	60691426	TCATCAATAAAACATAATAAC			II	
0.2250962	cg17165241	cg17165241	69692400	CCACATC	23810364	CCGCGTC	I	T
0.1527894	cg17166262	cg17166262	67633425	TTATTTACTTCRAACAACTCAA			II	
0.1375283	cg17167832	cg17167832	40617361	AATACCCATTTTCCAATAATTA			II	
-0.108043	cg17168875	cg17168875	13743444	ATAAACCATAAATACCATCCA			II	
0.1061571	cg17178175	cg17178175	69748353	CCATCTCAACCAAAATAAAAA			II	
-0.120377	cg17178900	cg17178900	24757439	ATACATA	18682492	ATACGTA	I	A
0.1672069	cg17180633	cg17180633	60646378	RAAAATAATAACTCAAAAAAA			II	
0.1091811	cg17181941	cg17181941	40626314	TATCACAAATAACCACAAACC			II	
0.1197638	cg17186103	cg17186103	43674488	AACATTTTCACTCAAAAAAAT			II	
-0.193682	cg17187785	cg17187785	26692361	CCTCCRTCTCCACAATATAACC			II	
-0.116786	cg17193417	cg17193417	51661351	TAACAAACCCCACCCTCCTCC			II	
0.1734882	cg17196051	cg17196051	58774337	ACCRATACATAAATAATTATT			II	
-0.19195	cg17196155	cg17196155	24754456	AAAAAAATACTATTAATTCCC			II	
0.1073738	cg17198051	cg17198051	69694432	AACCAAATATATATAACRAAA			II	
-0.11396	cg17205386	cg17205386	53759508	TCCACCCCCAACCAAAACTAA			II	
0.1006501	cg17207064	cg17207064	36718408	AATCATACAACTAAAAACTAC			II	

-0.123267	cg17207724	cg17207724	38676425	AAAAATA	64765509	AAAAATA	I	A
0.2298062	cg17209769	cg17209769	57677340	AAACTAACAAAACAAAATATC			II	
-0.112488	cg17214408	cg17214408	74666430	TAAAAAA	66699412	TAAAAAA	I	A
0.1075129	cg17216092	cg17216092	34794502	ACATAAAAAATTCCTATAACT			II	
0.1029227	cg17220055	cg17220055	70646350	AAACTAACAAAAAAAATTCAT			II	
-0.227171	cg17220237	cg17220237	73774471	AATCATCACRTTTTAAAACTCC			II	
-0.106441	cg17221315	cg17221315	42636396	CRCTTTATAAAACCTCTAACCT			II	
-0.115848	cg17225604	cg17225604	66787301	ATCTCTATATAACTAATACRAA			II	
0.102698	cg17240198	cg17240198	28741440	AACTCAACCCATTAAAAACCA			II	
-0.127634	cg17242351	cg17242351	34734432	AAATCCC	65731463	AAATCCC	I	A
0.1277869	cg17246929	cg17246929	28738380	AAAATCATACCAAAATACTCR			II	
0.197942	cg17248267	cg17248267	55762375	CRCCCAACCAAATAAAACTTT			II	
-0.118076	cg17250082	cg17250082	47751472	AACAACAACATCTACAAATAC			II	
0.1374457	cg17251423	cg17251423	57779473	CCAAACC	33693464	CCAAACC	I	C
0.1073603	cg17253407	cg17253407	26789304	CTACAACAAAAACCCTTAACC			II	
0.163192	cg17253981	cg17253981	39748337	TTAAAACATCRAAACTAAAAA			II	
0.1212957	cg17257516	cg17257516	45621509	CTCTAACACAAACCAATAACA			II	
0.1417145	cg17272838	cg17272838	49706393	AAAACAACCTCCCAAAATTCC			II	
0.1363982	cg17273096	cg17273096	39645372	AACCTAAAAAAACAAATTTAT			II	
0.1329828	cg17273683	cg17273683	24688344	TACAAAACCCATTATTAAATA			II	
-0.116315	cg17276853	cg17276853	64668397	CAACAAC	18768374	CAACGAC	I	A
-0.164343	cg17277199	cg17277199	44648340	TTTCCCA	74611303	TTTCCCG	I	C
-0.190402	cg17292337	cg17292337	34808478	CCCACCTCTAACTCTTAAAACT			II	
0.2197661	cg17294865	cg17294865	18639475	CAAACAACCCTAATACCAACC			II	
0.1190613	cg17295834	cg17295834	62803373	TTCCTTATTTCATTTATAAATA			II	
-0.194622	cg17302580	cg17302580	33720308	TAAAAACCTACTCTATACTCAA			II	
0.1150652	cg17312546	cg17312546	69604352	TCCTAATACCCTTAAAAAATA			II	
0.111391	cg17316073	cg17316073	55632466	ATCCTCTAAATTCAAAAAACA			II	
0.133077	cg17330048	cg17330048	48702307	AACTAATTAAAAATAACCAAC			II	
-0.138088	cg17330251	cg17330251	61784461	AAATAAAACTTTTAACTAAAA			II	
-0.183363	cg17331757	cg17331757	28761395	TACCTTTCTAAACCAAACCAAT			II	
0.1135171	cg17333767	cg17333767	61796381	AATCRCCATTTAAAATAAACR			II	
0.1069854	cg17333973	cg17333973	60796449	ATCATTCACACTTCAATATAAA			II	
0.1240088	cg17334266	cg17334266	64752491	AAACTAC	65758332	AAACTAC	I	A
0.122942	cg17335001	cg17335001	70662462	AAAAAAAAACAAAAACAAACTT			II	
0.1070034	cg17341345	cg17341345	52784434	ATCCTCTCCCTCTATTTTCATC			II	
0.2021699	cg17343184	cg17343184	62626346	CACAAAAATAACACAAAAACT			II	
0.1278659	cg17344932	cg17344932	37756330	ATATCAA	38659340	ATATCAA	I	A
-0.120085	cg17345036	cg17345036	50705397	AAAAAAA	55735450	AAAAAAA	I	C
0.1544649	cg17345450	cg17345450	35667417	AAAAATCCTCCCAAATAACAA			II	
-0.108032	cg17347178	cg17347178	65677341	CAAAAAAACTAACACAAAATA			II	
-0.255796	cg17348244	cg17348244	34619474	CTAACCTAACTACAACACCTA			II	
-0.207964	cg17351927	cg17351927	69628380	AAAAACCTCAAAATACAAATA			II	

-0.183388	cg1735587	cg1735587	32770399	TATACAACCRCTATAAATACA			II	
-0.122855	cg1736055	cg1736055	40713497	ATAACRCTACCAAAACTAACT			II	
0.1642425	cg1736781	cg1736781	44703447	AAACAAAATTTAACATAACA			II	
0.2170005	cg1736969	cg1736969	59740473	AAAACTAAAAAAACCACAAA			II	
0.2577129	cg1737061	cg1737061	38638395	ACATCTCTAACAATTTCTACA			II	
0.1294042	cg1738230	cg1738230	34648306	AATTCCACATAAAAAACCTAA			II	
0.1176763	cg1738412	cg1738412	14738462	ATCTACCTATTTAAACCAATA			II	
0.1129804	cg1738476	cg1738476	12738359	AATTTTCTTTATAAACTCRTCT			II	
-0.102915	cg1738570	cg1738570	72697330	AATATAACCRAAACCTATAAA			II	
0.2688403	cg1738624	cg1738624	56635354	TAAATTTAATAAATATTTCTTC			II	
0.1374567	cg1738647	cg1738647	58756404	ATAAAAAATAAATTCAAAAAA			II	
-0.461671	cg1738877	cg1738877	42751448	TAATAAAATTCACRTTAAATA			II	
0.1790711	cg1738981	cg1738981	70801395	TTCTCTCTAATTCATATCCTAA			II	
0.2848505	cg1739314	cg1739314	44749493	AACCTAAAACAAAAACCCTTC			II	
0.1082622	cg1739555	cg1739555	13802506	CTCCAAAAACATACTAAACTC			II	
-0.117889	cg1739928	cg1739928	60611360	TAAAAAC	63726326	TAAAAAC	I	A
0.7159346	cg1740444	cg1740444	64711377	CAACTATATTATAAATTCAAA			II	
-0.101443	cg1741308	cg1741308	33798377	AAAATTAATATATAATAAATC			II	
0.1192034	cg1741532	cg1741532	57742313	TACCRTATAAACTAAAATAAC			II	
-0.101641	cg17415381	cg17415381	38694432	ATAATCATAAACCTAATCTTC			II	
0.4214469	cg1742104	cg1742104	62610408	ATTAATAATTATCCAATTAAA			II	
-0.110457	cg1742254	cg1742254	50708387	TTTACTA	40618459	TTTACTA	I	A
0.1825851	cg1742291	cg1742291	54728465	TCATACTCCCACTATACTCTTA			II	
0.1261456	cg1742506	cg1742506	40649492	AAAAACRTCAAATAACATACA			II	
0.1117373	cg1742692	cg1742692	46713318	TTCCAAACACAAAATTCTAAA			II	
0.1278358	cg1744219	cg1744219	63790401	CAACTTTTAAAATCTTCACTAA			II	
-0.129264	cg1744335	cg1744335	60715486	CTAACTA	13669344	CTAACTA	I	A
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-0.101947	cg1744995	cg1744995	31684386	AAACAA	22617405	AAACAA	I	A
-0.125351	cg1745902	cg1745902	60658314	CCACAAA	48644424	CCACGAA	I	A
-0.182564	cg1746036	cg1746036	56761388	TATACCTCATTTACACTAATCA			II	
0.1075377	cg1746845	cg1746845	66656324	AAACATTACTCTATCTACCAA			II	
0.1690773	cg1747371	cg1747371	49701335	CTTAAATCACTTAAACCAACT			II	
-0.103002	cg1747478	cg1747478	19620473	AATAAACTACTATAATAAAAA			II	
-0.164304	cg1747479	cg1747479	58636369	ACTTCCRAATAACTAACAAAA			II	
0.200087	cg1747757	cg1747757	42763346	CTAAACCTAAACTTCATAAAC			II	
0.1641881	cg1748211	cg1748211	46717450	TAAAATT	40620377	TAAAATT	I	A
0.1062292	cg1748242	cg1748242	16662422	CCTTATCACCAAAATACAAAA			II	
0.1062172	cg1749019	cg1749019	35727500	CRATCAACCAATTTCCCCRAA			II	
0.1341359	cg1749130	cg1749130	54757498	TAACTTATAAAATAAATTCTA			II	
0.1174001	cg17504791	cg17504791	21760487	CAAAATTTATAAACTCAATAA			II	
-0.124868	cg1751548	cg1751548	22677494	CRAAAAACCTAACCTCTAAAA			II	
0.1050131	cg1751624	cg1751624	55616388	TTTAATTAACAATTCACATTTC			II	

0.1099072	cg17516997	cg17516997	20670464	ATCTACATTAAATAAAATTTA			II	
0.1048957	cg17519156	cg17519156	13806418	CACCATAATTTTATTACCTTAT			II	
-0.174568	cg17529386	cg17529386	53793338	AATAAAA	59806471	GATAAAA	I	C
-0.240002	cg17536720	cg17536720	30749407	CTCACCCCCATACCCATAACCA			II	
0.1868199	cg17537073	cg17537073	60713348	AATACAT	12623339	AATACGT	I	A
-0.140435	cg17543884	cg17543884	29697321	AAAAACC	47758315	AAAAACC	I	C
-0.124531	cg17544364	cg17544364	58678487	AAAATTATTTACCCCAAAACA			II	
0.1073387	cg17544584	cg17544584	61713469	CTTCCTACTAAAAAAATATTAA			II	
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-0.10435	cg17553149	cg17553149	50636422	AAAAAAC	40688384	AAAAAAC	I	A
0.1029873	cg17564498	cg17564498	73792452	TTTATAAATAACAAAATCCCA			II	
-0.124893	cg17566592	cg17566592	13668422	AAAATAACTAAACTACRAACA			II	
0.115022	cg17569842	cg17569842	47650435	TCACRAAATACAAATAACACT			II	
0.1367352	cg17581485	cg17581485	31794477	TATTTAAACCTCTTCTAACTTA			II	
0.1716151	cg17583957	cg17583957	61737317	CATTTACATTATTTCCTAAAAT			II	
0.101143	cg17586885	cg17586885	24687467	CACACAA	20660370	CACGCAA	I	A
0.2491621	cg17588704	cg17588704	11801433	CACAAAACCTAAACTAACAAA			II	
0.1166216	cg17588812	cg17588812	33720486	ACTACCA	49762315	ACTACCA	I	C
0.1463037	cg17590135	cg17590135	46682420	ATAACAA	64784322	ATAACAA	I	C
0.1290119	cg17593342	cg17593342	63762391	TAATAAAAAATTCAAATTAAA			II	
-0.115893	cg17597639	cg17597639	32787408	AACRAACCCTATTCCRAAAAA			II	
0.1272133	cg17601785	cg17601785	24640334	CACCTCACAAAAAAACCCTTA			II	
-0.100629	cg17611045	cg17611045	51783342	TTCAACA	12662447	TTCAACG	I	A
-0.197176	cg17611936	cg17611936	70725376	ACCTAAA	53803433	ACCTAAA	I	C
0.1326859	cg17613924	cg17613924	44667300	ACTTACT	21715415	ACTTACT	I	T
-0.13059	cg17619311	cg17619311	62762491	TTACTCT	33638303	TTACTCT	I	C
-0.269891	cg17626671	cg17626671	19642505	TACAATCTATCCTTACCCCTCT			II	
0.1304278	cg17631184	cg17631184	49774438	CTACTAAATAAAAACTCRCAA			II	
0.1180954	cg17633431	cg17633431	60767302	TTAACCAACTAAAAAAACAAT			II	
-0.10286	cg17639056	cg17639056	60754322	CAAAAAA	27808404	CGAAAAA	I	C
0.1097761	cg17643624	cg17643624	10698454	AAATAACAAAAAATTCTACTA			II	
-0.118511	cg17646499	cg17646499	21603415	AAAATACTTTATTTAAAAACA			II	
-0.148848	cg17655970	cg17655970	38694502	AAAAAAA	26658331	AAAAAAA	I	T
-0.179955	cg17658874	cg17658874	38622405	ATACAAATACATTTCTACCCA			II	
-0.187589	cg17662493	cg17662493	73732393	CACATCCCTTCCCCTATATCCA			II	
0.1207178	cg17687367	cg17687367	46774480	ATTAATTCTTAATAAATAACT			II	
0.1204482	cg17694130	cg17694130	11600347	CACTATT	35689408	CACTATT	I	T
0.1171219	cg17695537	cg17695537	62691303	ATACTTTCTATTAACTACTACC			II	
0.123436	cg17706972	cg17706972	40715497	CCCTAAAATACCAAAACATTT			II	
0.1380851	cg17707274	cg17707274	29773376	TTAATATTTTCTACTAATAACT			II	
0.3474425	cg17707870	cg17707870	43670432	CATTCCACACATTTCTAATTCC			II	
-0.191892	cg17711541	cg17711541	57621337	TAACAATTTATTAAACTCCTCR			II	
-0.144021	cg17713488	cg17713488	29754432	ACCTACA	57727428	ACCTACA	I	A

-0.205696	cg1771486	cg1771486	39643303	CTCTATC	48785319	CTCTATC	I	A
-0.124512	cg1771610	cg1771610	15612475	TATTTTA	40706329	TATTTTA	I	C
0.1715669	cg1772320	cg1772320	20761434	ATCTTATTCATCCCCTCTTCTA			II	
0.2935002	cg1773197	cg1773197	50780340	ATATAAC	11685308	ATATAAC	I	A
-0.151277	cg1773559	cg1773559	61740315	ATCTTATTTCTTTATATATTTC			II	
0.2140073	cg1773777	cg1773777	29669336	TATACCC	50711333	TATACCC	I	C
0.1029518	cg1773852	cg1773852	64607510	TTAAAACTCCTAACAATATTC			II	
-0.179426	cg1773861	cg1773861	33678338	AAAAAATTCTTACTAAAAAAA			II	
-0.10513	cg1774144	cg1774144	15746504	RAAACTTTTATTATACTTCCT			II	
0.1907637	cg1774487	cg1774487	51762459	CTTATCAAAAACTAACAAAAC			II	
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-0.113389	cg1775447	cg1775447	12657385	TACCTAC	72717470	TACCTAC	I	A
0.1365459	cg1775548	cg1775548	73631423	TACCAAATTATCAAACACCTA			II	
-0.313765	cg1775925	cg1775925	33732332	CATTAAA	49729500	CGTTAAA	I	T
0.115703	cg1775959	cg1775959	69703437	ATTTCTTTCTAATTAACCACRT			II	
0.1103988	cg1776126	cg1776126	70764415	ATCTTACAACTATTTAAATATA			II	
0.116604	cg1776356	cg1776356	44796313	CTCAAACATATACTAAATCAT			II	
0.1053252	cg1776483	cg1776483	29623345	CTTTCAAAATATCTTAATTTTC			II	
0.1095819	cg1776499	cg1776499	38698498	AACAAAACTAAAACTTCAACA			II	
-0.127015	cg1777657	cg1777657	30768498	CTAATAA	42792354	CTAATAA	I	A
-0.10074	cg1778044	cg1778044	41752359	ACCTACRACCTTAACAATAAA			II	
0.1083285	cg1778369	cg1778369	24653317	ACTTTACATCTAACTATTAATA			II	
-0.125004	cg1778525	cg1778525	31652419	AAAACAC	60723394	AAAACG	I	T
-0.106316	cg1779481	cg1779481	58733440	AACAAA	39617452	AACGAA	I	C
0.1237014	cg1779794	cg1779794	54673319	ACCRAAATTACTCCTCCACCC			II	
-0.346846	cg1780326	cg1780326	12663410	TAACACTAAACATCATCACRT			II	
-0.17923	cg1780411	cg1780411	71690317	CACTCAA	21626456	CGCTCAA	I	A
0.100799	cg1780818	cg1780818	22641331	ATAAAACTATAAAATTTATTC			II	
-0.204879	cg1781243	cg1781243	20662375	TTAACATTAAAAAATCACACC			II	
0.1294457	cg1781251	cg1781251	38646365	CATACRCATCTCTACCTTCTTC			II	
0.1763644	cg1781617	cg1781617	21802414	CCCAAAATCRATAACTACTAT			II	
-0.157809	cg1781752	cg1781752	74747366	AACTTAAATAAAACRCRTAAC			II	
-0.19515	cg1782006	cg1782006	39603403	TACCCCCACAAAAACATCRAT			II	
-0.135353	cg1782294	cg1782294	64808470	TACTAAC	10634487	TACTAAC	I	C
0.1125023	cg1782689	cg1782689	42747303	ACAATTACATTTACCACTAAT			II	
-0.125296	cg1783117	cg1783117	69692402	ATACTACCTCATTCTCTATTCC			II	
-0.145887	cg1783303	cg1783303	49649482	TTTCCTTAACCCAATAACACCT			II	
0.284	cg1783716	cg1783716	69810325	TATAAAT	71724461	TATAAAT	I	T
-0.172409	cg1783816	cg1783816	10653390	CAAACATCCCTAAAATCAAAC			II	
0.1739466	cg1783836	cg1783836	66669365	AAATTAAAAAAATAATCAAAA			II	
-0.151161	cg1783975	cg1783975	70682329	ATTATTACCTCAACATCTTCCT			II	
0.1208454	cg1784004	cg1784004	58761423	TTTACAAATATACTCAACAAC			II	
0.2335583	cg1784025	cg1784025	18672453	CTCTAACTTAAAATTAACCCTA			II	

0.1037852	cg17840997	cg17840997	52603312	ACRACTAAAATAAATTTTTCC			II	
-0.193425	cg17843418	cg17843418	42727506	TATCCAA	33790411	TATCCGA	I	C
-0.101041	cg17845680	cg17845680	70783337	CTTAATATCACTACTTAATAA			II	
-0.107316	cg17848407	cg17848407	51725388	RAACTCCCAAATATAATTACA			II	
-0.256878	cg17851276	cg17851276	36699438	AATCCACAAAACCAAAAAAAC			II	
0.1027952	cg17852326	cg17852326	64767390	CTACAATTAAATATATCAATA			II	
0.1536143	cg17855222	cg17855222	58603355	TAACAATATTTTCCTAATTCTT			II	
0.1179899	cg17862558	cg17862558	38697493	AACATATCTCTTCAAAAATAT			II	
0.1033866	cg17862903	cg17862903	23774440	ATAATACCAAACRAAATCAAT			II	
0.1307446	cg17867776	cg17867776	40605438	RCTTCCCRATAAAAACAAACT			II	
-0.192245	cg17871621	cg17871621	35794392	CTTAACCCCRAAACRCAACTA			II	
0.127314	cg17874109	cg17874109	52697443	TAAAACAAAAATTAAAATTCA			II	
0.2022412	cg17876294	cg17876294	40769337	TAATAACCAAAACRCTCTTCT			II	
0.1382723	cg17878501	cg17878501	26600357	TCAATACCATTACAACAAACA			II	
-0.109898	cg17880703	cg17880703	48690350	RCAACTAAAAAATACAAATAC			II	
0.1055588	cg17883068	cg17883068	67673459	ATAAATCAAAAACCAAACTAA			II	
0.1061789	cg17884766	cg17884766	31729411	AAAACTAAAAACTATAATCAT			II	
0.1032433	cg17885794	cg17885794	61754331	CCAATCACTAAAAAACAATCC			II	
0.1768849	cg17894362	cg17894362	65804408	CACAACAACCCTAACAAAACT			II	
0.1746683	cg17894577	cg17894577	64615429	CTTTCTTTTTACAACCTACTAC			II	
	cg17901463	cg17901463	13609457	TATCCCAATACCCCAATATCA			II	
0.1439167	cg17903506	cg17903506	46677482	AAACATAACTATTACATCCTC			II	
-0.15835	cg17906851	cg17906851	16669375	CCTAAAA	68732485	CCTAAAA	I	A
-0.132268	cg17911021	cg17911021	73700473	TTTCTAAATCTAAAAAAAAAC			II	
-0.197236	cg17913405	cg17913405	68658442	AAAAACA	51785358	AAAAACC	I	C
-0.115184	cg17915676	cg17915676	23747310	CCTTCCA	16603441	CCTTCCA	I	C
0.1471486	cg17922998	cg17922998	31729313	ACRAACCATCCAAACCAAAAT			II	
-0.113782	cg17929042	cg17929042	61732494	AAAATAC	61785438	AAAATAC	I	A
-0.384419	cg17929630	cg17929630	42778478	CATTTTC	24628430	CATTTTC	I	T
-0.107324	cg17932096	cg17932096	54680411	TAAAAAA	71634319	TAAAAAA	I	C
0.1426922	cg17934277	cg17934277	43775397	ATTTAATAATATCCCTATCCTT			II	
0.2281895	cg17943323	cg17943323	10725345	AATATCT	74710311	AATATCT	I	A
-0.121964	cg17951978	cg17951978	54721318	CCATCAAAAATTACRCTTTTCT			II	
0.1056198	cg17958516	cg17958516	26612425	ACAAAACCAACTACTTCCAAC			II	
-0.118963	cg17962638	cg17962638	57691346	TAACAAC	48753432	TAACAAC	I	C
-0.20511	cg17967673	cg17967673	42652479	CACCACA	47683506	CACCACG	I	A
0.1058573	cg17972013	cg17972013	55801377	CCAACCAATAATAAAATATAA			II	
0.1450306	cg17976473	cg17976473	18628445	TATAAAACCCAAAAAACTATA			II	
0.1107633	cg17991919	cg17991919	48806380	ATCACATAACATATAATAACR			II	
-0.228886	cg18001722	cg18001722	11803395	TTTTACRCACRAAAACTTTATT			II	
0.2323685	cg18013856	cg18013856	14741457	AAACCATAAAACTAAAATCRC			II	
-0.134231	cg18015035	cg18015035	55684336	AAAAACT	53622345	AAAAACT	I	A
0.2583807	cg18015625	cg18015625	51612387	AAACAAAAACATTTAATTCAT			II	

0.3126044	cg18021992	cg18021992	22634366	AACCTCATTATTCTTCAATAAT			II	
0.1125967	cg18025438	cg18025438	39724429	AAAAACC	53600384	AAAAACC	I	A
0.127504	cg18027903	cg18027903	64659303	TCTATACTTATTCTTAATCCTTA			II	
-0.26741	cg18029321	cg18029321	14773369	CACCTAA	15627427	CGCCTAA	I	T
-0.369439	cg18049365	cg18049365	20749317	CTTTCAAAAACTCTAAAATCAA			II	
-0.230151	cg18058072	cg18058072	19698435	CTCATTCATTTCATACTTTTTCT			II	
0.1021158	cg18065195	cg18065195	56632432	ACCRCTACTAACAACTAAACRA			II	
-0.15862	cg18065318	cg18065318	57722402	AATAATA	28716370	AATAATA	I	A
0.1752836	cg18066181	cg18066181	15764473	CTAATTAAATCAAAAACCCAAT			II	
0.1314448	cg18066206	cg18066206	40766387	AAAACTAAAAAAATTCTCRTTC			II	
0.1234475	cg18073702	cg18073702	10662424	CAACCAATAATATTAAATAAC			II	
0.1103124	cg18075691	cg18075691	44667386	TAAAAAC	40687509	TAAAAAC	I	A
-0.1171	cg18077580	cg18077580	65638428	ACAATCT	55721395	ACGATCT	I	A
0.1019554	cg18085660	cg18085660	18797349	ATATTATAAACTACATACRCTT			II	
-0.135857	cg18087477	cg18087477	46682331	RAAAACCATTAATTCTTTCTAT			II	
0.1058723	cg18087694	cg18087694	61657497	CTAATCCCTCACATCTTTTAAT			II	
0.1325563	cg18088906	cg18088906	67808397	TAATTTAAATATCACTTCTAAT			II	
0.1146267	cg18089380	cg18089380	35673462	ACTAAAAAATATACTATCACCA			II	
0.1660911	cg18089426	cg18089426	46749487	AACCTAC	21664493	AACCTAC	I	C
0.1980699	cg18093448	cg18093448	50789402	AACTAATACAATTTATTATACT			II	
0.1596284	cg18096251	cg18096251	15772317	AACACCA	31766326	AACGCCC	I	C
0.1004345	cg18098433	cg18098433	46705300	TAATAATATAACAACCRTCTTT			II	
-0.22747	cg18098534	cg18098534	45759375	AACCAAATTAATAATACTAAAT			II	
-0.185104	cg18101138	cg18101138	56696302	AAAACAA	33732501	AAAACAA	I	C
0.1557791	cg18101140	cg18101140	73696454	ACRAAACAACRAACCAATTTC			II	
0.1009825	cg18102738	cg18102738	16785412	TACTAAAACTACATCTCCAAAT			II	
0.1584307	cg18104070	cg18104070	74644413	CACCCATAATATACACATTTTT			II	
0.1092128	cg18109485	cg18109485	23629378	ATTTCTCRAATAACTAACAAAA			II	
0.1971397	cg18111114	cg18111114	51629438	TCAACTATAAAACATAAAATA			II	
0.1002852	cg18113731	cg18113731	67743477	AAATAATCCTAAACAAACCTCT			II	
0.1313249	cg18116815	cg18116815	20656325	CACTATTTAACCTATTTCAATC			II	
0.142206	cg18120259	cg18120259	60660316	AAAACATAATACAACCTACTA			II	
-0.140565	cg18127410	cg18127410	18628506	AAAAAAA	30793406	AAAAAAA	I	A
-0.148696	cg18128914	cg18128914	41774408	ACAAAAA	31634314	ACAAAAA	I	A
0.1679237	cg18129296	cg18129296	52643353	AACATTTCAAAACTTAAACTCT			II	
-0.11002	cg18129748	cg18129748	64665323	ATAAAAA	27793432	ATAAAAA	I	A
0.1102698	cg18129996	cg18129996	27733307	ATTTCAAAAATCTAACCATCCA			II	
0.105994	cg18132363	cg18132363	59669394	TTCAAAAAACRACAAAAAACT			II	
0.3001747	cg18137779	cg18137779	16712471	TCACAATAACCACTTTAATAAA			II	
-0.103404	cg18138788	cg18138788	67667410	CRACAACTAAAAAAAATTACT			II	
0.1010239	cg18142730	cg18142730	17650424	ATCACTACTTTATTTAATTACA			II	
-0.134865	cg18146506	cg18146506	31784507	CCAAAAA	35749469	CCGAAAA	I	A
0.1066548	cg18167946	cg18167946	49786505	AATAATAACCTCATCTCCCTAT			II	

-0.169742	cg18168924	cg18168924	65652445	AACATCTTATCCATAAAAATA			II	
0.137552	cg18170545	cg18170545	51703355	CTAATACCAAATATATAATAT			II	
0.2081508	cg18172516	cg18172516	47666425	ACAATCAATAACTCAACATTT			II	
0.2254567	cg18178836	cg18178836	62753314	TAATAAACACTCCCCCAAAAC			II	
-0.105449	cg18182148	cg18182148	65806464	TTTCCAA	14759469	TTTCCGA	I	A
0.1393242	cg18184218	cg18184218	39675302	ATTTTCA	60713458	ATTTTCG	I	T
-0.130776	cg18189112	cg18189112	24641487	AAACCACCACTTATAAAATTT			II	
0.1770639	cg18191743	cg18191743	39654422	CTACTCTATCACTATTAAACTA			II	
-0.118207	cg18197594	cg18197594	30777480	TTACCTT	22606501	TTACCTT	I	A
-0.103151	cg18206858	cg18206858	71800437	TCATCAAAACTCCAAATTCCC			II	
0.102721	cg18209359	cg18209359	39698449	CAACCTT	30614324	CAACCTT	I	C
0.1202112	cg18217622	cg18217622	63639332	AAATTTC	29753412	AAATTTC	I	C
0.1002821	cg18221341	cg18221341	44712443	CACAAATAATCCRCTCACTAA			II	
0.1273358	cg18229196	cg18229196	32720509	ACRTAATAACCTCTATAATAT			II	
-0.385677	cg18232235	cg18232235	37622316	ACCCAAA	19617432	ACCCAAA	I	C
0.1326065	cg18235746	cg18235746	74796359	TAAACCTACTCATAAAAATAT			II	
-0.12774	cg18236584	cg18236584	56748399	TAAAAATTTAACCCRAACAAA			II	
	cg18237398	cg18237398	54606493	AAAACCAAAACAAAAAAACC			II	
0.1007781	cg18237739	cg18237739	59617323	CCATTCCTAAAACTCCTAATTA			II	
-0.261718	cg18239511	cg18239511	31669324	CCCCAACCATAATCATAACAC			II	
-0.108923	cg18240390	cg18240390	34758345	ACTAAAA	20710362	ACTAAAA	I	C
0.1074727	cg18241555	cg18241555	36766333	AAAACAACAAAAACTAAAAA			II	
0.1149931	cg18243846	cg18243846	59632301	AAATCACTTCRAAATCATTTC			II	
0.1031601	cg18256949	cg18256949	70761332	CTAATCC	18774336	CTAATCC	I	A
0.108896	cg18263166	cg18263166	32613407	CTAAATCAACATACAACCACA			II	
0.1132903	cg18264092	cg18264092	51614455	AATAACTCAAAATAATTCTAT			II	
0.1776353	cg18285337	cg18285337	62704331	TACCAACTACRCAAAACCAAA			II	
0.1095606	cg18285636	cg18285636	42663455	AATAAAAACTCTATAAAAATA			II	
-0.147138	cg18288532	cg18288532	12763351	ATAATAC	24637492	ATAATAC	I	A
0.1206571	cg18302460	cg18302460	63637364	AAACCCCTCTATAACTAAAAA			II	
0.1052384	cg18310639	cg18310639	22750426	TATTCATTCTAACTCAAATTAT			II	
0.1210127	cg18313094	cg18313094	20750478	RAAACATCATAATCACTATCA			II	
0.117412	cg18313416	cg18313416	56641438	AAAAATCAAATCTTTTTTTCCC			II	
0.1184685	cg18319366	cg18319366	59609370	TTAACTCAAATTTCTCACTACR			II	
0.129956	cg18321929	cg18321929	38679509	ATAAACAATATAAAATTCCTA			II	
-0.110356	cg18322025	cg18322025	73790449	TAACAAAAATCTTCCCAAATA			II	
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-0.157782	cg18327128	cg18327128	43622441	ATCTTAA	72679507	ATCTTAA	I	A
0.1641619	cg18332814	cg18332814	24660360	CTTACAACTAATCTAACTCAA			II	
0.1491073	cg18332838	cg18332838	15750345	ATAAAATAAACAATTCTAAAA			II	
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0.2231824	cg18346634	cg18346634	25688486	AAAATCCRACTCCAAATTAAA			II	
0.2930605	cg18359218	cg18359218	63713492	AACTTCCTAAAACACTAAAAC			II	

0.1574388	cg18361425	cg18361425	38652398	AAACAATTAATCACCTAATAA			II	
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-0.108046	cg18383984	cg18383984	59712332	AAACAAA	62658412	AAACGAA	I	T
	cg18384097	cg18384097	54661343	TTAAAAACATCAAATCTATAA			II	
-0.184111	cg18391209	cg18391209	15607400	CCTAAATACTTAATACCAAAA			II	
0.1584497	cg18395354	cg18395354	50618432	ACACACTAAACCTAATATAAA			II	
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0.1351091	cg18397450	cg18397450	71715420	AAAACAA	39692388	AAAACAA	I	A
0.1265922	cg18400281	cg18400281	44685449	AAAACATTTATACRAAATCAAT			II	
-0.386823	cg18403673	cg18403673	35631307	AAACTAAAAACAACTCAACTA			II	
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-0.163195	cg18413218	cg18413218	62675325	AAATCTTTAAAACAATACCTTA			II	
-0.203665	cg18417245	cg18417245	30753390	ATTCCTTTCTTATAAACTTCTTA			II	
-0.11558	cg18417622	cg18417622	22740372	CRTAACTTAATACTACACRCTA			II	
0.119258	cg18418242	cg18418242	24632416	AACTAAATTCAATCTTACTAAA			II	
0.198792	cg18424635	cg18424635	21718331	TTAATAATAACCTTATACCAAA			II	
-0.138098	cg18431856	cg18431856	55604411	AATCCACRTCCTAAATAACATA			II	
0.1163236	cg18434356	cg18434356	72748422	ATAAATAATTTCCTAATTCRCT			II	
0.102613	cg18436272	cg18436272	17740354	AAAATAACTCTAACCTCATAA			II	
-0.12538	cg18437193	cg18437193	12788411	AACAAAT	58659490	AACGAAT	I	A
0.1348948	cg18437551	cg18437551	10800325	ATCRCCTAAATCAAATATAAAT			II	
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-0.189389	cg18444757	cg18444757	20699419	CRTATTTCCAACACAAAATTTA			II	
0.1230713	cg18446441	cg18446441	42799423	TCTATTCTCCTCCTACTCAAAT			II	
0.1377949	cg18456803	cg18456803	47788300	AATTTACATATTTAACCTAACA			II	
0.100613	cg18458353	cg18458353	22756322	CACAAAAAACAAAACAAACRT			II	
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0.1172266	cg18476566	cg18476566	30646465	AACAAATTTACAATAAAAACC			II	
0.111286	cg18480654	cg18480654	70607379	TAAAAAACAAACTATAAAAAA			II	
0.1148528	cg18486231	cg18486231	52645457	AAATACTTTCCTAACTATATAA			II	
0.1230933	cg18492943	cg18492943	17605353	TCAAAATTCTAAAACCTAATTA			II	
0.1581235	cg18497238	cg18497238	43603334	AACCTTTCCCTACTAAAATCTC			II	
0.1167981	cg18498115	cg18498115	74803328	CCAACCTAAATACTAATATACT			II	
-0.108598	cg18500448	cg18500448	18746310	AACATAA	21703329	AACGTAA	I	T
0.1322493	cg18502238	cg18502238	14718442	AAAAAAACACRTTACTTTCAT			II	
0.1390706	cg18503829	cg18503829	35600395	CACATAAAAAACACAAACCCA			II	
0.1276995	cg18504989	cg18504989	35754305	ACRAAAAACCAAAACAACTTC			II	
-0.112645	cg18509524	cg18509524	36778350	CCATAAAATACRCCCTTCTAAA			II	
0.1041792	cg18512930	cg18512930	43642477	RAAAAACTCCCRAAAAAATTCT			II	
-0.121647	cg18514705	cg18514705	18775345	CTCCAAAAACAATACTATATAT			II	
0.1095858	cg18526142	cg18526142	31777387	TCTATTTCATTAACCTATAAAA			II	

0.123915	cg18530748	cg18530748	27674480	CAATAACTACTAAAAACTAAC			II	
0.1993686	cg18538668	cg18538668	57613469	CATCCTCCTACCCTCTTTATTA			II	
0.1110601	cg18540674	cg18540674	47703489	TATAAAA	34638494	TATAAAA	I	T
0.1517766	cg18544888	cg18544888	56619423	ACTACATTACTAAAACCACCA			II	
0.1367189	cg18550212	cg18550212	47738353	AATAATATTACCTCTTCCTACC			II	
	cg18558968	cg18558968	24730370	TATAACA	62631352	TATAACA	I	A
-0.182236	cg18558969	cg18558969	32634441	TTATATTTCATTTATCTACATA			II	
-0.315104	cg18559901	cg18559901	33808339	ACCTCCTAACRAAACCCTAAA			II	
-0.176286	cg18561676	cg18561676	23642315	AAAAAAT	25610431	GAAAAAT	I	A
0.1179315	cg18566555	cg18566555	69619467	CTTCTACCAAATAATACCCCA			II	
0.1182747	cg18574144	cg18574144	41738380	AAAATCTCATAAAACTCAAAT			II	
-0.419786	cg18576044	cg18576044	68603321	RTAAACTCTACTTTTCTAATTC			II	
0.1205476	cg18578974	cg18578974	44742476	TAATTTACAAATATAAAAACC			II	
0.1211913	cg18586886	cg18586886	59686310	AAAAACA	25634375	AAAAACA	I	A
-0.102758	cg18587476	cg18587476	66713393	TTCCATT	16746438	TTCCGTT	I	A
0.1119716	cg18594054	cg18594054	42643354	TCTATACTTCTACAAAAATTTA			II	
0.1012937	cg18594701	cg18594701	16771328	ATCTCCCACACTAAACATATTT			II	
0.1022209	cg18595137	cg18595137	50743404	CAAATTTATACAAAATAATTC			II	
0.1120371	cg18595348	cg18595348	49600459	TTCAATTTTCCCATAAATCATA			II	
0.1605324	cg18596626	cg18596626	67608471	AAAAACC	56619403	AAAAACC	I	A
0.1184967	cg18596939	cg18596939	45791316	AAACCCAAAATACAAAATAAT			II	
0.1371964	cg18599206	cg18599206	22725391	AAACCAAATTCTCACACCATC			II	
0.111929	cg18609120	cg18609120	20639370	ATATTCTCTACAACTTAACCTC			II	
-0.109142	cg18612167	cg18612167	19683443	TACAAAAATTCTTACATCTAA			II	
-0.124897	cg18614735	cg18614735	72666418	TCAAACTAAAACTACTAAAAA			II	
0.1432321	cg18618815	cg18618815	72789442	TTCTTCTCAAAAATCCCCAAA			II	
0.287259	cg18621672	cg18621672	54794373	CCCTAACCCTAAAAACTACAC			II	
-0.101226	cg18621852	cg18621852	49649455	TCCTAAACAAAACATTCCAAT			II	
-0.123252	cg18625305	cg18625305	38786353	TAAAACATCCRAAAAACTTAA			II	
0.1420608	cg18628853	cg18628853	15752508	TACTATAAAAAAATAACAAAA			II	
-0.100158	cg18630644	cg18630644	30663428	AAAACAC	71604489	GAAACGC	I	T
-0.103641	cg18634211	cg18634211	65675489	ATTATCTTTTAAAATTTAAAAA			II	
-0.146431	cg18644703	cg18644703	24744359	ATATTAC	42742445	ATATTAC	I	A
0.1011642	cg18650219	cg18650219	26727330	CCTTCAAAATAAACAACTTAA			II	
0.1714313	cg18650367	cg18650367	44770510	TACAACATATATCTCCTTTAAA			II	
-0.139179	cg18667659	cg18667659	18600413	AAATTTC	47657432	AAATTTC	I	C
-0.12202	cg18668511	cg18668511	73803381	TACCCAAAACTCAATTAACAT			II	
0.1236123	cg18672030	cg18672030	61724489	TTCCAATTAATCACAAATTAA			II	
-0.10013	cg18676967	cg18676967	62800469	RAACACTCCATCAAAACCCCC			II	
-0.149826	cg18678645	cg18678645	30651474	RACCCRAATAAAAATATACRA			II	
-0.19206	cg18679504	cg18679504	24634453	ATCCCAC	45682460	ATCCCGC	I	A
0.1130465	cg18680181	cg18680181	55777484	TCCCTTAATCTCRTTAATTACT			II	
	cg18684755	cg18684755	48604510	AACAACATAACCAAATAACTT			II	

0.2581907	cg18698799	cg18698799	71781488	ACTAAATAAACTATTCCCAAA			II	
-0.323535	cg18699744	cg18699744	17610311	ATCAAAT	50803478	ATCAAAT	I	C
0.1004679	cg18707191	cg18707191	56623390	AAATCAATTACCAATAATTAC			II	
-0.110508	cg18709881	cg18709881	13716416	CACTACT	35614448	CACTACT	I	A
0.1010795	cg18709904	cg18709904	36760466	TACACATCCCRCTACACTAAA			II	
-0.165272	cg18710053	cg18710053	57759456	AATTAAA	30709321	AATTAAA	I	A
0.1138744	cg18710162	cg18710162	52787416	AACAAAATTACAACACAACAA			II	
0.1759358	cg18711535	cg18711535	17630435	CTTCTAAATCAAACTTCATTAC			II	
0.1867899	cg18715193	cg18715193	55607332	AAAACTTCCAAAATCCCCCAA			II	
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0.1067972	cg18720803	cg18720803	36780455	ACCCTAAATAATCAACAATAA			II	
-0.100907	cg18723276	cg18723276	24728328	AAATTAT	69768312	GAATTAT	I	C
0.1155358	cg18730865	cg18730865	44794322	AAACTACCCTATACTTTAACTC			II	
0.10712	cg18736835	cg18736835	62763467	TAAAAAAAACAATAAATATCA			II	
0.1566658	cg18748525	cg18748525	64734310	TATAAATCAATCTCACRTCCCC			II	
-0.163294	cg18755531	cg18755531	65673494	TACAATA	26705407	TACGATA	I	C
0.1009873	cg18756771	cg18756771	58784415	AATAAAAAACAATAAAACTAT			II	
0.145358	cg18756931	cg18756931	18673412	TACTCTCTATACCTAATCTACA			II	
-0.105717	cg18757172	cg18757172	21604380	ACAAACT	50633484	ACAAACT	I	A
-0.219723	cg18757817	cg18757817	46676349	TCCAATAAACATTATCTACCC			II	
0.1803087	cg18761958	cg18761958	59759492	ACAACCTATAACTACTCAACT			II	
0.1501355	cg18761976	cg18761976	13705477	AATCAAATAACTCACACTAAA			II	
-0.111995	cg18762806	cg18762806	18783464	CTCAACC	61769414	CTCGACC	I	A
0.1246113	cg18764164	cg18764164	54684365	ACCAACCCTAAAATATAACTC			II	
0.1054272	cg18764771	cg18764771	23773404	TTACTTTCRCCAAAAACTCTCC			II	
-0.140943	cg18765565	cg18765565	30701412	ATAAAAC	69737303	ATAAAAC	I	A
-0.183061	cg18770944	cg18770944	34736429	ACTAACTAAAAAACRCCTAAA			II	
-0.138546	cg18771553	cg18771553	30745384	AATACCAACCTATCCCCCCAA			II	
-0.106655	cg18771570	cg18771570	16795398	ATTTCRAAAACTTATAAACAC			II	
-0.196286	cg18771937	cg18771937	45603442	CCCAACAACATAAAACTACCT			II	
0.1217269	cg18773937	cg18773937	66607479	CATTTTACAAATATATCACCA			II	
0.1305732	cg18774170	cg18774170	15750484	TATTTAAAAATAAATCCCRTT			II	
0.2266313	cg18776460	cg18776460	59716352	TAACATAAACTCTAACTTACC			II	
0.1314995	cg18782604	cg18782604	33640410	ACTCTCT	69771399	ACTCTCT	I	A
0.1120118	cg18786224	cg18786224	15670369	AATCCRAACTCAAAATCCCAC			II	
0.1183402	cg18790340	cg18790340	21802416	CCCCAAATTTAATCTAAAAAA			II	
-0.528201	cg18792536	cg18792536	59607453	ATACCAC	37656490	ATACCAC	I	C
-0.112581	cg18797653	cg18797653	65706357	AATTCATAAACTACTTCRAAA			II	
-0.190787	cg18801505	cg18801505	29715318	CAACTAACAACAAACTACTCT			II	
0.2917731	cg18805164	cg18805164	51795502	CAAAAAA	49795427	CGAAAAA	I	A
0.1278639	cg18806716	cg18806716	34733372	CATTTCCCACRTATCAAACACC			II	
-0.1151	cg18808261	cg18808261	31775510	TTACAAAACRAAATCCTTTTCA			II	
-0.410905	cg18816122	cg18816122	40800307	ACTTTTA	60804314	ACTTTTA	I	C

0.116274	cg1881639	cg1881639	63781395	AAAAATCCTTACTCAAAATTA			II	
-0.101911	cg18822951	cg18822951	39802455	TACTAATAAACRCACACCATC			II	
0.5531551	cg1882826	cg1882826	45742508	CCACATAAACACAAAAAAACA			II	
-0.124472	cg1882836	cg1882836	68786375	CACTACTTAATAAAAAAACCA			II	
0.167147	cg1883224	cg1883224	32721320	CCTCATTTAACCRAAAACTAC			II	
-0.178863	cg1883261	cg1883261	64706315	AATAAATACACAAAAAATAAT			II	
0.1179463	cg1884235	cg1884235	62643339	CTTCCATCTACCTCTAAACAA			II	
-0.174288	cg1884325	cg1884325	23606377	CCAAAATCCRCCCCTACTCCT			II	
0.2723467	cg1884559	cg1884559	64729449	ATCTAAAATATACTCTTTAAA			II	
-0.2716	cg1884595	cg1884595	23655331	TCCAAAA	39745490	TCCGAAA	I	C
0.3927707	cg1884759	cg1884759	37742467	TAAATCAAAAACCCTCAACTA			II	
0.1978634	cg1886176	cg1886176	66694457	ATCCACTAAAAAAATAACCTA			II	
0.1067184	cg1886221	cg1886221	30730442	TTCCCACATACAAAATAAAAT			II	
0.1214975	cg1886412	cg1886412	54703465	AAAATAATACAACCAATTTAC			II	
0.1307789	cg1886621	cg1886621	71749347	AATACCRTCACTTATTTTTATC			II	
-0.142956	cg1886791	cg1886791	68708477	ATTCCCT	65731382	ATTCCCT	I	A
0.1040664	cg1887201	cg1887201	14605399	AAACRAAACAAACCTCTAACC			II	
-0.248603	cg1887350	cg1887350	40700434	AAATTAAAAATACCTAAAATT			II	
0.136863	cg1887396	cg1887396	54692329	ATAAAAC	10612501	ATAAAAC	I	C
0.110063	cg1887982	cg1887982	18622333	TAACTCACAACAACCAAAAAT			II	
0.1458839	cg1888634	cg1888634	15615488	ACAAAAAAAAACCAAACCCCA			II	
0.1030164	cg1888978	cg1888978	41772482	CTAATAAATAACAAATACTAC			II	
-0.114631	cg1889863	cg1889863	73652446	TATCCCTTTTAATTATTATTTA			II	
0.1047029	cg1890455	cg1890455	57804445	AACAAACAAAAAACTATCTAA			II	
-0.149414	cg1891220	cg1891220	12717429	CAAAAAC	33798456	CAAAAAC	I	A
0.1335448	cg1891285	cg1891285	73627398	TACACAA	52719449	TACGCGA	I	C
-0.152076	cg1891384	cg1891384	27768316	TTAATAAACATCCTACTATTCA			II	
0.1295932	cg18914751	cg18914751	22696464	CAATTATCCCTCTTATAACTAA			II	
-0.107751	cg1892198	cg1892198	26643444	AACTAAA	18749330	AACTAAA	I	A
0.1460382	cg1893091	cg1893091	67639417	AAAAATCAATACAACRCAAAA			II	
0.1242495	cg1893200	cg1893200	13771476	ATAAATTTTAACACAATACCT			II	
0.1036861	cg1893739	cg1893739	36698324	CRCTATCCCRAAAAAAATTCR			II	
-0.159431	cg1893890	cg1893890	28607449	ATCATAAACATAATACTAATT			II	
-0.323611	cg1894004	cg1894004	29738408	CAAAAA	18643318	CGAAAA	I	C
-0.127844	cg1894464	cg1894464	17610306	AAAAAA	24766383	AAAAAA	I	A
-0.340795	cg18949721	cg18949721	10737407	TTTTTACCACATATTAAAATAC			II	
-0.167408	cg1896408	cg1896408	60705361	CCTCTAAAAATCCCTACATTA			II	
0.1169479	cg1896615	cg1896615	60689504	ATAAAAATCTAAAATTTCAAA			II	
0.1027602	cg1897386	cg1897386	53621510	ACCTAAATAAATATTCCAAAA			II	
0.1653118	cg18974921	cg18974921	25750367	AAATTCTAAAAAATACACTAT			II	
0.110471	cg1898292	cg1898292	73759472	ACCATTACATTATTTAATTACR			II	
0.1118393	cg1898498	cg1898498	49726348	AATAAAAACTTCCATATAAAA			II	
-0.126469	cg1898905	cg1898905	47798444	AAAACCA	58669418	AAAACC	I	T

-0.12126	cg1899791	cg1899791	73799498	AAAAAACTCTTTAACACTAAT			II	
0.1092718	cg1900129	cg1900129	33738369	CAAAAAATCTAAATTCAAACC			II	
-0.133535	cg1900548	cg1900548	19753347	CRCTAATTATATTATACAATA			II	
0.1246907	cg1901755	cg1901755	12791403	TCATAAATAAACTCTCAAAAT			II	
0.1106395	cg1902457	cg1902457	66683313	ATAACTAAAACTAACAACCTT			II	
0.1685332	cg19026811	cg19026811	72688464	ACCAAAAAACTACCTCCAATA			II	
0.1042808	cg1902846	cg1902846	23709435	AATAAAAACAATTATATCAAA			II	
-0.100216	cg1903992	cg1903992	18772410	TTTAACACTCTATCCRTTCTCC			II	
0.1038544	cg1904367	cg1904367	28634462	AAACCTATAAATATCTAAAAC			II	
0.1249273	cg1904380	cg1904380	37690425	TAAATAAAACTAACTAACATT			II	
0.1547851	cg1904597	cg1904597	38642499	CAAATTCTCACACCATCCAAA			II	
0.1037239	cg1904693	cg1904693	62747452	ATTAAAA	56669392	ATTAAAA	I	A
-0.101625	cg1904766	cg1904766	39632473	AACCAA	19788466	AACCGA	I	A
0.1142505	cg1905055	cg1905055	53626330	ATTTCTAACCTTTATTATTATA			II	
-0.245096	cg1905415	cg1905415	50692499	ACAAAT	38620328	ACGAAT	I	A
0.1178374	cg1906169	cg1906169	16654445	AAACATAAATATAAACCATTC			II	
0.1094997	cg1906430	cg1906430	16806431	TCAAACTACTATATTAATCAT			II	
0.1210673	cg1907008	cg1907008	51641443	TATAAAATATCTTCCCTACCC			II	
0.1039726	cg1907749	cg1907749	59686444	TCAATTTCCCATATTCAAAAA			II	
0.1857898	cg19081571	cg19081571	39616332	TCCTCAA	64729355	TCCTCAA	I	A
0.1251172	cg19084031	cg19084031	22697405	ACACAAAATTTCCTCTAAAAT			II	
-0.100636	cg1908462	cg1908462	15678303	AAACCA	21616417	AAACCG	I	A
-0.343041	cg19089141	cg19089141	13650302	TTCTCACTTAAACRTATACTTT			II	
0.1099368	cg1910156	cg1910156	41708499	ACACAAAACTCATAACAAACT			II	
0.1220481	cg1910317	cg1910317	69780387	TCATATT	55632318	TCATATT	I	C
-0.166153	cg1910693	cg1910693	70727507	AATATAA	13769303	GATATAA	I	A
0.1088406	cg1911137	cg1911137	14791415	TAAAAACAACACTAACCTAAA			II	
0.1660802	cg1911235	cg1911235	43715460	ATCTCAATTCAAATTTCAAAA			II	
-0.115347	cg1911297	cg1911297	39655422	AATAAA	58802319	AATAAA	I	A
-0.113663	cg1911368	cg1911368	62787444	AAATATT	52670483	AAATATT	I	C
-0.107037	cg1911619	cg1911619	58774450	ACAAAAATATCTAAAATCAAA			II	
	cg1912198	cg1912198	17612323	AAAAAC	29675408	AAAAAC	I	A
0.126976	cg1913734	cg1913734	53769423	ATACTTT	68711421	ATACTTT	I	A
-0.177336	cg1914033	cg1914033	53809370	CAAACA	22730398	CGAACA	I	C
-0.105484	cg1914042	cg1914042	20787496	AAAATC	63779377	GAAATC	I	A
0.1001754	cg1914508	cg1914508	18765434	CATAAAAACAATATTATTAAT			II	
0.1651466	cg1914532	cg1914532	42631416	CTCTAACAAAAAAATAACCCT			II	
0.1145484	cg1915281	cg1915281	72749376	CTCTAAACACTAAAACAAAAA			II	
0.1092454	cg1915322	cg1915322	19720454	CTATAAATAAACATTTACCCR			II	
-0.12081	cg1915593	cg1915593	43749462	ACAAAA	39638415	ACGAAA	I	C
-0.207357	cg1915604	cg1915604	24621302	AAAACACRCCATTTATATTCT			II	
-0.127881	cg1916230	cg1916230	19617336	ACAACA	51760401	GCAACG	I	C
0.1637457	cg1916339	cg1916339	14795356	TTTTAAAACTAATTCTAATTAT			II	

0.1176264	cg19163939	cg19163939	32709467	ATTCTCCT	37750441	ATTCTCCT	I	A
0.1086566	cg19178509	cg19178509	70712376	ACTAAAATCAACRTAAACCTA			II	
0.125966	cg19179910	cg19179910	74661377	ACTAAAATACACACAACTTCCC			II	
-0.138453	cg19181528	cg19181528	25651436	ACAAAAA	10665457	ACGAAAA	I	C
0.1081491	cg19182919	cg19182919	41702481	TTTTAACTTTTTTAATTAACTTC			II	
-0.123399	cg19183166	cg19183166	34778379	TAATCAC	27645367	TAATCAC	I	A
-0.219592	cg19183395	cg19183395	69684305	TTCAACAAATTCTCCCCAAAAC			II	
0.1158299	cg19188207	cg19188207	64642350	CTTATAAAACCAATAAAACCCT			II	
-0.12934	cg19191272	cg19191272	48655375	CCACTCT	24616329	CCGCTCT	I	C
0.159168	cg19192626	cg19192626	32620442	ACACTAAACTAAAAAATTTTTA			II	
0.1089409	cg19194645	cg19194645	63739487	AAAAAAACAAACRACCTAAAT			II	
-0.139801	cg19196401	cg19196401	28656499	AACAAAC	64758359	AACGAAC	I	A
0.105971	cg19197744	cg19197744	60653364	AAATAAA	12766507	AAATAAA	I	A
-0.179268	cg19197888	cg19197888	49737495	ATACCTC	42794429	ATACCTC	I	A
-0.125684	cg19200589	cg19200589	18783416	TCCTTAA	21641317	TCCTTAA	I	A
0.1156462	cg19200953	cg19200953	57715418	TTTCCTATTCATATCRAATCTA			II	
0.1051227	cg19201144	cg19201144	12668447	RAATCACCCAAAAAAACCTAA			II	
0.1062704	cg19203575	cg19203575	41729330	CAAAACA	73749471	CGAAACA	I	C
0.1481211	cg19204924	cg19204924	52618403	AACCCTACAAACCTAAAAAAT			II	
0.1097174	cg19218082	cg19218082	46650473	CTAAAAA	58732404	CTAAAAA	I	A
0.1259654	cg19222397	cg19222397	53804325	AAATAATACAACCRTATAAAC			II	
0.1111079	cg19225953	cg19225953	62655484	TACTTATAACAACCCCAAACCC			II	
0.1081972	cg19229215	cg19229215	41615359	ACAAAAACTATAAAACTACCA			II	
-0.102041	cg19232382	cg19232382	57630337	AACTCCA	48795476	AACTCCG	I	A
-0.107568	cg19236328	cg19236328	16618399	CCTAAATTTAAAAACCACTAAT			II	
-0.203554	cg19236675	cg19236675	39622372	ACAAAAAATCCAATAACTAAC			II	
-0.103769	cg19239041	cg19239041	36808446	AAATATACTACTATAACAAACT			II	
0.3287034	cg19242610	cg19242610	72628304	CTAAAAAAATACCTACCCCCA			II	
0.2062804	cg19244032	cg19244032	27615359	TTCCCAAAATAATCCTAAACAA			II	
	cg19245941	cg19245941	59606503	AAATCAATATCCTAAACTCCTT			II	
0.252597	cg19249811	cg19249811	17795473	AAACATT	24793332	AAACATT	I	T
-0.15488	cg19255828	cg19255828	69638391	TACCAAA	46603391	TACCAAA	I	C
-0.108112	cg19259802	cg19259802	70606369	AAATAAATTTTTATTTCTTTTTA			II	
-0.114913	cg19263607	cg19263607	43620445	CACRATAAAAATCCRCTCCAA			II	
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-0.121016	cg19276736	cg19276736	74733353	ACTCACA	20648379	GCTCGCA	I	C
0.2211357	cg19285525	cg19285525	71768474	CACCCTCACCATAATCTAATAA			II	
0.2499465	cg19291696	cg19291696	13748308	TAAACTAAATTATATCCTCAAC			II	
-0.16347	cg19300195	cg19300195	10720447	AATAAAAATACTACCCAAAAT			II	
0.4303614	cg19300401	cg19300401	38724489	ACTATCAACAATTCTATATTTT			II	
0.1455556	cg19300549	cg19300549	18720498	TCCCTAACTAATTTCCTAACTT			II	
	cg19301897	cg19301897	29810355	CTATTATTCTTAAAACTATATA			II	
0.1292037	cg19303524	cg19303524	69647415	ACTCCAACTATAAATTCTAAAT			II	

0.1130758	cg1930649	cg1930649	16807337	AACCTCC	43714304	AACCTCC	I	A
0.1358398	cg1930898	cg1930898	11636377	CAAACCCCTAAATCAAAACTT			II	
0.1619087	cg1931137	cg1931137	60640379	TAAAATTTTCAAAACTAATAC			II	
0.1322046	cg1932328	cg1932328	63752427	CTTATATATCAACCAACCTTA			II	
0.1170384	cg1932579	cg1932579	16661434	CAAAAACTTCRAAAAACAACT			II	
0.1340421	cg1933198	cg1933198	72621403	AAAAACCAAAACTAATAATAC			II	
0.254488	cg1934029	cg1934029	51696419	CCACAAAAATCAAACRCTAAA			II	
0.1047919	cg1934487	cg1934487	68703407	TTTCCAATTCCAACTAATAAA			II	
0.1182027	cg1935305	cg1935305	23654413	CACAAACTTTAAAATTAAACA			II	
0.1167045	cg1936021	cg1936021	48673335	ATAACTTTTCTTAAATCCCATA			II	
0.1099373	cg1936247	cg1936247	31614361	TCTACCTACAAACTATAACCC			II	
-0.281949	cg1936277	cg1936277	36649386	AAAAAA	13798457	AAAAAA	I	A
-0.161336	cg1936717	cg1936717	35634328	AATCTCA	28751497	AATCTCA	I	A
0.1347609	cg1936785	cg1936785	54795417	CCTCTTTAAAACCTCAAACAT			II	
0.1794634	cg1937250	cg1937250	60705397	AAACATTTTTTAAACTACTTA			II	
-0.12695	cg1937334	cg1937334	37624483	ACCTCTATTTATATTTTCRTTA			II	
0.17375	cg1937541	cg1937541	29773383	ACTCTATAAACACTATCRCRA			II	
0.1006929	cg1937760	cg1937760	74654306	AATCACCTAAATTATTTATAA			II	
0.1129022	cg1938015	cg1938015	62608399	AAACAAAAATATTTACAATTT			II	
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-0.109234	cg1938937	cg1938937	60619466	CAATTAC	59765345	CAATTAC	I	A
-0.110812	cg1939255	cg1939255	35758373	AATAACTAAAAACATAAACRC			II	
-0.104561	cg1939819	cg1939819	65712353	AACACTA	42639385	AACACTA	I	A
0.1038683	cg1939845	cg1939845	71803437	AAAATCTCAAAAAAAAATTTA			II	
0.1443691	cg1940331	cg1940331	38619467	AAACAAAAACTATAAAAACC			II	
0.1018537	cg1940588	cg1940588	28672500	TTCCTCCAATCCAAAATCTTTT			II	
-0.121481	cg1940857	cg1940857	22647322	ACAATAA	26687438	GCAATAA	I	A
0.1200179	cg1941173	cg1941173	60751362	AAAAATTTCACAATAAAAAAC			II	
-0.509402	cg1941574	cg1941574	68625351	ATATCTCAACAATAAAATAAA			II	
0.1678464	cg1941831	cg1941831	60709383	ACACRTTTATTACCATAACRT			II	
0.1047959	cg1941852	cg1941852	40631412	AATTCTTTCATATAACATTCTC			II	
0.117084	cg1941929	cg1941929	39699342	TACCAAA	71736313	TACCGAA	I	A
-0.117625	cg1942657	cg1942657	74655465	TTCAATA	14802305	TTCGATA	I	T
0.1424689	cg1942860	cg1942860	46662383	TCCTTTACTAAATCCAAATCR			II	
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-0.152594	cg1944796	cg1944796	46763425	AATAATC	59680396	AATAATC	I	A
0.170133	cg1944796	cg1944796	24796508	AAATTTATTTTCTTAAAAAAA			II	
0.1061295	cg1944994	cg1944994	66788487	CCAAACCCTCTTTTCCTATAAC			II	
0.1280113	cg1945081	cg1945081	30628447	AATTTCCCTAAAATACTATCA			II	
0.1490498	cg1946319	cg1946319	69779335	AAACTAAAACTAACCTCAAAT			II	
0.1337909	cg1946944	cg1946944	19685405	ACACCCCTACCRAACRAATAT			II	
0.1040463	cg1947081	cg1947081	50687414	CRAAAATAAAATTAAACCTCR			II	
-0.125859	cg1947146	cg1947146	44792377	ATATTAAACTCCAAAAAAACC			II	

-0.120111	cg1947590	cg1947590	27728477	CCAAATT	32691488	CCGAATT	I	C
-0.10837	cg1947678	cg1947678	35650493	CTACTCC	46680357	CTACTCC	I	C
-0.108032	cg1948168	cg1948168	58680416	AAAAAAAAATATACAAACRA			II	
-0.311008	cg1948409	cg1948409	25692469	CTAACTATTCTCRTAAATCTTA			II	
-0.103584	cg1948430	cg1948430	26682315	AAAAAA	58741495	AAAAAA	I	C
-0.126198	cg1948786	cg1948786	61791398	CACTAAA	21674385	CGCTAAA	I	A
-0.224344	cg1949122	cg1949122	43711300	CAAATTCATATATCTAAATTT			II	
0.1263287	cg1949561	cg1949561	31707422	AAAATAAAAAACCCCCAAAA			II	
-0.127717	cg1950324	cg1950324	24659420	ACCTTCT	66736311	GCCTTCT	I	A
0.1205926	cg1950625	cg1950625	15645445	CACTCCCTTTTACCTTACACAT			II	
-0.143509	cg1950939	cg1950939	37622407	ACTCACC	20617345	ACTCACC	I	C
-0.115666	cg1951472	cg1951472	72789432	AAACAATAAAATCAACRTATC			II	
0.1366673	cg1951692	cg1951692	32758486	CTCCCTAAATACTCTACTAAC			II	
0.2203825	cg1952023	cg1952023	65796424	TAAAAATAAAATCCCTAAACC			II	
0.1136655	cg1952161	cg1952161	37671427	AAAAAA	54784313	AAAAAA	I	A
-0.114874	cg1952549	cg1952549	22736306	ACTATAT	55730490	ACTATAT	I	T
-0.1009	cg1952970	cg1952970	53619307	AATTAAA	36739481	AATTAAA	I	A
0.100453	cg1953678	cg1953678	37640352	AATAATAAAAACAATCCCATA			II	
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0.1129759	cg1953998	cg1953998	12758378	TAAAAAAATACATCAACTCCT			II	
-0.126609	cg1954593	cg1954593	59809335	TAATAAAATTTCTCAATATCC			II	
0.1035851	cg1955396	cg1955396	32663387	ATAAAAATATACTCTAAAATC			II	
-0.131566	cg1955677	cg1955677	10671472	CCATAAA	27751496	CCGTAAA	I	C
0.1159197	cg1956021	cg1956021	53731484	ACCTATTCRATAAATCAAATA			II	
-0.109607	cg1957077	cg1957077	32771462	ACCACAA	15679450	ACCGCGA	I	C
-0.178907	cg1957921	cg1957921	66676426	ACAACAA	62762448	ACGACGA	I	A
0.1076593	cg1958423	cg1958423	19601371	TAATACCACATTTCTCAAATA			II	
-0.173425	cg1958567	cg1958567	44725418	AAAAAACCCTAACTTTATTTC			II	
0.1931161	cg1959687	cg1959687	71733384	ACCTCTACACTACTAATAAAT			II	
0.1188229	cg1960541	cg1960541	42717455	CTTCATTATCCAAATTAAAAA			II	
0.143629	cg1960943	cg1960943	37692420	TAAAACCAATTTACTTATTCC			II	
-0.100154	cg1961075	cg1961075	47697491	ACCCCCT	27663422	GCCCCCT	I	C
-0.106024	cg1962362	cg1962362	13677339	TAAAACC	54604468	TAAAACC	I	A
0.1945831	cg1962898	cg1962898	70743474	CRTATACTACAAATAACTATA			II	
-0.113658	cg1963260	cg1963260	59792327	CRTCAAAACCRCATTCCCAAA			II	
0.1369313	cg1963540	cg1963540	68605351	AAAAAAAATAACTCCACTAAA			II	
0.1424907	cg1963662	cg1963662	43728500	AAAATCCTAACRCTACTTAAA			II	
0.1187162	cg1964082	cg1964082	63719500	TACRATCTAAAAACCCTAAAC			II	
0.1084995	cg1964132	cg1964132	28633339	AAAAAA	34644367	AAAAAA	I	C
0.1327665	cg1965070	cg1965070	51600390	TCAAAAATCTACACTCTATAA			II	
-0.219161	cg1965111	cg1965111	65652432	AAAATTAAACACAACAACTAC			II	
0.1255717	cg1965175	cg1965175	50649322	TATACCCCAACCAATCRTAAA			II	
-0.208803	cg1965324	cg1965324	43737438	CAAAACCTAAACTCTTATTAA			II	

-0.34337	cg19656425	cg19656425	41794410	ATCTAAATAACCCTAACATATA			II	
-0.187785	cg19678392	cg19678392	36727471	AAAATAA	70710392	AAAATAA	I	A
0.1279182	cg19683417	cg19683417	53760422	ATCACTTTCATAACAAATCCAA			II	
0.1722554	cg19683494	cg19683494	50780489	AAACAACTATTAAACAATTCR			II	
0.1464705	cg19689330	cg19689330	46677368	ACTAACTAACATCCCATTCTTA			II	
0.1324708	cg19689876	cg19689876	31612432	ACRAAAATAAAAACTACAAAT			II	
0.1016231	cg19691260	cg19691260	36743375	TAAACTACATACCAAAATAAA			II	
0.1052633	cg19696794	cg19696794	34711400	AATTTCTCTAAACTCCRTAATA			II	
0.109591	cg19705210	cg19705210	32679304	ATAACTCTATCCACAAAACCCT			II	
0.1341747	cg19707653	cg19707653	57743487	ACTAAAATTTATATATAATACC			II	
0.175631	cg19722082	cg19722082	15638325	CCTATAACTACTAAAATTAAAT			II	
0.1461662	cg19724567	cg19724567	47774317	AATAAATCAAAAAACCAAAAT			II	
0.3819413	cg19726630	cg19726630	38736359	ATTACCTATAACTTCTCTCAAT			II	
0.1553613	cg19726711	cg19726711	53789502	ATACATAAATCTAACCTATTTT			II	
-0.100863	cg19728223	cg19728223	63645353	ATAAAAACTTCCRCCTCACTTT			II	
-0.124238	cg19729930	cg19729930	20728450	ATACTTAAATACACCCTATAAA			II	
-0.101771	cg19730268	cg19730268	72622502	ATCACCAACCAAATCTTTCCAA			II	
0.1580333	cg19733736	cg19733736	63663437	TCTTCTACTAAATACCTTACTC			II	
-0.146807	cg19735421	cg19735421	44720402	CTCCAACAAAAAATAAATCCC			II	
0.1153455	cg19745930	cg19745930	60730367	TAAATATTTAATTTACTTAAAT			II	
0.10978	cg19749898	cg19749898	24694465	AAAAATA	44652349	AAAAATA	I	C
0.1079698	cg19752602	cg19752602	35665438	TCCATAATTTAAATACTCATAT			II	
-0.106479	cg19754833	cg19754833	17683336	CTCATCC	43763498	CTCGTCC	I	C
-0.224854	cg19755813	cg19755813	10773369	CCTACCT	26610429	CCTACCT	I	T
0.1133095	cg19758837	cg19758837	64717398	ACCACATCTAATTAATACAAA			II	
0.2009186	cg19759671	cg19759671	15716438	AACACAA	65697462	AACGCAA	I	A
0.1194863	cg19759847	cg19759847	43696369	CCAACTTTTCTAATTCTCAACA			II	
0.1746565	cg19766988	cg19766988	20616320	CCTCCCTAAAAACCAATTTTTT			II	
0.1385635	cg19770671	cg19770671	19680502	AAATTAAATCCAAATAACCTC			II	
0.3030837	cg19774683	cg19774683	50611302	CTTCATAAATTTCTCAACCACC			II	
-0.126982	cg19775763	cg19775763	22670481	AAATATA	73781407	AAATATA	I	A
-0.26681	cg19778375	cg19778375	53777447	ACACATA	20734362	ACACATA	I	T
0.1033849	cg19778647	cg19778647	50607419	CACTTAAATACTACTTCTTCCT			II	
-0.234619	cg19787013	cg19787013	50641413	CTATCAA	40741305	CTATCAA	I	C
0.2633759	cg19791271	cg19791271	59625487	CAAAACATAAAATCCCCTCTTT			II	
0.1274149	cg19798881	cg19798881	10622317	AAACAAC	42682438	AAACGAC	I	A
0.116861	cg19816075	cg19816075	31784354	TTCAATAACCCACATATACACT			II	
0.114136	cg19827875	cg19827875	67742337	ATAAAAT	31648360	ATAAAAT	I	A
-0.100019	cg19830372	cg19830372	21709404	AAAACAT	60749337	AAAACGT	I	T
0.1341548	cg19832565	cg19832565	13755419	TCTACAAAATCTAAAACATCTT			II	
0.1009627	cg19836199	cg19836199	26695382	TTTTAAATAATAAAATCCACAT			II	
-0.167368	cg19843891	cg19843891	29795448	AACACCA	62706410	AACACC	I	T
0.1055218	cg19844283	cg19844283	49775320	ACTCCAACATAACCACCTTATA			II	

-0.293505	cg1984757	cg1984757	70786455	AAAAAAAAAACCACTTATTCA			II	
0.1427361	cg1984873	cg1984873	22745427	TAAATATTCTTTACCTTCTAAC			II	
0.1215084	cg1984892	cg1984892	18686334	CTAACCCAAATACTAAACCCT			II	
0.1129137	cg1985821	cg1985821	59655427	CAAAAATTTCCTTTAACTAAA			II	
0.1026523	cg1986406	cg1986406	61679361	TTTTAATCAAAACCTATAAAA			II	
-0.151929	cg1987392	cg1987392	17781439	ATCAATAATTTTAACTTAACA			II	
0.1448436	cg1987609	cg1987609	71761486	AAAAAAAACCAACAAAAAAC			II	
0.1212	cg1988503	cg1988503	35712386	AAAACAATAATTCAATAAAAA			II	
0.158824	cg1988562	cg1988562	28772411	ATAATACTCTCTAAATCTACT			II	
0.118446	cg1988985	cg1988985	59725332	ACTTCAAATACCAATTCCTTCC			II	
0.124176	cg1989472	cg1989472	74609367	AACTCCATATCACCCCTATAA			II	
-0.15417	cg1989727	cg1989727	41718424	AAACAA	42744398	AAACGA	I	C
-0.155385	cg1989810	cg1989810	11674459	AAAATTTAATAAAAACTCTAA			II	
-0.135274	cg1989953	cg1989953	42755505	AACCACCATAACTAAAAACAA			II	
0.1837466	cg1990392	cg1990392	44719347	TACAACC	29742380	TACAACC	I	C
-0.12434	cg1990435	cg1990435	31611431	RAACACTAATAAATAAATATC			II	
0.1091401	cg1990725	cg1990725	21714440	ACAAAA	45748377	ACAAAA	I	C
-0.106937	cg1991273	cg1991273	17667498	ATTCTAAAAATTCCRAAATAC			II	
0.1629469	cg19921651	cg19921651	42773329	CCTTTAATATCAATAACCCAA			II	
-0.15143	cg1992750	cg1992750	15756427	AAAACAAAATATAATTACCRT			II	
0.1025258	cg1993000	cg1993000	17623415	ATATTACTATAAACTCAAAAC			II	
0.1086926	cg1993703	cg1993703	15742318	AAACTAAATCTTACTAAAACR			II	
0.1309586	cg19937061	cg19937061	31777487	ACTACAC	56706476	ACTACGC	I	C
0.1342466	cg1994746	cg1994746	53645471	ACATCACRACAATAACRACTT			II	
0.1154838	cg1995423	cg1995423	44758434	TCAAAACTTCCCACCCTCTTAA			II	
0.1736458	cg1995859	cg1995859	45670346	CATTCTCTATTATAATTAATAA			II	
0.1409395	cg1996061	cg1996061	50669464	ATAAAACAACTAAAAACATTT			II	
-0.239912	cg1996115	cg1996115	72760479	ACCAAA	52661376	ACCGAA	I	A
-0.204018	cg1996766	cg1996766	56696355	ACTACAA	29681401	ACTACAA	I	A
0.1967898	cg1997264	cg1997264	48651395	ATAAAAACTTAATAAAATAAT			II	
0.1005492	cg1997412	cg1997412	57652366	TATCRACAAATAAAAATAACT			II	
-0.120377	cg19975301	cg19975301	39678468	ACAACAT	29753506	ACAACAT	I	T
0.1965168	cg1997603	cg1997603	23677489	ACTTATTCRTCTAAAACACTA			II	
-0.137109	cg1997644	cg1997644	44698394	AAAATAAATCATTAATTCATA			II	
0.1829832	cg1997910	cg1997910	45742455	ATACCATACTTATATACTTAA			II	
0.1020062	cg19982031	cg19982031	70707453	CATTCCCAAAAACAAAAATCC			II	
0.1183572	cg1998394	cg1998394	63794307	ACTTTCATATCCCRTTAAAAA			II	
0.1149268	cg1998790	cg1998790	72739359	CCCTATTACATTAATTCTTTAA			II	
-0.163297	cg1999706	cg1999706	59762379	AACCTAA	22730465	AACCTAA	I	A
-0.107278	cg2000217	cg2000217	25675354	TAACTTACATACAAAAAAAAA			II	
0.1261015	cg20002901	cg20002901	18674314	ACCCTAA	73703502	ACCCTAA	I	C
-0.134478	cg2000665	cg2000665	60601461	CAATAA	55626498	CAATAA	I	A
-0.176318	cg20007021	cg20007021	61733478	CAAAAA	63671402	CGAAAA	I	A

-0.260576	cg2002014	cg2002014	32673453	CCACCAA	68605367	CCGCCGA	I	C
-0.105944	cg2002072	cg2002072	51764502	ACACCTAAACRAAACTTTATA			II	
-0.248572	cg2002203	cg2002203	44656440	CTATAAATAATTTCTATCCAA			II	
-0.103264	cg2002636	cg2002636	55661387	AACCCACTAATTAAAAATTCA			II	
0.1274414	cg2002794	cg2002794	63760366	AAAAAATCCTTCCTAAAATAA			II	
0.1775788	cg2003567	cg2003567	44729502	TCTAAACCAACAACAACCRCC			II	
0.1257024	cg2004569	cg2004569	42794428	AAAATCTAAACAAAATAACAC			II	
0.1077635	cg2004804	cg2004804	35687429	AACATAACCRTAAAACCAAAA			II	
0.105581	cg2005048	cg2005048	63714318	TAAACATCTTCTAACACACTA			II	
-0.105224	cg2005311	cg2005311	45641463	TAAAACC	31810473	TAAAACC	I	A
0.1126327	cg2006063	cg2006063	39792380	CTATACCTAACAAAAAATCTA			II	
-0.164771	cg2006415	cg2006415	49624409	TATAACATCTTTACAATCCTTC			II	
0.1030498	cg2006678	cg2006678	67725489	AAATATTTCTCATAAAAATAT			II	
-0.144632	cg2007331	cg2007331	47630313	CATAAAC	17625416	CGTAAAC	I	C
0.1388848	cg2007612	cg2007612	49774361	CCAATAAAAATCAAAATAAAA			II	
0.1134461	cg2007651	cg2007651	41782446	TTCCTAAAAACCTAACCCCRC			II	
0.1148425	cg2007864	cg2007864	66678384	CCTTCTAATACATACAACTATT			II	
0.1232282	cg2007880	cg2007880	66714495	AAAATCTAAATTTCCATTCCA			II	
0.1217049	cg2008745	cg2008745	53631452	AAATAAACATACACACCTTTT			II	
-0.192838	cg2008751	cg2008751	10682449	TAATACA	49799315	TAATACG	I	C
-0.118501	cg2008824	cg2008824	69751485	CTTTAACCRTTAAAACRTTTAC			II	
0.1321267	cg2008979	cg2008979	37764504	ATTAAACRATACTATAAATCT			II	
-0.169645	cg2009006	cg2009006	41707350	CCTAAAAAATATAAACTCTCT			II	
-0.110559	cg2009028	cg2009028	58795481	CTAATAA	67686425	CTAATAA	I	T
-0.147656	cg2009434	cg2009434	27791426	CCTACAAAAAAACCCCCTCAA			II	
0.4940095	cg2010607	cg2010607	49631492	ATAATAACCAATTCAAAAAAC			II	
0.1128095	cg2011452	cg2011452	72763473	ATAAATAACTCTCRTTTCCTAT			II	
-0.101819	cg2011615	cg2011615	33765311	TAAAATT	59601326	TAAAATT	I	A
-0.102207	cg2011979	cg2011979	55721375	TTAACTATCACCATAATCAAA			II	
0.1400142	cg20119891	cg20119891	50617369	TTTTAAACAATATCATTTCTAA			II	
-0.120975	cg2013286	cg2013286	38701360	TCCATAT	22791459	TCCATAT	I	A
-0.109139	cg2013774	cg2013774	63661307	TACAAAT	62647384	TACAAAT	I	T
0.1143575	cg2014139	cg2014139	63670429	ATCAACT	25809507	ATCGACT	I	A
-0.155691	cg2014276	cg2014276	73630387	TTTCTCTTACCRTACRACTACA			II	
0.1497231	cg20144261	cg20144261	63723458	AAATAATAAAATCCAACCCAA			II	
-0.136691	cg20164601	cg20164601	24804471	AAATTCA	68657454	AAATTCG	I	C
0.1037753	cg2018405	cg2018405	55689349	TAAATCACAAATTCATAATCA			II	
0.1138955	cg2018801	cg2018801	10758349	CCTTATTAACTAATTAAACTAT			II	
-0.26412	cg2018821	cg2018821	12636503	TCTTTCCTTCTTTTCCAAATCA			II	
-0.175316	cg2018849	cg2018849	45773423	CTATAATACCTAAAAATTCCC			II	
-0.118151	cg2018924	cg2018924	41702417	TAACCAC	58683406	TAACCGC	I	C
-0.100134	cg2019092	cg2019092	57708313	ATTCCTCCTAATAAATATTTAT			II	
0.2539717	cg2020518	cg2020518	29676313	TAATAACCRAAATAAACCRAA			II	

0.1100344	cg20207327	cg20207327	15787404	TAAAAAAACAACACACTTACT			II	
-0.100088	cg20208600	cg20208600	74785399	CCTAAAAAAAACRCTCTATTT			II	
0.1229516	cg20212912	cg20212912	45745470	ACAAATCAAATAAAACATAAC			II	
0.1401559	cg20214871	cg20214871	40789333	CCTACAAATTAAAATTCTACC			II	
	cg20218571	cg20218571	73790507	AATAAAAAACRACACCRAAA			II	
-0.109066	cg20223206	cg20223206	28672338	CAAATTAATATAATAAATACA			II	
0.107057	cg20223687	cg20223687	42650326	CTACTAC	16610447	CTACTAC	I	A
0.128695	cg20231299	cg20231299	36657311	TCCCAATATCAAAACTAAAAA			II	
-0.278328	cg20242889	cg20242889	15736503	TTCACAA	71710493	TTCACGA	I	C
-0.154994	cg20246113	cg20246113	54789496	AAAAACC	71748377	AAAAACC	I	A
0.2602279	cg20249327	cg20249327	11758417	CACCCAACACAACTAAAAACT			II	
0.1190189	cg20250341	cg20250341	67750401	CCCRAATCAACTACTTAAAAA			II	
-0.437658	cg20255370	cg20255370	26731480	TTCTCAT	30771301	TTCTCAT	I	A
-0.108152	cg20262330	cg20262330	47808302	ACTAAAATACCAACTTCAAAA			II	
-0.131343	cg20264068	cg20264068	48676422	CATAATA	70637481	CGTAATA	I	T
-0.101805	cg20264966	cg20264966	49718390	ACTAAAAATCATTTACTTTAA			II	
0.1823941	cg20267322	cg20267322	41696395	TTCCRTAAATATCCCTAAATA			II	
-0.120818	cg20269046	cg20269046	33757366	AAAACCA	20798360	AAAACC	I	A
0.1266826	cg20272648	cg20272648	41747302	AAAAAACTAAAATTTCTACTA			II	
0.1037337	cg20273260	cg20273260	67803443	ATCAAAATCTACAAACAAATA			II	
-0.139119	cg20276780	cg20276780	49660309	CRAACCCTCTAATAATTCCCTT			II	
-0.141348	cg20281601	cg20281601	56683470	CACTTCT	74788335	CGCTTCT	I	C
-0.157881	cg20282550	cg20282550	43628367	AACTAAA	30753492	AACTAAA	I	C
0.1208768	cg20284019	cg20284019	44796422	TACTTCTAATAAAAAACCAAC			II	
0.1239273	cg20284239	cg20284239	49746434	AATCACTATTTCAACTACACA			II	
-0.102751	cg20285546	cg20285546	31603433	CTACTCCCAAATATAACCAAA			II	
0.1029623	cg20287936	cg20287936	60624477	TTTAACTCCCACTTCTAAATAA			II	
0.1286322	cg20288617	cg20288617	50689426	AAACAAAACCTAATAACRAAC			II	
0.1251827	cg20289854	cg20289854	48606406	AAATAATATAAACAAACACAA			II	
-0.199656	cg20299670	cg20299670	72697402	CTTTCTTTCCATTAAAACAACA			II	
-0.256559	cg20300514	cg20300514	53768450	ACRCATTAAAACAAAACRAAC			II	
0.1220938	cg20300784	cg20300784	58697445	CTAAAACCCRAAACCACACAC			II	
-0.129821	cg20310608	cg20310608	53748416	ACTAAAA	22764447	ACTAAAA	I	C
0.1956587	cg20311002	cg20311002	67768324	CCCAACTTCCAATTTCTAACTC			II	
-0.121676	cg20311673	cg20311673	48606478	AAATATA	48723444	AAATATA	I	T
0.1444915	cg20312012	cg20312012	17683345	TATTTTATTTCCTCATACCTTA			II	
0.1099146	cg20312418	cg20312418	60802385	AAAACTAAATTCAAAATCAAA			II	
-0.133203	cg20321086	cg20321086	48745481	ACACAAA	53754400	ACGCAAA	I	A
0.1205382	cg20325573	cg20325573	39771403	AAAAACAAAAACATACACRAT			II	
0.1315153	cg20327845	cg20327845	24655434	ACCATAC	41653386	ACCATAC	I	C
0.1041821	cg20331155	cg20331155	58644321	AATAACAAAACCTCRAACCRT			II	
0.1078694	cg20332503	cg20332503	45620310	TAATCCAAACATCCAAAATCC			II	
0.1165327	cg20334115	cg20334115	33801340	AAAATTACTCTAAAAAAATAA			II	

0.2652687	cg2033601	cg2033601	58689457	AAATAAAAATCTTACRAAAAA			II	
-0.110233	cg2033799	cg2033799	28626323	CCAAACCCAAACAAAATTCCT			II	
0.112949	cg2034072	cg2034072	16728426	TCCTAACTCTACTCTAATTTTC			II	
-0.100745	cg2034086	cg2034086	11678484	CACTTAA	65669459	CACTTAA	I	A
0.1220489	cg2034438	cg2034438	44636396	TTTAAACCTCTACAAAAAAC			II	
-0.120852	cg2034766	cg2034766	68779491	CAACTAA	14756391	CAACTAA	I	T
-0.126595	cg2036418	cg2036418	49676321	TACCATTCRTATTACAACCAA			II	
-0.12558	cg2037018	cg2037018	70714459	CAAACAAACCTAAATCAAAAC			II	
0.1243628	cg20372591	cg20372591	61778393	TATCACCTCTACCTTTATATTT			II	
-0.124964	cg2037274	cg2037274	67706308	ATCCCAA	12660310	GTCCCAA	I	T
-0.120795	cg2037730	cg2037730	39711501	TATCTTT	16773420	TATCTTT	I	C
-0.29226	cg2038137	cg2038137	15777504	AAACAACTAATCTATATCTTC			II	
0.1719257	cg2038462	cg2038462	19794463	AACAAA	64625488	AACAAA	I	A
0.1142273	cg2038777	cg2038777	13726478	TACCTACTTTTTAAACTTTATC			II	
0.1076878	cg2038873	cg2038873	67755386	ATACTATAAATAAACAACTAA			II	
-0.175965	cg20390711	cg20390711	56715415	ACAAATA	53601482	ACAAATA	I	A
-0.14854	cg2039961	cg2039961	63653479	CCATAAA	28680319	CCATAAA	I	A
0.1127526	cg2040154	cg2040154	66684405	CAAACRCCAATTTCACTTTCTA			II	
-0.40049	cg2040278	cg2040278	66662387	TCTCCTA	33633366	TCTCCTA	I	A
-0.144107	cg2040393	cg2040393	34752304	AAACTAA	28762345	AAACTAA	I	C
0.206005	cg2040975	cg2040975	48623369	TCTATTAAATAAAACCACCCA			II	
0.1033579	cg2041155	cg2041155	25618398	ATTAAATAATAATCAAACCTA			II	
0.1081591	cg2041852	cg2041852	64762372	TAAACCT	39730349	TAAACCT	I	T
0.2038854	cg2042627	cg2042627	36706349	TATAAAAAACCCAAAACCAAA			II	
0.1177011	cg2043385	cg2043385	17795371	ACTCAAAAATAAAACTAACTC			II	
0.1197544	cg2043442	cg2043442	71609502	ATCTAAAATCTACAAAACTAT			II	
-0.106593	cg2044191	cg2044191	47727341	AAAACCA	67792481	AAAACCC	I	A
-0.10607	cg20450471	cg20450471	12656497	TATTATC	38620431	TATTATC	I	A
0.2137923	cg20453861	cg20453861	63637430	ACTTAAACACATAAAATAATT			II	
0.1983959	cg20457051	cg20457051	74687328	TAACCTTTTAAAATTTTCTTTA			II	
0.180906	cg2045903	cg2045903	27804461	CCATATACCTCCTAAAACTAA			II	
0.1000714	cg2046415	cg2046415	27634393	TAAATTTCTACCAAATTAAAA			II	
0.1094919	cg2046488	cg2046488	62676315	ACRAAATACTAACTTACTTTTT			II	
0.1035421	cg2046900	cg2046900	59735428	ATCATAAATCAACATATAAAC			II	
0.1801365	cg2046950	cg2046950	27692475	TAACTTCTAAATTAAATTTATC			II	
-0.140819	cg2047770	cg2047770	37713507	CACCCRCTTATACRTCTTATAA			II	
-0.295331	cg2047920	cg2047920	17633366	TTCAAATAAAAAAAATCAACA			II	
0.1886533	cg2048867	cg2048867	16785488	CTAAAAAACCCAATAACTAAT			II	
0.1047944	cg2049477	cg2049477	42605490	AAACCCTATATTCTACCAATA			II	
0.1035699	cg2050390	cg2050390	59775378	AAAAATCRACAATACCCCAAT			II	
-0.156506	cg2050391	cg2050391	41745467	AAAACTA	39679510	AAAACTA	I	A
0.1189358	cg2050680	cg2050680	21800380	TACAAAA	46796390	TACAAAA	I	A
0.1745426	cg2050727	cg2050727	25806371	AAAAACACCAATATATAAAAC			II	

0.1546832	cg2051003	cg2051003	11709493	TAAACCCTAAATTCTAACCRC			II	
0.1233997	cg2051341	cg2051341	68734497	ATAATTAAAAAAAACCTATCT			II	
0.127323	cg2052239	cg2052239	20643447	TCTATACTTCCCTCATTATACT			II	
0.1355735	cg2052878	cg2052878	28708301	TTCTCCTCTCRAAACTCAAAA			II	
-0.225969	cg2053084	cg2053084	47798492	TAAAACTATCAACCAATCCCC			II	
0.1683344	cg2053398	cg2053398	57741364	RAACCAACTCTACRTCTATCTT			II	
-0.190722	cg20536971	cg20536971	48795471	TCCTTTTTCTATTTACTAATAA			II	
0.19122	cg2054023	cg2054023	13606314	TCACTCACTAAAACTCTAATTT			II	
-0.369669	cg2054929	cg2054929	73796474	TCAAAAACAAAATATAATCCT			II	
0.2758084	cg2055001	cg2055001	20688329	AATCTAA	74727490	AATCTAA	I	A
0.116143	cg2055300	cg2055300	16702322	RCAAAAACCTATAAACRAACR			II	
-0.105632	cg2055437	cg2055437	70636447	CRAAATACATATTAATAATAC			II	
-0.172014	cg2055921	cg2055921	33655451	TTCTAAACCRAACAAATCRAA			II	
0.1369014	cg20561261	cg20561261	38732415	TAAAAACTCTTCTTAATTTATA			II	
-0.156943	cg2056193	cg2056193	32730395	TAAATTCCTCCCTATACCCCTC			II	
-0.166597	cg2056327	cg2056327	49686368	AACAAA	33708300	AACAAA	I	C
0.1134551	cg2056810	cg2056810	36666492	CATCAATTAACCCAATTCTAA			II	
0.2748303	cg2056842	cg2056842	12740464	TATCACTTATTCACTATCTTCT			II	
0.1140765	cg2056980	cg2056980	59676454	CTCATTAACTTCTTAAATAAC			II	
0.1507272	cg2057659	cg2057659	58762444	CCATACAAAAAACCTATAATC			II	
0.1032069	cg2058085	cg2058085	13714328	CCTATTTCCTACCTAAAAAAC			II	
-0.120312	cg2058187	cg2058187	71619415	TCTAAAA	65808494	TCTAAAA	I	C
0.1069377	cg20584841	cg20584841	54797458	CACCTACATACAACRATAATT			II	
-0.13306	cg2058499	cg2058499	74778381	AAAAAA	48629465	AAAAAA	I	A
-0.131308	cg2059201	cg2059201	11637351	AAAACA	15737394	AAAACA	I	C
0.120021	cg2059212	cg2059212	39750490	ATCTAAAAAAAATAAACTACC			II	
-0.3007	cg20592391	cg20592391	69708495	AAATCTAAAAATAAATATTTT			II	
0.158851	cg2059283	cg2059283	43730356	AACCCCTTTATAACRTCACAA			II	
0.1069165	cg2059677	cg2059677	36751506	AACTAACTAAATAAATATACT			II	
-0.110435	cg2061045	cg2061045	62753398	CCCTACC	39645307	CCCTACC	I	A
-0.127805	cg2061732	cg2061732	18710494	TTCCTCTCTCAAAACAACAAA			II	
-0.144514	cg2063381	cg2063381	73667326	CRCTTTATAAAAACTCTAACC			II	
-0.134706	cg2063980	cg2063980	35692332	TCCATTAATATTACCATCTTAT			II	
0.2325593	cg2064037	cg2064037	18642456	ATCCTTT	31658443	ATCCTTT	I	C
0.1369686	cg2064167	cg2064167	10738373	AATTTATCCTAAACCAAATAT			II	
0.1412884	cg2064344	cg2064344	42606486	TATTCRTTATTCCAATCAATCT			II	
0.1881453	cg2065164	cg2065164	47692461	CAAACTATTATTAAACCTATT			II	
-0.11995	cg2065312	cg2065312	32640330	ATTTAAAATAATAATATATAT			II	
0.1233282	cg2065770	cg2065770	12673404	ATAACAAAAATATCAACCACC			II	
-0.135671	cg2066291	cg2066291	39793457	ACAAAA	27705428	ACGAAA	I	T
0.1489976	cg2066304	cg2066304	73745465	TAATAATTCTATATAACRCTA			II	
0.1027895	cg2066444	cg2066444	44618449	TCCAAAA	49704310	TCCAAAA	I	C
0.1161782	cg2067625	cg2067625	24744337	TATCTCACTAACCAATAAAAA			II	

0.1138012	cg2067883	cg2067883	50695330	AACAATCCAATCAACACAACA			II	
-0.179733	cg2067898	cg2067898	63806509	TAACACCAAAATATTTACACA			II	
0.1056624	cg2067940	cg2067940	43772339	RAAAAAACAACTAAAATCTAA			II	
0.1176112	cg2068344	cg2068344	62708473	ACCTAAA	54684413	ACCTAAA	I	A
0.1896375	cg2068620	cg2068620	59637311	ATAAAACCTCRACCATAACTA			II	
0.1019867	cg2068627	cg2068627	71638430	AAAACAC	63712320	GAAACAC	I	C
0.1387974	cg2069561	cg2069561	70661373	AAACCATATAACTAAATAAAA			II	
0.1012762	cg2069927	cg2069927	71654483	TTCTACTAACCATATAATACA			II	
0.1020523	cg2070220	cg2070220	28808505	ACACTAATAACTCTCCRATAT			II	
-0.122303	cg2070496	cg2070496	21621390	CACCTAAAACTATCAATAACT			II	
0.1550421	cg2070589	cg2070589	15653321	TTCTACCTATTCRACATCTTTA			II	
	cg2071381	cg2071381	69709355	CCAAATT	13644459	CCGAATT	I	T
-0.113845	cg2072059	cg2072059	12740331	AAAAACC	28690392	AAAAACC	I	C
0.130006	cg2072403	cg2072403	59755484	TTATACATTCAATAAATCATA			II	
-0.258243	cg2073193	cg2073193	49698416	ACCCAAA	10682396	ACCCGAA	I	C
-0.11067	cg2073506	cg2073506	28732348	ACAACTCTAAATCATCCRAAT			II	
0.1954733	cg2074104	cg2074104	40687318	TTACCCAAAATAAACTACAAA			II	
-0.141503	cg2074152	cg2074152	34749417	AACRAACCCTATTCCRAAAAA			II	
0.1076451	cg2074648	cg2074648	73669372	CCCCTAAAATTAACAATCTCC			II	
0.1127151	cg2075139	cg2075139	11652370	ATAACTAAAACTCRACTCTAT			II	
0.3142838	cg2075602	cg2075602	53647446	AATCCRAAAAACTAAAAATAT			II	
0.109229	cg2076478	cg2076478	54722475	TCAATCACTATCCCTCRTACTT			II	
0.1120414	cg2076734	cg2076734	44648351	AAAACTAAATTCTCAATCATA			II	
0.1687727	cg2076985	cg2076985	44637311	CAATCATAAATTCCCACAAAA			II	
-0.101842	cg2077314	cg2077314	52728317	AAAAAA	13657389	AAAAAA	I	C
0.1125737	cg2077860	cg2077860	25686351	TCAAAATATCCTAACTTACTC			II	
0.2096466	cg2077891	cg2077891	60629456	AAAAAAAAATATACAAAACCC			II	
0.1280639	cg2078397	cg2078397	43801338	TCAATATATATCTAATTTTAAA			II	
0.1078657	cg2078948	cg2078948	74659383	AAACATACCAAAAACTACTCR			II	
-0.123295	cg2079079	cg2079079	26770430	RAAATATAAAAACCRACRCCA			II	
-0.281732	cg2079129	cg2079129	71714440	ACCACCACCATATCCAACTAA			II	
-0.117094	cg2079537	cg2079537	57723448	AACTACC	63695473	AACTACC	I	C
-0.302446	cg2079541	cg2079541	63659363	RCACACCACCACACCCAATTA			II	
0.2106094	cg2079806	cg2079806	69666477	AAAAAATAAACCCATATACTA			II	
-0.108476	cg2081175	cg2081175	53690493	AAAAAACAACATCTACCRAAA			II	
0.1579022	cg2081198	cg2081198	31628448	CTCAAAC	12625453	CTCGAAC	I	T
-0.227368	cg2081417	cg2081417	25742488	ACCAAAA	51751377	ACCGAAA	I	T
0.117727	cg2082104	cg2082104	48808387	ACAACCTCAACAATTACTACT			II	
0.1154289	cg2082171	cg2082171	57656364	AAAATCCTCATATAACACCTC			II	
0.1546395	cg2082352	cg2082352	35605502	ATATCCCCTAAACACACAAAA			II	
0.1485388	cg2082674	cg2082674	47760413	CAACCATCCAAAAATAACCTA			II	
-0.233938	cg2082828	cg2082828	31612369	AACCATA	74658363	AACCGTA	I	T
0.1014387	cg2083570	cg2083570	39713425	ACTCTAAAACRTCTAACCTAA			II	

-0.138759	cg2083920	cg2083920	72782462	ATCAAA	14649377	ATCGAA	I	A
-0.13485	cg2084486	cg2084486	31733489	AAAATATAACAATTCAACAAA			II	
0.1325819	cg2085098	cg2085098	46766420	CACAAACAAATTATATAACAA			II	
-0.147304	cg2085984	cg2085984	69633331	ATATTCRCTACAACCATACCC			II	
0.1072684	cg2086421	cg2086421	37637493	ACCAAA	29685483	ACCGAA	I	C
-0.12122	cg2087676	cg2087676	39770411	AATAAACTCAAAATAAACCRC			II	
-0.102029	cg2088488	cg2088488	37803322	ATTAAA	60728315	ATTAAA	I	A
-0.140573	cg2088736	cg2088736	25669327	TAAAAA	47748497	TAAAAA	I	A
0.1143295	cg2089393	cg2089393	30740505	AAAACATTACTATAATACTAA			II	
0.1464788	cg2089978	cg2089978	48636352	RTTTAAAACCTTAATTACCCA			II	
0.2443235	cg2090433	cg2090433	62603309	CRACTTAACCAAATCATAATA			II	
-0.15073	cg2090713	cg2090713	13706331	CCAAAA	19607309	CCGAAA	I	T
0.1077694	cg2090740	cg2090740	33773300	AAAAACTACAAAACTACTCTT			II	
0.1149626	cg2091036	cg2091036	23728464	TCCTAATATTTACATATACATA			II	
0.1471278	cg2091642	cg2091642	53682313	TAACCTAACCACAAAAACAAC			II	
0.1035536	cg2091707	cg2091707	17716311	CAAAACTATCATTAAACATTC			II	
0.2551301	cg2091749	cg2091749	70618476	TAAAAATCTTATCACTAACRA			II	
0.1058682	cg2092442	cg2092442	30640339	CRATCCAACCACRAAACTCCT			II	
0.1074037	cg2092739	cg2092739	13804374	AAATTACTACAAACCCAAACA			II	
0.1172974	cg2092765	cg2092765	13616379	ATTTTTACTTTTTACCAAACCC			II	
0.1677403	cg2094118	cg2094118	58669414	TCTACAACCTCCTAAACAAAC			II	
-0.129992	cg2094508	cg2094508	40674373	CCTAACC	29626407	CCTAACC	I	A
0.1030867	cg2094827	cg2094827	36623459	TACTTACACAAATAAAAATAA			II	
-0.120719	cg2094836	cg2094836	49686431	TCCAATT	19704373	TCCGATT	I	C
-0.112705	cg2095164	cg2095164	51768470	TTCTAAAAAAACCRATATCTA			II	
0.2759559	cg2096032	cg2096032	58758453	CCATAAAAAAACTTCTTTAAA			II	
0.1249079	cg2096915	cg2096915	30775370	ACTACTCTATCTAAAACRATC			II	
0.1118208	cg2097819	cg2097819	49784457	CTACCTTACCTTCTACCTCCCT			II	
0.1200039	cg2097892	cg2097892	68705431	CAAACA	13754460	CAAACG	I	T
0.1167104	cg2097915	cg2097915	38808325	CTACTAC	71720494	CTACTAC	I	C
0.1520174	cg2097938	cg2097938	40604470	AATAAAATTCCCATTCTTATA			II	
0.1900771	cg2098116	cg2098116	67601502	TCACTAATTAATACCTCTACA			II	
-0.116283	cg2098145	cg2098145	11725350	TCTACTA	40708411	TCTACTA	I	C
-0.114286	cg2098683	cg2098683	72743474	AAAAATCRCTACAAACATAAA			II	
0.1062389	cg2098743	cg2098743	63774318	TTTAAACTATATCTTTAAAAC			II	
0.1886873	cg2099115	cg2099115	38770375	ATCCCAACCTTCATTTTCAAA			II	
0.1075608	cg2099508	cg2099508	14801411	AAAACA	35782396	AAAACG	I	A
-0.122501	cg2099635	cg2099635	13809302	AACACA	61637328	AACACG	I	C
-0.141916	cg2100551	cg2100551	35610381	CCCAAA	44640449	CCCGAA	I	C
0.1328402	cg2100568	cg2100568	27653315	AATTTCCCCACTTTATCTCTTC			II	
0.1808829	cg2101205	cg2101205	14677460	CAAACTAATAATTTAAACCRC			II	
0.1060485	cg2101788	cg2101788	71619357	CACAACT	47602308	CGCGACT	I	A
0.3224225	cg2102831	cg2102831	71711491	TTTTTAAAACCACTTACAATC			II	

-0.397032	cg2103256	cg2103256	19687445	TTTCTAT	50644406	TTTCTAT	I	C
0.1056796	cg2103440	cg2103440	26684317	AATACTATCCCACAAACACAC			II	
0.1057419	cg2104009	cg2104009	70668361	ACAATAATATCTACAATAACR			II	
-0.101658	cg2104010	cg2104010	59656331	AACCACA	67614499	AACCGC	I	A
0.1039101	cg2104557	cg2104557	10792451	AATTACAAAAATATTTCACAA			II	
0.1357679	cg2104870	cg2104870	59735421	TTAAACATTTCTATCATTCTCA			II	
0.1710447	cg2104939	cg2104939	71773502	AATATCACATCTCRATAACTCA			II	
0.1393884	cg2105276	cg2105276	51790432	CAAAACC	70742444	CAAAAC	I	A
-0.115255	cg2105491	cg2105491	63721486	CCCTACACACATATATCRATC			II	
0.2289566	cg2105555	cg2105555	12765328	TAATCAATAAAAAATATTTCA			II	
-0.122895	cg2106278	cg2106278	38635332	ACATCAA	34689472	ACGTCAA	I	C
-0.25493	cg2107008	cg2107008	64787328	ATATTTAAAATAATACCTTCTT			II	
-0.306228	cg2107807	cg2107807	72651462	CCTAAAA	37638335	CCTAAAA	I	C
0.1020657	cg2108227	cg2108227	38628338	CAACCAT	64679354	CAACCGT	I	C
0.1243418	cg2109317	cg2109317	12741508	TTCTCATTAAAAAAAATTCCTT			II	
-0.112193	cg2109380	cg2109380	51790502	AAATAAT	51609351	AAATAAT	I	T
0.1313206	cg2109778	cg2109778	58700335	CTAAAATACTAAACCTAATAA			II	
-0.108679	cg2110587	cg2110587	34635360	TAAAAAA	37612334	TAAAAAA	I	A
-0.160566	cg2110648	cg2110648	50801389	TAAACTA	45649507	TAAACTA	I	C
0.2370687	cg2111472	cg2111472	10785309	ACTCACA	39705421	GCTCGCG	I	C
-0.105151	cg2111626	cg2111626	59722425	AACAAAT	30706349	AACAAAT	I	A
0.101202	cg2112160	cg2112160	23692348	AATATCTCTCTTCCTACTTAAA			II	
-0.139855	cg2112662	cg2112662	56731381	TATAAAATACTTTTTCTCAAA			II	
-0.116461	cg2113086	cg2113086	74646366	AACCAAA	24683387	AACCAAA	I	C
-0.368576	cg2113979	cg2113979	27621380	AAACTATCCCTTTCCTCCTTAA			II	
-0.154321	cg2114406	cg2114406	26735430	TTCTCATTCATAAACCCCACA			II	
0.1001192	cg2114862	cg2114862	39620319	AATATTCCTTAAAATCACRTAA			II	
0.1636967	cg2114935	cg2114935	27800342	TATTAACTCAAATCCTACAAC			II	
-0.106169	cg2115365	cg2115365	48737317	AACTACT	60749334	AACTACT	I	A
-0.101365	cg2115638	cg2115638	62695318	CCCATCC	38725337	CCCATCC	I	T
-0.158663	cg2115816	cg2115816	37710386	AAATTAA	13616441	AAATTAA	I	A
0.1226372	cg2115850	cg2115850	51683349	AACAACA	24639308	AACGAC	I	A
0.1151745	cg2116014	cg2116014	39644459	AACACTTATCTTATTATACTAC			II	
-0.188139	cg2116430	cg2116430	74616396	ACTAATA	19793383	ACTAATA	I	A
-0.203834	cg2116740	cg2116740	36707329	ACACCAA	28725425	ACACCGA	I	C
-0.12051	cg2116905	cg2116905	66643428	AAAAATTTATCAAATACTAAA			II	
0.1231564	cg2117568	cg2117568	33757409	AACCACRAACCAACTAAACRT			II	
0.1174456	cg2118609	cg2118609	22682417	ATTCCCAACAAAATACAATAC			II	
0.1020989	cg2118706	cg2118706	33657429	AATAAAAATAAAACTCCCAAA			II	
0.1044651	cg2118719	cg2118719	16608507	AAAAAACAAAACCAAACACRA			II	
-0.105599	cg2118777	cg2118777	22600395	AAAAACA	11635390	AAAAACA	I	A
0.107557	cg2118840	cg2118840	48623506	TAAAAACAAAAACACAACAAA			II	
-0.111199	cg2119512	cg2119512	24682453	TTCAATCACRACTTAATTTAAA			II	

0.1158072	cg2119733	cg2119733	14633388	CTACACC	50615402	CTACGCC	I	T
0.1028107	cg2119992	cg2119992	59607454	ATCCTTAACCTTCTCAAAACA			II	
0.2334414	cg2120227	cg2120227	54709323	ATTATCATCRACTTCATTTTT			II	
-0.261877	cg2120324	cg2120324	16695486	AAACCAAACTAAATAACTTCC			II	
-0.1245	cg2120795	cg2120795	28669333	ATAAACA	35692508	ATAAACC	I	T
0.1538031	cg2120827	cg2120827	43681422	CTTCTAA	16804410	CTTCTAA	I	A
0.1481028	cg2121064	cg2121064	15645328	TCRTTTTACCTTTAAAAACCTC			II	
0.1894664	cg2121742	cg2121742	67633484	TTCAAAAATACAATTTAAAAC			II	
-0.101107	cg2121754	cg2121754	29667425	CAATAAA	31734421	CGATAAA	I	C
-0.162021	cg2122184	cg2122184	11714457	CACCTAA	17682427	CACCTAA	I	C
-0.101983	cg2122957	cg2122957	72766402	ATTAACA	28702423	ATTAACG	I	A
-0.113122	cg2123248	cg2123248	13630343	CAACCTT	40804496	CGACCTT	I	T
0.1326327	cg2123403	cg2123403	44734473	CTATATACTTTCTAATAACCTA			II	
-0.404437	cg2123408	cg2123408	14786388	TACTATCTCAATTATTCACTAT			II	
-0.134377	cg2124244	cg2124244	17615461	RACTTTCAAATACCTCTATAA			II	
0.2346141	cg2124306	cg2124306	10697439	TTATTAACCAAATAACTTCCA			II	
-0.192065	cg2124413	cg2124413	42731360	CAAAAA	68807439	CGAAAA	I	T
0.1153308	cg2124772	cg2124772	44771401	TCAACCTACTTTCTAATCATAT			II	
-0.122465	cg2125197	cg2125197	28692399	AACTTTC	22688415	GACTTTC	I	C
0.1042213	cg2125729	cg2125729	11648326	CCTCCCCTTTATATACCCRACR			II	
0.1368731	cg2126554	cg2126554	22798463	AAATATCAAAAAAAATATATT			II	
0.1059971	cg2126591	cg2126591	54640409	CAATCCC	37717456	CGATCCC	I	C
-0.134398	cg2127227	cg2127227	54669345	ATATAAACTTCACRTATACTTT			II	
-0.166636	cg2128032	cg2128032	38729303	CATAACTTTTAAAAAATACCA			II	
0.100632	cg2129134	cg2129134	39752480	CCATCTTCAAAACTCTAAATT			II	
0.1816685	cg2129185	cg2129185	32715333	TAACAAACATAACAACTAAAA			II	
0.2211905	cg2129736	cg2129736	43669411	RTATTCACCCTAAATATTTTCC			II	
-0.112148	cg2130099	cg2130099	10605381	TAAAAA	14789475	TAAAAA	I	A
0.2676408	cg2130134	cg2130134	16715416	ACAACTCTAATATAAAAACAA			II	
0.1165125	cg2130428	cg2130428	54764434	TAAACCTATAATTTACACAAA			II	
0.122535	cg2132310	cg2132310	50718335	TAAACCACATCCTCCCAATAA			II	
-0.10641	cg2133181	cg2133181	39744307	TCTACAC	14634387	TCTACGC	I	C
0.1116381	cg2133230	cg2133230	26794493	CCRCCAATAACRACACCTCAA			II	
0.1182245	cg2134032	cg2134032	63719354	CCCAAAA	44756317	CCCAAAA	I	A
-0.10123	cg2134594	cg2134594	66710318	TTAAAAA	21782313	TTAAAAA	I	A
-0.156707	cg2138531	cg2138531	72739466	CCTTCTACCCTATATTAAAACC			II	
0.1585353	cg2138574	cg2138574	67616437	ACATAAA	74709458	ACATAAA	I	C
0.1393516	cg2139270	cg2139270	19729465	TAATCRACTAAACRAAATTTT			II	
-0.100378	cg2139754	cg2139754	31744475	ATCTATATTACTAAAAATATA			II	
0.1342022	cg2140085	cg2140085	43710318	CTTTTCACTTCTATATTATCCT			II	
-0.183855	cg2140493	cg2140493	60704396	AAAAAA	51742335	GAAAAA	I	A
0.111352	cg2140881	cg2140881	34738319	CTTATACTTTTTAACTTCRATT			II	
0.1696	cg2141490	cg2141490	15671471	ATTCTCCAACAATTTATAAATT			II	

0.1292825	cg21415227	cg21415227	65715345	AAAACACCTAATAAAACAAAT			II	
0.2126825	cg21435684	cg21435684	35794359	ATAACAC	57688310	ATAACGC	I	A
-0.107006	cg21436572	cg21436572	37779393	CATAAAT	35648401	CGTAAAT	I	A
-0.128001	cg21437417	cg21437417	29648403	TAATCCRAAAAACTAACACRA			II	
0.1381845	cg21440776	cg21440776	25778431	AATATAATTCAAATTCTCTTTT			II	
0.1622816	cg21442271	cg21442271	17615445	TATACAATATCCTCATTAACRA			II	
-0.142427	cg21445553	cg21445553	33647476	CAATAAC	14602378	CGATAAC	I	C
0.2191097	cg21446772	cg21446772	69795464	CCCTTCTATCTCCCACAATACA			II	
0.1862804	cg21446981	cg21446981	69682374	CTTTAAAAAACCCTAACTATTT			II	
0.17848	cg21450228	cg21450228	46640502	CTAAAATTACTTTTACAAAAA			II	
0.1092511	cg21450627	cg21450627	74746464	ATTAAAATACAAAACCTATAA			II	
-0.153065	cg21450784	cg21450784	55615448	AACATCA	70740454	AACGTCA	I	A
0.1174245	cg21461981	cg21461981	21782468	AAAAATCTATAAAAACTCCTC			II	
-0.106449	cg21471580	cg21471580	11682463	CATATAA	40651448	CATATAA	I	C
0.1055397	cg21474104	cg21474104	18751494	TTTAAAATCCCRAAAACATTA			II	
0.1387815	cg21474247	cg21474247	27742412	ACTTTTAACATTATCATAAAA			II	
-0.106571	cg21482472	cg21482472	69797492	CCCAACA	61690493	CCCGACG	I	A
-0.110409	cg21483883	cg21483883	37804335	ATTTAAA	36737432	ATTTAAA	I	T
-0.12067	cg21484940	cg21484940	20628314	AACCACT	57756386	AACCGCT	I	A
0.1241345	cg21490751	cg21490751	19684498	CAAAACTAACATACTAAAAAA			II	
-0.107307	cg21493951	cg21493951	27713418	TAAAACA	48651339	TAAAACA	I	A
-0.177075	cg21498547	cg21498547	45773411	TAACCACAAACAAAATAACTT			II	
-0.121878	cg21513803	cg21513803	32806307	CAAAAACAAAAAACATAAATA			II	
-0.140441	cg21524061	cg21524061	26665478	TCCRAAAAACAACCATTCCCT			II	
0.1412847	cg21526778	cg21526778	28675375	ACTACTTCTATTTCTAAAAAC			II	
0.1091157	cg21527078	cg21527078	42730477	ACAATCC	47738478	ACAATCC	I	T
0.1153879	cg21527616	cg21527616	38647423	CTATATCCTATAACCRAAACR			II	
0.1281613	cg21528927	cg21528927	14672460	ATAATCAATAAACRAACTTCT			II	
0.1080016	cg21529477	cg21529477	71704423	CRTTACCAAAAACTAATTACR			II	
-0.144249	cg21530267	cg21530267	59617486	RAAAAATCTACAATCATAATC			II	
0.1257265	cg21531389	cg21531389	41625395	TTAAATCACTAATACCAAAAA			II	
-0.123958	cg21535947	cg21535947	39635363	AAACTTA	52656337	AAACTTA	I	C
0.1234834	cg21537187	cg21537187	24764306	CTCCCTCTCTCCRTCATCCAAT			II	
0.1329616	cg21543434	cg21543434	25663371	AAAAACCCTAAAAAACCTAAA			II	
-0.120381	cg21548955	cg21548955	60786424	AACTTAA	38790471	GACTTAA	I	A
0.1031018	cg21552300	cg21552300	17661452	AACTATCRCTCCCACAAACAA			II	
-0.106889	cg21557146	cg21557146	62615452	AATTCAAATTCCTAAAACCAA			II	
-0.123711	cg21561701	cg21561701	32757473	CAAAAA	44642452	CGAAAA	I	T
0.4939809	cg21566433	cg21566433	50669491	AACRTTAAACAAATCTTTATA			II	
0.1113094	cg21574271	cg21574271	50724467	AAATTCCTTCAAATTCCTAAA			II	
0.1354442	cg21574822	cg21574822	12645459	TAATTTACRTATTACRTAATTT			II	
0.1396113	cg21578457	cg21578457	62623454	AAAAAATAACTCTTTACTATT			II	
0.2520058	cg21578644	cg21578644	11631406	AAAAACAATAAAAAATTCATA			II	

0.1010095	cg2158211	cg2158211	52731499	CACCAACATAAACAAAAATTA			II	
-0.134495	cg2158615	cg2158615	42654505	CTCATAA	16670326	CTCGTAA	I	C
-0.119195	cg2158700	cg2158700	66612314	AAAAAATCAAAAAACCTAATA			II	
0.1446179	cg2158941	cg2158941	22623481	AACTATAAAACCTAAATTTCA			II	
-0.216897	cg2159315	cg2159315	25634351	TAAAAAATACATATATATTCT			II	
-0.119574	cg2159340	cg2159340	12716411	CRTAAATAAACTCRATATAAA			II	
-0.102799	cg2159367	cg2159367	50643403	TAATTAACCTAAAAACTCRCT			II	
0.2365878	cg2159470	cg2159470	46660491	AATTACTCAATCACATTAAAA			II	
-0.111595	cg2159848	cg2159848	17665351	AATTTTAACTCATCCAATAAA			II	
0.113623	cg21605781	cg21605781	36656336	ACCAATCTTATTAACTTCTAA			II	
0.1215977	cg2160958	cg2160958	52647497	AAAAATAATATATTATATTAA			II	
0.1202484	cg2161083	cg2161083	55730303	AACAATTTTAACAATTTTAAC			II	
0.2732792	cg2161092	cg2161092	19687435	CAAATCACACTTTAAACTCCA			II	
0.1344649	cg2161362	cg2161362	10728413	AAACTATTCTTTATAATTTTCA			II	
0.1470962	cg21614201	cg21614201	42692387	AAAACATAAAACCTTTTTATC			II	
0.1081953	cg2161735	cg2161735	49799346	TTCRTCTTTCAAAATAATCCTT			II	
0.1270061	cg2162344	cg2162344	31708474	ACCAAATCATATTAAACCTTC			II	
-0.283477	cg2163084	cg2163084	13610445	TTTATCCATTTTCTTTAATTAC			II	
	cg2163494	cg2163494	38617440	TTAACAA	58629367	TTAACGA	I	A
-0.161901	cg2163587	cg2163587	52726337	AAACAA	47718377	AAACGA	I	A
0.2664737	cg2164205	cg2164205	46765335	AAAAAAAAACRTAAATTTTAA			II	
0.1013409	cg2164326	cg2164326	28801369	CCCRAAACTATACCTTATATA			II	
-0.102409	cg2164526	cg2164526	58727386	TCAAACTAAAAATTCCACAAA			II	
0.1543244	cg2164575	cg2164575	48612396	AAACAAATAACTAAACTAACT			II	
0.1023585	cg2164639	cg2164639	72635404	TAACTTCCAAAAACAAACAAA			II	
0.1709303	cg2164718	cg2164718	72714356	ACTAACCTTATTCCRATATCCR			II	
-0.111509	cg2164837	cg2164837	28640480	TAACCTC	14658488	TAACCTC	I	T
0.1203206	cg21655171	cg21655171	71731387	AAAAATTTAAAAAAATCCTTC			II	
0.1130258	cg2167071	cg2167071	22640468	ATTTTCACCATAAATCATTTAC			II	
0.106064	cg2167299	cg2167299	74799351	AAAAATAAAACAACCCTCATT			II	
0.1651715	cg2167946	cg2167946	39808413	TTCAACAAATCTAATCAACTC			II	
-0.10745	cg2169045	cg2169045	59707422	CTACCRATTTCTTTCTATTCTT			II	
0.1363128	cg21690921	cg21690921	14715322	AAAACATTCRAATCACTCCCT			II	
-0.130694	cg2169262	cg2169262	65690437	AAAAAA	49801463	AAAAAA	I	T
0.1460942	cg2169637	cg2169637	46777321	TCTCTAATATATATTTTATCCT			II	
-0.183444	cg2169776	cg2169776	72804500	ACTCCCATTCACACCTTAAAA			II	
0.1229213	cg2171237	cg2171237	29754329	AAAACTACACTACRTAATAAC			II	
-0.165693	cg2171772	cg2171772	71663496	RCRCACAAAATATACAATTAC			II	
-0.162539	cg2172279	cg2172279	60720343	CAAATCA	28699467	CAAATCA	I	A
-0.110352	cg21733531	cg21733531	33698309	ATAATCC	73719447	ATAATCC	I	C
0.2224078	cg2173506	cg2173506	37686370	AACCCAATTAATCAACATTCT			II	
-0.112021	cg2174128	cg2174128	42783350	TATATAC	70787499	TATATAC	I	A
0.2545014	cg2174151	cg2174151	32773475	AACAAAAAACCCCTACTTCTA			II	

0.1121395	cg2174199	cg2174199	38683447	AATAACATATACCTACAATCC			II	
0.1571288	cg21749951	cg21749951	72665489	AAACAACRAAAACCTAAACAA			II	
0.1222272	cg2175058	cg2175058	62758508	TTCCTCAATATAATATTATCTA			II	
-0.117666	cg2176258	cg2176258	63757329	TTAAAAACATTATTAATCCAA			II	
0.1041331	cg2176765	cg2176765	60616459	ATATATAAAATTTAATACCTC			II	
0.1672097	cg2177039	cg2177039	66640321	AAATCAAACRTCAAAACCTAC			II	
-0.139688	cg2177718	cg2177718	40634335	CATTAATATCTACAATCACTA			II	
0.1423106	cg2177898	cg2177898	15666369	AAATCACCCATTTCCTTTCTAC			II	
0.1314158	cg2178060	cg2178060	15696410	ACACCAAAAACCCCATTCAAT			II	
0.1206828	cg2178344	cg2178344	12680303	ACTAAAACTATTTAAACCATC			II	
-0.13848	cg2178367	cg2178367	60644498	TATTTACTAACCCTAACTAAA			II	
0.1175252	cg2179298	cg2179298	35623406	CAATTTCTACATCRCCTCAACT			II	
0.1091262	cg2179476	cg2179476	56615495	TAACTAAATAAAATAAACAAA			II	
0.140084	cg21805731	cg21805731	50674364	TCTTTCTAATCCCTACTCTCTC			II	
0.1158406	cg2180588	cg2180588	36696500	TAAATCTACACRTAACTAAAT			II	
-0.212596	cg2180992	cg2180992	47711327	TCTACCA	23679433	TCTACCG	I	C
0.1435485	cg21810411	cg21810411	29679377	ACCCTATAAATATTTCTAAAA			II	
-0.225851	cg21811911	cg21811911	48689493	CTCRAAACTACRAAACTCRTT			II	
-0.112993	cg2181285	cg2181285	39717419	AAAAATAAATTTAACTCTAAA			II	
0.1406311	cg2181455	cg2181455	16735421	AATATTACAATCAATACTAAA			II	
0.1096016	cg2182342	cg2182342	60751458	TTAACCCAATATTCTAATCTCC			II	
-0.286239	cg2182903	cg2182903	46608371	CCCCACC	13645391	CCCCGCC	I	C
-0.301794	cg2183093	cg2183093	31754304	AAAAATACCCTATATAAATCA			II	
0.1203685	cg2183118	cg2183118	65707402	CRCCTTCATTAAATTACCAATC			II	
0.1860765	cg2183377	cg2183377	73772414	AACTTTATCAATATTTTTCCAT			II	
0.1368726	cg2183950	cg2183950	44680459	AAAAAAC	47676368	AAAAAAC	I	T
0.1466432	cg2184163	cg2184163	55683413	CTAAAACCAAAAACTTACCAA			II	
0.1328647	cg2184292	cg2184292	66777402	TATCACRAAAAATATACTATA			II	
0.1044475	cg2184711	cg2184711	37664311	AAAATAATACTAATCCCAAAA			II	
0.1181465	cg2185433	cg2185433	11607314	TCATTATTAATTACCTAATCCT			II	
-0.100147	cg21855211	cg21855211	12780345	AAAATAAACCCCRTATACTAA			II	
0.1101924	cg2185956	cg2185956	19654372	CTACTTAAATTTCTTTTCTAAA			II	
0.1748837	cg2186067	cg2186067	50647478	CTAAATTCRCCTTACTAACTAC			II	
0.1532317	cg2186209	cg2186209	56698492	CRTCACACRACCAACACATAA			II	
0.1090682	cg2186401	cg2186401	40755448	AAATATTAAATTTATTCAACA			II	
0.1187366	cg2187003	cg2187003	37664451	ATCATCTCAAAAACCAAAAAC			II	
0.1074671	cg2188179	cg2188179	61795328	CRAAACAAAAAACRCCTAAAA			II	
0.2285498	cg2188511	cg2188511	73753465	TCCCAAA	56694324	TCCCAAA	I	C
0.1767368	cg2190232	cg2190232	60770320	ACACAAAAAACAAACCCAAA			II	
-0.122788	cg2190239	cg2190239	70630496	AAAATAAAACCTAAATTTCAA			II	
-0.109372	cg2190364	cg2190364	42616369	ACAAAA	58643484	ACGAAA	I	C
-0.119354	cg2191127	cg2191127	15730437	CCTCTCCTAAACACCRAAAAA			II	
0.220919	cg2191333	cg2191333	26716330	CTATAAC	71672317	CTATAAC	I	A

-0.126322	cg2191591	cg2191591	53602438	AAACTCA	24619471	AAACTCA	I	A
-0.114691	cg2192056	cg2192056	47651462	CCRAACTATATTCCTACAACT			II	
-0.106232	cg2192680	cg2192680	41692372	AACATAAACAAAAACTTATAA			II	
-0.239354	cg2192799	cg2192799	25632330	CCCAATCACCAAACCCACTAA			II	
-0.187237	cg2193171	cg2193171	24684390	ATAAAAT	25616423	ATAAAAT	I	C
0.1098549	cg2193198	cg2193198	73685456	AAATTACTCCTAATCAACACA			II	
-0.179032	cg2193236	cg2193236	26719328	TTAAACC	25696394	TTAAACC	I	A
-0.102406	cg2193739	cg2193739	69623491	TTTCAAATAATAATAAAACTC			II	
0.1097676	cg2193854	cg2193854	69691430	ATTCATAAAAATAAACACCTA			II	
0.146566	cg2194563	cg2194563	30642361	AATTCAA	56781505	AATTCGA	I	A
0.1385775	cg2194663	cg2194663	56710498	CCTAACAAAATTAAACAAACT			II	
-0.132747	cg2195172	cg2195172	42767403	CTACAAA	25663443	CTACAAA	I	C
-0.155773	cg2195465	cg2195465	24766355	CTCTAACCTAAAAACTCTAAA			II	
-0.107812	cg2195839	cg2195839	46665387	TAAACATAAACTCCTATAAAT			II	
-0.120381	cg2196979	cg2196979	63779384	AAACACC	44754485	AAACGCC	I	T
-0.151352	cg2197813	cg2197813	11782505	AAACATTTAACACCRTACTAA			II	
0.1501139	cg2199481	cg2199481	16603301	AAATTTAAATCACACTCTTAC			II	
0.1617525	cg2199565	cg2199565	63727351	AAATATTATTTTACTAATAATC			II	
-0.119883	cg2199606	cg2199606	29712302	ACTACCACRCCCTAACCACAT			II	
0.1948797	cg2199772	cg2199772	55681501	CTTAACA	70735507	CTTAACA	I	C
0.1921954	cg2200721	cg2200721	13793461	ACACAAACATCAATACTTTCA			II	
0.1282242	cg2201411	cg2201411	31741504	ACTCAAC	18749447	ACTCAAC	I	A
-0.171597	cg2201808	cg2201808	18651414	AAAATAATAAATTTTTACTAA			II	
0.1561897	cg2202608	cg2202608	60740480	CAATTTCCAAATAATTATTTTT			II	
0.1779488	cg2202901	cg2202901	40750308	TCCTACA	10720446	TCCTACA	I	A
0.1399077	cg2202987	cg2202987	29656450	CCTAAAAACAACTTATTTCAC			II	
0.1130586	cg2203202	cg2203202	62667465	AAAAAACTCATAAATAAAATC			II	
0.3389283	cg2203724	cg2203724	44755506	TATTCATTCTCTAACTTTAACC			II	
-0.163749	cg2204020	cg2204020	27756392	TCCAAAACCATAAAATTATAA			II	
0.1289569	cg2205163	cg2205163	32731457	CCTAATAACCCTTTCCTATAAC			II	
0.1856953	cg2205491	cg2205491	18731335	AAAAAAAACAATTTTTAAAAC			II	
0.1015039	cg2206404	cg2206404	72703306	CAAATACCTACTACTTAACTC			II	
-0.177348	cg2206840	cg2206840	66663338	CTTATTA	27656445	CTTATTA	I	T
-0.117384	cg2206944	cg2206944	74738411	CAAATCT	27704357	CAAATCT	I	C
0.1599643	cg2207642	cg2207642	61764309	AAAAACCCCTAAAAACTTATA			II	
0.2672325	cg2207661	cg2207661	12701365	ACTAAAAAATTCCACRAAATC			II	
0.1171459	cg2207731	cg2207731	39626373	ACCTCCTCCCTCATCAAATATT			II	
0.1276506	cg2207845	cg2207845	53692421	AAAAAAATTATCCTCATAAAT			II	
-0.100945	cg2208280	cg2208280	11799427	ATCACAC	20794463	ATCGCGC	I	C
	cg2208505	cg2208505	24730483	AAACTTA	57749407	AAACTTA	I	C
	cg2208735	cg2208735	12768443	ATTAAAAAAATATCACCTCCA			II	
-0.378596	cg2209492	cg2209492	37642502	AAACCCAACCAACAAAAAAC			II	
0.1103911	cg2209526	cg2209526	30706332	CATTAAAATATCTTAATTCTCA			II	

0.1183908	cg22105162	cg22105162	56718419	CTAACTAAACCAATTACATACA			II	
-0.222569	cg22106220	cg22106220	37606332	CAATAAACCAATAAAAATAAT			II	
0.1211602	cg22110158	cg22110158	56661428	CAATAAACAAAACACTAACTC			II	
0.1020842	cg22111167	cg22111167	47652314	ATCTAATTCCAAAATATTTTCR			II	
-0.105747	cg22111694	cg22111694	60693421	TACAAAACAAACTTCRTATTAA			II	
-0.185098	cg22117893	cg22117893	59706422	TTAAAATAACCACACCCTATTC			II	
0.1003012	cg22118297	cg22118297	15809455	CATTCCTCTACCCTCCAAATAT			II	
-0.163678	cg22121557	cg22121557	41734419	TAACAAC	40791476	TAACGAC	I	C
0.1536731	cg22127309	cg22127309	27724371	ACTCAAACCAAAAAAATCACA			II	
0.1160674	cg22140866	cg22140866	53785452	AACTAACTATCACTCCTACATT			II	
0.1504182	cg22142142	cg22142142	37691483	ATACRAAAAATCRAAAACCAC			II	
-0.123414	cg22143285	cg22143285	74665360	ACTTAATTAACACTACAAATTT			II	
-0.102394	cg22144900	cg22144900	73794378	ACACCCA	38745448	GCACCCG	I	A
-0.106306	cg22147163	cg22147163	47795484	RAAATAAACTTAAAACRCACA			II	
0.1193317	cg22151773	cg22151773	33752365	ATTACTTTTAATATCTATAAAC			II	
-0.148011	cg22152229	cg22152229	11755402	CAATACC	12615500	CAATACC	I	C
0.1419997	cg22159647	cg22159647	10709400	CCATCAAATAAAAATTACCAA			II	
0.1086847	cg22161115	cg22161115	38611463	AACTTCCAAAACTAAAATAAC			II	
0.1244215	cg22164009	cg22164009	49680432	CAAAATCAAACCTAAAACACT			II	
-0.147993	cg22172057	cg22172057	43740344	AAAAATAAAAACCACTTATAC			II	
-0.104427	cg22185043	cg22185043	38609393	AAAAAAA	50609306	AAAAAAA	I	A
-0.203054	cg22189786	cg22189786	50767389	CCTTTAA	72751456	CCTTTAA	I	A
-0.191217	cg22190023	cg22190023	37667321	AATCCTTCCCCACAAACATTAC			II	
-0.169921	cg22198853	cg22198853	61682431	TTATCTCC	12810408	TTATCTCC	I	C
-0.127408	cg22199969	cg22199969	73764363	AATAAAA	45746334	AATAAAA	I	C
0.1001351	cg22202381	cg22202381	73628497	TACATAATAATAACTTAAAAA			II	
	cg22203829	cg22203829	67639510	CAAAATTAAATTATCCATCTCT			II	
0.110246	cg22209918	cg22209918	30609421	CTACATAAAAACAATACTATA			II	
-0.145116	cg22210497	cg22210497	24779331	AAAAAAATTAAACACCTTTCA			II	
0.1143598	cg22214800	cg22214800	62789388	AAAAATCTCCTACTAAAAACA			II	
0.1078504	cg22216196	cg22216196	69605422	ATACTCA	58784418	ATACTCA	I	A
0.1270478	cg22222799	cg22222799	47789410	AAAACTTCTACAAACAAACAA			II	
0.1048878	cg22223119	cg22223119	39794491	CACRTAACATCAATCTTATATC			II	
0.1126444	cg22231758	cg22231758	13740491	AAACAAA	69793339	AAACAAA	I	A
0.1463968	cg22234930	cg22234930	32803418	TAAAAACAAATCAAAATATAT			II	
0.1093373	cg22236066	cg22236066	25762347	TAACCTCATCCTCTCTAAATTT			II	
-0.173289	cg22237018	cg22237018	27797434	ATACCTACCTTTCTAATAAAAA			II	
-0.173454	cg22237495	cg22237495	59714316	TTCTTACTCTTCACAATACTAC			II	
0.1600306	cg22237644	cg22237644	15786353	CAAATACTTACTATATACTTAC			II	
-0.114769	cg22242857	cg22242857	61748404	AATCAATATTTTTTATTTTATA			II	
-0.120672	cg22243109	cg22243109	39666377	TCAAAAC	19677413	TCAAAAC	I	A
0.1012938	cg22247748	cg22247748	20605478	CTCTTCTACAACAAAATCRACA			II	
0.1241471	cg22251684	cg22251684	59672310	AAATCTACTTTACTTAACTAAA			II	

0.1506361	cg2226089	cg2226089	17786473	AAAAACTACACTCAAACTCAA			II	
0.1417457	cg2226498	cg2226498	15656323	TAACTCCAAAAAATACAAAAC			II	
0.1000473	cg2227411	cg2227411	33784443	CTACACAACATCAACTTATTC			II	
0.1030949	cg2227808	cg2227808	56639356	ACTACAAAACTACTTCCCCTA			II	
0.127737	cg2228208	cg2228208	48656396	AAATCTCACRTCTCTACTAAA			II	
0.1236263	cg2229014	cg2229014	28751506	AACTCTA	70754366	AACTCTA	I	A
-0.104149	cg2229658	cg2229658	57770413	CRCTAAATTTCAAACTAAATA			II	
-0.275863	cg2230451	cg2230451	53635488	CCCTTTAATTAAAATCAAAAT			II	
0.1454996	cg2230600	cg2230600	71772431	ACAAAAAAATATTTTAAAAATT			II	
0.1171365	cg22316451	cg22316451	36810353	CTAAACTTTAAAATACRCTAC			II	
-0.201358	cg2231661	cg2231661	34764306	CCAACAA	67739463	CCAACGA	I	A
0.1026057	cg2232132	cg2232132	49710463	CAAATATACTTTCCAAAACTA			II	
-0.117895	cg2232582	cg2232582	43632388	TCTTAAATATCCCCAAAATCC			II	
0.1465127	cg2233580	cg2233580	39743399	CAAATCA	34757343	CAAATCA	I	A
0.3074989	cg2233686	cg2233686	55637506	CAAAATCTTAAACCCAAAAAA			II	
0.1686523	cg2233762	cg2233762	36714448	AACACCAATCTTTACATAAAA			II	
-0.165153	cg2234050	cg2234050	12808405	AACTTTC	24758434	GACTTTC	I	T
-0.237885	cg2234131	cg2234131	70701466	TCCRAAACCACTAAAAACTAT			II	
-0.115766	cg2234372	cg2234372	26622337	ACAATAA	59671385	GCGATAA	I	C
-0.127376	cg2235277	cg2235277	47718389	CRACRACRACTACACTAAAAC			II	
-0.111448	cg2236110	cg2236110	63806459	AAATATACAACACCAATTCTA			II	
0.1217917	cg2236489	cg2236489	57682467	TTATTAATTTCTCTACCCACTA			II	
-0.149448	cg2236770	cg2236770	65647306	CTAAAAC	59700369	CTAAAAC	I	T
0.1166649	cg22367981	cg22367981	25645372	CTTAAACTTCTTTTTAACTCTA			II	
0.2358912	cg2237309	cg2237309	35685405	TTTTCCCTTCAATTAAAAATCT			II	
0.1052707	cg2239004	cg2239004	59608335	ATAACAAAATACRCACATCCA			II	
0.6942551	cg22402121	cg22402121	23779301	TAAATAT	34774468	TAAATAT	I	A
0.1140352	cg2240810	cg2240810	60731414	ACTACCCAAATAATTAAAAAC			II	
-0.112226	cg2241118	cg2241118	47682498	AAATTATTCRTTCCTCCTATTA			II	
0.1224598	cg2242051	cg2242051	17693448	AAAAACAAAATTATAAAAATC			II	
0.135219	cg22422251	cg22422251	73660487	ACAACRATACTCTATAATTAA			II	
0.1227504	cg22428691	cg22428691	51644345	AACTACTCCTATCAACTATTC			II	
0.1174997	cg2243740	cg2243740	36771482	AAAACACTATAAACTCAAAAC			II	
0.1461534	cg2244261	cg2244261	62754307	CCTATCCAATAAATCAAAACR			II	
0.5093445	cg2244321	cg2244321	65611468	AAAACCTTCAAAACAAACATA			II	
0.1501974	cg2245040	cg2245040	27629332	TCCCTACAACCTCATAAATAA			II	
-0.124257	cg2245223	cg2245223	11725483	AAACTCC	42645456	AAACTCC	I	C
-0.112096	cg2245566	cg2245566	52783348	CAATCCA	41720477	CGATCCA	I	T
0.1152522	cg2247333	cg2247333	27676319	AAACCTATAATCTAAAAACTT			II	
-0.106885	cg2248116	cg2248116	66810335	CCATAAT	19775311	CCATAAT	I	A
0.2748025	cg2250230	cg2250230	47810318	ATAAATAAATATATCTCACAC			II	
0.2541334	cg2250814	cg2250814	59700445	TAATCAAAAACTATAACCCAC			II	
0.1202094	cg2250893	cg2250893	73600419	ATACAAAATAACCTTTTTAAA			II	

-0.116953	cg2250911	cg2250911	58605415	ACTAATT	63801383	ACTAATT	I	A
0.1104484	cg2253023	cg2253023	48703391	CAAACAAATAAAATCRAACTA			II	
-0.110653	cg2253428	cg2253428	44735506	CCAAACA	51738369	CCAAACC	I	C
-0.13292	cg2254125	cg2254125	14721442	AATAAAATAAAACCTAACAAA			II	
0.1673455	cg22542451	cg22542451	17773359	ATAAATCTTATCTACCTTAAA			II	
0.1026473	cg2254337	cg2254337	59706414	TCTATCCACCTAAATCCCATA			II	
-0.227996	cg2254392	cg2254392	63771360	AATTATTCTCAAACTAAATTTA			II	
0.1733639	cg22545121	cg22545121	62657346	CAAACCC	49710451	CAAACCC	I	A
0.1157399	cg2255081	cg2255081	72640301	CAAACTCTATAACTTACAAAA			II	
0.1201236	cg2256179	cg2256179	43675403	TTTATCCTACCTTAATACTATA			II	
0.1458736	cg2256381	cg2256381	35731370	ACAAACACTTAACACCTCTAA			II	
-0.153154	cg2256949	cg2256949	61810439	CCTAAAA	10741321	CCTAAAA	I	A
0.1204345	cg2257626	cg2257626	46701454	TTAAAAAACTATAAATTCCAA			II	
-0.122151	cg2257760	cg2257760	53709439	ATACCCCTAATAACRATAACT			II	
0.1047185	cg2257907	cg2257907	55763419	TCTCCTATTCTAAAAAATCTAA			II	
-0.128235	cg2258595	cg2258595	29749339	ATTATTATCCTAATATTCTAAT			II	
0.1149976	cg2258760	cg2258760	30659497	AAAAACCCAAATCATACTAAC			II	
	cg2258814	cg2258814	12768471	AATCCAA	16693306	AATCCGA	I	C
-0.107249	cg2258972	cg2258972	73648503	TCAAATAAACAAAAACCAACT			II	
0.1103241	cg2258982	cg2258982	63618321	TCTACCCCCACTAAATAATAA			II	
0.1016623	cg2259721	cg2259721	43696442	RAATCAAAACTTCAAAAACCA			II	
0.1065768	cg2260141	cg2260141	54726304	CAATAATTCCCATAACTCTCC			II	
0.1036603	cg2260326	cg2260326	27673429	TAAACAAATCTTACTCCTATA			II	
0.1206228	cg2261112	cg2261112	23694300	AAACAATAAAATATCTATTAT			II	
0.1032549	cg2261244	cg2261244	44674486	CTCAAAC	13747358	CTCAAAC	I	T
-0.106823	cg2262068	cg2262068	48767360	TCCAAAACTCAAATAACTTAA			II	
-0.115532	cg2262289	cg2262289	38644415	CCAAATCRCTACATACCTATA			II	
0.1558413	cg2262490	cg2262490	30641306	CATCATTCAAAACAATAACTA			II	
0.1132473	cg2262702	cg2262702	35617474	CAACTCC	36799401	CAACTCC	I	T
0.1016591	cg2263161	cg2263161	49803433	AAAAAAAACTAAATTACCACA			II	
-0.155254	cg2263252	cg2263252	35766468	ATACAAC	37606499	ATACAAC	I	A
0.1037528	cg2263463	cg2263463	18779345	AAATAAACAACTAAATCTATA			II	
0.1170984	cg22635491	cg22635491	63726451	CACCATA	34610498	CGCCATA	I	A
0.1289597	cg22637941	cg22637941	67726462	CTTAAAATTTTCAAACTCAAA			II	
0.1002604	cg2264081	cg2264081	20771450	ACTTTTAACCAATTATTTCCAC			II	
0.1112375	cg2264768	cg2264768	16783379	CCCAAAAAAAACAACTCCTAC			II	
0.1257066	cg2265314	cg2265314	62627395	CCTTCCA	48804333	CCTTCCG	I	A
-0.178109	cg2265395	cg2265395	39672463	AAAACA	52765451	AAAACG	I	A
-0.165277	cg2265705	cg2265705	31653389	CCTATATATACCCTAAAACTA			II	
-0.114334	cg2265926	cg2265926	64795501	ACAACCA	35739490	ACGACCA	I	A
-0.104045	cg2266093	cg2266093	47756478	CCTTCCT	13763395	CCTTCCT	I	A
0.2935995	cg2266429	cg2266429	29680347	ACRTCCAAAACACAAAAAATA			II	
-0.10875	cg2267260	cg2267260	11633459	ACATAAA	57720491	ACGTAAA	I	C

-0.228449	cg22673542	cg22673542	55723396	AAAAACCTTAAAATAACCTAC			II	
-0.107931	cg22676075	cg22676075	36774424	AATAAAA	49760474	AATAAAA	I	C
0.1119271	cg22678674	cg22678674	32674499	AACAATA	46613423	AACAATA	I	A
0.1014403	cg22678739	cg22678739	10612410	TTAATAACRACTTACTAAAAA			II	
-0.108005	cg22679014	cg22679014	27807312	RAAATAATTTCTTCATTCATCT			II	
-0.100055	cg22681709	cg22681709	46668356	TACTAATAACTCACTACACATA			II	
-0.217676	cg22681945	cg22681945	49730486	CAAAATAAAAAAACTAAATCA			II	
0.1038514	cg22682200	cg22682200	58691497	TTTCCRCACACAACRATAACTT			II	
0.105518	cg22683010	cg22683010	57666362	CTTCATACRCRACTTCATATTT			II	
-0.123427	cg22683036	cg22683036	19808382	TTTTCCATATTCAAATTATTTT			II	
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-0.163609	cg22696546	cg22696546	17676435	TAACRACTACRTAATACCTAA			II	
0.1653413	cg22699314	cg22699314	66748409	AAATTTACRCAAAACACAAAA			II	
0.1270798	cg22699620	cg22699620	49665394	ACATATTTCTTTTCCCRTTCAA			II	
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-0.153472	cg22700790	cg22700790	67694374	CCAAACT	53774307	CCAAACT	I	A
0.1082546	cg22700822	cg22700822	22648488	TTTAATCTAAATTCTATACACC			II	
-0.114425	cg22705954	cg22705954	53786440	AAAAAAAACRAACRCCTAAAT			II	
0.1143681	cg22708961	cg22708961	54703456	AACACTA	70629384	AACGCTA	I	A
0.115006	cg22711676	cg22711676	55697508	TATATAAATATCTAAATACAC			II	
0.1008368	cg22716262	cg22716262	70793361	AATTTTATTTCAACTTAACTTC			II	
0.394307	cg22717235	cg22717235	23800358	CCAAAAATTCCTAATCCCCAA			II	
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0.1023447	cg22727432	cg22727432	16809362	ATAACAAAACTAAAAAATTCC			II	
0.1100367	cg22730029	cg22730029	12650394	TAAACCCAATTATTCTACTAAA			II	
0.1941114	cg22730047	cg22730047	73676317	AACCAAA	15721361	AACCAAA	I	A
0.1077178	cg22732126	cg22732126	27620327	CAACCCTAACAAATCTTTAAA			II	
0.2367625	cg22741595	cg22741595	26754377	TCTATTCAAAAACCAAAATCR			II	
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0.1049562	cg22745624	cg22745624	70606419	ACRTATTTCAAAATCRAAACC			II	
0.1173385	cg22746865	cg22746865	60650501	AAACCTAAAACTCTAAAAACC			II	
-0.118266	cg22747650	cg22747650	63759321	ATATTAAACAAAAACTTAAAA			II	
0.1044173	cg22759261	cg22759261	31682388	ATTTCCATTAAAATATACRTTT			II	
0.1277982	cg22763593	cg22763593	41798424	AATAATAACTATAAAAAACTC			II	
0.2717314	cg22764591	cg22764591	19801466	AAACCCA	58622419	GAACCCC	I	C
0.311546	cg22771759	cg22771759	63691435	AATACCCAAAAACCACAAAAA			II	
0.1454968	cg22775600	cg22775600	69745429	CCTATAAACTAACTCAAAATT			II	
0.2774979	cg22777560	cg22777560	14786382	TTACACCAATAAATACATCATT			II	
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0.1451589	cg22786472	cg22786472	13717427	CCAATATAACTCTTCCTTAACT			II	
0.1263264	cg22786748	cg22786748	49745403	AACCAAACACAATCCCTATTCT			II	
-0.148722	cg22789318	cg22789318	70685378	AAAAACC	22676408	GAAAACC	I	T
-0.103867	cg22789982	cg22789982	31797416	AAAAAAT	59652457	AAAAAAT	I	C

0.1115251	cg2279087	cg2279087	46786313	ATCATATACCATATATCAAAC			II	
-0.120545	cg2279198	cg2279198	67764353	AATAAAA	57737497	AATAAAA	I	A
-0.10237	cg2279306	cg2279306	57707436	ACCAAAC	15678323	ACCAAAC	I	C
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0.1113901	cg2280201	cg2280201	74740492	ACATCCAACATTTAACATCAC			II	
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0.121536	cg2281261	cg2281261	12751429	CCCATAAAATAATAAAACTCA			II	
0.1050116	cg2281402	cg2281402	27604327	ATCAAAT	36741365	ATCGAAT	I	A
-0.115589	cg2281646	cg2281646	30630456	CTAAAAA	13682306	CTAAAAA	I	A
-0.15238	cg2282657	cg2282657	48779380	AATACTA	19609302	AATACTA	I	C
-0.135924	cg2282918	cg2282918	30777395	ATCRTAAAAACTCCACCTAAA			II	
0.1278018	cg2283347	cg2283347	69655472	AAAACTTAACCCCAACCATTT			II	
0.1723925	cg2283414	cg2283414	39767488	CAAAAACACTACAACTAAACT			II	
0.121069	cg2283454	cg2283454	73755435	TAAATCAAAAACTCTAAATTA			II	
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-0.100633	cg2285632	cg2285632	60663333	CAACATA	18745388	CAACGTA	I	A
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-0.113395	cg2289106	cg2289106	67760498	CAACACC	37743313	CGACACC	I	A
0.1107113	cg2290047	cg2290047	47648350	CTCTAAATAACCCTAAACCTC			II	
0.142488	cg2290440	cg2290440	63689409	CTCACTTTTATCTTACAACATT			II	
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0.1383104	cg2290729	cg2290729	25656423	CCACCCCTACAAAATAATACA			II	
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0.1606972	cg2291734	cg2291734	33807428	RCAATCTCCCTTCTACTAATAA			II	
0.105298	cg2291804	cg2291804	56689381	TTTCCCRAAAACACCCAATAA			II	
0.2218972	cg2292686	cg2292686	21730447	CTCTCTCAACATTTTCCCCTAC			II	
0.1252899	cg22931151	cg22931151	44794321	CTAAAACTTTAAAACATAATA			II	
0.1066338	cg2293145	cg2293145	33604408	TATTAAACTTCATTACAATAA			II	
0.2850172	cg2293380	cg2293380	53623508	ATCATTCTCAAATTTCCCTAAA			II	
0.1146722	cg2293542	cg2293542	58611458	CAAAATCCAAAAACCTAACTA			II	
0.1204156	cg2293625	cg2293625	29744499	CCCCTCTAATATAACTCTTTA			II	
0.1102591	cg2293735	cg2293735	10764462	TATAACCTCAAATATCRTATTT			II	
0.1082474	cg2293970	cg2293970	11632479	CAAATCCTAAACTAACTACCC			II	
0.1271241	cg2294480	cg2294480	24604355	TTTTTTTTTTTCTACCTTCAAA			II	
-0.11463	cg2294976	cg2294976	42718400	CRATACRTACAATAAAAATCC			II	
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0.118256	cg2295368	cg2295368	59715476	AACCTAAATTTCTCCTAAAAC			II	
0.1664849	cg2295663	cg2295663	25629423	ATTACAT	41654421	ATTACAT	I	T

0.1068175	cg22969108	cg22969108	51682366	ACAAATCATATTAAATCAATTC			II	
-0.222471	cg22970003	cg22970003	18714369	TAACTTATTCCCAATACTACTC			II	
-0.107723	cg22971216	cg22971216	27643360	AAAACTACTTCCCCTAACTTCC			II	
0.2320217	cg22972806	cg22972806	46726489	CACACAA	43680309	CACACAA	I	A
-0.115335	cg22979783	cg22979783	67806326	ATATAAC	24759318	ATATAAC	I	T
0.15683	cg22984587	cg22984587	37602338	AAATAAC	29733506	AAATAAC	I	C
-0.179294	cg22986662	cg22986662	32810386	AAAAAAC	62806350	AAAAAAC	I	A
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-0.112528	cg22992497	cg22992497	46762356	TCTAAAATTTATCAACAAAAC			II	
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-0.157546	cg22993195	cg22993195	44704364	AATAAAA	22743479	AATAAAA	I	A
0.5956249	cg22996768	cg22996768	43608419	TTCCATTATACCCTAAAACCAA			II	
0.1023701	cg22999620	cg22999620	31727365	AACAAAA	47793449	AACAAAA	I	A
-0.359266	cg23005102	cg23005102	68655481	AAAAAAC	54730315	AAAAAAC	I	C
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0.2277082	cg23009094	cg23009094	59611434	AAAATAC	51731434	AAAATAC	I	C
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0.1437973	cg23012310	cg23012310	50664382	AAATATT	30761362	AAATATT	I	C
0.1880468	cg23012654	cg23012654	12657463	ACAACAACTATCCTAAATAATA			II	
-0.236082	cg23019589	cg23019589	31615444	CAATTTAAATTAAACTCAACTA			II	
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0.1871668	cg23028740	cg23028740	49756401	ACTCATTCTTATTTTTCAAAAC			II	
0.1130295	cg23030200	cg23030200	37721486	AAACAAAAAATACCTCAAAAA			II	
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-0.111165	cg23037265	cg23037265	36602441	TATAATAAAATTAATAACCCTA			II	
0.1059931	cg23045277	cg23045277	61622368	ATCCTTAAAAACATATTCTTTC			II	
0.2055765	cg23051926	cg23051926	39676303	ATATACTACCAATTCCTTAAAA			II	
0.2737093	cg23053506	cg23053506	68659434	TAAAACC	44808484	TAAAACC	I	A
0.3082822	cg23058319	cg23058319	36693466	CCTAACC	67652467	CCTAACC	I	A
-0.102766	cg23061114	cg23061114	46647510	AAACCAA	28752344	AAACCGA	I	A
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0.2087563	cg23066280	cg23066280	72707452	CCAACCA	57736329	CCGACCA	I	T
0.1242616	cg23069046	cg23069046	53733425	CTTTCTTTACTTATAACAAAAA			II	
-0.164267	cg23074932	cg23074932	28749411	CRCCAAAAACTTAAATTTAAAA			II	
0.1060148	cg23075611	cg23075611	56645475	AATCCTTACAATTATCTTAACT			II	
0.1493584	cg23079063	cg23079063	39756485	CACTCTAAACATATCCTTATTA			II	
0.1257737	cg23084506	cg23084506	33767397	CCTTAAATCCTACCCACTTCCA			II	
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0.1091407	cg23090207	cg23090207	47796459	CTCTACCCTAAACAACRTCCAA			II	
0.1525276	cg23098068	cg23098068	12711505	CAAAACTAAAATTCAAAACTA			II	
-0.116795	cg23098789	cg23098789	23786356	RACTCAAAATACCCATCRCRAA			II	
-0.119492	cg23106045	cg23106045	27662435	TACTACCTAAAACCCTTCRCTA			II	
-0.105323	cg23109867	cg23109867	68739412	TCTATAC	57770329	TCTATAC	I	A

-0.112681	cg2311461	cg2311461	67614345	CTAAACC	58772358	CTAAACC	I	A
-0.126239	cg2311738	cg2311738	39656417	TTTAAATATAAAAAATACTTA			II	
-0.142172	cg2312325	cg2312325	26689339	AATACAT	64768303	AATACAT	I	T
-0.273421	cg2312851	cg2312851	34773406	ATAAATTTAATTCTTATCCTAA			II	
0.1274688	cg2313083	cg2313083	41611411	AAATACCATCCTTTTACTAAC			II	
-0.125638	cg2313674	cg2313674	17660464	CAACATT	66795481	CGACGTT	I	A
-0.106017	cg2314185	cg2314185	72804303	ACTTAAACCCAACCACCTAAT			II	
0.1005059	cg2315650	cg2315650	69727490	TATCAAATAAACTAATCAAAA			II	
0.11251	cg2315818	cg2315818	32629444	ATAACCA	12713425	ATAACCG	I	T
0.5681564	cg2315997	cg2315997	72704311	AAAATAAAAATTATTATAACC			II	
0.105302	cg2316259	cg2316259	59687470	AATTATATTCTCTAAAACCTTC			II	
-0.106733	cg2316742	cg2316742	59770497	CTCTAATTTCCCAATCTTTTAT			II	
-0.136118	cg2316852	cg2316852	67794317	CCAAAAAATACTTAAAAACCT			II	
0.10437	cg2317110	cg2317110	19799376	TACTTCTCCCAAAAATAATAT			II	
-0.103254	cg2317340	cg2317340	61624403	AAAATTT	63721342	AAAATTT	I	A
-0.125366	cg2317368	cg2317368	18794419	AAAACCT	62765313	AAAACCT	I	C
0.1132191	cg2317557	cg2317557	51749314	AAAACCAACCCAACAAAAATT			II	
0.1098408	cg2317661	cg2317661	59602301	TTCTACTCTTTAAAATCCACRC			II	
-0.130121	cg2318284	cg2318284	34670367	CATTCTA	65739445	CGTTCTA	I	A
-0.14455	cg2318731	cg2318731	59663416	AACCTTCCACCCATTAAAATT			II	
-0.163334	cg2318868	cg2318868	63604477	AACCTCC	25783483	AACCTCC	I	A
0.293646	cg2319576	cg2319576	44748359	RTATTTTTCTCTACTATCTTTA			II	
0.1072862	cg2320272	cg2320272	12694323	CATCTATAAATAATATAAAAC			II	
0.1201758	cg2320935	cg2320935	59758416	AAAACAAAACTAACTAACAAC			II	
0.1175476	cg2320994	cg2320994	37721439	AAAAAATACTATAAATTAATC			II	
0.1332673	cg2321052	cg2321052	49695350	TAACACATTTTCTTTATCTATT			II	
0.1207998	cg2321244	cg2321244	74799377	TTAATACTAAACCAATCCTCCC			II	
0.1268975	cg2321443	cg2321443	57770404	CTCAACAAATTTTAACAAAAC			II	
-0.107386	cg2321476	cg2321476	62803315	CAAATTA	22614428	CGAATTA	I	C
-0.143324	cg2321835	cg2321835	60646428	ACACTAT	18724379	ACACTAT	I	C
0.1647452	cg2321836	cg2321836	70727307	CCACAAAACCAAAAACTACTT			II	
-0.172759	cg2321855	cg2321855	45740474	AAACAAC	35708392	AAACGAC	I	C
0.1491842	cg2321895	cg2321895	58717327	AATAAATAACAAAAACAAAA			II	
0.1191912	cg2321925	cg2321925	26748333	ATAAAACCAAAATAAAACAAT			II	
-0.122508	cg2322435	cg2322435	55717393	AATACAA	30647326	AATACGA	I	C
-0.141787	cg2322691	cg2322691	23658400	ATCCCAA	43769447	ATCCCAA	I	A
-0.146432	cg2322852	cg2322852	12778419	TCATCAC	49678399	TCGTCAC	I	C
0.1508376	cg2323083	cg2323083	54682481	AAAAAACAAACTTAATTTCCT			II	
-0.189645	cg2323163	cg2323163	39659445	TCCTAAACATCTAACTTAATA			II	
-0.216168	cg2323341	cg2323341	15758300	CAAATAACTAAATACTAAAAA			II	
-0.100481	cg2323879	cg2323879	13741416	TCTACCT	64642364	TCTACCT	I	A
	cg2324214	cg2324214	36799442	CCCACAC	62803492	CCCGCAC	I	A
-0.114976	cg2324491	cg2324491	70620478	AAATACA	16603329	AAATACC	I	A

-0.138059	cg23247945	cg23247945	46605301	AAATTAA	54684461	AAATTAA	I	A
0.1122293	cg23248424	cg23248424	33740452	AAATAATAACACACCTTAAAT			II	
-0.101283	cg23250574	cg23250574	40613384	AAAACAT	62690339	AAAACGT	I	C
0.1170224	cg23256480	cg23256480	71759373	ACAACCC	63640366	ACAACCC	I	C
-0.127442	cg23259542	cg23259542	29766366	CCTCTCCTAAATAACRAATTAC			II	
0.1118174	cg23261171	cg23261171	18708502	CAACTCATTAACCCTTAACTCA			II	
0.1131959	cg23268630	cg23268630	63735467	AAAAAAAACAACTAAATAAAC			II	
	cg23281527	cg23281527	59606390	ACCAAAA	43696426	ACCGAAA	I	C
0.1509398	cg23288838	cg23288838	68682381	TAATACAATAAATAACCCCCCC			II	
-0.116822	cg23289024	cg23289024	58802339	CAAACTACRACCTAAAACCCCC			II	
-0.108791	cg23289854	cg23289854	23752376	CCTAACAACACCTCTACTAATA			II	
0.1621413	cg23290313	cg23290313	48724355	CCTTAAAAAAACCAAATCCTA			II	
0.2231183	cg23296792	cg23296792	72682370	TAAATATTTTAAAAAATTAAAA			II	
0.130327	cg23298862	cg23298862	11700305	CTTCCAA	34632345	CTTCCAA	I	T
-0.288898	cg23299919	cg23299919	19700344	TTCTAAC	20734385	TTCTAAC	I	A
0.1427254	cg23302740	cg23302740	44725301	ACATATATATATTTATCTATAT			II	
0.1080047	cg23302998	cg23302998	10626312	TAAAATCTCACTAAAAAAATA			II	
-0.138368	cg23305129	cg23305129	31657469	CCCCCAA	23720345	CCCCCGA	I	C
0.2197034	cg23305899	cg23305899	64730380	CTAAAAA	73795306	CTAAAAA	I	T
0.3399447	cg23331433	cg23331433	24708349	TCAAATCTTCTAAATACAATAA			II	
0.1885607	cg23333490	cg23333490	58633483	ACTCCAAACTAACCTACTCCTA			II	
-0.105266	cg23336481	cg23336481	21771471	AACCAATAAAAAACTCAACAT			II	
-0.102678	cg23337650	cg23337650	59667438	AACRACTCTCACCTCATCAACA			II	
0.1563255	cg23338388	cg23338388	49774469	ACCACAAAATAAAAAACACAA			II	
0.1708007	cg23345508	cg23345508	42759326	TAAAATATCAAAACATTTACA			II	
-0.120629	cg23348979	cg23348979	31695334	AACAAAA	42783446	AACGAAA	I	T
0.1113695	cg23351707	cg23351707	21606469	ACAAACTATTAAAAAAAACTA			II	
0.1814604	cg23352245	cg23352245	44763338	TAAATAA	73707305	TAAATAA	I	C
-0.136273	cg23364040	cg23364040	42654436	AATCAAC	56704416	AATCGAC	I	A
0.1565812	cg23371476	cg23371476	46780375	TAAAAAACATTTTCCATTTATC			II	
-0.200608	cg23371584	cg23371584	61718377	ACACTAACCACTAAAAAATAC			II	
-0.124922	cg23376554	cg23376554	41759380	TCATTTTTTTCRCCATCRTTATA			II	
-0.134971	cg23390118	cg23390118	14778329	AAACCAC	13618360	AAACCGC	I	C
0.6040583	cg23392381	cg23392381	29658437	TATTAACTCTACCRTTCCAAAA			II	
0.1174801	cg23400446	cg23400446	53742492	AAACTCCCTCTCTAAAATCAC			II	
0.102062	cg23401796	cg23401796	41668374	CAAAAAA	31702423	CGAAAAA	I	T
0.1469278	cg23402305	cg23402305	44670458	AATTATTCTTAAAACATTCTTT			II	
0.2350529	cg23404737	cg23404737	33614370	CTCTAATTCCCTCTTATATTAT			II	
-0.114487	cg23414861	cg23414861	60804361	AACCAAA	49684479	AACCAAA	I	A
0.1564485	cg23418075	cg23418075	63758467	CTCCTAACCAAAAACTCTCAAA			II	
0.1279255	cg23418968	cg23418968	22654362	TAAAACCAAATCATCTAAATCA			II	
0.2625141	cg23421392	cg23421392	14675470	ATTCTACAAACCACAAACTATC			II	
0.3088818	cg23421896	cg23421896	49705387	AATTCTTCCAAAAACATCAAA			II	

0.1380913	cg23429749	cg23429749	52632490	CRCAAAAAACATAACAACTAT			II	
0.4687389	cg23438516	cg23438516	50695345	AAATACAAACRCAATTTATCR			II	
0.1042161	cg23440389	cg23440389	18738325	TTACRTATTCATAACTCCATTT			II	
0.1606121	cg23441248	cg23441248	59728457	AAAATATAATCAACACACAAT			II	
-0.116748	cg23442198	cg23442198	23739407	ACCTAAA	62718433	ACCTAAA	I	T
0.1074091	cg23462305	cg23462305	74612343	TCTCCCTAAACRTTATATATTA			II	
-0.218009	cg23463680	cg23463680	22625473	ACAATATTAAATTTACCTAAA			II	
-0.156965	cg23464743	cg23464743	51804485	CRAACTAATTTTACATACACC			II	
-0.154369	cg23476877	cg23476877	66602389	AATCAAA	66725344	GATCAAA	I	C
0.1123167	cg23481024	cg23481024	16732386	TATTTTTCAACATAAACRACC			II	
0.1150312	cg23481862	cg23481862	74770344	AACACTAACTAAAACCAATAA			II	
-0.18342	cg23490161	cg23490161	59606495	CCCCAAT	34632365	CCCCGAT	I	C
-0.256442	cg23496178	cg23496178	69629438	AAAACTTTCRTCCTTACCCAAC			II	
-0.114969	cg23497306	cg23497306	38764414	AAATACA	53764352	GAATACA	I	C
0.1786569	cg23497569	cg23497569	45679428	CACAACTACCAATCCAACTAT			II	
0.1067709	cg23501005	cg23501005	20681329	TCAAAATACTAAAATACATAT			II	
0.1037101	cg23505044	cg23505044	20795336	CATAAAA	16688394	CGTAAAA	I	T
0.1197544	cg23508201	cg23508201	50687494	CAATCATCCTAAAACAACTCA			II	
0.2213913	cg23513018	cg23513018	42775378	AAAATACACAAAATACCTTTT			II	
0.1617854	cg23515496	cg23515496	63698447	ACAACCCCAACTAACRAAAAA			II	
-0.205702	cg23517115	cg23517115	25611479	AACTCTCAACACCTAACCRTA			II	
-0.20685	cg23517941	cg23517941	62643304	CCACAAA	23765336	CCACAAA	I	C
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-0.317347	cg23523359	cg23523359	40683383	ACCTTCCCTAAAATTATAAAA			II	
0.1047092	cg23543481	cg23543481	13689325	CCTATAAAAACRTAAATATAA			II	
-0.137428	cg23549902	cg23549902	36622495	AACTATT	65717441	AACTATT	I	T
0.106637	cg23550704	cg23550704	34740420	ATACTTTCTTCAACACACAAC			II	
-0.139113	cg23551722	cg23551722	73611464	CTAACTCCCAACTTAAAATTC			II	
0.3798285	cg23564471	cg23564471	57798316	AAAAACTAACTATCCTCCCAT			II	
-0.118603	cg23567120	cg23567120	36634317	AAAATAATCAAAAAAACCTCC			II	
0.192421	cg23579537	cg23579537	26799415	ATCAAAACAATACCAATCTAC			II	
0.1205034	cg23583501	cg23583501	31753327	CAACCTCTAAATCACCTTTCTA			II	
	cg23586272	cg23586272	54606442	TTCTATTAAAATAAAAAACTT			II	
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0.2996596	cg23590389	cg23590389	65610329	ATACATC	52657479	ATACATC	I	A
-0.167393	cg23591463	cg23591463	18644450	AATACAAAAAACACTTTTTCA			II	
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-0.116662	cg23595304	cg23595304	11609369	CATAAATACTTCTCTTTAAACC			II	
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0.1018863	cg23603995	cg23603995	14792375	TCCTTACCTACTAACTCCACCT			II	
-0.157871	cg23610373	cg23610373	27760360	AAACAAA	14661413	AAACAAA	I	C
0.1211841	cg23611697	cg23611697	50719487	CAACAAAATCTTCTAATAATA			II	
-0.103578	cg23616046	cg23616046	53728375	TCATTAACTATACRAACTATCA			II	

-0.106449	cg2362236	cg2362236	15693488	ATAACAC	67650322	ATAACGC	I	A
0.1155933	cg2363017	cg2363017	14642480	CTATTCCCCCTATCAAATAAA			II	
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-0.11833	cg2363434	cg2363434	45738341	CAAAAA	24724448	CGAAAA	I	C
0.2063085	cg2363657	cg2363657	41790318	AAATAAATTTTCAATATTTTCC			II	
-0.121689	cg2363804	cg2363804	54804489	AATCAATTAACATATTAATTA			II	
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0.1055954	cg2364227	cg2364227	48642510	TTCTCCAACCACACTAACCCC			II	
0.1955	cg2364908	cg2364908	27711488	AAAAAC	29791450	AAAAAC	I	T
-0.102764	cg2365608	cg2365608	49691371	TCAAAAA	66651389	TCAAAA	I	T
0.1162818	cg2365905	cg2365905	48605322	ATTCCAAAACTACTAATCCCT			II	
	cg2366438	cg2366438	50730307	AATAAATTTAAAAAACACTAT			II	
	cg2366477	cg2366477	29803410	CTATTCAAAAAAATACAACCR			II	
-0.116488	cg2367063	cg2367063	39727415	CCACCTC	71635485	CCGCCTC	I	A
0.104049	cg2367339	cg2367339	56774429	AAATAAAATCAAAAAACTTAA			II	
0.1045024	cg2367934	cg2367934	31602493	AATAAATCATACAATATCCAC			II	
0.1067154	cg2367937	cg2367937	57767364	CCAACCAAACCCAAAAAAACA			II	
-0.118741	cg2368174	cg2368174	65620344	ACCAAAC	25792325	ACCAAAC	I	A
-0.123984	cg2368186	cg2368186	25694317	AAACAAAAAAATTTACAAAAC			II	
-0.114733	cg2368301	cg2368301	66739327	ACTCCAA	21636467	ACTCCGA	I	T
0.1818705	cg2368380	cg2368380	72631320	TCTATAAACATTATCACCTACT			II	
0.2450945	cg2368743	cg2368743	65801402	AACCAAAATTACCAAAATCAA			II	
-0.119259	cg2369141	cg2369141	68601485	AACCTATTTCCATTTCAATAAT			II	
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0.1148244	cg2370515	cg2370515	51728396	AAAACCTCACAACCAACCAAA			II	
0.118448	cg2371201	cg2371201	41796445	AACTACA	17703398	AACTACG	I	C
-0.14912	cg2371390	cg2371390	53693410	ACCTAAAAAAATACRATCAAA			II	
-0.104132	cg2372707	cg2372707	29693481	ACACAAATCCAAAAAAATCTT			II	
0.108564	cg2373060	cg2373060	11773436	TCACCAA	10627324	TCGCCAA	I	A
-0.107721	cg2373262	cg2373262	27652365	CTTCCCAACATCCAAACCCAC			II	
-0.144422	cg2373339	cg2373339	35610394	AAACAAATAACAACCCCTTAA			II	
-0.109582	cg2373719	cg2373719	63690442	ATATTAA	30723353	ATATTAA	I	C
0.1380024	cg2374223	cg2374223	56640382	CTCATCACTAATTAAAACRCC			II	
0.1378801	cg2375882	cg2375882	64672430	TCTACAA	66743443	TCTACAA	I	C
0.1073673	cg2377222	cg2377222	52666371	AACACTAACTCAAACCTATCT			II	
0.167632	cg2379321	cg2379321	10789310	TCCCCCA	53791392	TCCCCCA	I	A
0.1423491	cg2379333	cg2379333	67739465	TCATCAACATTTTATCTCTCAA			II	
-0.290078	cg2381248	cg2381248	14714457	ACATTTTCCCAAAAATCCAAA			II	
-0.149912	cg2381339	cg2381339	59678432	ACAATTAAACCAATTATTTAA			II	
0.1278294	cg2381902	cg2381902	70699431	ACTTAAAAAAACCTTTAAAAT			II	
0.2120784	cg2382795	cg2382795	64759481	CAACCAC	60656358	CGACCAC	I	A
-0.134105	cg2382868	cg2382868	49800321	AACRATAAAACCACAACCACT			II	

	cg23835894	cg23835894	64778312	TTCTAAC	28624444	TTCTAAC	I	A
0.2591873	cg23835923	cg23835923	36600420	TAATAACRTCAAAAACCTCAA			II	
0.1027181	cg23838005	cg23838005	29808339	TAAACCCRACATTAACATTTCT			II	
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-0.117015	cg23855392	cg23855392	19709465	AAAAAAAAATCRAAACATCTA			II	
0.1697864	cg23856611	cg23856611	37808387	CAATTATTACTATCAAAAACA			II	
0.1563925	cg23863670	cg23863670	43604369	TCCATAAAACTAACTTTACTCA			II	
0.1105232	cg23864202	cg23864202	57781427	ACTTTAAATTATATAACCTCCR			II	
0.1400386	cg23869232	cg23869232	28782332	TAAAAACATAACTTTACACAC			II	
0.1145879	cg23873996	cg23873996	17694510	TACAACCAAAAATAAAAAACT			II	
-0.202617	cg23876149	cg23876149	63806393	AACTAAA	64756379	AACTAAA	I	T
0.123224	cg23878260	cg23878260	60638333	AATCCTCATTCTATACCTTTAC			II	
0.1008308	cg23881926	cg23881926	30680503	ATAAAAA	42733395	ATAAAAA	I	A
0.2019672	cg23887839	cg23887839	48673495	CCCAATTTAAAACCAATCATA			II	
0.312647	cg23892766	cg23892766	48640474	TAAACAAAAACAAAACCAAAA			II	
0.1114869	cg23895439	cg23895439	67722339	TTAAACTAAAATAAAAACCAA			II	
0.1362621	cg23899527	cg23899527	21750485	TTAATAACAACRCCTCATCTTC			II	
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0.1105111	cg23910458	cg23910458	12614492	CAAAAACTAAACAATATTTAA			II	
-0.106022	cg23915527	cg23915527	32806360	ATCTTTACTATATTTATTTTCTC			II	
-0.10389	cg23918315	cg23918315	36794403	AACAACCTTACAATAACTTCCT			II	
-0.101648	cg23924370	cg23924370	63705465	ATTATAT	47704307	ATTATAT	I	A
-0.144466	cg23926439	cg23926439	69633370	TCCAAAA	54786464	TCCGAAA	I	C
-0.100537	cg23928165	cg23928165	56691490	TAACACT	34772365	TAACGCT	I	T
-0.118118	cg23928763	cg23928763	30742476	CCACAAA	40630333	CCACGAA	I	A
	cg23929036	cg23929036	13644375	TAAAATCTACCCAACRACAAA			II	
-0.115205	cg23930313	cg23930313	52704340	TAAAACRAAACRATTAAAAAC			II	
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-0.114914	cg23942717	cg23942717	16778433	CTAAACC	34674323	CTAAACC	I	A
0.360688	cg23947654	cg23947654	71638364	CCCRAAATTCCCCAACCTATAT			II	
-0.135437	cg23948391	cg23948391	44670393	ATAACCTAACRTTCAAATTAA			II	
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-0.106509	cg23948993	cg23948993	39790306	AAAAACC	12633348	GAAAACC	I	C
0.187797	cg23958704	cg23958704	47736360	CRTCRTAAACRTACACCAAAC			II	
0.1175073	cg23959772	cg23959772	61661388	TCTTCCCTCATATTTATTTCAA			II	
0.1299093	cg23966361	cg23966361	22690431	RCRCCTAAAACAAAACCAAAC			II	
0.1024268	cg23971182	cg23971182	54750474	TTACTATTTCCCAAACCTTTTA			II	
-0.115086	cg23974473	cg23974473	63659338	AAAACCAAAATAAAAATCTAA			II	
0.1659187	cg23976981	cg23976981	29800510	AACRTCTCTATTAAAAAATACT			II	
0.1014723	cg23981702	cg23981702	22734320	AAAAAATCTACTTCCCAACAA			II	
-0.117035	cg23985370	cg23985370	59733300	TAACAAT	33766476	TAACGAT	I	T

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0.2568897	cg24007926	cg24007926	29756506	AAACAAA	46755377	AAACAAA	I	C
0.1079503	cg24009067	cg24009067	72650436	AAAACRACAAAACATCCRAAA			II	
-0.107308	cg24013589	cg24013589	26810484	CTCTAAATAAAAACATCCCCTC			II	
0.2407884	cg24014558	cg24014558	44688390	TCTATACTAACTTCRCCAAAAA			II	
0.2240797	cg24016855	cg24016855	26718464	TAAAAAACTAATCCCACACCTA			II	
0.1251823	cg24018148	cg24018148	73806350	AACTCCTAAACTAAAATCTTAC			II	
0.144685	cg24032445	cg24032445	17682431	CCTAAACTAACCCACAAACAA			II	
-0.104399	cg24033103	cg24033103	32630505	AAAAACC	22792481	AAAAACC	I	C
-0.121738	cg24033122	cg24033122	13790358	AAACTCTAAAAAAACCRAAAA			II	
	cg24033503	cg24033503	12682383	ACAATCA	13644361	ACGATCG	I	C
0.2342547	cg24036791	cg24036791	12614397	CAAAAAA	47768375	CAAAAAA	I	A
-0.101315	cg24046087	cg24046087	53665466	ATACAAA	59795326	ATACAAA	I	A
0.1246463	cg24046616	cg24046616	72694474	TAAACCTAACCATAAAAAAAT			II	
-0.152976	cg24051234	cg24051234	52757446	CTCTACTAACTTTAAACCAAAT			II	
-0.114375	cg24051749	cg24051749	70679390	AACCAAAATTAATCAAAACCT			II	
0.207155	cg24057558	cg24057558	71674454	CRACCTCTAAAAATAAACCAC			II	
-0.121165	cg24060917	cg24060917	24667399	CTATATCCACATCAAATCTCCC			II	
0.3124983	cg24062389	cg24062389	70637368	AAAAAATACCAACTTTAAAAT			II	
-0.153278	cg24065641	cg24065641	25672361	CCATCCTATTTATCTCCTTTTCA			II	
0.1003518	cg24076588	cg24076588	31766373	CTACAACTACAACTCTAAATTC			II	
0.1220903	cg24076747	cg24076747	22733497	CCTAATATATATTACAAATATC			II	
-0.330413	cg24077401	cg24077401	42744339	RAACTCCTAACCTCAAATAATC			II	
-0.16159	cg24080129	cg24080129	67640506	AATCAAAAATCTTTATTTACAA			II	
-0.155763	cg24082680	cg24082680	51756305	TCAAATTATTTTCAAACATTAA			II	
-0.15482	cg24084927	cg24084927	47735449	TCTTTTTAAATAAAATCTCACT			II	
-0.150233	cg24097094	cg24097094	63650427	ATACTAATCAAACAATCACAA			II	
-0.103163	cg24100293	cg24100293	62648337	AATTACTATTACTTCTTTATCA			II	
-0.168524	cg24100357	cg24100357	38660364	ACTCCCA	59766507	ACTCCCG	I	A
0.114746	cg24100841	cg24100841	54650349	TACATAACCRAACTATCTATAA			II	
0.1413137	cg24103044	cg24103044	31723420	ACCCCACCCCAAATAATACAA			II	
-0.242505	cg24114014	cg24114014	54677411	AATAACC	59640472	AATAACC	I	A
0.1170067	cg24115019	cg24115019	64600307	AAACAACAAACCCTCTTCCAA			II	
0.1072057	cg24116380	cg24116380	18614375	AAAATATCCTTCTCCCATCTAT			II	
-0.101098	cg24117504	cg24117504	56702336	ACTTTTTTCCTACTATACACAA			II	
-0.114441	cg24120210	cg24120210	27697486	ACAAAAA	71668435	ACAAAAA	I	A
-0.121263	cg24126849	cg24126849	70700395	AACTTAA	37676493	AACTTAA	I	C
-0.145249	cg24127414	cg24127414	42665471	AACTACRTAAAATTTTACATTA			II	
-0.115252	cg24130284	cg24130284	41607326	RTTCTAAACTACCTAAATATAA			II	
0.119629	cg24134182	cg24134182	47714360	AAAATAATACAATTACTTTAA			II	
0.1881254	cg24139874	cg24139874	59650333	ACTCTTCTCTCTTTAAAAAACA			II	
-0.164774	cg24142775	cg24142775	29730323	TTTCTAA	54661507	TTTCTAA	I	T

0.2370199	cg24154853	cg24154853	54680357	AAAACAT	72777479	AAAACGT	I	C
0.1151772	cg24156181	cg24156181	35765340	AACCTCAATCCTAATCRCATTT			II	
0.1416696	cg24158878	cg24158878	73610478	ACCAAATATCAAAATAAATAA			II	
-0.1313	cg24160421	cg24160421	41739424	ATCACTACAAAATATTTACCCT			II	
-0.205138	cg24166916	cg24166916	13752399	AACCTTAAAAAACTAAAATT			II	
0.1280712	cg24169486	cg24169486	47650434	AACTCTTATAAACCACTAATAT			II	
0.1161285	cg24170085	cg24170085	55767342	CTCTAAA	20663507	CTCTAAA	I	C
0.132541	cg24181174	cg24181174	60718359	TAACCAAAAACATCAAACAAA			II	
0.1201942	cg24181662	cg24181662	72677445	ATAAACAAAACCCTAAAACAT			II	
0.1426881	cg24183504	cg24183504	47684365	CRTTTTAAACACCTTATATTTC			II	
-0.102058	cg24184022	cg24184022	22600456	TCTCCAC	71690340	TCTCCGC	I	A
-0.128428	cg24185656	cg24185656	56687360	CTTTACC	55750345	CTTTACC	I	A
-0.130815	cg24192559	cg24192559	54676328	CACTAAT	72666434	CGCTAAT	I	C
-0.115823	cg24192660	cg24192660	40765501	ACAAAAT	62705329	ACGAAAT	I	A
0.132902	cg24199384	cg24199384	29724343	TTATAATAATTTATTACAACAA			II	
0.1190358	cg24205048	cg24205048	22657328	CATTTAAAAAATAATCACCTCC			II	
0.1449503	cg24208588	cg24208588	52723466	AAAAAACTAATTATCTTTTAAA			II	
0.1163542	cg24210810	cg24210810	37769364	TTATACACCAAACATCTATAAC			II	
0.1020708	cg24233679	cg24233679	60729308	AAAAAACCTCRAATATCAAAA			II	
0.1223294	cg24238409	cg24238409	13672463	CTACACATTTCAAATTATACAA			II	
-0.120229	cg24264239	cg24264239	51699370	ATTATTAACTAAAATCCAAAA			II	
-0.169577	cg24265722	cg24265722	30724305	TAAAAACCTAAAAACCTAAAA			II	
-0.101063	cg24280832	cg24280832	57670475	CTAAAAA	16687490	CTAAAAA	I	A
0.1071697	cg24284460	cg24284460	16800439	TTTCCRAAAAAATATCTTAAAA			II	
-0.247938	cg24284539	cg24284539	18760487	TCTCAAA	54751387	TCTCGAA	I	A
-0.113005	cg24287218	cg24287218	17713396	CAAAACTATAATCTTAAAAAC			II	
-0.120173	cg24289452	cg24289452	30605485	AAATACA	63790501	AAATACA	I	A
0.1072662	cg24296187	cg24296187	21741468	CTATATTTTTCAAACTCAAATA			II	
0.2614737	cg24299087	cg24299087	38674411	CAAAAATTAAATAAACAACAC			II	
0.1809598	cg24299306	cg24299306	44711379	AAATAAAATACCCATTAAATTA			II	
0.10316	cg24304617	cg24304617	73697392	CCTTTTTAACAATAACCTAAAA			II	
0.519186	cg24309769	cg24309769	31759311	ACCRATACAAACCCTAACCAA			II	
0.1224775	cg24311643	cg24311643	56688344	TACCACATAATCCRACAAACTC			II	
0.1001408	cg24312520	cg24312520	27670303	TTTTCTAACTTTATTTTAATTTC			II	
0.1494268	cg24320034	cg24320034	59641444	CCTCCTA	47739385	CCTCCTA	I	C
0.1662725	cg24321971	cg24321971	62765508	TCAACRCCTATAAAATAAACA			II	
-0.130968	cg24324837	cg24324837	15742383	AACTACC	13698310	AACTACC	I	T
-0.113582	cg24325991	cg24325991	31734427	AAACTAAAACTTTCCCAACTCA			II	
0.1973034	cg24330456	cg24330456	40790492	ATACAAA	71730422	ATACGAA	I	C
0.1206515	cg24343430	cg24343430	28716473	AATTAAAACCAAAAATATATA			II	
-0.167129	cg24355182	cg24355182	71711502	AACAAAA	12653509	AACGAAA	I	C
0.187304	cg24359926	cg24359926	20672497	AAAATAAACTAACTACAAAAA			II	
0.1184008	cg24360871	cg24360871	71656418	TAATAATATTCTAATTCACRCT			II	

0.1382847	cg2436339	cg2436339	31666380	TAAATATCACAACRCCRAAAA			II	
-0.108406	cg2436362	cg2436362	48790407	AAAAAAATTACRTTAAACCCT			II	
-0.106169	cg2436784	cg2436784	48762444	CATAAAA	37767480	CATAAA	I	C
0.1375162	cg2436795	cg2436795	47744433	ACTTAAAACACTTAAAATAA			II	
-0.110148	cg2438424	cg2438424	27644355	AAATACT	36635317	GAATACT	I	A
0.1069801	cg2439293	cg2439293	57755443	CTCTTTACACCAATATCCTATT			II	
-0.143861	cg2439331	cg2439331	64658453	AAAACTC	28662378	AAAACT	I	A
-0.122935	cg2439934	cg2439934	68718419	TATCCCT	55710367	TATCCCT	I	C
0.1096056	cg2440624	cg2440624	67648488	CAATAAAAATTTCACAATCTA			II	
0.1284152	cg2440820	cg2440820	44687303	CTAAAAATAACAATAACCATC			II	
-0.40997	cg2441715	cg2441715	72680508	AAAATACTTTCTATTATCCCTA			II	
0.1061104	cg2441960	cg2441960	59679345	AAATAATTTTCCTTCTCTAAA			II	
-0.129184	cg2442190	cg2442190	43631335	CTAAATCCAAACCCRCAACTA			II	
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0.1227915	cg2443968	cg2443968	53698457	AAACTACACRAAAACRCRCCT			II	
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-0.191916	cg2445011	cg2445011	52684506	CRATCTTACCAAATATATCTA			II	
0.3149379	cg2445187	cg2445187	39659345	TAACAAAAACAACTCCTTTTA			II	
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0.1281903	cg2445711	cg2445711	23806421	AAAAATATAACCTACCAATAA			II	
-0.120346	cg2446012	cg2446012	22710467	AAATTTA	12605372	AAATTTA	I	C
-0.105014	cg2446130	cg2446130	37723323	TCTATACCTCAATTTCCTCTCT			II	
0.115118	cg2446450	cg2446450	48775334	ACCTACAAATTTTAAAACTAA			II	
0.1697233	cg2446532	cg2446532	60633364	AAAAAATCAAAATAAAAAATC			II	
0.2809118	cg2447046	cg2447046	22782397	AATACACTTTCTTTCCCACTCT			II	
-0.162027	cg2447121	cg2447121	26675310	AACCAACRTAAACAACAAAAT			II	
-0.174173	cg2447603	cg2447603	58697331	AAAAAA	28755447	AAAAAA	I	T
0.1618155	cg2447812	cg2447812	64749312	AAAAAAAAATCACAACCTAAA			II	
0.1265233	cg2447938	cg2447938	54699405	AATATATATAAAAAAACACTA			II	
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0.1021696	cg2449449	cg2449449	27809338	CCACACCTAATCACCAATAAC			II	
-0.218957	cg2450622	cg2450622	61722487	ACCTCCA	69724377	ACCTCCA	I	C
0.1020429	cg2450776	cg2450776	68607444	AACAAAATAACCAAAATATTC			II	
-0.330506	cg2450842	cg2450842	66660332	TAAAAAC	36656493	TAAAAA	I	A
0.1805693	cg2452276	cg2452276	34629506	CAACCTCTAAAAACACRTCTA			II	
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0.1136181	cg2453634	cg2453634	21699463	TACTCACRCTAAAAAAACCCT			II	
-0.145725	cg2453678	cg2453678	11672327	ACAAAA	35767456	ACGAAA	I	A
0.1203994	cg2453959	cg2453959	41691439	TTAATCCACACTACAAACCTA			II	
0.1091792	cg2454155	cg2454155	40673371	CCRACCAACTAACCTCAAAAC			II	
-0.217508	cg2455021	cg2455021	45679347	AACAACA	47717394	AACAAC	I	A
0.1380206	cg2455675	cg2455675	33642301	AATCAACTACCTACTAAATAA			II	

0.1463248	cg24567694	cg24567694	42736321	TCACAAAAAAAACTACTTAAC			II	
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0.2178702	cg24577594	cg24577594	35619362	ACCCTTACCAAACTAAATCACA			II	
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0.1233577	cg24586205	cg24586205	21656447	TTTCAAAATCAACTCTACCACA			II	
0.1444506	cg24587185	cg24587185	39810504	TATAATAACTCATACTTTAAAA			II	
-0.106306	cg24592527	cg24592527	70651325	AATCCAA	40737350	AATCCAA	I	A
0.1000795	cg24592576	cg24592576	21710401	TATTTAATAAAACCTAAAAAC			II	
-0.129252	cg24593918	cg24593918	61624328	AACAATCRAACTAATTTACAT			II	
0.1017056	cg24594633	cg24594633	52750506	TAAATCAAAAACAAAAACRTC			II	
0.1648728	cg24597825	cg24597825	35631360	ACACCTA	74648484	ACACCTA	I	C
0.100055	cg24599709	cg24599709	30746490	AACAAAAAAATCTAATTTCAA			II	
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0.1298109	cg24609101	cg24609101	50675301	AATAAATTTACTACACCAAAC			II	
0.1686951	cg24613956	cg24613956	61737472	CCATTATTCCAATACTAAAATA			II	
0.1040105	cg24625984	cg24625984	22730469	RATACCRAAACAAAATCRCAA			II	
0.1024079	cg24629232	cg24629232	16694492	AATCTCAAATATATCTTTATAA			II	
0.2779493	cg24636332	cg24636332	22607313	AAAACAA	74769447	AAAACAA	I	A
0.1282465	cg24636969	cg24636969	10804440	ATATAAA	12717471	ATATAAA	I	A
0.1731954	cg24637044	cg24637044	28656357	AAAAACC	39746472	AAAAACC	I	T
0.1056609	cg24648384	cg24648384	31751309	TTACCTTCCCAAACCCRTAAAA			II	
-0.105223	cg24648715	cg24648715	71797347	AAAAAACACAAACCTATCCCR			II	
0.1764359	cg24650913	cg24650913	65768461	AACTATATAATCCTATAAACTA			II	
-0.213338	cg24652615	cg24652615	52635432	ACTACAC	74687433	ACTACGC	I	C
0.1089135	cg24655706	cg24655706	20762315	AACATAAATTCTATAATCAATA			II	
0.1143229	cg24661168	cg24661168	59699382	AACTAAATCCTACACAAATTC			II	
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-0.101284	cg24670453	cg24670453	28689388	ACTAAAA	55775453	ACTAAAA	I	C
0.1026502	cg24672777	cg24672777	55760423	CACAAAA	48672464	CACAAAA	I	A
-0.107984	cg24674504	cg24674504	11728364	ATAAAAC	29619326	ATAAAAC	I	C
-0.158532	cg24680632	cg24680632	11688465	TTAACTT	71701313	TTAACTT	I	T
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0.1944229	cg24680742	cg24680742	27802424	AAAAAACAATATAAAAAATAT			II	
0.1339304	cg24686551	cg24686551	68782416	AAATCTCTTTTACTTTAAAAAA			II	
0.1045592	cg24686553	cg24686553	36667388	TTACTCTATCATATAAATAAAT			II	
0.1110779	cg24687805	cg24687805	48707310	ATTACAACATACCTCACAACTT			II	
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-0.212084	cg24691167	cg24691167	23766456	TTATCAA	54758300	TTATCAA	I	A
-0.164017	cg24691330	cg24691330	45715405	TTACCCTTTATCCTATCCCTTA			II	
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0.5347426	cg24694833	cg24694833	20694418	CAAAACCCTACAATTATAAAA			II	
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0.104286	cg2472105	cg2472105	28716403	ACTAAATTCACTATATAAAAA			II	
0.2778124	cg2472257	cg2472257	50656303	CAACAACAAATTCTACCCATA			II	
0.1537847	cg2472552	cg2472552	32785398	AAAATAAACRTATAACRCTAT			II	
0.1942942	cg2472983	cg2472983	59719371	ATACTTCTACRACTCAAAACA			II	
0.1317488	cg2473673	cg2473673	60699433	CTACAAACTAAAAAAACTATC			II	
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0.1300964	cg2475309	cg2475309	74793327	ATATCCCACCCCCAAATATTA			II	
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0.1055082	cg2475545	cg2475545	24624480	CAACAA	55695461	CGACAA	I	C
0.3936825	cg2476058	cg2476058	69733370	ACATTAAAATATAATACAATA			II	
0.1148415	cg2476578	cg2476578	52708465	CACRACTAAATCATACTCCRC			II	
0.2873369	cg2476938	cg2476938	24754359	AATAATACCAAAAATCTAATT			II	
0.127893	cg2478197	cg2478197	32606446	ACCTCAATTAAACATATAAAA			II	
0.1435989	cg2478617	cg2478617	41677319	CCTCRTCCATCTACTTAACCAA			II	
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-0.217953	cg2480022	cg2480022	64678343	TACTACAACTATAACRACTCA			II	
0.1334046	cg2480926	cg2480926	50603507	AATAAACACCCAAATCAATTA			II	
0.110381	cg2481073	cg2481073	41786312	CTCATAA	59756367	CTCATAA	I	A
0.1080827	cg2481926	cg2481926	15679456	TATAAAATAAAAACAACTAAT			II	
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0.1124521	cg2482437	cg2482437	12641307	TCAAACRACAACCRTCACAAA			II	
0.102296	cg2482447	cg2482447	46719372	TCTAAACAAAAACACTACTTT			II	
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0.1329395	cg2483439	cg2483439	10618304	ACCATATATATTCACTAAAAA			II	
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-0.158539	cg2483806	cg2483806	38702310	CAAAAA	31642452	CGAAAA	I	C
-0.111748	cg2483831	cg2483831	27744377	CCCATTTTCCTTCTCTCTTTAT			II	
0.1059957	cg2484593	cg2484593	71800302	CCACATCCTAAACATAAACAA			II	
0.2096146	cg2484600	cg2484600	16757458	ATAACCCCTAACCTTCCAAAT			II	
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0.1124531	cg2485922	cg2485922	69663383	TCTTTCTATAACCAACTAAAA			II	
0.1529288	cg2485964	cg2485964	12639454	TCAATCTCAAAATCCTAAATA			II	
0.1416759	cg2486139	cg2486139	16740353	ATAAAAATCTCTACTCAATCT			II	

0.1026492	cg24861747	cg24861747	28663414	ACCAAAAACRACACTATATTA			II	
0.1247197	cg24865482	cg24865482	48699411	ACCTCATATAATTATCRTAAA			II	
0.1143962	cg24866764	cg24866764	29671350	CCAAAATAATACATCTACAAA			II	
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0.1266774	cg24870391	cg24870391	44690397	TTAACTTCCTAAAATCTAAAA			II	
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0.1247513	cg24882709	cg24882709	60703325	AAAAATATATATCCTAATACT			II	
-0.168555	cg24883219	cg24883219	44800449	TAAAATTAACCTCTATAATAA			II	
0.1047212	cg24886788	cg24886788	14800312	ACCATAACAATCACAAACCAA			II	
-0.10628	cg24888257	cg24888257	43667408	AAAATA	38600394	AAAATA	I	A
0.1889035	cg24893378	cg24893378	44810332	TTCTAAAAATACAAACTCCCT			II	
0.1518573	cg24896460	cg24896460	70722452	ATAAATATATATTTATATTCAC			II	
0.1331706	cg24897392	cg24897392	59659411	CTCTAAATCTCTCTACCAAAC			II	
0.1006311	cg24900563	cg24900563	53796500	AATCAAACTTAAACAAACATC			II	
-0.120211	cg24906015	cg24906015	47620370	ACAAACATAATTTCTATTTTCT			II	
-0.108453	cg24908198	cg24908198	58770325	TTTTCAC	17807473	TTTTCAC	I	A
0.1040526	cg24911283	cg24911283	55669478	TCATAAATAATATACTATAAA			II	
0.1428739	cg24911837	cg24911837	36781471	AATTCAATCAATAAAAACCAA			II	
0.1032126	cg24912023	cg24912023	25801336	AATCCTATAATTACTCCRATTT			II	
-0.125767	cg24912560	cg24912560	47689501	RATTTAATAACCTAAACCACC			II	
0.1014787	cg24913168	cg24913168	64614493	AAACAA	59706366	AAACGA	I	A
0.2746815	cg24917131	cg24917131	33787301	TTAAAAACAATTATCAAACTA			II	
-0.183655	cg24923430	cg24923430	17678303	ACATATA	63754349	ACGTATA	I	C
-0.147485	cg24923931	cg24923931	38724324	ACTCAAC	55774308	ACTCGAC	I	A
0.1053319	cg24925741	cg24925741	20633404	CRACCAAAATCATTTCACCCA			II	
0.1082575	cg24926185	cg24926185	62631457	AAAACCTATTTCTTTAAACTA			II	
0.1131032	cg24927769	cg24927769	57729426	AACACACTAAAATTAAAATTA			II	
0.1080373	cg24933157	cg24933157	32625369	TAATATTTAAACCTAACCATA			II	
0.1014532	cg24940951	cg24940951	38653505	CAAAAATTCCATCTACAAAAC			II	
0.4240594	cg24941469	cg24941469	15772351	CTACACRTAATACTTACRAAC			II	
0.1032996	cg24941603	cg24941603	69621483	ACAAATC	10765423	ACAAATC	I	C
0.2837002	cg24946117	cg24946117	46801340	TCAATCCCAATCCCAAAAAAT			II	
0.2042333	cg24947637	cg24947637	72609377	AATAAA	19674510	AATAAA	I	A
-0.107381	cg24948743	cg24948743	22636366	CAACCCC	15613336	CAACCCC	I	A
-0.217292	cg24955829	cg24955829	13663506	AACTTAAACTTTCTAATACTA			II	
0.2255872	cg24955955	cg24955955	20670468	ATCTACCTAATCTACTAAAAA			II	
0.1770026	cg24957518	cg24957518	67780307	AAAAAACCTCCCATCCCTATA			II	
-0.218721	cg24958687	cg24958687	10629423	ACAATACATTTTCCTAAAAAA			II	
-0.178882	cg24960960	cg24960960	17612325	ACCAAA	37779367	ACCGAA	I	C
0.1008669	cg24961286	cg24961286	72637374	TACAAATATCTTCCTTACCAA			II	

0.1532111	cg2496636	cg2496636	49617431	CCTAAATCRTATCTAAACCAA			II	
0.1029734	cg2496886	cg2496886	19687446	TAATACTAACTATTCCTATTCA			II	
0.3433301	cg2496949	cg2496949	15736439	AAACTTTCACAACTTTATTAA			II	
-0.172073	cg2497472	cg2497472	28661329	ACAAAA	20728454	ACGAAA	I	A
0.1037127	cg2497521	cg2497521	18722400	ATTTTATAACAATATAAATAA			II	
0.1587471	cg2497916	cg2497916	44756319	RCRACAACAAAAATCACCATT			II	
-0.151917	cg2500624	cg2500624	42722446	TACAAAA	55680418	TACAAAA	I	A
-0.161482	cg2500772	cg2500772	69692414	ACCAATA	68723455	GCCAATA	I	C
0.1820286	cg2501375	cg2501375	25682361	TCCAACCTTATATAAAATTAA			II	
0.1136842	cg2501422	cg2501422	49645350	TAAAAAACRACCATTATATCT			II	
0.1029758	cg2501503	cg2501503	67632390	TCCTATTTACTCAAACCAAAA			II	
0.1295277	cg2501722	cg2501722	29608371	TTACCAT	46697347	TTACCGT	I	A
-0.230319	cg2501762	cg2501762	27739443	AAACCTA	28777354	GAACCTA	I	C
	cg2501797	cg2501797	47616304	CTATTAA	59810484	CTATTAA	I	A
-0.189537	cg2502699	cg2502699	72730386	TAAAAA	38693418	TAAAAA	I	A
-0.100786	cg2502944	cg2502944	37766331	AAAATTATTATCCACCATATA			II	
0.1041565	cg2503494	cg2503494	48777493	AAAATCCTACAAAATTCACAA			II	
-0.174083	cg2503563	cg2503563	61738421	CCACAA	30677325	CCGCGA	I	A
0.1700986	cg2504657	cg2504657	23646384	AAAATATACACTCCACTCACA			II	
0.1091462	cg2505940	cg2505940	42669397	CCACCCRAACAATCCTCAAAA			II	
0.1265304	cg2505969	cg2505969	61613414	TCATAATAAAAAAACCACAAC			II	
0.1189612	cg2506513	cg2506513	12621490	AATCRCCATCTAAATAATTCT			II	
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-0.152017	cg2508536	cg2508536	57758371	AACAAAATCTACRCTAAATTC			II	
-0.284095	cg2509909	cg2509909	19746429	AATACTTTCCAAAAAAATTAA			II	
0.1252843	cg2510341	cg2510341	40688342	TAAAATTCCAAACTAAATAAT			II	
0.2072613	cg2510423	cg2510423	26625304	CAAAACAATCACTAAAACTAA			II	
0.1011076	cg2511418	cg2511418	24629421	CAACATTCCTACTTTCTACCCA			II	
0.1168226	cg2512356	cg2512356	37785319	CCTTTATAATCAACCACAACA			II	
0.4028873	cg2512630	cg2512630	24616484	TCTATATTACCCAAACTAATC			II	
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-0.164192	cg2513464	cg2513464	21646334	CTAAAATAATCTAACTAAATA			II	
0.1037503	cg2513875	cg2513875	39780366	CTACACA	11757314	CTACACG	I	A
0.1908996	cg2514021	cg2514021	60681365	TAAAACCACCTAACTTTAATA			II	
-0.117294	cg2515375	cg2515375	57695325	CRAACCAAAAACRAATATCTA			II	
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	cg2516554	cg2516554	18794378	AACAAA	49604510	AACAAA	I	A
0.1135628	cg2517111	cg2517111	19601447	TTAAAACCAACCTATCTCTAC			II	
-0.137459	cg2517411	cg2517411	42628414	TAAATAACCACATACCTAAAC			II	
0.1047553	cg2517433	cg2517433	24627320	ATCTTTTATAACTAACTACCTT			II	
0.1210031	cg2517460	cg2517460	67697330	AACTAAA	21705410	AACTAAA	I	A
0.1080126	cg2518117	cg2518117	45797474	AACATCACAACATTCTTACTT			II	
0.1117523	cg2518614	cg2518614	71800390	TTATATTTATATATATATACAA			II	

0.1184387	cg25194822	cg25194822	29809481	TTAAAAATACTTCTTTCTTAAA			II	
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-0.174074	cg25202367	cg25202367	61615420	AACCAAAACAAACCCCTTCTA			II	
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-0.161097	cg25205438	cg25205438	18792373	AAAAAAAACTACTACCTTCCR			II	
0.1664214	cg25217276	cg25217276	63639328	ATTAATTCTTCCTTCCTCTTTTA			II	
0.134693	cg25219495	cg25219495	71607444	CRCTAAACCTAATCCACAAAA			II	
-0.204593	cg25220063	cg25220063	30798484	AAAAAAC	26616353	AAAAAAC	I	C
-0.163391	cg25225155	cg25225155	46784473	TTCACTA	11652474	TTCGCTA	I	A
-0.108481	cg25226891	cg25226891	74719354	CCAATAACCRCCTAAAAATTA			II	
0.1041216	cg25227803	cg25227803	65744387	CTCTAAAAATTCTAACCATAA			II	
0.1006835	cg25242423	cg25242423	57751408	AAAAACTCCTAAATTAAAAAC			II	
-0.133002	cg25243082	cg25243082	55626484	TAACAAA	43698461	TAACAAA	I	A
-0.24251	cg25246894	cg25246894	12721379	CTCTAAAAAAAAACACAAACC			II	
-0.187922	cg25247689	cg25247689	23714413	TCAAAACTTACCAAATTACTTC			II	
0.1266949	cg25249286	cg25249286	36623314	TCTATAA	71712407	TCTATAA	I	A
0.1473061	cg25249362	cg25249362	17794346	AATAACRAAATCCAATCTATA			II	
0.1003583	cg25252017	cg25252017	36690375	TCAACAATATACTTTAAATCCT			II	
0.1050739	cg25252197	cg25252197	42767506	TAAACAAAACCCAAACATATA			II	
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0.1016147	cg25281849	cg25281849	53728444	ACTACTAAAATATACATTACTT			II	
0.4904483	cg25283336	cg25283336	20702363	TTTCAAAAAACAATATACACA			II	
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-0.130671	cg25291250	cg25291250	32617420	TTCATTATATCACACACAAAAT			II	
0.108933	cg25296938	cg25296938	39603442	ATCTTACCAACCACRCAAAATA			II	
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0.1342644	cg25307332	cg25307332	20611310	CTTTAAATCTCAATTACCTCAT			II	
0.1088001	cg25312054	cg25312054	48710475	TAAAACAAAAAATCAATACTA			II	
0.1070181	cg25312970	cg25312970	14611497	ACCCCACAAACCRTCTATACA			II	
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0.1130057	cg25326289	cg25326289	69638390	AACTCTA	20604404	AACTCTA	I	A
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0.1918439	cg25336892	cg25336892	12802321	TCAAACACAAACRAACAAAAA			II	
0.2491737	cg25339052	cg25339052	74719359	TAACCTACAAACTATATTTAAC			II	
-0.118507	cg25340688	cg25340688	53782363	AAACTAA	38662399	AAACTAA	I	A
0.101261	cg25345738	cg25345738	41694346	TTATATCTATATCATACTTCTC			II	
0.1466835	cg25356468	cg25356468	40666356	TTAATACAAAATCRATTAAATC			II	
0.114548	cg25357666	cg25357666	67661507	AACCTCAAACAACAAACAATA			II	
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0.1043493	cg25369262	cg25369262	60723452	CTAATCACCAAAATAATATCA			II	

0.1104254	cg25371267	cg25371267	46633425	ATATCTAAATAATCAATCAAT			II	
0.1700462	cg25372296	cg25372296	66787371	AATACTA	66810354	AATACTA	I	A
0.1575176	cg25375162	cg25375162	65732308	AAACTTTAAACCAACCTATTT			II	
0.122825	cg25376032	cg25376032	45623463	ATAAAA	19763424	ATAAAA	I	A
0.1964592	cg25381253	cg25381253	28714405	ATCTCTTCTTCATATCAAATCC			II	
0.1050662	cg25382821	cg25382821	26632370	ACTTTTCATAATCTCRAATACA			II	
-0.244342	cg25388952	cg25388952	24657323	CAAACTACAATATATATAAAA			II	
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0.1081036	cg25400378	cg25400378	25778421	CCTAACT	42739471	CCTAACT	I	A
0.1851405	cg25408960	cg25408960	67762367	TTACTAAAAAATATAATAACR			II	
0.1930005	cg25410789	cg25410789	19742358	ACAACTCTAACAAATATCRAA			II	
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0.1413963	cg25424279	cg25424279	44730478	AACTTTTCATAACTCACAAAA			II	
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0.1379996	cg25434864	cg25434864	63772451	AACTCCA	59708488	AACTCCA	I	C
	cg25436245	cg25436245	60784379	TCCACAA	51657370	TCCACGA	I	T
0.108284	cg25437886	cg25437886	14705510	TAATAATAATACAATCTTTCT			II	
0.1026028	cg25438876	cg25438876	46644374	TCCTAAAATTTTACCTAAAAA			II	
0.1592988	cg25445671	cg25445671	38619346	TACAAATCCCAATTCRAACTA			II	
0.1012682	cg25446460	cg25446460	25720424	CATAATAACTTATACATTATA			II	
0.1220195	cg25450121	cg25450121	23733451	CCRACTCAAAATAACAAACTC			II	
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0.1028102	cg25455408	cg25455408	56705368	CTTCACCTAACTAAAAACAAA			II	
0.111756	cg25462858	cg25462858	19638351	AAACTATATCTTCATCTTCCTC			II	
0.1772217	cg25467833	cg25467833	56651484	ACAAATAATAAAAATAACAAC			II	
-0.170766	cg25468618	cg25468618	69778302	AAAAAC	23627486	AAAAAC	I	C
-0.100805	cg25468928	cg25468928	31686334	ATATTTTAACAAAACATACTA			II	
0.1092607	cg25469418	cg25469418	47711344	CTAACTC	68633335	CTAACTC	I	A
-0.169213	cg25470758	cg25470758	73769489	ATAAAAT	72647366	ATAAAAT	I	C
0.1079484	cg25481160	cg25481160	13663473	AAATCCCTATCAAATAAAAAT			II	
0.1186213	cg25483907	cg25483907	22723355	CAAAAAAAAAACCAATATTAA			II	
0.1010242	cg25488284	cg25488284	57793476	TAAAAAACATATATATCCATA			II	
0.2350157	cg25498731	cg25498731	73789377	CTAAATTTTAACTCTCCTCTAT			II	
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0.1548585	cg25535982	cg25535982	14607324	CTTTTATCTTTTCATTTCTTACT			II	
0.2274309	cg25536467	cg25536467	34807466	TTCTAATAACAAATAATCACC			II	
0.1444024	cg25538571	cg25538571	64636442	CAACACAACTAACCTTCCAAT			II	

0.1357291	cg25542319	cg25542319	49701389	AATAATATAATCAAAAATAAA			II	
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0.1133862	cg25544384	cg25544384	16604387	CATCRTAACAATAACAATATA			II	
0.1038274	cg25546488	cg25546488	53758452	TTTCCTTCCTATAACAAAATAT			II	
0.1117507	cg25547135	cg25547135	23714488	TACCTTTTCAAAACCATTCTTC			II	
	cg25551699	cg25551699	13644385	ATTCCCAATACTTAATACRTAA			II	
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-0.178199	cg25593194	cg25593194	33751503	CATACCCAAATTCATTCCCTAA			II	
-0.119999	cg25594826	cg25594826	27779474	ATATATTAAACTCAAATAATCA			II	
0.1547919	cg25596287	cg25596287	35611367	TCTTCAAAATTTCAAATATTCC			II	
0.1545402	cg25597117	cg25597117	58743426	ACCAAACTAAAAACCTTCAAC			II	
0.1079204	cg25597623	cg25597623	32647412	CCCTAAAAATATACCCAATAA			II	
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-0.199193	cg25601709	cg25601709	25670452	ACTCTCAACCTCATTTTCCATA			II	
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0.1165841	cg25607216	cg25607216	47759413	AATCCTCATTCAAAAAACTAA			II	
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0.1075931	cg25613061	cg25613061	23731348	TTAAAAT	38682366	TTAAAAT	I	C
0.1890648	cg25614253	cg25614253	12786346	TAAAAAC	70791391	TAAAAAC	I	A
0.1379604	cg25618559	cg25618559	67639508	RAAAATATAAAACACCCACCT			II	
-0.136244	cg25618731	cg25618731	19602485	AAACAACCCTTAAACCTAATT			II	
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	cg25635000	cg25635000	13644333	CCCTAACAACCATAAATTTTAT			II	
0.1308822	cg25636466	cg25636466	54810503	CCACAATATTATATCACCACAT			II	
0.1047102	cg25641515	cg25641515	10757490	AAAATATCTCCTCATAATCCTT			II	
0.1318529	cg25642955	cg25642955	33807370	ACCAAAACTCTAATTCCCTAA			II	
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0.1027218	cg25659902	cg25659902	32630357	TTCTAAAAAATCTAACTTAACT			II	
0.1097613	cg25664050	cg25664050	50613420	AATAAAATTTTTATAACATCT			II	
0.192666	cg25666210	cg25666210	13665497	AAAAAAACAAAACTCTCTTAC			II	
0.1051006	cg25671242	cg25671242	26733308	AAAAAATCTCCAAACTCCAAA			II	
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0.1231503	cg25674883	cg25674883	24782425	AAAAATTCAACCTATAAAACA			II	
0.1665294	cg25677394	cg25677394	43683426	TACCTAACAAATTACTACCTAA			II	
0.1080056	cg25687874	cg25687874	33636301	TATCCTTAACAAAAAAAACAA			II	
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0.1444655	cg25692139	cg25692139	26791369	AAATCCAAAAATAACCTAACA			II	
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-0.252943	cg25697727	cg25697727	66760371	TAAAATA	35687481	TAAAATA	I	A
0.1350674	cg25701646	cg25701646	20738426	AAAAAACCCAAACTAAAACAA			II	
0.1202706	cg25705492	cg25705492	42733480	TCCATTA	11778350	TCCATTA	I	A
0.1082855	cg25707745	cg25707745	43624350	ACCCACATACAACTTTACCAA			II	
0.1240943	cg25709335	cg25709335	29620365	AAAACTCTCAATAAAAAATCC			II	
0.1217234	cg25710298	cg25710298	31786453	CTACAAACCAAATTCATACATA			II	
0.1110531	cg25718748	cg25718748	34656411	ATTATAAAAAACCTAAAAAAT			II	
0.1807215	cg25735490	cg25735490	58601483	TAACACT	28662440	TAACGCT	I	T
-0.207898	cg25736251	cg25736251	63709335	TAACCAC	50624488	TAACCGC	I	A
-0.132158	cg25736982	cg25736982	42624311	ACAACTCTAATAAATCCTTTTA			II	
0.1134816	cg25738176	cg25738176	31778309	RATTTAACCCTCRATCRAACAA			II	
-0.105478	cg25746134	cg25746134	45616428	CTCACCC	71657317	CTCACCC	I	A
0.1480687	cg25747670	cg25747670	54620484	CAACCACRTAAATAACCRCTA			II	
0.1110699	cg25749254	cg25749254	65713432	CAAATAAAAACTTTTAATATA			II	
-0.105481	cg25753631	cg25753631	22639435	TAAACCA	43710382	TAAACCA	I	A
0.1166782	cg25753720	cg25753720	32777378	TCAATAAACTCATACTATAATA			II	
0.1139895	cg25755851	cg25755851	57716321	AATAACTTCAAACCTTAATTTC			II	
-0.180408	cg25757140	cg25757140	55763352	AATTACTCTTCTAATTTAATTC			II	
0.1049095	cg25763212	cg25763212	40639344	CCCTATCCAAATAAAATCTTAA			II	
0.124741	cg25765192	cg25765192	10671490	ACATTCATTCATAAAATCCACA			II	
0.1702272	cg25771052	cg25771052	13616491	AAATACTCTTACCTCAACCTCT			II	
0.1121719	cg25771113	cg25771113	48691468	ACTTTAAATTTTTATTTTCTACC			II	
-0.216629	cg25771854	cg25771854	36780433	ATTCATAAATAAATTAACCTCT			II	
0.1090947	cg25780024	cg25780024	73614460	TACTATTTAAATCACRTAAATA			II	
0.1569482	cg25781755	cg25781755	67767325	TTTACTTTAAATATTAAATCRT			II	
	cg25783987	cg25783987	13644438	CCTCACTTACCTTAAAAAATAC			II	
0.1073111	cg25784280	cg25784280	20699410	CATAATCCTTCCTCCCACCATA			II	
0.1444913	cg25788793	cg25788793	68742426	ACAACTCRACAATACCCRACT			II	

0.1144449	cg2579013	cg2579013	24628433	TATTCTATTCTCTTTTAAAAC			II	
-0.144634	cg2580435	cg2580435	56611493	TAATAAATAATAATTTAAACA			II	
-0.125582	cg2581750	cg2581750	31787453	ACCTACAAATAACAAATATTC			II	
0.1038076	cg2582562	cg2582562	69600381	AAAATAACCATAATCTCCRAA			II	
0.15821	cg2582767	cg2582767	53622440	TAAAAAAACTCCAATAAAAT			II	
0.1064329	cg2582896	cg2582896	72722475	CTTAATATTTAATCCTAACAA			II	
-0.159721	cg2583241	cg2583241	54781444	AAAAAA	42720419	AAAAAA	I	A
-0.120549	cg2583292	cg2583292	43714394	CCAAAAT	36726440	CCGAAAT	I	A
-0.109874	cg2584803	cg2584803	69774465	CCTACAA	29642457	CCTACAA	I	A
0.2035818	cg2585609	cg2585609	22744405	AACAATAACTCACTACTTAAC			II	
0.1257849	cg2587351	cg2587351	27674380	TTCAAAAAAATAATTCTAAAC			II	
-0.427604	cg2587939	cg2587939	28614346	CAAAAAACRAAACTCAATTCC			II	
0.240307	cg2588095	cg2588095	50802381	CRCCCCTCAAAAACCTAACAA			II	
-0.144562	cg2588647	cg2588647	65601307	ATCAAAA	44698438	ATCGAAA	I	A
-0.120569	cg2588886	cg2588886	16784456	AAAAATATCTACAATACCCAA			II	
0.1227987	cg2589258	cg2589258	57739357	TATTCRAACRATATTACAATAT			II	
-0.11038	cg2589660	cg2589660	41801497	TAAAACT	48769415	TAAAACT	I	A
-0.142231	cg2589704	cg2589704	11768491	AATCTACCATTTCCTTCAAAA			II	
-0.195589	cg25910261	cg25910261	15796467	ATCTATAAAAAAAACAACACT			II	
0.1226353	cg2591200	cg2591200	47703395	AAAAAAACRCAAATTTTAACR			II	
0.1931987	cg2591452	cg2591452	27699304	ATACRATAAAAATCCRATATC			II	
-0.154428	cg2591992	cg2591992	37687374	CAAACA	18734419	CGAACA	I	A
-0.391462	cg2592939	cg2592939	14621300	AAAACACAAACTTTCCTATTA			II	
0.151659	cg2593286	cg2593286	72731368	TTCCAAC	14691388	TTCCAAC	I	A
-0.162782	cg2593721	cg2593721	64668503	TACAACT	31790314	TACAACT	I	C
0.1243055	cg25937451	cg25937451	41673508	TCAAATAAACTACCACCAATA			II	
-0.107867	cg2595121	cg2595121	33737452	AAAACA	37624370	AAAACG	I	C
-0.185296	cg2595171	cg2595171	14715421	CAAAATATCTATAAAAATTCT			II	
0.1060335	cg2595426	cg2595426	73614359	AATTTTAAAAACAAACTTCCT			II	
-0.157405	cg2595453	cg2595453	70697407	AAAATACTAATCAAAAATCCC			II	
0.1024307	cg2595608	cg2595608	32617505	ATCTTACTAACATACTCAAAC			II	
0.1018619	cg2595610	cg2595610	33647352	AACTTTCCATCCTAACTTATAA			II	
0.1552505	cg25959131	cg25959131	39609353	TTATCTTAACTAATCCTTCAAT			II	
0.1570581	cg2596421	cg2596421	74775451	ATAATACTACAACAACAATAT			II	
-0.141615	cg2596690	cg2596690	40606387	ACAAAAACTCCCRTATAAATC			II	
0.1485974	cg2597776	cg2597776	66729380	RAAAAAACTATAATCTCTACT			II	
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-0.12471	cg2598535	cg2598535	18673434	ATACTCT	24707378	ATACTCT	I	C
0.251114	cg2598545	cg2598545	57639456	AACAACAAAATATAAACRTAA			II	
-0.141614	cg2598745	cg2598745	27789451	TTTAATA	10603416	TTTAATA	I	C
0.106554	cg25996061	cg25996061	26777302	AACCCAACCTCAAACCTTTCT			II	
0.1046607	cg2599607	cg2599607	14794347	CTTACCACTAAAAATCTAATT			II	

0.1029992	cg25997306	cg25997306	67738491	ACTCCTATATATATTTCTCTAT			II	
-0.175188	cg26000542	cg26000542	13707418	CCCAACCRCCAAACCTAATAA			II	
-0.138714	cg26000619	cg26000619	49723391	CTCAAAT	32777403	CTCGAAT	I	A
-0.126158	cg26004771	cg26004771	43686443	TAAAAAA	49758509	TAAAAAA	I	A
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0.1005767	cg26027052	cg26027052	15694442	AACTTCACTCTCTAAAATCATA			II	
	cg26027669	cg26027669	67758452	ACCTTTA	36725493	ACCTTTA	I	A
0.1396387	cg26034313	cg26034313	51738305	TTCTCTAAATCACATCTTAAAA			II	
0.5282301	cg26035071	cg26035071	30783484	CAACTCCRCAACCAAAATCTA			II	
-0.117613	cg26035633	cg26035633	61612472	AATAACTACCTCAAAAAAACT			II	
0.1478252	cg26037936	cg26037936	22744448	CTAATCCCAACAAATTCTAAA			II	
0.2255244	cg26038514	cg26038514	11809492	AAAAAAAACAAACCCTCAATA			II	
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0.1481614	cg26067096	cg26067096	71710417	CTCRCACTATATTAAAACTAA			II	
0.1239161	cg26069044	cg26069044	12603426	TACAAATAATATTAATACAAC			II	
0.1444794	cg26069539	cg26069539	31662423	AACAAAATCAATATTAACTAC			II	
0.102263	cg26069973	cg26069973	46804344	ATTTTAAATCCCAATTTAAACA			II	
-0.17533	cg26076233	cg26076233	44657335	ACATAATAAAATCTCAATATA			II	
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0.1433165	cg26086902	cg26086902	55766497	ATTTCTC	21660459	ATTTCTC	I	A
-0.136479	cg26088294	cg26088294	60663334	TAAAAAC	73801426	TAAAAAC	I	T
0.1446812	cg26089705	cg26089705	62735412	AAATAAAACCAACAACATCTA			II	
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0.1169806	cg26103179	cg26103179	47663399	CRAAACATCAAATACCCTTAT			II	
0.1822625	cg26103306	cg26103306	59764449	TTACCTAAAAACTTAACAACC			II	
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0.1186487	cg26116326	cg26116326	25741478	TCTCTTACTCTACCTTAAATCA			II	
0.1222908	cg26120902	cg26120902	64650457	AAATCATTATAACACAAATAT			II	
0.1882641	cg26124596	cg26124596	57687319	RAATAACTCAACACCCACTAT			II	
0.1076929	cg26126295	cg26126295	25720316	RCAAAAAACAACCTAAAATTA			II	
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0.1412832	cg26140475	cg26140475	42804422	TAAAAAAATTACAAACRATCT			II	
0.1019545	cg26144567	cg26144567	23648361	TATAAAC	37618434	TATAAAC	I	T
0.1207222	cg26158270	cg26158270	45735423	CTACTCCCAAAATACCCCTAT			II	
0.1170293	cg26161057	cg26161057	16681300	ATAAATTAAATAATTTTAAAA			II	
0.1702114	cg26166854	cg26166854	22682412	AAAACAATCAAAATTCACACT			II	
0.1239429	cg26169783	cg26169783	21710418	AAAACTAAAACTCTACAAAAA			II	
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0.1508851	cg2617465	cg2617465	53648435	AAATACTCTAAAAACCTTCTT			II	
0.1464899	cg2617544	cg2617544	67607446	ACTCCTCACTTAAACATACTA			II	
0.1390514	cg26177041	cg26177041	21601334	ATTCATTTCCAACCTTCTACTT			II	
0.1429689	cg2617709	cg2617709	34651357	CCAAAATCACTCAATTAATAA			II	
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0.1528952	cg26181731	cg26181731	39672354	ATTCCCCAAACATAACTATTA			II	
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0.1477403	cg26188621	cg26188621	61802303	CAACCACCAATCAAAACTCAT			II	
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0.1018702	cg2620159	cg2620159	30699308	TCTCCRTAAACTACRAACCTT			II	
0.1005002	cg2620967	cg2620967	24801488	CCCTAAAACRAACAAAACAAC			II	
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0.1038982	cg2622011	cg2622011	59617342	AAACCACRTCACCCCTCAAAA			II	
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0.165228	cg2625158	cg2625158	33790464	CTTACATAAACAACCAATTCT			II	
0.1003007	cg2626476	cg2626476	12612401	ACAACATAACTACAAACATAA			II	
0.1076044	cg26276301	cg26276301	58641425	CRTTTACATATCACCCATACC			II	
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0.1210888	cg2628279	cg2628279	50743508	ACTAACA	35771465	ACTAACA	I	A
0.1388886	cg2628683	cg2628683	56743399	CATCCCT	52663310	CATCCCT	I	A
0.2770569	cg2628708	cg2628708	70697461	ACCTAACCCAACTAAACCCAC			II	
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-0.138707	cg2629577	cg2629577	27637485	TAAACTCTTAATATCATAATT			II	
0.3007739	cg26296371	cg26296371	32610338	TATCAAATTTAATCCCACCCT			II	
-0.129741	cg2631025	cg2631025	19693331	CTTTACACCTAATTAACTCCTT			II	
0.1195459	cg2631042	cg2631042	66734380	ATTAAAC	50763482	ATTAAAC	I	A
-0.148466	cg26310551	cg26310551	26661506	TAAAAA	36664364	TAAAAA	I	A
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0.2025616	cg2632273	cg2632273	60620301	ACTAAAAACTATAATATCTAA			II	
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-0.135056	cg2632863	cg2632863	30791406	TAAAAAT	17743418	TAAAAAT	I	A
0.1377713	cg2633080	cg2633080	63768469	TCAAATAAACTATCTACCAAA			II	
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0.1143692	cg2634520	cg2634520	24719508	AATAAATTTCCTAAAAACTAA			II	
-0.100685	cg2635265	cg2635265	25639317	TTATATTCTTACCCCAAAACC			II	
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-0.114448	cg2635575	cg2635575	26645385	CRCTTACTCTACRTAATAATA			II	
0.1349538	cg2636143	cg2636143	26635492	AATAAATACTTAAATAAAAAA			II	

0.1811543	cg2636153	cg2636153	38608410	AAAAATAAAAATCATATACCT			II	
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-0.112302	cg2637925	cg2637925	38675371	CACAAA	61735303	CACGAA	I	A
-0.341548	cg2638745	cg2638745	44610504	TTTTTAAAACAAAATCTCTCTC			II	
0.1009895	cg2638850	cg2638850	37715492	CAAACTATACAATAAAAAATC			II	
0.1742955	cg2639179	cg2639179	61735467	AAACAAATTCCCATCCAACAA			II	
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0.1214261	cg2639569	cg2639569	65681467	AAAAATCAACCCAAAAACAA			II	
0.1206271	cg26395761	cg26395761	52649436	TACRTACAAACTTCAATAAAC			II	
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0.1754072	cg2640982	cg2640982	12685507	TCCAAAAAAATACTAATCCAA			II	
0.1117378	cg2641319	cg2641319	33663333	CTTATTAATCCCAACTCAAAC			II	
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0.2589192	cg2642246	cg2642246	50734334	ACTACRAACACCRTCCATCAA			II	
0.106645	cg2642276	cg2642276	39603443	CCAATACCTACAAAAAAACCT			II	
0.1090406	cg2642901	cg2642901	38702376	CACAAAAACTCACAAAACAA			II	
0.1475817	cg2642902	cg2642902	34655409	AATCCRACCTATAATTTATTAT			II	
0.1396711	cg2644005	cg2644005	59636307	ACATTCAAAAAAACTCCTACA			II	
0.1158334	cg2644014	cg2644014	57664313	RCCAACCTCCTTATCCTTATCC			II	
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0.1707134	cg2645025	cg2645025	23687451	AACCAA	51794485	AACCAA	I	C
0.1820357	cg2645134	cg2645134	74750436	CAAAACTTATACAAATCTATA			II	
-0.154327	cg2645173	cg2645173	47622446	ACACAC	16697437	ACACAC	I	A
-0.149711	cg2645618	cg2645618	59694308	ACATTTCTTTTCCCTATAATAA			II	
-0.133356	cg2645716	cg2645716	43639448	AAACAAATTCCCRTACCCCAA			II	
0.13715	cg2645874	cg2645874	18645396	AACTCTTTTCTAACTAACTAA			II	
0.1057395	cg2646126	cg2646126	58808317	AATTTACRTTTCATTTTTCTTT			II	
0.1065996	cg2646171	cg2646171	47652340	AATAAACCCCCATTTCTACAA			II	
0.1724367	cg2646205	cg2646205	48657505	ACTAATACCAAAAATATTACA			II	
0.1587134	cg2646515	cg2646515	22688368	ACCAACCATAATCTTACTAAA			II	
0.1290464	cg2646560	cg2646560	15791438	CAAATA	11686361	CAAATA	I	T
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-0.317008	cg2647711	cg2647711	24774328	ACAAAAAAACCTCTAATACAAA			II	
0.1056041	cg2649491	cg2649491	43673381	ACAATACCAACACACAAAAAC			II	

0.1390049	cg26497631	cg26497631	49677468	TCTTACAAAATTACAAAATAT			II	
0.1011625	cg2649896	cg2649896	34658301	ACCAACT	55807442	ACCAACT	I	A
	cg2650081	cg2650081	69624364	AATATAAAAACTTAAACTAAC			II	
0.1303562	cg2650426	cg2650426	69779320	ATAAAATCCAATAAACCAACC			II	
0.1794722	cg2650461	cg2650461	54705308	ACAAAAAAACCTCRCAACCTC			II	
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-0.12939	cg2650763	cg2650763	53661308	AACCACC	62741421	AACCACC	I	C
-0.146613	cg2651246	cg2651246	38741327	TAAAAAC	41740366	TAAAAAC	I	C
-0.189739	cg2651374	cg2651374	30608337	TAATTAAAATATCTCTCCTAA			II	
-0.224408	cg2651568	cg2651568	30779505	CACCATAAAATATATCAACTA			II	
-0.110484	cg2652001	cg2652001	21677360	ACCACAA	23712417	ACCGCGA	I	C
0.1048059	cg2652546	cg2652546	25746318	AATTCTATTTTAAAAACTAAC			II	
0.1332426	cg26531231	cg26531231	34794479	AACTCATCAAACRACTATAAC			II	
-0.115156	cg2653170	cg2653170	49604443	CAATCTCAAACACTTCCRAAA			II	
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0.1293284	cg2654781	cg2654781	55630445	CTAAAAATCCAACTATTCCRA			II	
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0.144706	cg2655505	cg2655505	55781355	TACTCCA	56735502	TACTCCA	I	T
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0.115959	cg2655727	cg2655727	57621386	CTCCCACACCCAAAATAAACC			II	
0.1148004	cg2655775	cg2655775	55671425	TATAAAATAACCCATAAAAAC			II	
-0.350882	cg2656618	cg2656618	51692407	ATTCTTAAAACAAAACCTAAA			II	
0.1272978	cg2656738	cg2656738	35810338	TTCCAATACTACTACATCATA			II	
0.1222554	cg2656773	cg2656773	46682415	ATTCAACCCCAAATTTAATTC			II	
-0.11811	cg2657071	cg2657071	31716491	AAAAAAACCAACTTAAATTCT			II	
-0.156605	cg26570901	cg26570901	71802374	ATAAAAA	49785337	ATAAAAA	I	C
-0.110723	cg2657635	cg2657635	11695399	TCAAAATAAACAACCTCATAC			II	
-0.132087	cg2658334	cg2658334	33799355	CCCACAA	36642399	CCCGCAA	I	A
-0.170121	cg2659008	cg2659008	24751415	AACTTACCCAAAAAACACTAT			II	
0.2091301	cg2659010	cg2659010	61648332	TTACTCCAAAATCTCAAACCA			II	
0.1265721	cg26599871	cg26599871	46766455	ACTACCRCRCAAATTCAAAAA			II	
-0.111223	cg2660118	cg2660118	34774405	ACAACAT	48758480	ACAACGT	I	T
0.1072002	cg2660327	cg2660327	56671362	TCCCTACTAAAATATCCTTTAA			II	
-0.100423	cg2660658	cg2660658	29720320	CCCACCT	58680349	CCCGCCT	I	C
0.1118857	cg26607031	cg26607031	53770489	TATATACTACCTTACTCCAAA			II	
-0.183559	cg2660762	cg2660762	65650307	AATACAA	74790425	AATACGA	I	C
-0.127374	cg26618441	cg26618441	44629409	TCTTTACCRCAAATTCTTTCRT			II	
-0.256172	cg2662053	cg2662053	72664469	ACTAAAA	62672337	ACTAAAA	I	C
0.1487561	cg2664092	cg2664092	55773392	AATAAAAACTCCCTCTATCAA			II	
0.205133	cg2664277	cg2664277	71617460	TCTAAATTATTTAAATCCAAA			II	
-0.118137	cg2664396	cg2664396	22660445	AACCCTA	65702504	AACCCTA	I	A
-0.130554	cg2664404	cg2664404	50714320	ACAAACA	56650334	ACAAACA	I	C

0.1156634	cg2664467	cg2664467	35767342	AAAATACATAATTAACTCCTA			II	
0.1888946	cg2664543	cg2664543	61731305	TTACCTTTTCCAAAAACRACA			II	
0.1097748	cg2664818	cg2664818	69716389	TTAACATCCTCTAAAAACAAA			II	
0.2338095	cg2665128	cg2665128	21716506	CACCTACCACCCTCCCTACAA			II	
0.1510522	cg2665130	cg2665130	69748313	TATCCTA	57691326	TATCCTA	I	T
0.1442543	cg2665850	cg2665850	17793361	AATACCTACAACCTTCRAAAT			II	
-0.103001	cg2665980	cg2665980	67781376	CAAACAC	70743379	CGAACGC	I	C
	cg2666503	cg2666503	32769455	ATACAAC	73635397	ATACGAC	I	A
-0.112183	cg2666709	cg2666709	58684433	AAACRTTTTTCCTCCCTTAAAT			II	
0.1888096	cg2667364	cg2667364	20643483	CCCTCTAAAAATACCCTCTAA			II	
0.1270596	cg2667533	cg2667533	25790323	AAAAATAACATTTATATAATA			II	
0.1032393	cg2667644	cg2667644	29735503	AAACTAACCCCRCTCCAATTT			II	
-0.146686	cg2667900	cg2667900	24802369	CTTAAAA	37789498	CTTAAAA	I	A
0.1294638	cg2668060	cg2668060	29604349	AAAAATCAAAATCTATAATAT			II	
-0.162797	cg2668436	cg2668436	50792331	TTTAAAA	19714383	TTTAAAA	I	T
-0.120265	cg2668717	cg2668717	60616472	RAAAAATAACRACAACTTACA			II	
0.4980344	cg2669040	cg2669040	41734414	AAACTAAAAAATCTAAATAAA			II	
-0.106097	cg2669332	cg2669332	56719484	ACRAACCCTATTTCRAAAAAA			II	
0.1110657	cg2670091	cg2670091	54775355	CRATAAAAATAATATCTCCRA			II	
0.1442463	cg2670559	cg2670559	44686317	TAATCRCTATCAAATATACRC			II	
0.1708494	cg2670576	cg2670576	56712347	CTATTTA	55669349	CTATTTA	I	C
-0.184148	cg2671555	cg2671555	19747404	CAAAACC	16738355	CGAAACC	I	C
-0.163577	cg2671690	cg2671690	47627353	ATTAACA	66605321	ATTAACA	I	A
-0.15311	cg2671755	cg2671755	42807306	TAAACAA	54764402	TAAACAA	I	A
-0.132859	cg2672502	cg2672502	19733366	CTACTTC	10692372	CTACTTC	I	A
0.1275628	cg2673054	cg2673054	60736495	TTACCCAAATCTACTCTTCATA			II	
-0.123233	cg2673424	cg2673424	51800501	CTACAAAACCATTTTTAATTA			II	
0.1339008	cg2673802	cg2673802	21643304	AATCACTACACCCRACCTAAA			II	
-0.102594	cg2673914	cg2673914	57760454	AACACCT	20729387	AACGCCT	I	T
-0.21807	cg2673932	cg2673932	15674421	ACCTTCTCTCTCTCTAAATCTA			II	
-0.206128	cg2674468	cg2674468	25706443	ACAAAA	32762320	ACGAAA	I	A
-0.129807	cg2675164	cg2675164	43756408	AAAAATT	56742483	AAAAATT	I	C
-0.126482	cg2675390	cg2675390	45736477	CACAAA	19683378	CACAAA	I	T
-0.170196	cg2675722	cg2675722	52677329	CATAAAACCTTATAAAATATC			II	
0.1033576	cg2676394	cg2676394	21756503	AACCTTCATTTTTAAACTTACT			II	
0.1033697	cg2676797	cg2676797	69641403	AAAAAAAACAAAACCATCTAT			II	
0.1231449	cg2677238	cg2677238	47753436	CACATTATCTAAATCACATCC			II	
-0.146737	cg2677512	cg2677512	44723436	CRATCTAAAAAATAAAACTTA			II	
0.2381559	cg2677678	cg2677678	29600381	AACCCCTAAATCACTAAAATT			II	
-0.102223	cg2678420	cg2678420	38639415	TCAAAA	29731349	TCGAAA	I	A
0.2697506	cg2678661	cg2678661	41696393	AATTAAAATAAAAAACCAAA			II	
-0.107442	cg2678738	cg2678738	18622475	TCTCACT	38648505	TCTCACT	I	T
0.1047878	cg2678821	cg2678821	63738432	ATCAAAAAACAATCAATAATA			II	

-0.109541	cg26791257	cg26791257	25630315	ACAATTC	64734485	ACGATTC	I	A
0.1049179	cg26794700	cg26794700	25603505	ACCATAACATATAACCRATATA			II	
0.1511274	cg26796043	cg26796043	51642431	TATATTCC	66716324	TATATTCC	I	A
0.1786346	cg26796083	cg26796083	70615357	TCTTACAATACCATCCTTACTA			II	
0.1032344	cg26800883	cg26800883	38756410	TTAACATACCTAAATAACCATA			II	
0.1410035	cg26801241	cg26801241	35631475	TTAATCAAACCAAATCAAATAT			II	
-0.140603	cg26802063	cg26802063	64604428	ACAAAAT	71645485	ACAAAAT	I	A
-0.101276	cg26803268	cg26803268	21803377	TAACAAT	47640414	TAACGAT	I	A
0.1201543	cg26809868	cg26809868	40618348	TAACAAACTAACTTCTATCCAA			II	
0.1527593	cg26811705	cg26811705	14659426	AAAAAAC	30701330	AAAAAAC	I	A
0.1425784	cg26813483	cg26813483	58803504	TAACATCRATCCCTAAAAACRT			II	
0.1963193	cg26815032	cg26815032	10657320	CCATCCTTCATTAAAAAATATA			II	
0.1106654	cg26817755	cg26817755	38804485	ACAACCACAAAACATTTCTAT			II	
0.1032529	cg26818786	cg26818786	13611506	TCAAACAACTTTTTCTTTCTCT			II	
-0.122788	cg26820259	cg26820259	40647335	CATTCTAATTCACATCCCCCAA			II	
-0.103577	cg26822175	cg26822175	43780356	CATTCAAAATAACACAATAAC			II	
0.1384075	cg26826183	cg26826183	38808475	TTTTATACATTTACTTATTTATT			II	
0.2136557	cg26828599	cg26828599	55632485	CAAATACTTTTTCCCTAAATAT			II	
-0.115445	cg26841048	cg26841048	10786344	TCCCTATAATTTCRCTAAAATC			II	
0.1279871	cg26843807	cg26843807	74679492	CATCAAACAATAAAAAATTCA			II	
0.1452947	cg26854588	cg26854588	20690445	AAATCAAAATTCAAAAAAACC			II	
0.131018	cg26855015	cg26855015	34739493	AAAAACTATTAATTTACAAACA			II	
-0.104862	cg26856631	cg26856631	31766367	TACAACAAAACATAATCAACC			II	
0.1919323	cg26864826	cg26864826	14772371	TCCTTTTATAAATACAATATAC			II	
0.1232764	cg26871180	cg26871180	67801384	AAAATCATAAAATAATCAAAC			II	
-0.136899	cg26873880	cg26873880	65743318	ACTTCTCTCATACTTTAAAAAC			II	
-0.127081	cg26874229	cg26874229	66674405	CAAAAAA	42694358	CAAAAAA	I	A
0.124374	cg26879644	cg26879644	72640510	AAAATTCTATCAATCCTAAAAA			II	
-0.180401	cg26881268	cg26881268	42661402	ACACAAACTTCATAACTACACA			II	
-0.196227	cg26882525	cg26882525	14744359	AAATCACACACTCAAATACCTA			II	
0.1193291	cg26915799	cg26915799	21626380	TCCACCTACTAAACAATTTTTC			II	
-0.103181	cg26915952	cg26915952	30713425	TAAACAA	36747372	TAAACAA	I	A
0.1313547	cg26925980	cg26925980	23688339	AAAATTCAATAACTATATCACC			II	
-0.118217	cg26927544	cg26927544	17756352	TTACCAA	60699427	TTACCGA	I	A
0.1455062	cg26928789	cg26928789	60716382	AAAAAAAAAACACTTCTAAAA			II	
-0.14427	cg26929925	cg26929925	48754322	CAAAATT	25803318	CGAAATT	I	A
-0.131245	cg26930498	cg26930498	36600316	CACRTAAAATATAACCCACCCA			II	
-0.177116	cg26936989	cg26936989	69669477	ACTCCCAAAACATCACTATCTT			II	
0.104432	cg26939946	cg26939946	22713399	TCAAAATCCCTAACAAAAACTA			II	
	cg26940725	cg26940725	67799462	ATCCATTAACATAAACRAATTA			II	
-0.656263	cg26941787	cg26941787	70637510	CAAAAAAATCTTCTAACTTTCT			II	
-0.108884	cg26941870	cg26941870	63650347	TACAAAA	65750312	TACGAAA	I	T
0.1273714	cg26942829	cg26942829	24618335	CCCAAAAAAAAATATTCTATA			II	

0.1135057	cg2694597	cg2694597	21758419	CAAAACATTAAAATTATAAAT			II	
0.1300477	cg2694905	cg2694905	59707352	TCCATTCAATAAATCACTACT			II	
0.7126956	cg2695170	cg2695170	42739502	ACTTAAA	49667370	ACTTAAA	I	C
0.1069575	cg2695529	cg2695529	38625407	AAAACTAAAAAAACRTCATCA			II	
-0.136627	cg26955881	cg26955881	63760457	CAAAAAAACAAATCCTAAAA			II	
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0.1261153	cg2697004	cg2697004	43685411	ACTAAACCCCTCTAAAATTAT			II	
-0.115731	cg2697255	cg2697255	16777377	TAATAAAAAACCTCAAATACR			II	
0.1063399	cg2697518	cg2697518	57631400	TCAATAA	36712464	TCGATAA	I	A
0.2281658	cg2697837	cg2697837	22712463	AAACCAACACAACCAAACCTA			II	
0.1357068	cg2698015	cg2698015	59747386	AAATATTACTAACTTAAAATT			II	
0.1170523	cg2698093	cg2698093	24794368	TCTTCAAAATTCCACATTACC			II	
-0.108996	cg26982601	cg26982601	50742459	AAAAAA	23730422	AAAAAA	I	C
0.1447473	cg2698792	cg2698792	16658418	TCCTTAATCCCAAATAACTTA			II	
-0.120466	cg26991571	cg26991571	42649388	ACAAATA	18632350	ACGAATA	I	C
0.3363984	cg2699550	cg2699550	39753355	AATAACTTTCTCCTAATCACR			II	
0.1329498	cg2700023	cg2700023	73632481	CAACATCAAACAAAAAAATTC			II	
-0.132846	cg2700049	cg2700049	55698357	ATAAACT	66762343	ATAAACT	I	A
0.2458925	cg2700050	cg2700050	74713304	CTACTAAATTCTCTTTTACTAC			II	
0.1522497	cg2700511	cg2700511	39757339	AAATAAAAACATCCCCACRAA			II	
0.1258447	cg2701015	cg2701015	74726465	AAACAAATACTACAAAAATAA			II	
0.1091702	cg2701443	cg2701443	43626331	TTTTCCTTTAAAATAAATTTCC			II	
0.1079788	cg2701830	cg2701830	30775481	TCACTTTAATATACTACTCTTC			II	
0.4661825	cg2701898	cg2701898	55730337	ATAAATACCTAAAACCTCTTC			II	
-0.234236	cg2702034	cg2702034	37797354	CTACTCC	21763385	CTACTCC	I	T
-0.139674	cg2702336	cg2702336	29785438	AACTCCT	37634479	AACTCCT	I	T
-0.172794	cg27023871	cg27023871	37744504	RAAAAACAAAATTCCCACRAA			II	
0.1157741	cg2702440	cg2702440	40638350	AACAAAAAATTACTTAATATA			II	
0.1117509	cg2702619	cg2702619	40729374	AAAAATACTATAACTAAAAAA			II	
-0.128863	cg2703214	cg2703214	60613493	TCAAAAA	22725397	TCAAAAA	I	A
0.1009908	cg2703599	cg2703599	58804463	AAAAAAACAACAAATACAAA			II	
0.1176778	cg2704959	cg2704959	56651508	TCAAAACATCTACRAATAAAA			II	
-0.295952	cg2704964	cg2704964	65639453	TTTCTAC	36691449	TTTCTAC	I	T
0.1201226	cg2705040	cg2705040	72697501	CCCAACCTCATCCTTCCTAAA			II	
-0.154761	cg2705329	cg2705329	61762319	AAACTTC	21655443	AAACTTC	I	A
-0.106483	cg2705848	cg2705848	71679446	TAATATACTAAACRAAATATA			II	
0.1139106	cg27061791	cg27061791	49754427	ATTCTAAAAAATAACRTATCR			II	
-0.156861	cg2706942	cg2706942	52798451	AAATACA	14672356	GAATACA	I	C
-0.136684	cg2707039	cg2707039	16613327	CTTTCCCRTAATAAAACTACC			II	
-0.104222	cg2707115	cg2707115	49759419	TACTACA	74642481	TACTACA	I	A
0.1437456	cg2707334	cg2707334	28774445	ATATTTAAAAAACAACTAACA			II	
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0.103161	cg2707450	cg2707450	63669414	TCTTTTCCAATTCCACAATACT			II	

0.1104968	cg2707499	cg2707499	25671495	AAAACCRCACCCCAACCCCTA			II	
-0.192191	cg2707909	cg2707909	18698302	AACATTCTTTACRATATCACC			II	
0.1944752	cg2707919	cg2707919	22628361	AAAACACTCATACCATACRAA			II	
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	cg2708124	cg2708124	33704307	CCCATTT	13644439	CCCGTTT	I	C
0.1335551	cg2708308	cg2708308	26697460	AAAAAT	69671508	GAAAAT	I	A
0.1321464	cg2708402	cg2708402	33774509	CTAAAAACAAAATAACTTACR			II	
0.1044698	cg2708423	cg2708423	55610395	ATTTAAATAATATTTCRAAAA			II	
0.1687777	cg2708615	cg2708615	40698319	ACRTACCCCRTAAAAATCAAA			II	
0.1171716	cg2708630	cg2708630	55662450	AAAAAATAAAACCACAAACC			II	
0.1878473	cg2709224	cg2709224	58623436	AACTAAACTATTAATCAATTT			II	
-0.210022	cg2709743	cg2709743	26787346	ATACAA	56786397	ATACGA	I	T
0.1181056	cg2710014	cg2710014	41639327	ATCRAATATCATTCAAACAAA			II	
0.2300423	cg2710729	cg2710729	33650305	ACCTTATCACCTCTACCATCA			II	
0.1304287	cg2710796	cg2710796	61804348	AAAAATAAAAACCTCATAAAA			II	
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0.2084748	cg2711586	cg2711586	22626378	CAAACCA	14698339	CGAACCA	I	T
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0.1104102	cg2712054	cg2712054	62612508	CCAAAACCCRTTAAATCCCTA			II	
0.1207931	cg2712270	cg2712270	44638414	AATCAACTAAAAACAAAAATA			II	
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0.2110692	cg2713579	cg2713579	38624406	AAAAACATCATAATCTTCCAA			II	
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-0.114523	cg2714005	cg2714005	20615401	AACCACA	35637328	AACCACC	I	T
0.1533047	cg27141751	cg27141751	69713489	AACACTATTAAAACTTCTATC			II	
-0.486374	cg2714180	cg2714180	55690505	AAAACCAAAATCAAAATTCCC			II	
0.1673579	cg2714534	cg2714534	33750455	CTCAAAAATACCRTATCTATC			II	
0.1451889	cg2714545	cg2714545	56637356	AATATAATCTACTATCCATTTC			II	
0.1112444	cg2714755	cg2714755	67807427	ACAAACA	29706375	ACAAACA	I	C
-0.22887	cg2714907	cg2714907	11611421	AAACTAAAAAAACCCTACRCC			II	
0.1456082	cg2714997	cg2714997	40726435	CCTCATACCTAAATATACRTC			II	
0.1073868	cg2715167	cg2715167	44778424	TACRACCACTAATATTCAAAA			II	
-0.120831	cg2715177	cg2715177	30703368	CCCTAAC	64807415	CCCTAAC	I	C
-0.101843	cg2715221	cg2715221	48629373	ACAACA	11693393	ACGACG	I	A
0.1516035	cg2715651	cg2715651	73639456	TCATAAAAAATATACTTAAAA			II	
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0.1180523	cg2715998	cg2715998	14676344	TCATATTTTCCAATAAAATAA			II	
0.1057225	cg2716617	cg2716617	72774459	ACTCAACCATAACRATAACCA			II	
-0.129049	cg2716667	cg2716667	68632365	AAAAAA	44726414	AAAAAA	I	A
0.1241864	cg2717314	cg2717314	18733325	CAACTAA	35674409	CGACTAA	I	A
0.1261226	cg2717511	cg2717511	18779347	AAATAACCTAACRTCTCTCCA			II	
0.1107465	cg2717715	cg2717715	20601316	TCCAAACATAAAAAAAACTAT			II	

-0.116053	cg2717829	cg2717829	25683343	AATAATAAAATCCCTACAAC			II	
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0.1088335	cg2717981	cg2717981	53803352	TAATACTAAACRCCCCTAAAA			II	
0.1164251	cg2718137	cg2718137	69721302	ATAAATC	55727389	ATAAATC	I	T
0.1391373	cg2718303	cg2718303	71680393	AAATACATTCCTAATTCATAC			II	
0.1280446	cg2718651	cg2718651	58668500	AATACTAAAAAACCAAAAAAC			II	
0.1199025	cg2719002	cg2719002	53748501	AAAAATTAACTCTACAATATT			II	
0.1424553	cg2719969	cg2719969	41754334	AAAAATACAAAAACCAAAAA			II	
0.112103	cg2720025	cg2720025	58746331	TAAAAACAACAACATAACTAT			II	
0.1122703	cg2720089	cg2720089	66639482	CRTCACRAATACTAATATAAT			II	
-0.235307	cg2720291	cg2720291	29707314	RCACTAATCATCRTACTAACC			II	
0.102164	cg2721496	cg2721496	27609506	TTATAAT	15718384	TTATAAT	I	C
0.139533	cg2721918	cg2721918	57769383	AACCACAAAACTCTTTCCCCA			II	
0.1400692	cg2722614	cg2722614	16780412	CACATCA	38724384	CACGTCA	I	A
-0.119659	cg2722774	cg2722774	31712431	ATAATAA	37619383	GTAATAA	I	C
0.1251567	cg2722827	cg2722827	25764475	AACCTCTACAAACACRAACAT			II	
0.1201915	cg2723076	cg2723076	49780490	ACCACTAAAAAACACCACTAC			II	
0.1165243	cg2723236	cg2723236	27709322	CAAACAAATTTAAAACCATTC			II	
0.1544836	cg2723315	cg2723315	13736483	TCTAAACCATAAATACACATT			II	
-0.230283	cg2724497	cg2724497	74728376	AACAATT	33694484	AACAATT	I	A
0.1153097	cg2724769	cg2724769	44759351	ACAAAA	31768322	ACGAAA	I	A
-0.101796	cg2724858	cg2724858	16718309	ATAAAACTAAACTTACCCTAA			II	
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0.3104981	cg2725798	cg2725798	20738498	ATACAATAATACTATCTTAAC			II	
-0.116059	cg2725856	cg2725856	65616364	CRCTATCCAAATCTACAAATC			II	
-0.175262	cg2726173	cg2726173	54743425	AAAACAAATAATTAAATACCA			II	
0.1122667	cg2726399	cg2726399	19633313	ACTTAAAATAACACTTAACAA			II	
-0.170758	cg2726432	cg2726432	39635355	AATACAA	46659312	GATACAA	I	C
0.103133	cg2726883	cg2726883	74723367	TTAATTATAAAACAAAAACTC			II	
-0.209012	cg2727224	cg2727224	35664454	ATATACAATTATTTAACAACA			II	
0.2376561	cg2727322	cg2727322	45740413	TCACAACTTAATTCAATCTAA			II	
0.1060884	cg2728239	cg2728239	14747339	CATACACAATTCCCTACACAC			II	
0.1063636	cg2728412	cg2728412	64691332	ACCCAAATCRCTTTCRAACAA			II	
-0.15487	cg2728419	cg2728419	47622464	ACAATACTAACCRACAACACT			II	
-0.109848	cg2729130	cg2729130	33710361	ACCTCCATCTTATAACTAAAC			II	
0.1078797	cg2729146	cg2729146	51768317	TAATTCCCACCCTAATTCCCA			II	
0.1248415	cg2729209	cg2729209	72810314	ATATTCTTAAAACTTTCCTAAA			II	
0.1338452	cg2729222	cg2729222	41607394	TATAATCCCAAAAATCCCTAA			II	
0.1003638	cg2729565	cg2729565	29685464	AATTCTCTCTAATCAACCCTAC			II	
0.1245906	cg2729755	cg2729755	25602349	AAACCAACTATAAAACCATTC			II	
-0.183867	cg2729834	cg2729834	26760337	AAAACTA	39706440	AAAACTA	I	C

0.1164799	cg2730778	cg2730778	26809452	AAAAAC	58752493	AAAAAC	I	C
0.3257825	cg2730873	cg2730873	33793335	TTTAAAACCAAACTTAAAATA			II	
-0.130635	cg2732662	cg2732662	66679486	ACCACTA	63773438	ACCGCTA	I	A
-0.159344	cg2732867	cg2732867	11704424	AAAAAATAACAAAAAATACC			II	
-0.120306	cg2733000	cg2733000	14736422	CTTACCCCCAAAACAACAACR			II	
0.1063729	cg2733129	cg2733129	54688488	CRCCTCTCTACRAAACATCCT			II	
0.1058112	cg2733658	cg2733658	12720447	TAACACA	71636304	TAACGCG	I	A
	cg2733883	cg2733883	13644452	CCRCTCAACCCAAACCTATAA			II	
-0.24691	cg2734291	cg2734291	33666436	CCCACCT	15745448	CCCACCT	I	A
0.2263276	cg2734752	cg2734752	61768307	TTCCTTA	42802448	TTCCTTA	I	A
-0.132761	cg2734851	cg2734851	66743491	ACAACA	58797317	ACGACG	I	T
0.1055437	cg2735057	cg2735057	16797429	CTACTATACTTAATAAAAAAA			II	
0.1165702	cg2735571	cg2735571	60743476	AATTCCRAATCTAAACCACTA			II	
-0.15809	cg2736252	cg2736252	44659426	AAAAAA	29653431	AAAAAA	I	A
0.1975835	cg2736298	cg2736298	63766336	AATCACAACCACAACTATTTT			II	
0.1092125	cg2736314	cg2736314	27793347	ACAAAA	21680509	ACGAAA	I	C
0.1765362	cg2736599	cg2736599	20770382	ACAAACACAACAATAAAAAC			II	
-0.191054	cg2736676	cg2736676	21651349	ACACTAA	14699327	ACGCTAA	I	A
-0.119132	cg2736909	cg2736909	46808467	CACAACA	44740455	CACGAC	I	A
0.10013	cg2737145	cg2737145	11810404	ACATTTCCCCCACAAAAACAA			II	
-0.108972	cg2737245	cg2737245	18690453	CAAAAC	19678397	CGAAAC	I	T
-0.218545	cg2737853	cg2737853	31615459	AATATTAAACACCAACATTTT			II	
-0.113443	cg2737940	cg2737940	44699377	TTATTAA	48766488	TTATTAA	I	C
-0.111252	cg2738341	cg2738341	29768342	CTTCRTTAAATATCAAACCAC			II	
0.1097521	cg2739181	cg2739181	54750357	CATAACA	56763451	CATAACG	I	A
0.1074677	cg2739290	cg2739290	71676300	TAATCCTAAAACACTATAACR			II	
-0.102402	cg2740540	cg2740540	59651484	ATCCTCT	70740307	ATCCTCT	I	A
0.1274582	cg2740607	cg2740607	59665410	TATCCTTCAATATTCAAATACC			II	
0.2226923	cg2740817	cg2740817	39791422	ACAAAA	12749411	ACGAAA	I	A
0.1171927	cg2741285	cg2741285	28717352	AATAATATTATAAAATATCAA			II	
0.4139948	cg2741486	cg2741486	44664477	ACTCAAA	21610445	ACTCAAA	I	C
0.1331104	cg2741633	cg2741633	71665371	ACTTATAATTACTAACTTCTT			II	
0.1081323	cg2742234	cg2742234	53700466	AAATACAAACACAACCAACCA			II	
-0.129537	cg2742774	cg2742774	16749426	ACAATAA	30747495	ACGATAA	I	A
	cg2743104	cg2743104	26641373	AACCTAC	32768334	GACCTAC	I	T
0.2458772	cg2743347	cg2743347	42614354	ATAAAACCAAAAACAATATAA			II	
-0.116237	cg2743436	cg2743436	42682384	CTAAAACAACAAATAAAACCT			II	
0.1045666	cg2744086	cg2744086	56672320	AACTACTTAACATTATTTTACC			II	
-0.112798	cg2744135	cg2744135	14756460	AAACTTAAAAACCAAAACCAA			II	
0.1038696	cg2744333	cg2744333	28752456	AACACRTCTTAAAACTACACC			II	
0.4482122	cg2745074	cg2745074	50802392	TTTCTATCTCTTACTCATAATA			II	
-0.140723	cg2745136	cg2745136	24611496	AACRAACTATCAAATCRATTA			II	
-0.102541	cg2745225	cg2745225	58690410	ACAAACTTATCCCTTTATTTAC			II	

-0.106571	cg2745292	cg2745292	55621476	AAACCA	40702446	AAACCG	I		T
0.1142153	cg2745410	cg2745410	73724445	AACCTCAATAACTCAAACTAA			II		
0.1382517	cg2746125	cg2746125	62610464	CTAAAATCACRTAATACAACC			II		
-0.1578	cg2746787	cg2746787	14632431	TACTACTCCTCACTAAATACC			II		
0.280302	cg2746888	cg2746888	29620403	AAAATA	12793431	GAAATA	I		A
-0.12149	cg2746973	cg2746973	38713346	AAACCTA	31774471	AAACCTA	I		A
0.2742402	cg2748142	cg2748142	44744456	CRCTTCRAAAACAAAATTTCT			II		
0.1109793	cg2748466	cg2748466	21666391	AAAAAA	11780432	AAAAAA	I		A
-0.120887	cg2748510	cg2748510	17605506	ACATAA	20768326	ACATAA	I		C
0.1030461	cg2748874	cg2748874	48773302	TACATCTCTAATCCCTTCCTTA			II		
0.1109278	cg2749416	cg2749416	20717367	AAATAA	20632490	AAATAA	I		A
0.148219	cg2749489	cg2749489	61748336	AATAAAAAACTTACCCTACAT			II		
0.2578897	cg2750229	cg2750229	62806352	ATCCCAA	62687463	ATCCCAA	I		C
-0.100242	cg2750395	cg2750395	45729369	CAAAAAACACRAAATCCAAA			II		
0.1188539	cg2750818	cg2750818	42743387	AATCCTCTAACACCAATAACA			II		
0.1004396	cg2750912	cg2750912	34691381	CTCTATCCAATTTATTCTATT			II		
0.2236403	cg2750996	cg2750996	30789337	ACTCTAATAACCRACAATACC			II		
-0.180011	cg2751403	cg2751403	50745409	TAAAAA	46671445	TAAAAA	I		C
0.1185526	cg2751433	cg2751433	39653495	CAAAACTTCCAACAAAATTAA			II		
-0.307141	cg2751692	cg2751692	19682423	TCAAAAACCCTAATTCAAACT			II		
-0.111673	cg2751756	cg2751756	45782402	AAAAAT	45698475	AAAAAT	I		C
0.1187139	cg2752054	cg2752054	67703307	TTTATTTAACTTTCCTCTTAAT			II		
0.32875	cg2752116	cg2752116	34808321	AAAAAA	50637434	AAAAAA	I		C
	cg2752642	cg2752642	10643372	ACAAAA	64765396	ACGAAA	I		A
0.105091	cg2752677	cg2752677	30783419	ATTTTTAAACTTCTCATCTATA			II		
0.1361911	cg2753385	cg2753385	34615334	AAAAACTCATTAATAAAACAA			II		
-0.120861	cg2753719	cg2753719	17804389	CRAACCAAATATATTCTCAAT			II		
-0.153181	cg2754189	cg2754189	73804305	TTATTATAAAAATACTCRCTA			II		
0.1015756	cg2754234	cg2754234	72691401	CCACCCT	52700469	CCACCCT	I		T
-0.223978	cg2754304	cg2754304	11634337	CCCCRAAAAAAACTTACCAAA			II		
0.1131514	cg2754467	cg2754467	66683447	AAAACRAAAATACAACTATCA			II		
-0.171346	cg2754611	cg2754611	35768310	AAACACAACTATTATTTATAA			II		
0.2814462	cg2754918	cg2754918	60697329	AAAAAAAAATTACAAAACCA			II		
	cg2755066	cg2755066	32793334	TCACAAA	54606331	TCGCAAA	I		C
-0.103826	cg2755392	cg2755392	12790451	CACCCTC	64639473	CGCCCTC	I		A
-0.182746	cg2755778	cg2755778	19616307	CATAAAATAAACTCTACRAAC			II		
0.1471479	cg2756758	cg2756758	42654353	TATTAAAAATTAATAAATATT			II		
-0.161503	cg2757212	cg2757212	19647409	AACCCAA	51674379	AACCCGA	I		C
0.1363796	cg2757562	cg2757562	15736467	ACTCCACACCCCTAACTCCTTA			II		
-0.10963	cg2757714	cg2757714	16659309	CAAACTA	44767473	CAAACTA	I		A
0.1016914	cg2758232	cg2758232	14704347	CAATCCRACAATAAATAACTA			II		
-0.140945	cg2758330	cg2758330	27634389	AACCTAC	32665472	GACCTAC	I		A
0.1131933	cg2758514	cg2758514	24620463	AAACCAACACACCTAACTTAT			II		

0.1156557	cg2758835	cg2758835	48702341	ACTACAACAAACAAAAAATCT			II	
0.1291422	cg2759810	cg2759810	72641436	AAATATATAACTTCCCRTATA			II	
0.1123894	cg2760157	cg2760157	26690489	AACTAAAAAAAACTTCAAAAA			II	
-0.162521	cg2761232	cg2761232	51801389	AAAAACTACCRATAAACAATT			II	
-0.134924	cg2761448	cg2761448	62601359	TCTAATA	47732508	TCTAATA	I	A
0.148048	cg2762172	cg2762172	62733489	TTCAACATCACACCAAACTAA			II	
0.1096166	cg2762199	cg2762199	41605444	AATAAACAAATATTAACTTCT			II	
-0.307871	cg2762513	cg2762513	15722311	AAAATATCATTTCTAAATAAC			II	
0.2281281	cg2762618	cg2762618	16807466	ACCAAAT	66634378	GCCAAAT	I	C
-0.100636	cg2763919	cg2763919	49621366	AAAATCTATTCCRAAATTTCT			II	
0.1057788	cg2764025	cg2764025	73669303	AAAACCATCCCCCTTTATACTT			II	
-0.174941	cg2764247	cg2764247	58749395	AAATAA	48615364	AAATAA	I	C
0.1097667	cg2764821	cg2764821	25667382	AAAAAATAACCCAAATATATA			II	
0.1062943	cg2764827	cg2764827	67670425	CTATACACATTAAAAACCTCC			II	
-0.143215	cg2765521	cg2765521	27784335	TACTCCA	25657320	TACTCCG	I	A
-0.102379	cg2765904	cg2765904	50766426	AATTAAT	51699366	GATTAAT	I	C
0.1852823	cg2765979	cg2765979	58690368	TATTACCTCTAATTTAAAACCR			II	
-0.123543	ch.22.4827	ch.22.4827	62659432	AACTAACTACAAATACTCACC			II	
-0.129173	rs10033147	rs10033147	53636471	CCCACTC	37774439	CCCACTC	I	T
0.148117	rs1019916	rs1019916	43769491	TCTCACAACTCAAATCCCATC			II	
-0.121469	rs10457834	rs10457834	15748350	TTACTTCACTATTTAATTCACT			II	
-0.299441	rs10774834	rs10774834	22788456	TATAACT	30718329	TATAACT	I	T
-0.166876	rs10796216	rs10796216	14622465	TAACTAA	41635319	TAACTAA	I	A
0.2946505	rs10882854	rs10882854	47771383	CTTAAAC	39668349	CTTAAAC	I	C
-0.143493	rs10936224	rs10936224	34619331	TCTTTCA	30630453	TCTTTCA	I	T
-0.153106	rs11034952	rs11034952	58692423	AATCATC	44652497	AATCATC	I	C
-0.174347	rs11249206	rs11249206	60753422	TAAATCTCCCCTCTCTTATTCC			II	
-0.158488	rs13369115	rs13369115	44627385	ACTAACA	74780462	ACTAACA	I	A
-0.18639	rs133860	rs133860	52724359	TCTCACTCATCCCTCTCCCTTT			II	
0.140877	rs1414097	rs1414097	23759362	CCCACTA	39621311	CCCACTA	I	C
-0.222741	rs1416770	rs1416770	28667385	AACCTACTATATTAAATCTTTC			II	
0.1094236	rs1467387	rs1467387	45739435	AACCCAATCCAAACCAATATT			II	
-0.316369	rs1484127	rs1484127	33780375	CACTAACCAACCTACATAAAT			II	
-0.157557	rs1510480	rs1510480	69633374	TCACCTTCCATTAATTACTTCT			II	
0.3207767	rs1941955	rs1941955	33709340	TAAACCCTACTAATTCATAAA			II	
-0.477242	rs2032088	rs2032088	63663495	TTACTTCTATAACACCACACTT			II	
-0.329962	rs2125573	rs2125573	25698376	TTCTCCAACCATTCAACCTAA			II	
-0.307094	rs213028	rs213028	10622451	ACCTCCT	24684377	ACCTCCT	I	T
0.2962424	rs2208123	rs2208123	12714403	AATATAC	19761497	AATATAC	I	T
-0.286562	rs2235751	rs2235751	17621345	ATCCCAAAACAAACCTCCCCA			II	
0.3074717	rs2385226	rs2385226	46691371	TTACCAT	17623494	TTACCAT	I	C
-0.342941	rs2468330	rs2468330	23632464	ATCACACTTTTCATCACTCCAT			II	
0.1626822	rs2521373	rs2521373	12625304	CTACTACCTAATTAATAACAC			II	

-0.287038	rs264581	rs264581	52695345	AACCATTTACAAAAATAAAAA			II	
0.2879038	rs2804694	rs2804694	13748334	CTTATTCCCATCATATTTCACT			II	
-0.104655	rs2857639	rs2857639	23793421	TAAAAAAAAATTCAACCTTCT			II	
0.3117841	rs3936238	rs3936238	42802473	AATACCC	29627504	AATACCC	I	T
0.1435546	rs4331560	rs4331560	10654345	CATAACATTTCTCATCCAATA			II	
0.1676485	rs4742386	rs4742386	34623456	TCATAAATCACCAAATCTCCT			II	
0.4692939	rs5931272	rs5931272	39615340	ATCTAACAATTTATTCTCATCC			II	
-0.147488	rs6471533	rs6471533	11697340	TAACTAC	55602361	TAACTAC	I	C
-0.102864	rs654498	rs654498	36707408	CTAAAAA	15665335	CTAAAAA	I	T
0.1497186	rs6626309	rs6626309	15806372	CTTTCTC	69767339	CTTTCTC	I	T
-0.160248	rs798149	rs798149	48789496	ACACAACCTCCAATACTTCCA			II	
0.1563471	rs845016	rs845016	37661486	TAAACTAATATACCAATTTAC			II	
-0.368202	rs877309	rs877309	54760445	CCCCAACCCAAAACCTCTATA			II	
0.1587971	rs9292570	rs9292570	48712372	CTAAAAT	14806497	CTAAAAT	I	T
0.1279564	rs9363764	rs9363764	36689314	TAACTCCCTACCACCTAAAAC			II	
0.1298546	rs939290	rs939290	70759471	ATTTTATTTTCACTTTCCACAA			II	
-0.452934	rs951295	rs951295	11711409	AACAAAC	39778441	AACAAAC	I	C
0.1704655	rs966367	rs966367	16795360	ATAACTCCTTTAACTTTAAACA			II	

COLOR_C	FORWAR	GENOME_	CHR	MAPINFO	SOURCES	CHROMOS	COORDIN	STRAND
	CACGCTC	37	2	237027592	TGAGAAA	2	236692331	R
	TCTCTAA	37	X	103810908	CGCTAAC	X	103697564	R
	TATACAC	37	14	22989583	CGTCCTG	14	22059423	F
	TCTCTGT	37	2	1165351	CGGGGTC	2	1155351	F
Red	CCCTCCC	37	16	629015	CCCCCTG	16	569016	R
	TTTTAAA	37	1	167127353	ATGCAAT	1	165393977	R
Red	CCCTGAG	37	6	31650808	CGGGGGC	6	31758787	F
	TCTGGAT	37	1	23521272	CCTGGGA	1	23393859	F
	ACATTGT	37	4	123506194	TTTGAAG	4	123725644	F
	GAATTAG	37	16	11099199	TGGCTAA	16	11006700	F
	GCCACCT	37	8	59170968	CGTCTGT	8	59333522	R
	TTCTGGC	37	12	54090754	CGCAAAA	12	52377021	F
	ACAAATG	37	16	3511787	CGTGTTT	16	3451788	F
	AGCCCTG	37	8	144399335	CGCACAC	8	144470710	R
	TTATGCT	37	7	87027887	CTGTATC	7	86865823	F
	GTGCTGA	37	6	169539646	CGCCGCA	6	169281571	R
	CTTATCG	37	19	56688439	GGAGGAC	19	61380251	F
	GTCCATT	37	1	223575793	TCTTTCT	1	221642416	R
	AATGTAT	37	16	24712522	CTGAAGC	16	24620023	F
	TGGGGTT	37	2	46040236	CATGCAG	2	45893740	F
	TTTGTTG	37	2	242835364	CGGGTCT	2	242484037	R
	TTGAATC	37	1	55504649	GAAAGCT	1	55277237	R
	TTCATTT	37	16	86377053	TTACAAG	16	84934554	R
	TTGGGTG	37	2	237079099	ACCCTGT	2	236743838	R
	GTTTTCA	37	1	161391807	CGCCTTG	1	159658431	F
Grn	CTCGATC	37	4	122853693	CGGCGCA	4	123073143	R
	AAACCTC	37	16	5121151	CGGACTA	16	5061152	F
	GGCTTCT	37	1	53040491	GAGAATC	1	52813079	R
	GCTGGGC	37	17	78472159	TAGGAGT	17	76086754	R
	ACTATGT	37	1	233089275	CGGTAAC	1	231155898	R
Grn	CACCAGA	37	12	132944010	TGCACAA	12	131454083	F
	ACTGCAT	37	1	160121487	ACCTTCC	1	158388111	R
Red	CCAAGGA	37	13	112996967	CTGGGGT	13	112044968	F
	CTCAAAA	37	18	59218797	GATCCAA	18	57369777	F
Grn	TGGGGAA	37	15	22993172	TCCTCTT	15	20544613	R
	CCCGTTC	37	16	420108	CGCCCAC	16	360109	R
	TAATGTG	37	1	161280266	CGGGGAA	1	159546890	R
	ACAGAAC	37	10	73857843	CGCTGGC	10	73527849	R
	CTGGTAA	37	5	146784171	CGTCCCT	5	146764364	F
	CCTTCCG	37	12	75784855	CGGGACA	12	74071122	R
Red	GTGTCCG	37	16	1069760	GTGACCG	16	1009761	F

	TCAAAAC	37	6	32466447	CGGCAGA	6	32574425	F
	AGGTGAA	37	Y	21664296	AGACTAA	Y	20123684	R
	TGTAGGG	37	6	166251659	CGAGATC	6	166171649	R
	GGCCCCA	37	6	32033006	CGATCTT	6	32140984	R
	TATGTTC	37	1	95703607	GTCACTC	1	95476195	F
	GCAATTT	37	1	34645109	GGCCAAA	1	34417696	F
Grn	GCATGTG	37	5	135416412	GATGCGC	5	135444311	F
	CAGAAGC	37	15	71747687	CAAATCA	15	69534741	F
	ATTCTAG	37	13	43252734	CGGGATC	13	42150734	R
	TGCAACA	37	6	56507796	CGAATGC	6	56615755	R
	GGCACAC	37	15	62899159	GTGCTCC	15	60686451	R
Red	AGATGCA	37	1	9409810	CTTCCGT	1	9332397	R
Red	TTAAATC	37	8	1245703	TTTCATG	8	1233110	R
	GGGCTGA	37	6	133663589	CGGAAGC	6	133705282	F
	TCAGCTC	37	2	24344064	CGGGCAC	2	24197568	R
Grn	CGATCGT	37	20	29551622	GGCTCTT	20	28165283	F
	TCCATGG	37	16	81254719	CGGAGGC	16	79812220	R
Red	GGCCCGC	37	3	10149974	ACCTGCT	3	10124974	R
	CAGTCTG	37	3	117719971	GCAAAGT	3	119202661	F
	TGTGTGA	37	4	13922944	CGTGGCC	4	13532042	R
	CCAGGCT	37	1	3446295	CCATGCC	1	3436155	F
	ACCACAC	37	3	124531371	CGCTCCC	3	126014061	F
Red	CACAGTT	37	1	54822031	CGCCAGC	1	54594619	F
	AATTCTT	37	6	139861189	TAAAGGC	6	139902882	R
	GATATTC	37	22	41492007	CGTGTTG	22	39821953	F
	GAGGCAC	37	17	19291120	CGCCAGC	17	19231713	R
Red	TCTTCGA	37	13	113496682	CGCTCCA	13	112544683	R
	TTTTTTTT	37	6	72199637	TTCACAT	6	72256358	R
	GCCAACA	37	4	6665199	TTAAAAC	4	6716100	F
	ACAAGTC	37	5	158466226	CGGACCC	5	158398804	R
Grn	GCGGCCT	37	6	32552246	CGGGCGC	6	32660224	F
Red	CCATTGG	37	Y	21239348	CGCACGT	Y	19698736	R
	CGCGAGT	37	X	129300008	GCACAGT	X	129127689	R
	CTGCTGG	37	12	31255279	TCCAGGT	12	31146546	R
Red	ACCCCTT	37	6	30652268	GGCAGCT	6	30760247	R
	CTGGCAG	37	12	122233375	CGGCAGC	12	120717758	F
	AAATATA	37	3	64307530	TCTGAAA	3	64282570	F
Grn	CTCTGCA	37	12	1609346	GCCCGGC	12	1479607	F
	AGTCTTT	37	10	120516119	CTACTCT	10	120506109	F
	AATTCTT	37	17	928957	CGGGGGC	17	875707	R
	CTAGGGT	37	1	36021674	TGTGTTC	1	35794261	F
	TCACAAT	37	15	22904606	AGGCTGC	15	20456047	R
	AGGGGAC	37	8	1339852	AAGTGAC	8	1327259	F

Red	AATAAAT	37	10	26931912	CGGCAGC	10	26971918	R
Grn	TCCCCAA	37	X	12993156	CGGGCCC	X	12903077	F
	TACTGGC	37	3	129116393	TGAACAT	3	130599083	F
	GACGGGA	37	17	77922972	GCTGGAC	17	75537567	F
	TCATGTC	37	4	1986542	CGCCCCC	4	1956340	R
	TCAGAAT	37	1	150779776	CGCCTCG	1	149046400	R
	GTGGCCT	37	18	47016218	CGAAGTC	18	45270216	F
Red	CGTCTCC	37	12	126346041	CCGTTTC	12	124911994	R
	GCTAAAT	37	2	128569347	CGTCCAC	2	128285817	F
	CCCATCT	37	1	217306763	ACCCAGA	1	215373386	R
	GCAGAGA	37	17	724374	CGGGCCA	17	671124	F
	GACAGCC	37	8	4183880	CGACGAT	8	4171288	F
	AAGCCGC	37	6	156983315	AATTCCT	6	157025007	F
	CAAAGCC	37	5	140563151	CGTCCAC	5	140543335	R
	TTCCTGT	37	Y	14649908	CGGACAA	Y	13159918	R
	ACTTGTA	37	21	46220161	CCACCTA	21	45044589	F
	GGCTAGA	37	16	28300253	CGGGAGC	16	28207754	F
	GAGGAAA	37	16	88238863	CGTTGGC	16	86796364	F
	GCTCCTT	37	17	39222690	CGTGTGG	17	36476216	R
	TAGAAAA	37	11	103584918	CGGTCTC	11	103090128	F
	GCTCTGG	37	2	231855218	CGGCTGC	2	231563462	R
	TGACGGC	37	20	61047376	CGCTCAG	20	60480771	F
	CTGAATG	37	8	131453955	ATTCATC	8	131523137	R
Red	CTGTGAC	37	8	141555295	TAGAAGC	8	141624477	F
Red	TGTCGTC	37	11	67383545	CGCCGTC	11	67140121	R
	CTTCCGG	37	22	38071168	GCCCGGC	22	36401114	R
	TCGTGCC	37	10	62144786	CGGATGC	10	61814792	F
	CTTTCTT	37	8	2021420	GCTGGGC	8	2008827	R
	GGGTGGC	37	9	90620271	CGGAATC	9	89810091	R
	AGCAACC	37	19	50861774	AGGTTCG	19	55553586	R
	GCATGCA	37	15	22442000	CAGTTGA	15	19943364	R
Red	AGTGGTG	37	1	161582581	CGTTTCG	1	159849205	R
Red	TGCTGAA	37	1	235099120	CGCGCTG	1	233165743	F
	CTCATTC	37	2	61977683	TTCAATA	2	61831187	R
	CTGGCAG	37	4	190230730	CGGGCCC	4	190467724	F
	TGAGGCC	37	1	247803166	CTATAAT	1	245869789	F
	CCAAGGC	37	17	15340112	CCTCTCA	17	15280837	R
	CCCTCTG	37	10	135341933	CGGGGCT	10	135191923	R
Red	CAGTGAC	37	16	89152443	CGGGAGA	16	87679944	R
Grn	ACCGCCG	37	11	58736081	TGTTTGC	11	58492657	F
	ACAGCAT	37	6	57178623	AGTTGCC	6	57286582	F
	AGATTTG	37	1	169671116	CGATGAC	1	167937740	R
	GAACAAA	37	8	29033680	TTTGTAA	8	29089599	F

	GCCTGGT	37	1	236915027	CGGGGA	1	234981650	F
	CAAAATC	37	6	37682596	CGGCTGC	6	37790574	F
Red	GTTTCTC	37	4	155254194	CGACTGT	4	155473644	R
Grn	GAACTTT	37	1	8377787	AGCCTGT	1	8300374	F
Red	AAGCCTT	37	6	38202492	CGTCTTG	6	38310470	F
Grn	GTCCGGC	37	12	115109730	CGGCCAC	12	113594113	R
	GGGATCC	37	18	77236278	GCAGCTG	18	75337266	F
	CCCACCC	37	9	135454197	CGGCTTT	9	134444018	R
	CTATCTG	37	1	156974025	CGAGAG	1	155240649	R
	GGAGGA	37	11	57195187	CGCCCCC	11	56951763	F
	GGAGAA	37	19	51017311	CCTGTGC	19	55709123	R
	CTCCCCC	37	6	32186049	GCTGTCT	6	32294027	R
	TCTCTAC	37	16	16963007	CTCATAT	16	16870508	F
	GCCCCTT	37	19	58609269	CGGGGTC	19	63301081	F
	GGAAAG	37	2	10501297	CGCCTGG	2	10418748	R
	GCCTTAA	37	3	111721343	CGGTGTA	3	113204033	R
	TGACAGC	37	15	24722944	AGGGCG	15	22274037	R
Grn	GCGTCCC	37	16	30572815	CGGCAGT	16	30480316	F
	CCGCCTC	37	3	13974800	GAAAGG	3	13949801	F
	AAGTGGA	37	6	29908976	CGTAGCA	6	30016955	F
	CCTAGAG	37	1	145589534	TAATATT	1	144300891	F
	GAGGAG	37	4	178364342	CGTGCGA	4	178601336	F
	TAGTCCA	37	7	8476098	GTACAAA	7	8442623	F
Red	TTGGAGA	37	5	16509323	CGCCTAG	5	16562323	F
	AGAGAG	37	6	33040769	TACAGAA	6	33148747	R
	CGAAAC	37	7	140135611	AAGCTGC	7	139782080	F
	GCTGATC	37	8	2178551	CGAGTCC	8	2165958	F
Grn	CTAGGTC	37	X	100807848	CGCGCTT	X	100694504	F
	CTTGCAC	37	8	23712355	CGGCTAT	8	23768300	R
	GGGCTGC	37	1	2847213	CGAGGC	1	2837073	R
	TGTAAAA	37	7	138162679	CGGAAA	7	137813219	F
Red	ACTTAGC	37	2	119887680	CGCAAG	2	119604150	R
	GTAAGAT	37	2	220197716	TCAAGGA	2	219905960	F
	GCCTTTT	37	6	32493873	TGATCCA	6	32601851	R
	AGAGAAT	37	8	599525	CGGGGC	8	589525	R
	CCACCTG	37	10	49348564	TCAGTGC	10	49018570	F
	AGGTGA	37	2	208199465	TTCCTAT	2	207907710	F
Red	CCCTGCG	37	2	176936581	CGCCCAC	2	176644827	F
	TTCACTG	37	1	64434320	CGGGGG	1	64206908	R
	CCCAGAA	37	1	59221344	AGGGGCA	1	58993932	F
Red	GCGGCTG	37	19	1120191	TCCACGA	19	1071191	R
	GCGTCGG	37	17	76676366	CGGTCTT	17	74187961	F
	TCTATGA	37	12	19604192	CGAGCTG	12	19495459	R

	CACTTCT	37		2	1625268	CGGACCT		2	1604275	R
	ACTTGCA	37		19	40904851	GGGATAA		19	45596691	F
	TGCTGGA	37	Y		21036986	CGGTAAC	Y		19496374	R
	GCTTTT	37		4	152096720	CGGTTCT		4	152316170	F
Grn	GTTCCTC	37		19	41531916	GGTATCC		19	46223756	F
Red	ACTCAAA	37		2	48844908	GGGAAA		2	48698412	F
	CAAATTA	37		7	65610409	TGTGCAG		7	65247844	R
	ATTTTCT	37		3	150826472	CTGTGGC		3	152309162	R
	ATATGAG	37		2	26701355	CGCCCTT		2	26554859	R
	TGCATTT	37		13	36049807	CGCTGGT		13	34947807	F
	AGTCACA	37		6	44119147	GGCATCT		6	44227125	R
	GGCTCGG	37		16	67686943	CGGCTCC		16	66244444	R
	GTGGGGT	37		7	106505961	TCGGAAT		7	106293197	R
	GCTCCTG	37		16	67918840	TCACCGA		16	66476341	F
	TTTACTT	37		6	32223341	CAGAACA		6	32331319	R
	AAGGCG	37		6	164137946	CGTGGCC		6	164057936	R
	GATGAAA	37		10	3894968	CGTGAGT		10	3884968	F
Red	CCCTTCT	37		16	88094415	CGCGTGC		16	86651916	R
	AAAGGAT	37		1	209607166	TAACTAG		1	207673789	F
	CCTTATG	37		4	56274131	CGGCGTG		4	55968888	R
Grn	ACGCACC	37		16	89167792	CGGTCAC		16	87695293	R
	CCTGGGA	37		6	43737136	CAATGTG		6	43845114	F
	GGCAGGA	37		9	139616839	GGGATG		9	138736660	F
	CACATAA	37		1	118239410	CGGCTCA		1	118040933	F
	CTCCTCG	37		5	170845058	GTTTGTC		5	170777663	R
	GGGGCA	37		16	87616248	GTGCTGG		16	86173749	F
	ATCACTG	37		3	195578280	AGATGTT		3	197062677	F
	ATAATTT	37		12	49763288	GGTCACA		12	48049555	R
Grn	TGTCCAG	37		19	54899778	GGGGCA		19	59591590	F
	AATTCAA	37		5	9765708	CGCCCAC		5	9818708	F
Red	GGGCCCA	37		1	209405064	CGCGCCC		1	207471687	F
	CTGGGAC	37		1	230250356	CGAGGTC		1	228316979	R
	CTCCATG	37		11	6590092	CGCCCCC		11	6546668	R
	TCTCTAT	37		8	103138381	CGTCACC		8	103207557	F
	CCTGGTA	37		2	65355269	AGAATGC		2	65208773	R
	TGTTGCA	37		7	104881282	AATATGC		7	104668518	R
	CCCCCGT	37		17	17109740	CGCCAGC		17	17050465	F
	TTGTGAG	37		2	879464	CGGGGTC		2	869464	R
	AATCAAG	37		5	169548502	CGGCACT		5	169481080	F
	AAAGTTC	37	Y		6312218	CGGACTG	Y		6372218	R
Red	AGCCTGC	37		10	129949058	TCCATCT		10	129839048	F
	TTCAAAA	37		6	156717406	CGGTCTG		6	156759098	R
	AGATCCA	37		22	41983798	AGGCCTG		22	40313744	R

Red	GGAGCTC	37	13	114741241	CGGGCCT	13	113759343	R
	TACAAAC	37	8	72917147	TAAATCC	8	73079701	R
	ATATTTG	37	4	83955429	CGCAGGC	4	84174453	F
	GGATTCG	37	17	79961522	CGGGGAA	17	77554811	R
Red	TTCGAAA	37	5	74908170	TCCAGCC	5	74943926	F
	GCTGGAT	37	2	153468347	CAGGGCT	2	153176593	R
	CGTGATT	37	16	10772249	CGGCCTC	16	10679750	F
	TAACAGC	37	7	134250149	GAAGTCT	7	133900689	F
	CGCCTCC	37	19	50837025	CGCTCTG	19	55528837	F
	GCGTGGA	37	6	31124550	TCAGAGA	6	31232529	F
	TCCCCAG	37	6	26305371	GAAAACT	6	26413350	F
	GAGCACT	37	5	178549790	CGCCAGC	5	178482396	F
	TATTTTC	37	12	94640673	AATTGCC	12	93164804	R
Grn	TGTGAGG	37	13	112166963	GATAATC	13	110964964	R
	TTTCCTT	37	18	5193969	CTGGTAG	18	5183969	R
	CCCTTCA	37	20	44168629	CGACTTA	20	43602043	R
	CCCAACC	37	17	48267062	CGGCCAC	17	45622061	F
	TCCTCAC	37	15	89786496	GAAGGCA	15	87587500	F
	AGCCACC	37	4	182862370	GATCATG	4	183099364	R
	AATGCGC	37	16	57149847	AGGGGTC	16	55707348	F
Grn	GCGGTGA	37	1	59042065	CGCACGC	1	58814653	R
	AAGGTGC	37	13	100651721	GAAGAAA	13	99449722	F
	TTCCCAG	37	10	134066136	AGGACAC	10	133916126	R
	CGAACTT	37	4	189330030	CTTCCTG	4	189567024	R
	ACCATGC	37	Y	17568445	ACCCAGC	Y	16077839	F
	AGTGGCC	37	17	78958651	GCCAATG	17	76573246	F
	CCCAGGC	37	18	76073021	AGGGTTG	18	74174009	R
	GCTGTAG	37	6	142007733	CTCAGTG	6	142049426	F
	CAATTGA	37	10	63240299	ACTATGG	10	62910305	R
Red	GATGTGT	37	1	113285940	GGAGGTA	1	113087463	R
	CCCGGCG	37	10	4868386	CACCAGC	10	4858386	R
	TCCAGAA	37	9	132458129	CGGGAAA	9	131497950	F
	GGCTGCT	37	7	1787944	CGGCTGC	7	1754470	R
Red	GCTGACC	37	2	239889410	CGCCAAC	2	239554347	F
	GAAGAAT	37	4	1941849	CGCAGAC	4	1911647	R
Grn	GCCACTT	37	7	31006	GGAAAAA	7	126078	F
	CTGCTAA	37	8	2337813	GACCATT	8	2325220	R
	CAATTTG	37	15	101084442	TAGAAAC	15	98901965	R
	TAGTCAG	37	7	80352237	CGCAGCA	7	80190173	R
Red	TCCCGAC	37	X	106567457	CGCCCCC	X	106454113	F
Red	TTCCCGC	37	4	190906046	CGCCCTA	4	191143040	R
	CAACACT	37	22	43811071	ACGAGGC	22	42141015	F
	AGGGACT	37	2	186727863	CGCAGAT	2	186436108	R

	GCAGAA	37	17	31340147	CGTGCTT	17	28364260	R
Red	TTAGGTC	37	16	10856534	CGGCTGC	16	10764035	F
	ACTGAGT	37	13	80755568	CGCGTGT	13	79653569	R
	TGCTGTG	37	12	45703832	AATAAAT	12	43990099	F
	GCGCAC	37	9	137298813	CGGGTG	9	136438634	R
	CACCACA	37	15	72530044	CGGAAG	15	70317098	F
	TGGTATC	37	7	158032120	CGGAGC	7	157724881	R
Red	CACATGT	37	16	88990161	CTGCTGT	16	87517662	R
	CTCACGT	37	16	31343428	ACTCAGA	16	31250929	R
	AGGTAGT	37	1	8083892	AACGCA	1	8006479	F
	AGGGCTC	37	12	10954529	TGGGCTT	12	10845796	R
Red	CTGGACT	37	16	1052756	GACGGC	16	992757	R
	GTAAATG	37	X	103498585	CGTATCA	X	103385241	F
Red	GGGGAG	37	1	20915592	CAGGAC	1	20788179	F
	TTGGCAG	37	1	248100591	GTGTGTA	1	246167214	F
	TATTACA	37	6	30072616	GCAGCTC	6	30180595	F
Grn	GGGGCG	37	6	159360761	GCAGCA	6	159280749	F
Red	TGAAAA	37	2	234847769	CGCGCAT	2	234512508	F
	ACTGTAT	37	1	248636313	AAGTAGT	1	246702936	R
	GGCCTTT	37	6	166260532	CGGCAG	6	166180522	F
	TCTTGCT	37	16	23916466	ACTTACT	16	23823967	R
Red	GCGGCTC	37	14	106094144	CGGCCCT	14	105165189	F
	AGCAGA	37	14	37445440	CGGTAG	14	36515191	F
	GGCGACT	37	11	13986348	CGGGTAT	11	13942924	F
	ATTCACG	37	1	248790981	GACAAG	1	246857604	F
Red	AGCCGAT	37	1	6086018	CGGCAC	1	6008605	F
Red	AGGTCCT	37	1	49364657	GTCCAAG	1	49137244	F
	CCACTAA	37	X	35937697	TCACAGG	X	35847618	F
	GCTACCA	37	15	39876248	CGCACTA	15	37663540	F
	TTAAAAA	37	16	86326446	CGACCGT	16	84883947	R
	TGCTCCT	37	1	146552329	AACGGA	1	145018953	R
	GCGCAG	37	8	10584169	GGCACA	8	10621579	F
	GCTTGTT	37	1	215179216	CGGCATT	1	213245839	F
	CTGGCCG	37	1	27676652	GGACGA	1	27549239	F
Red	CCACGA	37	18	76725495	GAACGG	18	74826483	F
	TCTGCTT	37	2	234847683	CGAGCTG	2	234512422	F
	GGAGGA	37	7	158246263	CGGCAG	7	157939024	R
	GCCTGAT	37	1	207849914	CCCAATC	1	205916537	F
	AAAAGT	37	11	67383662	CGATGG	11	67140238	F
	GATGATC	37	19	57179660	TGTGACG	19	61871472	F
Red	CCCTCTC	37	12	116044025	GTGCCTT	12	114528408	R
Red	TGGGTGG	37	16	33483591	AAAGCG	16	33391092	R
Red	GCTTGGC	37	17	56565644	CGGGCC	17	53920643	F

	ACAGTCA	37	19	38039666	CGGCCTC	19	42731506	F
Red	CCTGGCT	37	19	5909063	TGTCCGC	19	5860063	F
	ACCCTAC	37	14	52466952	GGGGTTA	14	51536702	F
	TAACACT	37	2	166930521	TTCCTTT	2	166638767	F
	CAGCCCT	37	14	105293199	CGCCCTC	14	104364244	R
	CTTACCT	37	1	152196674	CTAAGAC	1	150463298	F
	GGTTTTC	37	3	177451285	AACATCA	3	178933979	F
Red	TGCTTGG	37	6	32847704	CGCGTCT	6	32955682	R
Red	ACTCTTA	37	17	73316505	CGGGCAC	17	70828100	R
	CATAAAA	37	2	230675880	CGCCTAG	2	230384124	R
Grn	CCTCAAA	37	7	27206907	TGACACA	7	27173432	R
	CTTCTCG	37	2	857746	AACCTGA	2	847746	F
	GCCCTTT	37	X	70323289	CGCCTGG	X	70240014	F
	TGCCCAA	37	1	36852956	CCCTTCT	1	36625543	R
	ACTGACA	37	18	11947875	CGGCCAA	18	11937875	F
	CGGGATC	37	4	187761401	CGACAGT	4	187998395	R
Red	TCCAGGC	37	1	207991122	CGTCCAT	1	206057745	F
	TGCCCAA	37	2	48962273	CGCAGAC	2	48815777	R
Red	CATTACA	37	14	99613313	CGCTTGG	14	98683066	R
	AAACCAA	37	10	16933505	CGGGCCA	10	16973511	F
	CCCATCA	37	22	20464947	CTCATTC	22	18844947	F
Red	CGCCCAG	37	6	30039142	CGGCCCA	6	30147121	F
Red	AGGAGTC	37	21	46237117	CGCGCCC	21	45061545	R
	ATCTTCA	37	21	28215206	AGAAGAA	21	27137077	F
	TGGCGCC	37	12	8025861	TAGGAGC	12	7917128	R
	CTGGGCT	37	7	150093664	GTGCTGC	7	149724597	F
	TGAAACC	37	4	121991345	CGCTCAG	4	122210795	R
	CACACTC	37	1	19810215	AACTCCT	1	19682802	F
Red	ATACAGA	37	X	101854294	CGGAATT	X	101740950	F
Grn	GTCCTAC	37	6	31797416	ACGAGAT	6	31905395	F
	CTGCAGA	37	16	90124400	GGCTTCT	16	88651901	R
	GAAGGCT	37	16	88990188	ATGGAGC	16	87517689	R
	AAGCTGC	37	1	161409970	AGTGGTG	1	159676594	F
	TTCATAG	37	6	32605043	CGGGGCA	6	32713021	R
Red	GATAAGC	37	5	140475652	CCAGCAC	5	140455836	F
Grn	CTGTAAA	37	X	39680221	AAATACC	X	39565165	F
	ACACATT	37	15	45493530	CGGACAA	15	43280822	F
	AGATGAT	37	1	217314284	CAGGGAA	1	215380907	F
	GCTATTT	37	6	16690986	GCTCCAG	6	16798965	F
	GACCGGC	37	3	183952212	CTGCACT	3	185434906	F
Red	CAGCTTC	37	14	106374554	AAGAAGA	14	105445599	F
	GACTTCT	37	8	98956478	GACCCCT	8	99025654	F
	CTGCATT	37	7	129499233	CGGAACA	7	129286469	F

	AGACTGA	37	14	103862143	CGGAGTC	14	102931896	R
	GGAAGC	37	6	32627885	CCTGTGT	6	32735863	F
	TACTTAT	37	5	142444988	TACATTG	5	142425181	R
Grn	CCGCTGT	37	1	47799638	CGGGCTG	1	47572225	F
	TAATACT	37	12	66139263	CGGGAG	12	64425530	F
Red	TTCAGGG	37	19	24270468	GGGAGG	19	24062308	R
	CGCACTC	37	4	3669900	CTTGGAC	4	3639698	R
	TGGCTAA	37	X	55935071	TTTACAC	X	55951796	R
	CATCTCA	37	7	151384763	ACCTGAG	7	151015696	F
	TTTTTTT	37	13	95309323	TTTTCTT	13	94107324	R
	CACGGTC	37	3	13246006	AGGCAGC	3	13221006	R
Red	GCGCTCT	37	16	2892766	AGGTTGA	16	2832767	R
Grn	ACGGAC	37	1	201488725	GGATTAC	1	199755348	F
Grn	GTATTCG	37	1	40598394	CGCCTCT	1	40370981	R
	TCTGGAT	37	18	43305784	CCACTCT	18	41559782	R
Red	CCAGCAC	37	1	201258280	GAATACC	1	199524903	F
	TCCAAGT	37	1	245314273	CGCCTCG	1	243380896	F
	GGGGCCC	37	10	729711	TGGTGAC	10	719711	R
	TCTTCTC	37	1	221056674	CGAGGAC	1	219123297	F
	GGGGGCC	37	16	1393766	CGCTCAG	16	1333767	R
Grn	TCTGTTT	37	5	4101132	CTGTTGG	5	4154132	F
Grn	AGCTACA	37	3	195709661	CACATTA	3	197194058	R
	TATGAGT	37	5	140226474	GTATTTC	5	140206658	F
	AAGGATC	37	3	195849513	AAGAAGC	3	197333910	R
	GGGTTCG	37	16	27487047	GCCTTTC	16	27394548	F
Red	TTGTTGG	37	5	140242159	CGCCAGC	5	140222343	R
	AACTGTT	37	17	80169878	AACCATT	17	77763167	R
	TTCACTT	37	3	115376349	CGGACTA	3	116859039	F
Grn	GGGCGGT	37	6	164255524	GGTGGCC	6	164175514	F
Grn	GCAGGCC	37	1	17216009	CAGGGCC	1	17088596	R
	ACTCTGC	37	1	54163070	CGGTGGC	1	53935658	R
	TCTACGG	37	22	42394853	CAGGAGC	22	40724799	R
Red	GGGCGAC	37	1	45279684	CGAGTTT	1	45052271	R
Red	ACGAGCT	37	6	170686343	CGCAGGC	6	170528268	F
	TGCCCTT	37	Y	9478342	CGCCTGG	Y	10088342	R
Red	AAAAAAT	37	16	23765258	CGCTTTA	16	23672759	F
	AGTACTG	37	19	15568935	CGGCCCC	19	15429935	R
	AAATCGT	37	1	162760584	TTCCGAA	1	161027208	R
Red	CGGCCTA	37	16	55363058	ATGCAGC	16	53920559	F
	CCGCATG	37	16	85620244	TGATACT	16	84177745	F
	TGCATCG	37	16	17516862	CGGGGAC	16	17424363	R
	GTGCGGT	37	15	40268610	CGGCACA	15	38055902	R
	AATCCTA	37	4	169535985	CGGTAAA	4	169772560	F

Red	GCCGCGC	37	6	33378345	AGGGGAC	6	33486323	R
	CCACGCT	37	5	140564161	CGGCCCC	5	140544345	F
	CGGGCCC	37	2	44313980	ATTTCTG	2	44167484	R
	TGTCTAC	37	2	240723304	GCTGGAA	2	240388241	R
	ATGAAAC	37	7	96899839	TGAGGTC	7	96737775	R
	TATTGCC	37	X	24169878	TACTAAG	X	24079799	F
	TTTCAAT	37	8	15094114	CGGGACA	8	15138485	F
	TCTTACA	37	14	52816915	CGCCTCT	14	51886665	R
	GCAGTGT	37	22	32599511	CGCACCG	22	30929511	F
	CCACCAG	37	9	129377854	ACTTCCG	9	128417675	R
	AGCAGGA	37	10	115465924	GATCTAT	10	115455914	R
	GGCCCGA	37	7	2883003	CCTGCCT	7	2849529	F
	ATTTCTC	37	15	49277592	CGTGGGA	15	47064884	F
	AGTTCCC	37	11	106239635	CGGTGTT	11	105744845	R
Red	TTGCTGG	37	16	818807	CAGGGGC	16	758808	F
	ACTAAGT	37	14	101539195	AAATGAC	14	100608948	R
	AACTTTA	37	12	32437813	CGCGAAC	12	32329080	R
	GGCATAC	37	17	41521676	CGAACAA	17	38877202	F
	TCCGCAG	37	10	118387327	CGCCCAG	10	118377317	R
	CTTTCGG	37	4	183601697	CGGTGGA	4	183838691	R
	CTTTGTG	37	6	158053980	TCTGTTT	6	157973968	R
Red	GCTGGGC	37	20	62221766	CGGCCTC	20	61692210	R
	AGGCTGA	37	22	37593672	GAAAAGC	22	35923618	R
Red	GGGACAA	37	7	56855195	CGCCTCC	7	56822689	F
Red	GTCCTAT	37	14	101175302	CGTCACG	14	100245055	F
	GTAATAT	37	11	127007896	CGCACGC	11	126513106	R
	GCCCGGC	37	4	1186469	CAAAGAC	4	1176469	R
Grn	TCTCAGT	37	11	85645743	CGGCCTT	11	85323391	R
	AGCTCCC	37	6	31095800	GCAGGGC	6	31203779	R
Grn	TCTCGCT	37	X	129254804	CAGGTGC	X	129082485	F
	GGGATGC	37	14	105695807	CGGGCCC	14	104766852	R
Red	ACCAGAC	37	5	140553091	CGCCCTC	5	140533275	F
	ACAGTGC	37	2	19549980	GGGGCCA	2	19413461	R
	ATTCTCA	37	15	65032199	CGGTCAC	15	62819252	F
	CGACCCC	37	2	241611991	GCCCGAC	2	241260664	R
	GTAATGA	37	2	52759434	CGGGTGT	2	52612938	R
Grn	GACGGGA	37	16	2867446	CGCCGCC	16	2807447	R
	TATGTCA	37	20	11869467	CAGAGTT	20	11817467	F
	TCATGCT	37	11	101313190	AGAATAC	11	100818400	F
	TGAATGA	37	5	140563213	CGCCTGA	5	140543397	F
Red	TCCCTCT	37	12	119592035	CGCGCCC	12	118076418	F
	ACACCTG	37	12	122116709	TGCTTCC	12	120601092	F
	CGGGCGC	37	11	1262311	CGGTCAC	11	1218887	R

	CAGGGAT	37	7	2582200	CGTCTGG	7	2548726	F
Grn	CGAAGAC	37	7	150020401	CGCCCAC	7	149651334	F
	TCCGGAG	37	5	140568075	CGGTTTC	5	140548259	R
	CCGGCTC	37	5	1856932	CAGGCAC	5	1909932	F
	CACTCAG	37	12	66025635	AAACATC	12	64311902	R
	TCCCTTTC	37	7	27206461	GCCCTGG	7	27172986	F
Grn	ACGCACC	37	7	56242554	CGGCCCG	7	56210048	R
Grn	GGGGGCC	37	6	30039025	CCTGGAA	6	30147004	R
Red	CTCCTGTC	37	8	145938564	CGGTCTG	8	145909373	R
	CTCAACA	37	2	27887409	CGCTTTG	2	27740913	F
	AAAGCCA	37	17	65072689	CGCAGCC	17	62503151	F
	GGAATGA	37	2	241230376	CGGGCAC	2	240879049	F
	GAGAGGC	37	3	184241840	TGAGGGC	3	185724534	R
	CCGTCAG	37	2	121372064	CGCTCTG	2	121088534	F
	GCAGTAC	37	8	2075820	CAAAAAT	8	2063227	F
	CGTGCAG	37	16	21199840	CGTCGTT	16	21107341	R
	TTACTTAC	37	9	126772537	GTGAAAA	9	125812358	R
	ACTGCTC	37	12	1042034	CGTACTA	12	912295	R
	CGGCTGC	37	1	2885134	CGGACCA	1	2874994	R
	GCTGGGC	37	7	25899194	CAGATTC	7	25865719	R
Grn	TTGTACC	37	X	123094675	TAACTTA	X	122922356	F
Red	TCTGTACC	37	17	75405842	CGCCATT	17	72917437	R
	CAGTAAC	37	6	152126441	TGATCCA	6	152168134	R
	GATGGGC	37	19	51866949	CGCCTCA	19	56558761	F
	AAACGTC	37	16	85123554	ATCTGAT	16	83681055	R
	AATACAA	37	20	4983091	CGGTTTC	20	4931091	R
	CAGGAGC	37	21	38580129	CCATACC	21	37501999	F
	CCTAGAA	37	6	32489203	CGCAGTC	6	32597181	R
Grn	AGGTTTG	37	7	4911022	CAGCCAC	7	4877548	F
	GGCCCGA	37	7	157260189	CGGGTTA	7	156952950	R
	CAGGAGA	37	12	26522758	CGGGCTG	12	26414025	R
Red	GTGACTC	37	21	40176597	CGGTGCA	21	39098467	R
	GTTCATT	37	5	140248564	GTTGGTC	5	140228748	R
	CTGTTAC	37	3	177182762	CGTTGGG	3	178665456	F
	TTGTGGA	37	2	33827715	AGTGGCT	2	33681219	R
Red	GCAGGGC	37	2	239925497	CGGAATC	2	239590434	F
	GAGGATC	37	22	40573054	GGGACTT	22	38903000	R
Red	GTGCGAC	37	19	49700021	CGGCGAC	19	54391833	F
	CACAGTC	37	2	190119363	CAGGGTC	2	189827608	F
	CCGGGCT	37	5	178565001	CGGGTGC	5	178497607	F
	TCTTCAG	37	3	187664092	CGCTTGC	3	189146786	R
	ATCCAGG	37	4	9479622	CTCAAGC	4	9088720	R
	GGGGCCA	37	6	34524766	CAGCAAC	6	34632744	R

	CAACCTC	37	2	136496804	CGTAAAC	2	136213274	R
Grn	TCACGGT	37	8	144810339	TGGCTGG	8	144882327	R
	GACAGTC	37	15	61091220	CGGCATG	15	58878512	R
	TCTGAAT	37	13	77090294	CCCTGAT	13	75988295	F
	TCTGCAG	37	17	57915740	CGCTTTT	17	55270522	R
	CGGCAGT	37	2	238322334	TGCCTAA	2	237987073	F
	TCCTAAG	37	2	192198841	TTCATTC	2	191907086	R
	TTCCTGT	37	3	14289162	CGAGTTA	3	14264166	R
Red	AAAGATC	37	16	87856264	CGCGCCG	16	86413765	R
Grn	TTGCGCA	37	17	17109239	CGGGTCG	17	17049964	R
	GAGGCCT	37	6	30652688	CGGGAGA	6	30760667	F
Red	GTGTCTC	37	1	3081226	CGCCTGC	1	3071086	R
Red	CGGCAGC	37	2	177017449	TTGATCT	2	176725695	F
Red	CGCCCTG	37	5	140237151	CTACTCT	5	140217335	R
Red	TTCAGCC	37	12	123259789	CGCCAAT	12	121825742	R
Grn	AAGCTTT	37	2	176936397	TTATTCG	2	176644643	R
	AAAAGCC	37	13	41593385	CAAACAT	13	40491385	R
	CTCTTAT	37	1	206729040	TGCCAGA	1	204795663	R
Red	TCAGGCC	37	7	158703106	CGCGCTC	7	158395867	R
Red	CAGGCGC	37	17	3771578	CGTGGGC	17	3718327	F
Red	CTGGTCT	37	3	133502909	CGGGTGC	3	134985599	F
	TGCGTGT	37	16	73099565	TCTCCCC	16	71657066	R
	GCGAGGC	37	3	49236800	CCCTGGG	3	49211804	R
	GCTGAAA	37	8	79885164	CGCCTGT	8	80047719	F
	AGCCGTT	37	20	52786323	AAAACAA	20	52219730	R
	AGTCTCA	37	Y	14648161	CGCTGTG	Y	13158171	F
	CCAGATC	37	4	24745718	CGCTTCT	4	24354816	F
	GGAGTGA	37	5	175299260	GAAAGGC	5	175231866	F
	AAATGAA	37	2	174827779	CGTGCAT	2	174536025	R
Grn	GTATACA	37	X	37430689	CTCCCCT	X	37315608	F
	TTCTCCT	37	4	187630905	CTTCTGC	4	187867899	F
	GGCTGTC	37	19	21264896	CGTGCCC	19	21056736	R
	GCTTCCC	37	19	54275893	CGGCACA	19	58967705	R
	CAGCGCC	37	8	72917363	GTCCGGA	8	73079917	F
	TGGGAGC	37	16	2334163	CGCACCA	16	2274164	F
	AGAAAAC	37	13	41186645	AGACTTG	13	40084645	R
Grn	CGCGGGT	37	6	29895074	CAGCACC	6	30003053	R
	CCCTTCA	37	6	29898751	CGGCAGT	6	30006730	F
Red	CCCCGCG	37	8	1431308	CGGTGCA	8	1418715	R
	GCGGGGC	37	6	29895005	CGCCCTT	6	30002984	R
Red	TCAGGCC	37	16	86411222	CGAGCCT	16	84968723	R
	CGCCGCG	37	Y	9234365	CGGTGCC	Y	9294365	R
	AGAGGTA	37	7	28447591	CGAGGGC	7	28414116	F

	AAAGTGA	37	14	59947673	AAGATCA	14	59017426	R
	AGCCTGA	37	16	4295972	TGACTGT	16	4235973	F
	CTGTACT	37	7	135433715	TCCATGT	7	135084255	R
	GTGAAAA	37	1	12893344	CGATTGG	1	12815931	F
	CATAAAC	37	1	85809159	CGCATGG	1	85581747	F
	CTTTGGG	37	5	176958396	TGCTGTT	5	176891002	R
	AAAATCC	37	4	154622943	AATGCTG	4	154842393	F
	GTGCTTG	37	19	48246266	CGACGCA	19	52938078	F
	GGCTGGC	37	5	3116792	AGTGAAC	5	3169792	F
	CCTCACT	37	19	52514445	ATCACCA	19	57206257	R
	TCCAGGG	37	5	140725147	CACCAGT	5	140705331	F
	AAACAGC	37	3	13420826	CGAGGAA	3	13395826	F
	CCGTGTT	37	3	54353711	CGCTCTC	3	54328751	R
	TATGTGA	37	5	123589203	CGTTGGC	5	123617102	R
	TTATGAG	37	11	93467095	CGTAGTA	11	93106743	R
	GCTAGGC	37	8	33342441	GGAGCTC	8	33461983	F
	AATTATT	37	X	25019025	CGGGCCA	X	24928946	F
	GCCACCG	37	22	32057065	AGCCTGT	22	30387065	R
	CTCCCAG	37	16	33734837	CGCCCAC	16	33642338	F
	TATGTTT	37	6	169857450	AAAGATA	6	169599375	R
	ATGGTGA	37	2	8829827	AGCTAGC	2	8747278	F
	GGTAGCT	37	7	150018095	CGAGGAC	7	149649028	R
	TGAGTTT	37	2	67102333	GAGGGTT	2	66955837	F
Grn	CCGGCCG	37	8	144809598	TCGGCCT	8	144881586	R
Grn	ACTGGAC	37	4	7763618	GCTCCTC	4	7814518	R
Red	TTGCCGA	37	12	115134918	CAAAGGA	12	113619301	F
	GTTTGGT	37	15	75953954	CGCATAG	15	73741009	F
	GAGGCCT	37	12	5195150	AGTCACT	12	5065411	F
	GTTCCGT	37	2	1657462	CGGACAT	2	1636469	R
	TGCGAGT	37	13	110747452	CGACTAT	13	109545453	R
	GCCTGGG	37	17	13447853	CGGCGCA	17	13388578	R
Red	GCTGCCG	37	13	111281479	TCGTCAG	13	110079480	R
	CTTGCTG	37	3	25833304	CGACCAT	3	25808308	F
	GAGTTGG	37	16	1880436	CGGTTCA	16	1820437	F
	AACATCT	37	15	39875777	CAGCACC	15	37663069	F
Grn	CTGAAAT	37	4	1202930	CGCATGT	4	1192930	F
	GCCTGTT	37	16	84743502	CGGGAGT	16	83301003	F
	TCACCCT	37	2	43521066	CGGGTCA	2	43374570	R
	TTCCAGA	37	7	98960493	CGGAATC	7	98798429	F
Grn	ATGTCTA	37	6	74063982	AGGCTTT	6	74120703	F
	GGCCCGC	37	6	30227583	CGCCTCC	6	30335562	F
Grn	GCACAGC	37	11	498864	CATCAGA	11	488864	F
Grn	GCCGCAC	37	6	35733710	CGGCTCA	6	35841688	R

Grn	CAGGTCC	37	17	8250623	ACTGCCC	17	8191348	R
	GTGAGTG	37	9	130705120	CGGCTCC	9	129744941	R
	TGTCATT	37	4	155254497	CGGCAGC	4	155473947	R
	TAGAAGA	37	7	108101162	CGTGCAT	7	107888398	F
	TCGAAAA	37	17	80246403	CGGACTT	17	77839692	R
	GCTCCAG	37	2	3315680	TGGGGCA	2	3294687	R
	ATTACCT	37	15	93629544	CGCAGGC	15	91430548	R
	TCTCTGA	37	6	1686746	TGGCCAT	6	1631745	R
Grn	ACCTGTG	37	16	15018856	CGCCTGC	16	14926357	R
	CAATAGT	37	4	146018691	ATACCGT	4	146238141	R
	CCCAGTT	37	3	75657183	CGTGGTG	3	75739873	R
Grn	CTTGGAG	37	6	101847656	CGGGGCT	6	101954377	F
	CAGTTCA	37	X	42638571	CATTGAC	X	42523515	R
Red	TCACCTA	37	16	25075152	CAGTTCT	16	24982653	R
	CGTGAGA	37	11	783889	GAAGGAT	11	773889	F
	GCGCGGC	37	22	24384245	GAGTCCT	22	22714245	F
	GCCATTG	37	17	54230996	AATGAAA	17	51585995	F
Red	GCTGGCA	37	20	43343365	CGGGAGC	20	42776779	F
	TGTGATA	37	16	51465744	CGGTATA	16	50023245	R
Red	GAAGAGC	37	8	43131353	GGCGGAC	8	43250510	R
	TTGCGGC	37	2	91634652	CAGCAGC	2	90998379	F
	TCTCTGA	37	8	1365659	CGGGGCT	8	1353066	F
	GGGGTGC	37	15	92459894	TTTCCCA	15	90260898	F
	TCAGTGG	37	2	242919814	CGCACAT	2	242568487	R
Grn	TGCGCCC	37	15	25123688	TTATACG	15	22674781	F
	AGGCCGA	37	6	28446840	CGCAGCT	6	28554819	R
	GAGTCAC	37	7	129933014	CGGGGAC	7	129720250	R
Red	CGGCACT	37	3	195578240	CGCGGCA	3	197062637	R
	TCAATAT	37	16	21740820	ACCAAAC	16	21648321	R
	ACCATAT	37	14	58762197	GCTGATA	14	57831950	R
	CTGTGAT	37	6	33041229	CTGAGTC	6	33149207	F
	CAGGTTA	37	6	32526702	CGGGAGC	6	32634680	F
	AAGTCAC	37	6	1706830	CGCAGGC	6	1651829	F
Grn	AGACAAT	37	4	4866091	TCCACAA	4	4916992	F
	ACAGAAC	37	15	48741995	AAATGGA	15	46529287	R
Grn	CGAGTCG	37	6	35754906	CGCGGAC	6	35862884	R
	AGCTTAT	37	7	1018969	CGCATTT	7	985495	R
	CCTGCTC	37	11	71276654	CCTGATC	11	70954302	R
	AAATACA	37	5	122836394	AACTATG	5	122864293	F
	GTGAAGA	37	11	121626930	TCTGTGC	11	121132140	F
	CACCTGT	37	6	73973719	TAAATTT	6	74030440	F
	CGTTAAC	37	9	100070007	CCCGAAC	9	99109828	R
Red	GAAAACA	37	14	28733613	GAAGAAC	14	27803364	R

Red	ATCACTA	37	14	106806179	ACCAGGC	14	105877224	R
	CTTGGAT	37	12	133036016	CGCCCTG	12	131546089	R
	GGGTTAA	37	17	79792936	CGTGCAG	17	77386225	F
	GTCATGC	37	16	87465786	ATTCTCC	16	86023287	F
	ATTAACC	37	5	145304100	CGGAACC	5	145284293	F
	GGGAGAC	37	6	166108110	CGCTGCT	6	166028100	F
	CTGCCCT	37	16	12156525	ATTTCCT	16	12064026	F
	ATATGAT	37	20	62439108	CGCTTGT	20	61909552	R
Grn	ACTAGTA	37	5	140480872	TAAAGCC	5	140461056	R
Grn	CGAGATC	37	X	8434367	TCGGTAG	X	8394367	F
	CAGAGCC	37	6	28863428	GTTACTA	6	28971407	F
	GGTGTCA	37	8	37005619	GCGAAGC	8	37124777	R
	CCAGGAT	37	X	76648652	CGGGGGA	X	76565308	R
	GCTGAAC	37	13	19692744	CGGGCAC	13	18590744	R
	GCCCAGC	37	8	15093686	CGGAGGC	8	15138057	R
	TCCCATT	37	7	94954059	CGGGGAC	7	94791995	F
	CCTGATC	37	5	149493008	TCACCTG	5	149473201	R
	GGCCCGC	37	2	54087008	CGGACCC	2	53940512	F
	TATTAAC	37	16	82660328	CGGGGGA	16	81217829	R
	TGATCCA	37	1	6660403	CAGCCAC	1	6582990	F
	GCTGCTC	37	7	105223849	AGGCCGC	7	105011085	F
Red	GCCGCGA	37	16	86465884	CGGGGGT	16	85023385	R
	CAGGTTA	37	8	980822	GTTTGTC	8	968229	R
	TAAACCA	37	14	94491763	CGCCTGA	14	93561516	F
	TGTCCTC	37	22	38201848	TCTTGAT	22	36531794	F
	CTGACAG	37	1	8085193	CGGTGAC	1	8007780	R
	TCTCCTT	37	6	100650602	GTAGCAA	6	100757323	R
	TGTGTTT	37	16	8995926	AACAATC	16	8903427	R
Red	TCCTAAA	37	16	11655159	AAGAGGC	16	11562660	R
	GGGGAAC	37	1	2121521	TCTCAAC	1	2111381	R
	TTCTGCT	37	16	88308391	GTTATTA	16	86865892	R
	CCCTCTC	37	1	25040257	CGTCCAT	1	24912844	F
Red	GGAGCTC	37	X	125687041	CGCGTGT	X	125514722	R
	TACTTAG	37	5	155548458	TTGATTA	5	155481036	R
	CCCCAAG	37	5	148541626	GTTTGCT	5	148521819	R
	CCTGATT	37	1	112107941	CGAGGTT	1	111909464	R
	CCTGACC	37	12	58934471	CGGAAGT	12	57220738	R
	GGACCAT	37	8	142239716	CACTGGA	8	142308898	F
Red	CTTGGAT	37	5	140480770	GTACTAG	5	140460954	F
	CGTAGGC	37	3	138725204	CGCCTCG	3	140207894	R
Red	ACGTCAG	37	1	2121724	CGGCGTC	1	2111584	R
	GGGTTGT	37	1	899182	CGGTCTG	1	889045	F
	TTTCCAG	37	12	54623795	ATTTATT	12	52910062	F

	TGTGTGT	37	1	40203715	TTTCTTT	1	39976302	R
	CCAATGC	37	2	152214027	AGTTTTT	2	151922273	F
	CTGTCAT	37	7	102783873	GCTGAGA	7	102571109	F
	GGGAATC	37	20	36932385	TGCAGCC	20	36365799	F
	AATTCCC	37	6	32829208	CTTCATT	6	32937186	F
	CATGTGT	37	6	148644988	CGCCCTG	6	148686681	R
	ATCAGCA	37	15	86270435	ACTTACA	15	84071439	F
	TCTCTCC	37	20	68396	GCCATGA	20	16396	R
	GCACTGG	37	1	24522592	CGCTTTC	1	24395179	R
	TTCATTT	37	6	30079177	CGCAAGT	6	30187156	R
	TGCCTTA	37	7	82435009	CGGAATA	7	82272945	F
	TACAAAC	37	11	84028562	TTGGATG	11	83706210	R
	CACTGCT	37	1	51986254	CGGGCAA	1	51758842	R
	TGGGTTG	37	2	190151266	CGGGAGC	2	189859511	F
	GCTCCGC	37	X	9432530	CCCCCAC	X	9392530	R
	AGGAATA	37	12	15907517	ATAGCTA	12	15798784	R
	GAACTCA	37	6	100896803	AATGTCC	6	101003524	F
Red	GGCACAT	37	17	973713	TTGCAAA	17	920463	F
	GTGGCAC	37	6	49605296	TATATAT	6	49713255	F
	CTTCCCA	37	6	33053608	ACAGTCT	6	33161586	R
	GACTGTG	37	19	46584209	CACTTCC	19	51276049	R
Grn	TTAAGCG	37	X	71351858	GAGAGG	X	71268583	F
	AGCTTCA	37	19	49689673	CGGCTAG	19	54381485	R
	TGCTTGA	37	2	224967286	CTATTGC	2	224675530	F
	CTCAGCG	37	11	108408962	GACCTCC	11	107914172	R
Grn	TCAGCAA	37	7	2768561	AGTGCCT	7	2735087	R
	TGTGTGG	37	6	101847541	CGTCATC	6	101954262	R
Grn	AGCGCTG	37	19	12831888	CGGCCAC	19	12692888	R
	TGGCATA	37	Y	22917894	CGGAACT	Y	21327282	R
	GACACCC	37	X	95940519	CGCGCAA	X	95827175	R
	GCATTTA	37	9	103788959	CGCCATC	9	102828780	R
	GGACCGT	37	17	65487462	ATGTAAC	17	62917924	R
	AATTCCA	37	12	68704235	GGTGTGA	12	66990502	F
	TTATATT	37	5	86707074	CGGTGTT	5	86742830	R
	TGGTCAG	37	15	52331471	CGCCTGG	15	50118763	F
Grn	GGAACCC	37	3	138739874	CGTGTCC	3	140222564	F
	AGGCACC	37	3	12792283	CGACTGA	3	12767283	F
	CTCAGGC	37	1	17674864	ACCCATA	1	17547451	F
	ACACACA	37	X	70151117	CGCAATC	X	70067842	R
Red	GCCGCGA	37	17	20687681	CGCGCCA	17	20628273	F
	AAGTGCA	37	14	59198210	CGCAGAC	14	58267963	R
	TCCTATT	37	15	59904009	CGGGAAC	15	57691301	F
	GCCATTG	37	10	93174498	CTTTATT	10	93164478	F

	ATTCATC	37	1	151665715	CGAGCCA	1	149932339	R
	CATCTTC	37	1	149212475	CGAGCCA	1	147479099	R
	TCCCAAA	37	11	114165695	AAAAAAT	11	113670905	F
	CACTCCA	37	16	85163406	CGGACAA	16	83720907	F
	TCTTTCT	37	4	129212177	CCTTTTC	4	129431627	R
	AAAATGA	37	16	474430	CGCGAAC	16	414431	F
	AAGTTTG	37	9	94182501	CGTGTTC	9	93222322	R
	AGACCAT	37	10	45072520	GAAACAC	10	44392526	R
Red	GTAAAGC	37	8	143660412	CGGTTTG	8	143657414	R
	AGTATGA	37	2	192161142	CGTCAGA	2	191869387	F
Red	CCGGGGA	37	21	47010818	CGCCCCA	21	45835246	R
Red	AACCTCA	37	15	78505051	CAGCGGT	15	76292106	F
	TGTAGAG	37	11	13938802	CGTGCAT	11	13895378	R
	TAAGTGG	37	1	27284253	CGCAATT	1	27156840	F
	ACAATTA	37	3	170451961	GAGACCC	3	171934655	R
	AATGCTC	37	5	79040203	CGTGCTA	5	79075959	R
	TTCCTCA	37	10	76642824	ATTATTT	10	76312830	F
	CCTCCAG	37	4	159091837	CGCTGTC	4	159311287	F
	TCTGGAG	37	10	81320623	CGTGCAG	MULTI	MULTI	R
	CAACACA	37	11	12284949	AACGAGA	11	12241525	R
Red	CACGGCC	37	1	29189789	CCGGGTC	1	29062376	F
	GCAGTTT	37	1	12100631	CGAGGTT	1	12023218	F
	AGACTAA	37	6	29648736	CGCCCCT	6	29756715	R
Red	CAGTGGC	37	17	79459563	CGCTCAA	17	77074158	R
Red	GGGAACC	37	X	19002980	CGGGGGC	X	18912901	R
Red	TGGCGGC	37	5	5887361	TCGGTGG	5	5940361	F
	CTGAGCG	37	2	172972681	CGCCCTG	2	172680927	F
	GTTTTCC	37	6	31651094	CGGTGTC	6	31759073	F
	ATCCGCT	37	16	4001959	GTCCATG	16	3941960	F
	AAATAAA	37	6	30588193	CGAAGTC	6	30696172	R
Grn	CTGCAGG	37	8	111214984	GCGGCTG	8	111284160	F
Red	GTTCCAT	37	10	43846539	CGCGAAT	10	43166545	F
	TAAGTCT	37	17	37385773	CGCCTCG	17	34639299	R
	AGATGAT	37	6	30022807	CGGCTAA	6	30130786	R
	AAATGAT	37	8	117587078	TTCTCTG	8	117656259	R
	GCCACCA	37	21	15434350	GGGGGGC	21	14356221	F
	AGGGAGC	37	10	43577025	CCATGGG	10	42897031	F
	CCTCCCT	37	12	56114155	CGCCTGG	12	54400422	F
	TTGTCAG	37	16	20780262	CGGTTAT	16	20687763	F
Red	GGGGCGC	37	16	1276278	CGTGGCT	16	1216279	R
	ACTCCTC	37	7	148321082	CGTCACA	7	147952015	F
Red	AGCGCCC	37	21	15352848	CGCCGCT	21	14274719	F
	GCATATA	37	10	135052900	TTCTTAC	10	134902890	R

	TCACATC	37	10	27232252	CGGTAAC	10	27272258	R
	CCGCGGT	37	X	152989807	CGTGCAG	X	152643001	F
Grn	CCCGGTC	37	X	70474483	GCAGGCC	X	70391208	F
	ACACGCT	37	10	15355978	CAAGGCA	10	15395984	R
	CCCTGGG	37	3	136069371	AGAGTAC	3	137552061	F
Red	ACTCCCG	37	10	130831421	TAAAGAC	10	130721411	R
	AGAGACA	37	10	48828109	AGGGGGA	10	48448115	F
Red	AGGCACA	37	3	48694451	GGGCCCT	3	48669455	F
Grn	CAGGTCC	37	14	99641151	CACCTTG	14	98710904	R
	AGCTTAG	37	10	75576192	CGGATTG	10	75246198	R
	GAGATAC	37	15	51390542	ACACGCT	15	49177834	R
	CCATAGA	37	1	170898554	CGGTGAA	1	169165178	R
	AATGAAT	37	3	39234924	AGCAGGA	3	39209928	R
	GATTGCC	37	4	154386540	CGCTGGT	4	154605990	F
Red	CCGCAAC	37	10	52434778	CTGGGAC	10	52104784	R
	CAAAGTC	37	11	93913200	CGTTGTA	11	93552848	R
Grn	CCGCCAG	37	11	50257496	TGCCGGT	11	50214072	R
Red	AAGCCTT	37	13	112157919	CGCCGCA	13	110955920	R
	AACCCAC	37	4	87849250	CAACATC	4	88068274	R
	TAGAGAC	37	6	37616410	GCCTAGG	6	37724388	R
	TTTAAAA	37	10	15212066	ATTTGCC	10	15252072	F
	CATTCCT	37	11	134608598	CGCACAC	11	134113808	R
Red	CCGCCGC	37	X	17879424	CGCAGAC	X	17789345	R
	AGTCCCA	37	19	24270073	GGGGTCC	19	24061913	F
	GCATGGC	37	5	1246274	CCACACG	5	1299274	F
	GGAGGCT	37	5	16895511	CTGAGGT	5	16948511	R
	AAGAAAA	37	16	90148388	GGAAATT	16	88675889	F
	GGCAAAC	37	1	4036953	CGCACCC	1	3936813	F
	TACTGAG	37	17	48256402	CGATCGG	17	45611401	F
	TATGCCG	37	5	1054262	CGGCCCA	5	1107262	F
Red	TCCCGGC	37	1	1144658	GTGCCTG	1	1134521	F
	ACCCGTC	37	8	1140574	TCACCAA	8	1127981	F
	ATAAGTA	37	2	152804107	AGAAACA	2	152512353	R
	TTTGCCT	37	16	55866890	CTCTCTC	16	54424391	F
	CAACATA	37	5	32223673	ATTCCAT	5	32259430	R
Red	CTGCTTC	37	5	126409227	CTGAGAT	5	126437126	F
	GGCTTCG	37	6	31650790	CGGTCGC	6	31758769	R
	GCCCTGG	37	5	33937182	CGCCAGC	5	33972939	R
	GGGCCAA	37	7	1955432	AGTGTTG	7	1921958	F
	GGCTGCA	37	5	140710469	CGGCATC	5	140690653	R
Red	TGGGTTT	37	16	33956717	GTTTGTG	16	33864218	F
	GGTTAAT	37	11	61732658	TACCATC	11	61489234	F
Grn	TGCTTTG	37	17	1390182	CGGCCTC	17	1336932	F

	GAGCTGC	37	3	169649593	TGGTGGC	3	171132287	R
	GTGAAAT	37	13	94885861	CGCTGGA	13	93683862	R
	AGGATTT	37	5	140220686	CGGAAGT	5	140200870	F
	CTTGGCT	37	14	95731916	CTCACAG	14	94801669	F
	CGATGCC	37	2	66801399	CGAGCTG	2	66654903	R
	GCTTTTC	37	2	207931932	AAGCATT	2	207640177	R
	CTATGAT	37	Y	16945913	TCATGAT	Y	15455307	F
	AATGTCA	37	7	39646802	CGACCAC	7	39613327	R
	TACTGGA	37	19	56349119	TGGCCCC	19	61040931	R
	TAATATT	37	10	60567288	CTCATAT	10	60237294	F
	TTTCAGC	37	3	177397780	TGCCCTT	3	178880474	F
	GTGGCAT	37	Y	23561638	CGGCCTA	Y	21971026	F
	TGCCTCC	37	7	150412715	TCCATTC	7	150043648	F
	TGGTGAA	37	7	158056848	AAGCCTC	7	157749609	R
	GATGAAC	37	5	169123192	CGGCCCC	5	169055770	R
	ATGCTTC	37	10	131209556	CGCCATC	10	131099546	F
	TCCTAAT	37	16	55866842	CGCATCT	16	54424343	F
	CCTCGGG	37	6	53219672	TTCCTTA	6	53327631	F
	TAGGAAA	37	6	36887307	AGCCATA	6	36995285	R
Red	CAGTCAT	37	15	22383188	CGTGCAC	15	19884552	F
	GGGGAAC	37	5	33321127	CGAGAGC	5	33356884	R
	GCTGGGC	37	6	31650786	CGCTTGA	6	31758765	R
	TTTTCCTC	37	7	46851524	GTAAGCT	7	46818049	F
	TCAGATT	37	12	76577488	AGACAGC	12	75101624	F
	CAAGTTA	37	17	41521655	AGACTGC	17	38877181	R
	AGTCGGC	37	5	41869679	CGGGTTA	5	41905436	R
Grn	AAGGGTC	37	16	75563489	GGCACCA	16	74120990	F
	TGGATCA	37	12	93140078	GAGCCTT	12	91664209	F
	GCCATCC	37	6	150266173	CGTGACC	6	150307866	R
	AGTGTTA	37	17	13502304	TGATTAA	17	13443029	F
	TCCCTGC	37	15	89354338	ACAGGGC	15	87155342	R
	CTCAGAC	37	10	134833335	GCGGGCA	10	134683325	F
	AGCATTG	37	Y	9384707	CCGGGCC	Y	9994707	F
	GTGGCCA	37	5	140530028	CGGGTTG	5	140510212	F
Red	CCGCACC	37	16	857454	CGCCTGT	16	797455	F
	CAGGGAC	37	21	36419648	TGCAGCT	21	35341518	R
Red	GCGTCCT	37	12	75784884	GATTGGC	12	74071151	R
	CCGGGCC	37	19	10747142	GGGCCTG	19	10608142	R
	AGGTTTC	37	5	125808164	CGCTGCC	5	125836063	R
	GACCTGC	37	16	90114563	GCCTGTC	16	88642064	F
	AAATGTC	37	16	63072440	CGCCCTA	16	61629941	R
	CGGACAC	37	6	32941126	GCGCCCT	6	33049104	R
Grn	CAGTGGC	37	7	46202794	TGCCACC	7	46169319	R

	GATCTCA	37	6	32367970	GTAAGAT	6	32475948	R
	CACTTGG	37	15	44223008	AGAACTC	15	42010300	R
	CGGCGGC	37	19	39056126	CGGGCAT	19	43747966	R
Grn	GCAGCCC	37	19	39056216	GCCGGGC	19	43748056	R
	GGGGCCA	37	1	221055401	GTCCTTG	1	219122024	F
Red	GGGCGCA	37	1	226111372	CCCACGG	1	224177995	F
	ACCCTGC	37	15	60966344	ACAGAAA	15	58753636	R
	TCCACAA	37	21	28340304	CGCTCTG	21	27262175	R
	CATTGTA	37	15	74275622	CACATTT	15	72062675	R
	TCTTTGC	37	8	1203186	TGGCTGG	8	1190593	R
	TTTTTGG	37	6	149806235	CGGGGGC	6	149847928	F
	TGGATGC	37	8	6876781	CGGCATT	8	6864191	F
Grn	CCGCTCC	37	2	48844916	CGCACCT	2	48698420	F
	CTGAGGC	37	17	15083645	CGCAAAC	17	15024370	R
	TTTCTAT	37	8	22250005	CGTCACC	8	22305950	R
	CAGCCAC	37	12	106484618	CGCTCTT	12	105008748	F
	GAGTAAA	37	5	2135054	CGCAGCC	5	2188054	R
	TGGAGTC	37	20	6514844	CGTAACT	20	6462844	R
	GGAGGAC	37	8	1365502	ATAAAAC	8	1352909	F
	GAAAGAA	37	18	56117145	CGAATCC	18	54268125	F
	TCTAACC	37	12	48356074	CTTTGCA	12	46642341	F
	ATAAAAT	37	2	135594780	AGAGCAC	2	135311250	F
	ACATTTC	37	5	59072686	CGTGAAA	5	59108443	R
	CTGGAGT	37	2	39319447	GGGAGGA	2	39172951	R
	TAAACAC	37	7	157348266	GCAGTCA	7	157041027	F
	CCGCGCG	37	20	58515583	AGGCGCC	20	57948978	F
	CTCAGTG	37	12	122297408	CGGCAGC	12	120781791	F
	CATCATC	37	12	10251536	GCATGTC	12	10142803	R
	TAAGAGT	37	3	97887864	CGCCAAT	3	99370554	R
	AGGCTGC	37	12	10095902	TCCTGCG	12	9987169	R
	GTTTTTG	37	17	57918600	GTTTTTT	17	55273382	R
	TTCCATC	37	10	78319050	CGCAGGA	10	77989056	F
	CCACCTC	37	12	52206773	CGCGGCT	12	50493040	F
	GCGACAC	37	1	247802739	CGCCTCC	1	245869362	R
	GGGACAA	37	20	61731334	CTGCAGA	20	61201779	F
	ATTTCCA	37	Y	22680010	AGTTTAG	Y	21089398	F
	AAATCAC	37	10	128086694	AGCCATT	10	128076684	R
	ACAGCAC	37	2	241834907	GGACCTG	2	241483580	F
Red	CGCCCAC	37	21	18984770	CGCCGCC	21	17906641	R
	CAGCATG	37	10	130279912	GCATTAA	10	130169902	F
	TCCCCAG	37	2	37996000	TGTGTCT	2	37849504	F
	AAACAAA	37	2	229291442	CGGTAAA	2	228999686	F
	GGCGCAC	37	6	170338826	CCTGGGA	6	170180751	F

	GCATGAA	37	16	69310261	CGCTGCT	16	67867762	F
	ACCCTGA	37	5	95478736	CGTGGAC	5	95504492	R
Grn	CAAAATA	37	16	57333902	TCCTAGG	16	55891403	R
	TGGCTAC	37	16	67978429	CCTTCGT	16	66535930	R
	GGAGCTT	37	4	3043199	CGCACTG	4	3012997	R
	CGTCACA	37	1	247569605	AGAGCAC	1	245636228	R
Grn	GCAGGAC	37	5	179588673	CCGGCAC	5	179521279	F
	TGAGATG	37	1	11761416	TGCCACT	1	11684003	R
Red	GGCTGTG	37	11	5959923	CAGCTGA	11	5916499	F
Grn	ACGCGGC	37	2	231855524	GTTGCAG	2	231563768	F
	CCCCCAC	37	12	132637860	CGCCTCC	12	131203813	R
	GATTCGC	37	15	100890963	GATGCAA	15	98708486	F
Red	AGTCCTC	37	X	105421602	CGTGCTG	X	105308258	F
	ATAACTT	37	2	11674057	CGCAGGC	2	11591508	F
	CTTCAAC	37	11	41735702	TCCCTAC	11	41692278	R
	CTGGGAT	37	2	47761452	CGGCTTT	2	47614956	R
	GGGAAGC	37	10	1975000	CGTAGCT	10	1965000	F
	GAAGGCC	37	7	86337918	CGTGGCA	7	86175854	R
Red	ACTTGGT	37	11	977280	CGGCCAT	11	967280	R
Grn	GTGGCTT	37	7	154998107	CGGGGAA	7	154629040	R
	GAACCTG	37	X	39547825	GCCTGGG	X	39432769	R
	ACACTGA	37	16	87339708	CGGCAGC	16	85897209	F
Red	TATATAT	37	7	72723152	ATTTTTT	7	72361088	R
	GAGACTC	37	1	93913524	GCAGTGC	1	93686112	F
	AATGACC	37	12	72149634	CGGGTCA	12	70435901	F
Grn	GGCACCC	37	10	124578366	TCCTCGC	10	124568356	F
	TGTCTTA	37	4	7844918	CGGTTCG	4	7895818	R
	GTGTTAC	37	17	25583370	AGGAGCC	17	22607497	R
	AGAGATC	37	1	227692291	CGGCACA	1	225758914	F
Red	GGTCGGC	37	X	150067276	CGCCCCC	X	149817934	R
	TGTGGGG	37	16	87367481	CTCCAGG	16	85924982	F
	TATCATG	37	3	183382726	GCAACTC	3	184865420	F
	CAAGTTA	37	13	41593416	ACACCAC	13	40491416	F
	ACCACCA	37	15	92661549	CAGCCAA	15	90462553	R
	CCTCCAT	37	5	170024515	CGACCAT	5	169957093	F
	AGAGAAT	37	6	21033836	CGGGAAA	6	21141815	F
	GGCTGTG	37	12	95671146	CGGGCAA	12	94195277	R
	CGCAGAT	37	16	55794731	GCGGGCC	16	54352232	F
Red	GGACCCT	37	6	32938824	CGCCTCT	6	33046802	R
	GGAGATC	37	5	177548615	TCTGAAG	5	177481221	R
	CTGCGGT	37	16	87491587	CGGGTCG	16	86049088	R
	TAAGATT	37	12	83125178	CGTTAGT	12	81649309	F
Red	GGGTCCT	37	17	74002944	CGAATTC	17	71514539	R

	TGACAGA	37	2	88716767	TTTCTTC	2	88497882	F
	TGCTGTC	37	19	292245	TCACAGA	19	243245	R
	AAAGGA	37	4	13514574	CATTTGT	4	13123672	R
	CTGTAGC	37	3	129799733	ATTCACC	3	131282423	R
Grn	TCTCTGG	37	10	86016643	CGGCTTC	10	86006623	F
	GCTTTCT	37	10	671406	CGGCCTT	10	661406	R
	TTGGTAA	37	7	136989898	CGCTAAC	7	136640438	R
	GTATCCC	37	X	8696915	CGCCCAA	X	8656915	R
	TGACATT	37	15	52526871	CGCAGCA	15	50314163	F
	TCCTCCG	37	3	125473844	CGCCCAG	3	126956534	R
Red	GGAAGCC	37	1	182921851	GTCGCTG	1	181188474	F
	TTTTTAT	37	8	11664728	TGAGATG	8	11702137	R
	TATTAAA	37	15	40268421	GATTATG	15	38055713	R
	CGGCTTC	37	4	190960010	CGGGGTC	4	191197004	F
	GTAATTT	37	2	242986091	CGCCCCA	2	242634764	R
	TCCTGAA	37	16	3613509	CGACCTC	16	3553510	R
	CCAGTTG	37	11	2924899	TGGCTTC	11	2881475	F
Red	AGAATAC	37	5	140762957	CGTGCCC	5	140743141	R
Grn	AGCCCTG	37	22	19420170	CGCCCTG	22	17800170	R
	GGGTTGT	37	10	79284013	TTCGACA	10	78954019	F
	CTGAGAA	37	11	103480630	CGTGGGC	11	102985840	F
	GTGTTGG	37	16	80972238	CGGTCGT	16	79529739	F
Red	TGGCTCA	37	6	16181250	CGGCCGC	6	16289229	R
	GTCCCGT	37	6	32489963	CGTGTCC	6	32597941	R
	CAGACAC	37	11	20119229	CGGAGCT	11	20075805	F
	CCTTTCT	37	2	135214041	AGATCTC	2	134930511	R
	GGGGGTC	37	1	221057236	CGGGTGC	1	219123859	F
	TCCCTAT	37	2	178970574	CGCAAGT	2	178678820	R
	CTTTATT	37	2	38099030	CGCTGCA	2	37952534	F
	TTTGGGA	37	1	152161885	AAAGTCC	1	150428509	F
	TGGCATA	37	10	99449502	CGGGATC	10	99439492	R
	TGACAGA	37	15	78535419	CGCTGTT	15	76322474	F
Red	GTGGATG	37	5	2253242	CGCGAGC	5	2306242	F
	AGCGTGA	37	6	169470822	TCTCTAA	6	169212747	F
Red	CTAGCAC	37	3	48698519	CGCTGGC	3	48673523	F
	GGGAATC	37	19	35800589	CGCCGGC	19	40492429	R
	TTGGGTG	37	11	68625231	CGTCCTT	11	68381807	F
Red	GATATAT	37	8	28174814	GGTGTGG	8	28230733	R
	TTAAATC	37	18	32289550	CGATACA	18	30543548	R
	TGCTCCC	37	6	32606884	CGCCAAC	6	32714862	R
	GAGACGC	37	3	23243300	AACTTCC	3	23218304	F
	ATCCTAG	37	8	61626185	CAAACCT	8	61788739	F
	GTGGCCT	37	Y	9214477	ATTCACG	Y	9274477	R

	TGGAAAC	37	21	46912386	CGAGCGA	21	45736814	R
Red	GCAGGCC	37	2	233251773	CGTTCTG	2	232960017	R
	ACAGAAC	37	11	119887950	CTTTGGA	11	119393160	R
	ATTCTTA	37	2	178853377	TGAACAA	2	178561623	R
	CATGCAT	37	16	87339553	CGGGACT	16	85897054	F
	TTGGTGC	37	12	56365894	CGGTTGA	12	54652161	F
	GGAGAGC	37	17	48267239	TGTGCTC	17	45622238	F
	TTTCCGTA	37	6	22113516	CGCAAAA	6	22221495	R
Red	GGGGTCC	37	10	134720057	CGCTCCA	10	134570047	R
Red	CTGCCCT	37	1	4771682	GCTGGGC	1	4671542	R
	CAATGAA	37	X	119133091	CGGTTGG	X	119017119	R
	AAGGCTT	37	8	72917432	AGTCACC	8	73079986	F
	AACGGGC	37	3	171523157	CGGCCAT	3	173005851	F
	CCGCCTC	37	1	246304208	AGATAGA	1	244370831	F
	TTAAGTC	37	16	14051717	CGGAGTC	16	13959218	R
	GCTGTTTA	37	11	111312361	CGCTTTTC	11	110817571	F
Red	TCCTTTCC	37	X	19140359	CGCCTCC	X	19050280	F
	TCCATCT	37	20	10492319	CGCAGAT	20	10440319	F
	AGAAATA	37	17	20840716	GAGCCAC	17	20781308	F
	TGAGCGA	37	6	88757302	CGCCTAC	6	88814021	F
Red	CGGGTGC	37	19	1525453	CGCAGCC	19	1476453	F
	TCCTTCC	37	11	110225729	TCCTTCC	11	109730939	R
	GTGACCA	37	4	186061165	CGGACTT	4	186298159	R
	ATCCTAT	37	8	100885941	TTGAAAA	8	100955117	F
	TCTGATG	37	6	31382931	CGCCTGG	6	31490910	R
	CCCCAGG	37	19	55735946	GGTCTGC	19	60427758	F
	GCAGCCC	37	1	16345207	GGACAAA	1	16217794	R
Red	AGTTTCA	37	20	57427650	ATCCTGG	20	56861045	R
	CTGCGGT	37	7	51539131	GCGGGAC	7	51506625	R
	GAGGTAC	37	19	5346237	GGTGGGT	19	5297237	R
	ATCAAGC	37	8	129082086	CGAAAGA	8	129151268	R
	CGTCATT	37	16	11410036	CGCTGGT	16	11317537	R
	GCACAGC	37	1	115826274	CGCCCAC	1	115627797	R
	TCAGCTC	37	3	31118948	CGCACTA	3	31093952	R
Red	GGACGTG	37	19	19323996	TATCCTTC	19	19184996	F
	ATTATTA	37	6	32605694	CGGATGT	6	32713672	F
Red	AGCTGCC	37	6	47210376	CGCCCCG	6	47318335	F
	CCTTGGG	37	6	32605283	CGGTGGT	6	32713261	R
	GTAGAAC	37	13	111281129	GTCATCC	13	110079130	R
Red	CTCATGG	37	X	43741601	CAGGCCC	X	43626545	F
	CCCATGG	37	6	74064298	GGAATGC	6	74121019	R
	CAGCAAA	37	16	66545712	CGCATGA	16	65103213	F
	AACTGGA	37	11	45734486	AGGCTGA	11	45691062	F

	GTCTCGC	37	4	2366485	GGGGTGA	4	2336283	R
Grn	CCCCAAG	37	8	145657956	GGCCCAC	8	145628764	R
Red	CGTTATA	37	17	79614795	CGCCCTC	17	77225200	R
	AAGGACC	37	4	1520151	CGGCCTC	4	1489445	R
	CTCCACG	37	1	161349006	AGCAGCT	1	159615630	R
	TGCCTGT	37	16	67687392	CGGAGTC	16	66244893	R
	CACACAC	37	12	117799749	CACAATG	12	116284132	R
	TACAATT	37	6	36515676	CGCACAT	6	36623654	R
	AATACCC	37	2	197944718	TCAATAA	2	197652963	R
	GGAAGAT	37	16	65105516	AAATAGC	16	63663017	F
	CAAGGGA	37	12	4829617	CGGCTTT	12	4699878	R
	TAAGTAA	37	16	55176084	CGTGAGC	16	53733585	R
	AACATTC	37	16	11374865	CAGGAGT	16	11282366	R
	TCTCAGG	37	6	29855338	AGGCCCC	6	29963317	R
	AAAGACA	37	11	79608291	TTAGCCG	11	79285939	R
	TGTTGGA	37	16	27437892	GGAGTCT	16	27345393	R
	CCTAGGG	37	20	36932397	CGCATGC	20	36365811	F
	ACTTCAT	37	16	53856169	AAGTCAC	16	52413670	R
Red	TGTGCGA	37	14	81879375	AGGCCGT	14	80949128	R
Grn	TTTCTCT	37	2	98357802	GCTTTCC	2	97724234	F
Red	GCTTCAG	37	1	1229351	CGCCCCG	1	1219214	R
Red	CGCCGCC	37	19	10679729	CGCAACT	19	10540729	F
Red	GAGGCCC	37	18	14748285	TTCAAGA	18	14738285	R
	TAAAAAA	37	7	55516872	GCATGGC	7	55484366	R
Red	GTGCCTT	37	14	98629206	CGGGCGT	14	97698959	F
	TAACGGC	37	6	29944670	AATTCCT	6	30052649	F
Red	GCCCTGG	37	2	202483740	GGCGTAA	2	202191985	R
	ATCCTGT	37	19	14586979	TGGGTGC	19	14447979	F
	TCCCCTG	37	15	71532066	CTACCAC	15	69319120	R
Red	GCCACAT	37	11	1947791	GCAGGGC	11	1904367	F
	TACAGTT	37	2	87040878	CGTTGAT	2	86894389	R
	GCATCTG	37	17	1975245	CGCCGTG	17	1921995	R
Red	GCCCGGC	37	8	21905599	TGGTAGA	8	21961545	F
	GCCACCA	37	11	30741136	CGGCGAC	11	30697712	F
	GCACAAT	37	2	224897425	CGTCAAA	2	224605669	F
	GCCATTT	37	20	57394000	GAATCCA	20	56827395	R
Red	GGCAAGC	37	16	88497077	ATTCTGA	16	87024578	R
	ACCTCAT	37	1	28560936	CGCCCAG	1	28433523	F
	CGGCTGA	37	5	76010658	CGCCTTT	5	76046414	R
	TGTGTGC	37	17	1553585	CGCAGCC	17	1500335	F
Grn	AGCAGCC	37	12	124929991	AGCAGGT	12	123495944	R
	AATGATG	37	1	15733844	GTCAGCC	1	15606431	R
	CATCACA	37	21	45658538	GTGAAGC	21	44482966	R

	GAAAGGT	37	6	21277954	CGGTGAA	6	21385933	F
	TGCCTCC	37	6	11702389	CGCATGC	6	11810375	F
Red	CCACAGA	37	Y	9193029	CGCATGC	Y	9253029	F
Grn	TCACCGT	37	17	1029917	CGGCGTC	17	976667	F
	CTCACCT	37	17	48268233	CGGACGC	17	45623232	F
	CCTTCAG	37	1	48173399	CGGAGAA	1	47945986	R
Red	CCCGCTC	37	20	61905353	CGGCTGT	20	61375798	F
Red	ATTGCTT	37	10	6183455	ATCCGGG	10	6223461	F
	TTGCACT	37	2	108159066	CGGCAAT	2	107525498	F
	TTCATTT	37	7	116738693	CGTGGGA	7	116525929	F
	CAGAAGT	37	8	38033655	CAGGCTA	8	38152812	R
	ATGGCGC	37	7	1976457	GTGCTGC	7	1942983	F
Red	CCTGTAA	37	22	37493737	CGGTGGC	22	35823683	R
Grn	GTAAAAA	37	12	54408664	CGAATGC	12	52694931	F
	CAGGGAA	37	4	186033378	CGCTGTA	4	186270372	F
Red	CACGTGG	37	10	133981681	GCCAGAA	10	133831671	R
	ATAATGT	37	5	140740607	CGACAAA	5	140720791	F
	GGATTCT	37	16	75232330	GACTGCT	16	73789831	R
	TCCCCTT	37	6	28557411	GATAAGA	6	28665390	F
	GCCTGTC	37	6	37598264	AGCCCAT	6	37706242	R
Red	CGAATTT	37	1	147801721	CGGAACC	1	146268345	F
	TATTGCT	37	2	80329553	CGAGGGA	2	80183064	R
Red	CACGGCT	37	6	33245490	CGCGCAC	6	33353468	R
	TAAATAT	37	1	94445292	CGGATAC	1	94217880	R
	CCGTGAG	37	19	491572	TCTGCCT	19	442572	F
	GTTGTAC	37	6	28185726	TGAAACA	6	28293705	F
	GACTCAT	37	16	15583606	AGTTTTC	16	15491107	R
	AGTCACA	37	12	125223679	AAGATTC	12	123789632	R
Red	GCGTTCC	37	13	114964125	CGGGGAC	13	113982227	R
Red	AGCGGGC	37	X	12993214	CGAAGTC	X	12903135	F
	CAGGGGC	37	7	2425741	TCCTGCA	7	2392267	F
	ATTTAGA	37	Y	15817871	AGGTCTT	Y	14327265	F
	GACACAC	37	6	150211725	CGGGGGC	6	150253418	F
	TCTCCTC	37	13	114797865	CAGTACA	13	113815967	F
	GGGCTCC	37	17	67457828	CGGGATC	17	64969423	R
Red	CATTCTG	37	1	234908226	GTCGGTG	1	232974849	F
	TCACCGC	37	13	111474862	CGGACAC	13	110272863	F
	AGACCAC	37	5	1007359	CGCTACC	5	1060359	R
	AGAACTC	37	1	92415048	CGGTTTT	1	92187636	F
	TACTTAA	37	6	166610956	CGGCTGC	6	166530946	F
	AGTGACC	37	1	227947250	CGCCTGT	1	226013873	F
	CGGCATC	37	8	1472227	AGCTGTG	8	1459634	R
	CAGGTCT	37	16	81353400	CGCTCAT	16	79910901	R

Grn	GCCCAGA	37	20	33762673	ACACCAC	20	33226334	R
	TTAATCT	37	16	24759640	CGGCAAC	16	24667141	R
Grn	CCGCGCA	37	13	102106348	CGGCGTC	13	100904349	F
	CCACCCT	37	19	1456886	CGCCAAC	19	1407886	R
	AAGTTGA	37	8	49502967	AAAGCA	8	49665520	F
	AAGAAAC	37	8	41707736	ACAGTTA	8	41826893	F
	CTCCACT	37	17	41522069	CGGAAG	17	38877595	F
	CGCACAC	37	7	150020125	CAATACA	7	149651058	F
	TTAAGTT	37	11	55431152	CCCAGGA	11	55187728	F
	GGGAGCC	37	8	43131535	GTGGAGC	8	43250692	R
Grn	CCACGCC	37	X	153237590	GAGATGC	X	152890784	F
	GGATGAC	37	10	69609995	CGAATTT	10	69280001	R
Red	CCCGCCC	37	6	32633015	CCCTTTC	6	32740993	F
Grn	TCCCTCC	37	X	70474012	CGCCCAG	X	70390737	F
	TGAAATT	37	1	247803637	CGGCTCT	1	245870260	R
	GCAGCAC	37	17	75315081	GAAAAGT	17	72826676	R
	ACTCAGT	37	1	177896505	CTTTGTT	1	176163128	R
Red	GCCTTCA	37	2	129494558	CGCCCAC	2	129211028	R
Grn	GGTTGGA	37	1	146550796	GCTCCAC	1	145017420	F
	CCACAGC	37	6	26615071	AGAAATT	6	26723050	R
	AGTGAAC	37	11	10331045	GGAGGGT	11	10287621	F
	GTCACTG	37	10	114635839	CGGCCCC	10	114625829	F
Red	CTCTGCC	37	16	1328562	GCTCTCA	16	1268563	F
Red	AAAAGTC	37	15	53045142	TTGGTAT	15	50832434	R
	AGGGCGC	37	19	44860820	AATTCTG	19	49552660	F
	AGAATCC	37	9	2013970	CGTAATG	9	2003970	R
	CTTGTGG	37	7	18330092	TACCCGT	7	18296617	F
	AAAAAG	37	2	11196659	AGACGAT	2	11114110	R
	AGAACTC	37	1	110654497	CGTGCAT	1	110456020	R
Grn	GCAGGAT	37	6	25882463	CGGGGCC	6	25990442	F
Grn	CGCCGGC	37	20	57465448	GAGTAGC	20	56898843	R
	TTGCTCA	37	8	11839764	CGGGGAC	8	11877173	R
	CAGACCC	37	22	50007725	CGGGGCC	22	48393729	R
	CCATCTG	37	11	2365581	CGGACTT	11	2322157	F
	TCCCCCA	37	10	131412643	GATCGTC	10	131302633	R
	CAGAGAT	37	13	66919912	CGCAGGC	13	65817913	R
	CCCACGC	37	16	87588893	CGGACTC	16	86146394	R
	TTGGGGA	37	4	104021583	TCTTTTC	4	104241032	F
	TGTAGAG	37	8	6913030	TCTTCTT	8	6900440	F
Red	TGGCTCT	37	16	90038083	CGATGGC	16	88565584	F
	CCCAGAT	37	7	29519323	GGATGCA	7	29485848	R
Red	AGCTGGA	37	11	1957880	CACTTAC	11	1914456	F
Grn	CCAGTAA	37	16	46603015	CTGTCGG	16	45160516	F

Grn	CGGAGCA	37	6	30038975	CGCCTGG	6	30146954	R
Red	CCAGAGC	37	11	688091	CCGGGGA	11	678091	F
	CACAAAA	37	18	76549840	CGACACC	18	74650828	F
	GCATATG	37	3	196347230	CGGAAGA	3	197831627	F
Red	GAGGTCC	37	12	34547930	CGGGAGA	12	34439197	F
	CCCCCAT	37	6	29819602	TCCAGAC	6	29927581	R
	TGTTGTT	37	16	6844322	CGGGCTA	16	6784323	F
Red	GTTGAAG	37	16	88496788	CCGGAAC	16	87024289	R
Red	TAGGCGC	37	1	4008051	AGGGTGT	1	3907911	R
	GCGTGCC	37	10	43846574	CGGTCTC	10	43166580	F
	GGAAACT	37	15	74281983	TACTTCTC	15	72069036	F
	TATGGCT	37	3	108125523	CGCAATG	3	109608213	F
	AGTCACA	37	19	7525578	CGGGCGA	19	7431578	R
Red	GGCGGTC	37	12	52473731	CGCCGCC	12	50759998	R
Grn	GACACCC	37	5	140536920	GAAAACC	5	140517104	R
Red	GTCCCGC	37	19	50249776	GGTCCCC	19	54941588	F
	TCATCCA	37	5	140501661	CGAGGCC	5	140481845	R
	ATTGGGA	37	10	49810606	CGGGCCA	10	49480612	F
	AGTAGTT	37	13	94725495	CGATGGT	13	93523496	R
Red	CCCACAG	37	6	30039175	CGCAGCC	6	30147154	F
	CAAGGAT	37	5	140481256	AGGCCTA	5	140461440	R
	CCCAAGA	37	6	28446794	CGGGGAC	6	28554773	F
	AAGCGCC	37	11	9781412	TACATGC	11	9737988	F
	ATTTTAA	37	6	80838251	CTGCCAA	6	80894970	R
	TAGTGGG	37	13	36049380	GAAAAGC	13	34947380	F
Red	GGGGACC	37	7	55516724	AATACCA	7	55484218	R
Red	TGCAGCC	37	X	31284813	GGGGCAA	X	31194734	F
	TAGTTGG	37	1	65611925	CGGAGTT	1	65384513	F
	TATGCAT	37	4	54548670	CGACAAC	4	54243427	R
Red	CCACGCT	37	11	60534991	CGGGGCT	11	60291567	F
	ACCTACT	37	1	3153293	CGGGCTC	1	3143153	R
Grn	TTTTTGTC	37	22	16868045	CGGCTTT	22	15248045	F
	GCCTCCA	37	6	31731881	ATGAATC	6	31839860	F
	AGTGGCC	37	2	173118470	CGCACCG	2	172826716	R
	CATCAGA	37	6	47065652	CGGGAGC	6	47173611	F
	TTCATCG	37	5	178684658	CGCTGGA	5	178617264	F
	AGATGTG	37	1	207842833	GGAGGAT	1	205909456	R
	CTCAGGT	37	20	4128752	CGCCCGG	20	4076752	F
	GGAGTGC	37	22	46481099	CGGCCAC	22	44859763	F
Grn	ACGGGCC	37	15	101095730	CCTCCTTC	15	98913253	R
	CAGTTCC	37	1	19261678	CGGAGGC	1	19134265	R
	GGTAGGT	37	1	38701867	CGCAGGA	1	38474454	R
	AAAGTGC	37	22	50630972	CGGAGGA	22	48973099	R

	AGGCAGA	37	4	185677549	CTCATCA	4	185914543	F
	ACATCCT	37	2	36656950	TTCCCAA	2	36510454	F
	TATCACT	37	15	33692812	GAAATTT	15	31480104	R
	GTCCAGG	37	7	101556171	TGCTCTT	7	101342891	R
	CAGCTAA	37	10	7652712	TCACTTA	10	7692718	R
	GATGAGC	37	3	10436869	CGGAAGT	3	10411869	F
	AGGGTGC	37	16	819064	TGTGTCT	16	759065	F
	CTTGTCT	37	11	128323520	CGGATCA	11	127828730	F
Grn	TCCAACT	37	6	32805548	CGGCAAC	6	32913526	F
	GGCGGCC	37	Y	14074417	CGCTCCT	Y	12584417	F
	ACCACGT	37	1	161368947	TAGTTTA	1	159635571	F
Red	CTGGCGA	37	Y	9363365	CAACGCA	Y	9973365	R
	GTGATTT	37	17	54509207	GAGAGCA	17	51864206	F
Grn	AGGAGGA	37	15	62516405	GGCGGGA	15	60303697	R
	AACGGGC	37	X	153626979	CGGGGGA	X	153280173	R
	ATAGGCT	37	3	187704482	CGGGGTA	3	189187176	F
	GGACCCC	37	9	140247365	GTGGAAC	9	139367186	F
	CTTGAAA	37	20	21003839	CGGGCTT	20	20951839	R
	TAGCCAT	37	3	100889156	CATGGTG	3	102371846	F
	GTTCTAG	37	6	84153455	CGCCACC	6	84210174	R
	GGGCAGC	37	16	75143200	CGGGCTC	16	73700701	F
	ATACCAG	37	10	34391256	CGGGGAT	10	34431262	R
Red	CGGCCGT	37	10	77159055	AGGAGTC	10	76829061	R
	AAATTCA	37	14	67729501	TTTAGTG	14	66799254	R
	TGCAATA	37	2	213587996	CACCACC	2	213296241	F
	AGATACT	37	3	54119792	CGCTGCA	3	54094832	F
	CAACCTG	37	3	15311154	CGGAGGT	3	15286158	R
	ACATCCG	37	6	44243750	ACCAGCA	6	44351728	R
Red	ACAATAC	37	12	124939480	ATATGCA	12	123505433	R
	CCTCCCA	37	7	76094015	CTAAACC	7	75931951	F
	AGTCGGT	37	12	118313817	ATACATT	12	116798200	R
Grn	GCCTTTG	37	6	25882590	CAGACGC	6	25990569	R
	CCCTGCA	37	1	235147744	TTCACAG	1	233214367	R
	TTCTCTG	37	4	25099040	CCTTGGG	4	24708138	R
Red	CAGCGGA	37	19	42592983	TTACATT	19	47284823	R
	ATTATCA	37	5	140537884	AAGTTTA	5	140518068	R
	CGTTCAG	37	7	27163820	TGAGTCA	7	27130345	R
Red	CCTCTGC	37	21	44258195	CATGGGT	21	43131264	F
	CCTCAAC	37	12	96251912	CTGAAAT	12	94776043	F
Red	GAGCGCC	37	2	62857522	CGCCCCC	2	62711026	F
Grn	GTATAAT	37	2	239030728	CGGTCGG	2	238695467	F
	GGAGTGA	37	6	30040291	CGAGAGC	6	30148270	F
	TGGTTTG	37	5	80716263	AGTCTCC	5	80752019	F

	ATGCAGA	37		17	40700314	CGCCTCT		17	37953840	F
	CGCTGGA	37		19	50735340	CGGGGCT		19	55427152	R
	AAAACAA	37		1	16679780	CGGACTT		1	16552367	F
	AAGTCAC	37		7	75666768	CGTGCTG		7	75504704	R
	GACTTTG	37		17	10002773	CGGATCA		17	9943498	R
	ACGGATA	37		16	89337953	CGGCATT		16	87865454	R
	GCGAGGA	37		2	95999906	CGGGTCA		2	95363633	R
	GGCTGAC	37		19	39055712	GGAGCTC		19	43747552	R
	ATAACAA	37		18	33485300	CGCCAAC		18	31739298	F
	TGAACCC	37	Y		15016101	CCTCTGC	Y		13525495	F
	CAGAACT	37		20	4795621	TCACCTG		20	4743621	F
	TCCCTGT	37		19	58868858	CGGAACC		19	63560670	F
Red	GCTGATC	37		5	140595072	CGTCCGC		5	140575256	F
Grn	TCCGGGG	37		8	49427283	CGGCCTG		8	49589836	R
Red	TGGAGAA	37		3	195870092	CGGGGAC		3	197354489	F
Grn	AAGTGAC	37		4	141391200	TCAGAGC		4	141610650	F
	CACACAC	37		16	89555682	CGCCCTG		16	88083183	F
	CTGCCGC	37		1	202129894	AAAGCAC		1	200396517	F
	CCTGGCT	37		5	131762326	GGATGGA		5	131790225	F
Red	GGTTTCC	37		7	2769253	CGCAAAC		7	2735779	R
Red	GAGCGGC	37		12	54389264	TGTGTCG		12	52675531	F
	AAAGATA	37		4	96012317	CGCAGAC		4	96231340	F
	TTCTATC	37		18	76473146	AATGGAC		18	74574134	R
	CACATTT	37		10	28720006	CGGTGGC		10	28760012	F
	ATGGTCC	37		18	13916330	TTTTGGG		18	13906330	R
	AGCCCGC	37		11	9549286	CAAGGGT		11	9505862	F
	TGGCTTT	37		10	7859623	CGGATTT		10	7899629	R
Grn	GGACTGC	37	X		71351803	GATCTGT	X		71268528	R
Grn	CGGTGCC	37		18	77623598	GAGGGGC		18	75724586	F
	CCACTTC	37		2	85832389	GTACACA		2	85685900	R
Red	TGGGACA	37		6	28584103	GAGGCCA		6	28692082	F
Grn	GAGATTA	37	Y		2803070	CGGCCCC	Y		2863070	R
	GCTTTAC	37		5	1868279	CGGCACA		5	1921279	R
	ACTCTGC	37		16	88849875	GTCCCGT		16	87377376	F
	TCACGAT	37		10	43882723	CGGACAT		10	43202729	F
	ATCCTCC	37		11	95888212	ATTTACC		11	95527860	F
	CCCAGGT	37		6	31275741	AAGGACA		6	31383720	F
Red	TGCAGGC	37		10	54538505	CGCCACC		10	54208511	R
	TGAACGC	37		12	54376094	AAGGGAC		12	52662361	F
	CGTTTAA	37		18	77508326	AGCAAAC		18	75609314	R
	GGCTTTC	37		7	2071723	CGGGCCT		7	2038249	F
Red	TGGCTGC	37		6	30458102	CGGCAAC		6	30566081	F
	GCGCCGC	37		19	1071622	CGGGGCC		19	1022622	F

	GAAGGAT	37	16	67550511	CTATTTC	16	66108012	F
	GTGTTGC	37	6	159360705	GGCTGAC	6	159280693	F
Red	CCTGCCT	37	17	48263173	TTCTGGG	17	45618172	R
	GTTCAGA	37	16	55867072	GGAGGG	16	54424573	F
	GCAGGAC	37	19	6476951	CGGCCAC	19	6427951	F
Red	GCGTCTT	37	1	248100585	AGAGCAC	1	246167208	F
Red	GAGATAA	37	16	857863	GCCTGGG	16	797864	F
Red	TCCAGGC	37	Y	22737896	TGACTGT	Y	21147284	R
Red	AGGGCAC	37	19	40421743	CGGCCCC	19	45113583	R
	CCCACCA	37	8	124688770	CGGAAAT	8	124757951	R
	CACACCC	37	1	51986130	CGCTTAC	1	51758718	R
Red	CGCCTGC	37	Y	2658057	GCCAGGC	Y	2718057	R
	CTCGGAG	37	7	37123550	AGCTTGC	7	37090075	F
Red	GCCTGGG	37	2	198650880	CGCCCCC	2	198359125	R
Red	CAGAGCC	37	20	61813415	CGGGCAC	20	61283860	F
	GCAAACC	37	11	86230664	CGCTGTT	11	85908312	F
	AGCTGTC	37	10	32229887	CGGGGGT	10	32269893	R
Red	AGTTCTG	37	12	38938054	TGGGAAA	12	37224321	F
	GCTTTTT	37	2	69538690	CGGGAAT	2	69392194	F
	CTCCAAC	37	13	24337521	CGGGGCT	13	23235521	R
	ACAAACC	37	2	220233953	AACATTT	2	219942197	R
Grn	GAGCGAC	37	20	61447110	CGCCGTC	20	60917555	F
	CCAGGCT	37	10	17259531	AAGGCAT	10	17299537	F
	TCTGTGG	37	13	112860456	ATAATGG	13	111908457	R
	CTGTGCA	37	17	74679597	CTGGGGC	17	72191192	F
	ACCAGCC	37	4	722598	AGGAGCC	4	712598	R
Red	GCACCGC	37	6	149778058	CGCGGGT	6	149819751	F
	TGGAGGC	37	5	149493099	TGTCCCA	5	149473292	R
Grn	CTGCTTC	37	16	12192430	GTCTGTA	16	12099931	R
	CCTGGGC	37	11	4615063	CGAGCTG	11	4571639	F
	TGGGTGA	37	11	7695433	CCAGGCC	11	7652009	F
	CATCTAC	37	3	19987815	GAACTGA	3	19962819	R
	TGCACAC	37	17	77707066	TCATGTC	17	75321661	F
	CTCTGTC	37	2	27403477	GGGAAAT	2	27256981	F
	ATAGAGA	37	7	8477597	CGGGGAC	7	8444122	F
	CTTGTGA	37	11	57195350	GCTTTTG	11	56951926	F
	TCAAAAC	37	3	193506005	AAATTCA	3	194988699	R
	AGAAATT	37	6	24903167	CGGTCAG	6	25011146	R
Red	ACGGGAA	37	15	35086967	TGCCAAG	15	32874259	F
	GGGATTC	37	X	100183878	CGGGCCA	X	100070534	R
	AACAACC	37	1	112154295	CGGTTAA	1	111955818	F
	GGCAAAA	37	10	118459383	ACAGTTC	10	118449373	R
Grn	AAGGAGC	37	6	28584155	CGCGGTT	6	28692134	F

	GGGGAGC	37	10	64344052	ACTAATG	10	64014058	F
Red	TTTGGAG	37	4	183062301	CGGTCCC	4	183299295	F
	AGCCTGA	37	22	30783737	CGGCAGC	22	29113737	F
Red	AAAATAA	37	5	177387597	GCTCCTC	5	177320203	F
	GGAGGAA	37	7	64034943	CGTGCTC	7	63672378	R
	TTCCAGC	37	10	4386802	CGCAAGT	10	4376802	F
	TTAATAA	37	6	29893605	CGGAAAA	6	30001584	R
Red	GAGGGCC	37	12	132638107	CGGCCAA	12	131204060	R
	GTTGATA	37	5	98108198	TCCCCAA	5	98136098	F
	GAGGAAT	37	3	118491179	CGCTTTC	3	119973869	R
	GGGGCCT	37	11	132910642	TGACTTC	11	132415852	F
	TTGCACA	37	13	106756690	GTTTCTG	13	105554691	F
	ATAGAAT	37	1	208135621	CGTGCTG	1	206202244	F
	CGTTAGG	37	16	21311480	CGGATTT	16	21218981	R
	AAGAAAT	37	7	65512561	AGCTCCT	7	65149996	R
	GTTGGGG	37	22	50492970	CGCTCAC	22	48835097	R
	TTGGCCG	37	7	157996423	CCCATCC	7	157689184	R
	AGTAGCT	37	7	64451426	CTCATTG	7	64088861	F
	TGGAAGC	37	12	54385275	CCAGCTT	12	52671542	R
	TGTCACA	37	6	126074639	CGGTGAC	6	126116332	R
	TGCTCTT	37	8	11995002	AATTTCC	8	12032411	R
	GATCCTC	37	17	46591291	CTGTTCC	17	43946290	R
	TGGAGCT	37	10	45065415	TAGCCCA	10	44385421	F
	GTCCTCG	37	11	118842390	CGCGGTC	11	118347600	F
	TCTGGTG	37	10	70977210	CGGTTGC	10	70647216	R
Red	GCCTCCG	37	16	87339657	CGGGTCA	16	85897158	R
Red	CAGCATC	37	X	106871544	CAGGTAT	X	106758200	F
	CTCCAGA	37	6	32408596	TATTACT	6	32516574	F
	GCCGGGC	37	9	138377834	CGTCTTG	9	137517655	R
	GCGAATT	37	16	14380714	AAGGCTC	16	14288215	R
	CTTAACT	37	1	22143533	CGCTGAG	1	22016120	F
	CATCTTT	37	1	207840521	CGCCATC	1	205907144	R
	ATACTCT	37	7	17691191	CGTGCCA	7	17657716	R
	AGGCAGC	37	11	660455	CCTGAAG	11	650455	R
Red	CTCCCTA	37	1	147801103	CGGAGGC	1	146267727	R
	GTCTTTC	37	6	91145465	CGGCTTT	6	91202186	F
Red	GTGGCTG	37	6	30652396	GCAGGGC	6	30760375	R
	TCATATA	37	1	152333423	CGCAAAT	1	150600047	F
	CCAGAAC	37	8	145014989	CGCCAAC	8	145086977	F
Red	ACAGACC	37	1	6190318	CGGCGGA	1	6112905	R
Red	GGCCCGA	37	1	223566761	CGCTGCA	1	221633384	R
	ACACAGC	37	7	2768911	GGGGCCC	7	2735437	F
Red	GTACCGT	37	8	82530967	GGGAGAA	8	82693522	F

	AAAAAA	37	1	241800323	CGCACAT	1	239866946	R
Red	CACTGGC	37	16	2749496	GGGCCCT	16	2689497	R
	GCAGAGC	37	6	3527443	CGCTTAC	6	3472442	R
	TAAAATC	37	1	212761056	CGGTTAA	1	210827679	R
	AAAGAA	37	1	222440048	AGGCTAC	1	220506671	F
	CCCCTCC	37	5	148942547	CGGCAG	5	148922740	R
Grn	CTTAAAA	37	1	11979188	CGGGGCT	1	11901775	R
	GCGCCGC	37	8	144668756	AGGCACC	8	144739899	F
	GTTCAAA	37	11	8754370	ATGGCAT	11	8710946	F
Red	GAACTAC	37	1	182669315	CGGCGGT	1	180935938	F
	ATTAATC	37	2	186988953	CGGTTCT	2	186697198	R
	GCCACGT	37	4	190236439	CGAGTGA	4	190473433	R
	AACTGGC	37	1	184909381	CGGCACC	1	183176004	F
Red	CCCCACA	37	17	80970799	TGGACTG	17	78564088	F
Red	ACGTGAC	37	17	5019989	CGAGTCG	17	4960713	F
	ATGAGCA	37	7	104619961	CGGGCA	7	104407197	R
	GGCCCAC	37	16	55794910	TCCGCAC	16	54352411	R
Grn	CACCAAC	37	3	197385493	CTGTGCT	3	198869890	F
	GTATTAA	37	13	47613485	CAAGCTC	13	46511486	R
	TTCTATG	37	12	102626348	TTCTGTA	12	101150478	R
	CCAGTAC	37	11	61007964	CGGGGAC	11	60764540	F
	GTGAGA	37	6	32549361	GGAAGTC	6	32657339	R
Grn	CCTGCGC	37	1	248100427	CGGCCAC	1	246167050	F
	GGCATAC	37	10	80008319	TCCCTAT	10	79678325	R
Red	GTGGCGC	37	X	117250962	CGCTACA	X	117134990	R
	TGCGACG	37	16	27298091	CGGCCTT	16	27205592	R
	TTAGTGG	37	6	33039804	TTAAACC	6	33147782	F
Grn	AGACCCC	37	8	11538245	GTGAGCA	8	11575654	F
Red	CGCCCAG	37	19	2251061	CGTGGCC	19	2202061	F
	CGGAAGC	37	6	32606445	CTTCCTT	6	32714423	F
	CCAAAAC	37	5	140535469	ACTTTTT	5	140515653	R
	GTAAGTT	37	20	61821263	GAGAGGC	20	61291708	F
Grn	GCAGCCA	37	11	76751369	CGGACCC	11	76429017	F
	CGGGCGT	37	17	40805777	GAGCCAC	17	38059303	R
	AGTTTAT	37	11	109786133	CGTTCTG	11	109291343	F
Grn	TGGTTGG	37	5	166354050	CGCCGTC	5	166286628	R
Grn	AGCTGGC	37	16	88975960	GGACGCC	16	87503461	R
Grn	AGGTGGC	37	4	798711	GCAGCCA	4	788711	R
	AAACAA	37	6	13915058	AAGTATT	6	14023037	F
	AGGGTCC	37	6	76147474	TGGAATG	6	76204194	F
	CACATGG	37	6	29980240	CGTGTAC	6	30088219	R
Red	CGGACTT	37	7	95026106	CGCCCTT	7	94864042	R
	CTTTCCA	37	1	48458049	TCTTTAA	1	48230636	F

	GACCAAC	37	1	56721795	CGTGGCA	1	56494383	F
	TCAGCCA	37	5	38765698	ATATGAT	5	38801455	F
	TCCCATA	37	1	27977270	CGGGGGC	1	27849857	R
	TTTTTTTA	37	1	92099858	CTTGAGC	1	91872446	F
	CTTTACA	37	15	82469848	CGCACTT	15	80256903	R
	CTCACTC	37	2	54483498	CGTGCTG	2	54337002	F
Red	TGGCGGC	37	7	1000210	AAGAGCT	7	966736	F
	CCTGTAT	37	13	19692715	CGTGTCT	13	18590715	F
Grn	ACGGCAC	37	7	4911051	CGGCCCG	7	4877577	F
	TTGAGTT	37	2	102510535	AGCTTGA	2	101876967	R
	CTTAGGC	37	4	62707027	CGTGAGC	4	62389622	R
	AAGAATT	37	4	186760378	CGGGGTA	4	186997372	F
	GGCCCAA	37	2	33951647	ACTCCCC	2	33805151	R
	GCTGTCA	37	6	131148736	CGGGGAC	6	131190429	R
	TGTGTGT	37	1	153854324	TGGAGGC	1	152120948	R
	GAAGCAC	37	5	112608004	CGGCCAT	5	112635903	R
Red	GGTGCGC	37	1	2847220	GGGGTGC	1	2837080	R
	AGGCATG	37	10	95656819	CGCAGCC	10	95646809	R
	GAACACT	37	16	88201606	CGCCCGC	16	86759107	R
	GTGGGAC	37	3	46618527	CGGCATG	3	46593531	R
	TCAGGGA	37	6	30899162	CGGCAAT	6	31007141	R
	GGATGTT	37	10	65442289	CGTCCAT	10	65112295	F
	CCAGAAC	37	11	131936494	CGCTCCT	11	131441704	R
Grn	CAAGGAC	37	1	1133248	CGCCCCG	1	1123111	F
	TTACTGG	37	7	94953770	CGCTCAC	7	94791706	R
Red	CCTCCCT	37	2	68017838	CAGACTA	2	67871342	R
Red	CTCAAGC	37	2	241719496	AATGTGG	2	241368169	F
	ATACTTG	37	2	152872424	GCCCACC	2	152580670	R
	GTGCCAG	37	Y	2655740	CGTAACA	Y	2715740	R
	ACCCTCT	37	17	146926	CGCCCCA	17	146926	R
Red	GGGAGGC	37	14	71131956	CGCTCCC	14	70201709	R
	TACCTGC	37	8	6876155	CGCCCTG	8	6863565	F
	CAGCACC	37	7	45002736	GAGTCCG	7	44969261	F
	TTTCTTAC	37	2	174057774	CATCAAA	2	173766020	R
	GAATGGC	37	16	89048704	CGGGCAC	16	87576205	R
Red	CTGGGCC	37	10	3138534	CGGCCTC	10	3128534	R
Red	AGCACGC	37	10	6183528	CGCCCTG	10	6223534	F
	AGCAACC	37	13	75980679	TCCAAGG	13	74878680	R
	ATGGGTA	37	Y	9170562	ACTACCC	Y	9230562	R
	GAAGGCA	37	14	101270817	TTCATGT	14	100340570	F
	CTCAGCG	37	5	125931362	CTTTAAT	5	125959261	F
	AATCACC	37	21	46225890	CGTGGGT	21	45050318	R
Red	AGGGAAC	37	17	70636940	AGACCTG	17	68148535	R

Red	CCAGGGC	37	5	37836246	CGACTGC	5	37872003	R
Grn	AACTTCC	37	2	119496171	ATGAATA	2	119212641	F
	GAGCCAA	37	3	149310862	TAGGGAA	3	150793552	F
	ATGAATG	37	1	217306700	CGCCCCA	1	215373323	F
Grn	TCACGTC	37	5	759544	CGCCGCG	5	812544	F
	GGCTCAG	37	21	45246164	CGGGCAC	21	44070592	R
	CAGCTGT	37	4	54729555	CGCAGGA	4	54424312	R
	AAGCTGC	37	1	184808004	CGGCAGA	1	183074627	R
	TTTAAAA	37	21	46629219	CGGCTTC	21	45453647	R
	CACCCGT	37	22	38435259	CCTGACA	22	36765205	F
	GGACCCC	37	22	22902047	CGCGGCC	22	21232047	R
	TGCATCA	37	5	55148534	CGGTTGC	5	55184291	F
	TTTTCAG	37	16	1722957	ATGTGGG	16	1662958	F
	GTAAACA	37	1	246785611	CGGTTCT	1	244852234	F
	GTACCCT	37	19	3458194	GGCCATA	19	3409194	F
Grn	GTCCGGG	37	10	119292300	CGCCTCC	10	119282290	F
	GGCTCAA	37	16	636227	CGGGCCC	16	576228	F
	AGTTGAC	37	1	94240208	CGACCTG	1	94012796	F
	AGCAGAC	37	8	98610472	CGGCCCC	8	98679648	R
	GCGCGGC	37	16	8963642	CCAGTGG	16	8871143	F
	AGGAAGA	37	6	149806273	CTGCCCT	6	149847966	F
	TTACTTT	37	17	57918500	AAACAAA	17	55273282	F
	TAAATCA	37	4	185749877	AGTCACA	4	185986871	F
	GGTGTGC	37	10	124578263	CCACTGG	10	124568253	R
	CAATTTC	37	1	230645569	CGGCCCA	1	228712192	R
	AAGAGAC	37	7	44163975	ACTTAGG	7	44130500	F
Red	CTACCTG	37	14	74194516	CGAGTGC	14	73264269	R
Grn	TTCTAAC	37	20	4665645	CGCCGCC	20	4613645	R
	ATTATGA	37	8	49892745	TTGAGGT	8	50055298	F
	TTTGTTT	37	1	205912819	CGGGGTC	1	204179442	R
	TAAATGT	37	4	16609513	TGGCACG	4	16218611	R
	GACTGAA	37	11	110627909	CGCATAC	11	110133119	F
	CTTAGAA	37	19	52023213	ACAGCAA	19	56715025	F
Grn	CCGGCCC	37	X	19140658	CGCCGCC	X	19050579	F
	TGGTCTG	37	17	16593582	CGCCAAC	17	16534307	R
	GGGTCGT	37	15	96869027	CGGCTCA	15	94670031	R
	ACCTTGA	37	2	11850727	CGTACCA	2	11768178	R
	CAAAACA	37	2	102589889	TTGGGCA	2	101956321	R
	GAATGTG	37	13	43988852	TCTTTTG	13	42886852	R
	TGCTCAG	37	22	46480891	CTGAGGC	22	44859555	R
	GAGAGAA	37	4	167021679	CGGTGAT	4	167241129	R
	GGGTTTG	37	6	44039484	CGGAGAC	6	44147462	F
	CTGTTCA	37	1	7259290	GCTTCCC	1	7181877	F

	GGAAAAT	37	16	78218445	CGGTGAT	16	76775946	R
	ACTAGCC	37	1	31136147	CGGCACC	1	30908734	R
	GACATTT	37	6	82459454	ATGCCAA	6	82516173	F
	GACACCA	37	16	1107501	AGAGGG	16	1047502	R
	GTCATTA	37	1	94559714	CGTCAAG	1	94332302	R
Red	AGGCCGT	37	6	116886211	CGCGCCT	6	116992904	R
	AGTGAAA	37	2	85390041	AGGTTCA	2	85243552	F
Red	CCCGGGC	37	19	45849853	CTGCTGG	19	50541693	R
	TTGTAAC	37	6	44039689	CGGGCTT	6	44147667	R
Red	GGGGGA	37	6	170554795	CGCGAG	6	170396720	F
	TGGGGGA	37	10	72593165	AACAAAA	10	72263171	F
Red	TAAGCCT	37	11	28399977	AAAAGC	11	28356553	R
Red	CCCTGCT	37	17	18023971	CGGGGTC	17	17964696	R
	GTTAGCG	37	16	2164019	CGGGCTA	16	2104020	R
	ACCTGAG	37	16	87234895	CTGCTCC	16	85792396	F
	ATGCTCT	37	3	185412244	CGAGCTA	3	186894938	F
Red	TGGAGAA	37	1	221055665	CGCCGCC	1	219122288	R
	CTGTCTC	37	2	237654635	TTTCAGA	2	237319374	F
Red	GCTTTCC	37	10	79596240	CGCCCCG	10	79266246	F
	TCAATTT	37	7	20010777	CGCTAAG	7	19977302	R
Red	CCACGGT	37	16	88885124	CGGCGCC	16	87412625	R
	GAATCGC	37	3	31494586	CGCCCAC	3	31469590	R
	AACTGGC	37	12	3948619	GGCCATT	12	3818880	F
	TTTAAAG	37	11	14495049	CGGCCTA	11	14451625	F
	AGTAAGC	37	11	12181467	GGACGCT	11	12138043	R
Red	ACAGAGT	37	17	78830472	CGCACAC	17	76445067	R
	GCCACAA	37	12	52762005	CGGTCAA	12	51048272	F
	TAAGAGA	37	4	54187654	CGTGGCA	4	53882411	F
Red	CTCCGGG	37	10	131770171	AGCGTCG	10	131660161	F
	GGGGCTA	37	4	76932862	CTGAGAT	4	77151886	R
Red	ATGTGGC	37	7	817454	ACAAAGT	7	783980	R
	CAAAGCC	37	5	135416205	AGTGACA	5	135444104	R
	GCAGCTG	37	4	81387148	CGGTAGC	4	81606172	F
	GTTCCAG	37	1	161334734	TATTTCT	1	159601358	R
	ATTTAGT	37	17	80860250	TAACCCT	17	78453539	R
	CAGGCTG	37	5	158086454	TTCAATA	5	158019032	R
	TAAGAAC	37	11	111312453	GTTATTG	11	110817663	R
	TAGTTAA	37	5	159203122	CGGGGAT	5	159135700	F
	TATTTTT	37	1	179322762	CGACAAC	1	177589385	R
	GCGCGCT	37	19	50931622	GCCCTTT	19	55623434	F
	ACTTACC	37	2	209010890	CGGGAAC	2	208719135	F
	GGACACT	37	1	8298617	CGCCTTT	1	8221204	R
	AGCCCCT	37	11	29358540	CGCTTGG	11	29315116	F

	GGAACTC	37		11	77299962	CCTCTTC		11	76977610	F
	GCTTCAA	37		6	86862059	ACACAAT		6	86918778	F
Grn	GGGCGCA	37		3	126261298	GCCGCTG		3	127743988	F
	GAGGCTC	37		17	27703877	CGCCTGC		17	24728003	R
Red	TGAGGAC	37		19	29218101	CGGGGTC		19	33909941	R
Red	GCTCCTT	37		11	13986162	CCTTGGC		11	13942738	R
	TGTGACT	37		1	33169558	CGCGAGC		1	32942145	R
	CCAGTGG	37		7	72982668	GCAACTT		7	72620604	F
	AAAAGGC	37	Y		9387798	CGCTGGG	Y		9997798	R
	ATTTAAC	37		13	53382856	CGTGTGT		13	52280857	F
	GAGTAAA	37		14	38071768	CGCACAC		14	37141519	R
	AAACTGT	37		13	100517027	GAGTCAC		13	99315028	R
	CTGCTGC	37		10	134460392	CGGGTGC		10	134310382	R
Grn	ACACAGC	37		19	24270007	TGGACAA		19	24061847	R
	AAAGGGA	37		19	54216680	CGGTAAC		19	58908492	R
	AAATGGA	37		1	235787279	CGGCTCA		1	233853902	R
	GAGGTGC	37		16	2749387	CGCGGCA		16	2689388	R
Red	GGGGTCT	37		19	36485360	CCGTCAG		19	41177200	F
	CGTAGCG	37		6	127797022	CGGCAAC		6	127838715	R
	GGGGCCC	37		3	49236808	CGCGGCC		3	49211812	R
Red	GAACGGC	37		19	1071208	GCGCGTG		19	1022208	F
	TTTGGTC	37		6	130774523	CGGTAGC		6	130816216	R
	GGAAGAA	37		17	74911808	GATTTTA		17	72423403	F
	CCCTTTC	37		1	230513809	CGTGTGA		1	228580432	R
	GATGATC	37		11	2418102	GTCCGGG		11	2374678	F
	GCAGCAC	37		19	14843922	TCTGATA		19	14704922	R
	GCTATGC	37		8	116663921	CCACACA		8	116733095	R
	CTGGAAA	37		1	196743672	TTTTTGA		1	195010295	R
	ACTTTCC	37		1	109741037	CTTGGGC		1	109542560	F
	TTTTAAG	37		10	18425598	TTAGTAT		10	18465604	F
	CAACTCT	37		6	29973221	CGCAGGC		6	30081200	F
	CTGTAGT	37		17	32581220	CGGGAAT		17	29605333	R
	AGCCGTG	37		9	96623111	CAGGCTG		9	95662932	R
	GAAATAC	37		4	183167912	TATGAAT		4	183404906	R
	GCTGTAT	37		11	34393106	CGTGTGA		11	34349682	F
Red	CCCTAGC	37		6	28584172	GACCGGC		6	28692151	F
	ACAATTT	37		19	52452317	GTTTGCG		19	57144129	R
	GGCTTCT	37		19	13113482	CGCAACT		19	12974482	R
Red	GCACCGC	37		5	14406732	CTTATCG		5	14459732	F
	CGGCCTC	37		11	67383862	TGGGGTG		11	67140438	R
	AAAGCAA	37		8	11212812	CGGGTCC		8	11250222	R
Red	GAACAGT	37		17	75315486	CGCTCCC		17	72827081	F
	AAATCAC	37		17	2308689	AGACATC		17	2255439	F

	TGGATGG	37	13	113407548	CGCCCCT	13	112455549	F
Red	CCAGGGC	37	2	198365150	CGCCTCA	2	198073395	R
	CAGTTGC	37	16	28079611	CGCCTGG	16	27987112	R
	ATGTCCA	37	19	55173030	CGCCCAG	19	59864842	R
	GCGCCGC	37	7	158712832	CGGAGGC	7	158405593	F
	GAAACA	37	10	5047487	CGGCAGC	10	5037487	R
	TTTCTAC	37	10	13696795	CGGGGAC	10	13736801	R
	TGTGCTG	37	8	142427117	GACTATG	8	142496299	F
	AGGCTTG	37	17	76895722	CGCTGCA	17	74407317	F
Red	CCCAGAC	37	10	116019713	GACAGGC	10	116009703	F
Grn	GGCTGCT	37	Y	7142046	GCTGGAT	Y	7202046	F
	GAAAGAT	37	2	109636680	CTTTTAA	2	109003112	F
Grn	TTTTTGA	37	5	180645302	AAGGAA	5	180577908	R
	TCTCTTG	37	6	32633354	CGGGACT	6	32741332	R
Red	GTGCGGC	37	2	97136556	CGCCCTC	2	96500283	R
Red	GCTGTGC	37	16	30485684	GGAGAGC	16	30393185	F
Grn	CACTCAC	37	22	42394638	CGGGGGC	22	40724584	F
Red	AACGGGA	37	4	132647861	TTTTGGC	4	132867311	R
	ATTGTTT	37	1	168215442	CGGTGCT	1	166482066	F
Grn	CTGGCGG	37	2	238647913	GCCGACT	2	238312652	F
	TAAAGGA	37	15	44507997	CGGACAT	15	42295289	F
	CAAAGGC	37	19	54269519	CGGGCAC	19	58961331	R
	CTGGGTC	37	6	15509388	CGGGGAC	6	15617367	R
	TCTCAAT	37	3	197209034	CGCTCAG	3	198693431	R
Red	CAGGCGC	37	12	133003907	CGTCACC	12	131513980	R
	GGCTGGC	37	4	58061991	GCATGGT	4	57756748	F
Grn	TTTTTAG	37	19	53018151	AGCTCAT	19	57709963	F
	TGTTTCA	37	16	67471172	CGCTGGA	16	66028673	F
	AGAGGAA	37	2	109622481	CGGGCTG	2	108988913	R
	ATCCTTC	37	6	34105785	GCATCCA	6	34213763	R
	TGTCTGG	37	10	15110983	CGCCAAC	10	15150989	R
Red	GCGGTCG	37	X	153236825	TGTTTCG	X	152890019	F
	CTTGACA	37	16	70808233	CGTGAGA	16	69365734	R
	GGGTGAC	37	19	11276691	ATTTAAT	19	11137691	F
	AGACAAT	37	6	32628953	CGCTGTC	6	32736931	R
	TGACCCG	37	6	22878214	CTTATCT	6	22986193	R
Red	AGTGTGG	37	1	234908381	CGGCCAC	1	232975004	F
	AGAGCCC	37	16	930179	CACAGGC	16	870180	R
Red	GCTCCCT	37	4	186960991	CGGCACC	4	187197985	R
	CGCCTAG	37	17	77923314	CGGGGCT	17	75537909	R
	AGTGAGC	37	1	246668601	GTGAGTG	1	244735224	F
Grn	CCGACGC	37	4	1994761	CGAGCTG	4	1964559	R
Red	ATATGCT	37	11	76998857	CGATGGT	11	76676505	R

	ATTCCTG	37	2	189064557	GGAAAG	2	188772802	R
	TTACAGG	37	3	10182561	CGGTAAT	3	10157561	R
	AAGGCCC	37	7	42896398	CGGAACA	7	42862923	R
	TTTGTGC	37	11	119341250	CGGCTGC	11	118846460	F
Grn	CTTGGGG	37	11	58598444	CGGGATC	11	58355020	F
	AGAAGA	37	14	24098569	AGCAAAT	14	23168409	R
	ATTCTCT	37	14	41469306	CCCTCTG	14	40539056	R
	TTCCCAG	37	9	141105974	CGGCAGC	9	140225795	F
	TGGAACT	37	13	113109379	ACCCCCA	13	112157380	F
	AAGAAA	37	6	32829144	GGGTAAC	6	32937122	F
	ATATATA	37	12	94761621	CGGGCTT	12	93285752	R
	AGATTAA	37	5	140562819	GGCTGCT	5	140543003	F
Red	CGCTCCC	37	Y	2804320	TGTGCCC	Y	2864320	R
Red	TCACTCT	37	X	134654334	GCTAGGA	X	134482000	F
	AGAGGG	37	5	17360014	TTCTGGG	5	17413014	R
	AACAGA	37	5	87389026	CGGGGA	5	87424782	R
	GTTGGTG	37	10	33016632	GCAATTG	10	33056638	R
	TAAAGTC	37	10	108921320	GCCCTCT	10	108911310	R
	GGGGCCC	37	17	34539744	CGGGAAC	17	31563857	F
	TTTAACT	37	10	81895943	CACCCTG	10	81885923	F
	CTCAGGT	37	14	22362071	GTCTGGG	14	21431911	F
	AGGGTCC	37	14	52783454	CGTAGCT	14	51853204	R
	GCTTAGG	37	15	45493327	TGGAATG	15	43280619	R
	CACATCC	37	15	97311928	AGCCGTT	15	95112932	F
	ATCATTC	37	17	17580647	CGAGGG	17	17521372	R
Red	GCCATGT	37	8	43132451	CGGCTGC	8	43251608	F
Red	CCTCAGG	37	1	9099298	CGGAGCC	1	9021885	F
	TGGAGCA	37	4	72670093	AATCTGT	4	72888957	R
Red	CTTCTTT	37	12	66262214	AAGCCCC	12	64548481	F
	CAAGCTG	37	15	22921184	CGGAAA	15	20472625	R
	TCCTATG	37	7	18906433	ACCACAC	7	18872958	F
	CATTTCT	37	3	72570318	CGGGGTC	3	72653008	R
	AGGAACA	37	7	50347487	CGACAGT	7	50318033	F
Red	GGGTGCC	37	14	104394831	CGCCTGG	14	103464584	F
	CAGGGTC	37	6	30459317	AACCAGC	6	30567296	F
	ACCATTC	37	3	150187338	TCCCTTT	3	151670028	F
Red	CCGAGCT	37	3	123166882	CGGCCGC	3	124649572	F
	GTGGCTT	37	15	63116514	CGGTTCC	15	60903567	F
	TGGCTCA	37	8	2122339	CGGCGCC	8	2109746	F
	GAAATCT	37	1	8083186	CCAGATG	1	8005773	F
	TTGAAGG	37	3	187086530	CGACCCT	3	188569224	R
	CCAACGC	37	3	139252106	CGCACAC	3	140734796	R
	TAGATAG	37	2	160764918	CGGCCAC	2	160473164	F

Red	AGTCGCT	37	2	132587079	CGGCCTC	2	132303549	R
Red	CAGCTGG	37	14	102415401	CGGCCTG	14	101485154	F
	ACAGTCA	37	7	38880852	CGTGAGC	7	38847377	R
	GCCCGCG	37	17	15652854	GTGGAGC	17	15593579	R
	ATGTACA	37	16	3570555	CGCAAGC	16	3510556	R
	AGGGGGT	37	3	13922158	GGTTGGG	3	13897159	R
	AAGTGAC	37	6	32362638	CGGGCTG	6	32470616	R
	GCCAGGC	37	22	46451319	TATGTCT	22	44829983	R
	ACAGGCA	37	20	61160996	GGCAGCC	20	60571441	R
	ATACTCT	37	1	8940460	CGGGATC	1	8863047	R
	CTATGTA	37	1	28573052	CGAAGCA	1	28445639	R
Red	CCCTCAG	37	19	57630446	TGCAGTC	19	62322258	F
	TTTTGTTC	37	11	103453960	CGGTCTT	11	102959170	F
	CCTGAAC	37	5	126409372	CGGAAAA	5	126437271	F
	ACACGTT	37	1	39513326	CGCTCCC	1	39285913	R
Red	CGTGAAG	37	16	841550	CGACTTC	16	781551	R
Red	ACGGGGC	37	19	1852165	GGAAGCT	19	1803165	R
	TATCACT	37	7	94045725	TTCCAAT	7	93883661	F
	ATTTCCA	37	7	73446865	TGTCATT	7	73084801	R
Red	CAGGTCC	37	11	118842387	CGGCGCC	11	118347597	F
	TCAACTT	37	2	240965916	CGGCCGC	2	240614589	F
	GCAGTGC	37	17	33390854	CGCAGTC	17	30414967	F
	TATGACC	37	5	90458832	TTTTTCTT	5	90494588	F
	ACTCATA	37	1	161676469	CTGACTA	1	159943093	F
	ATGCCCC	37	16	85028831	CGGGAGT	16	83586332	R
	GTAGTGA	37	8	69497246	GTCCTAA	8	69659800	F
	AAGACAC	37	14	91883268	CGGGTCA	14	90953021	F
	ATTTCTCT	37	8	25166343	CAAGAAT	8	25222260	R
	GGTAGGT	37	10	28970534	GTGTCTC	10	29010540	F
	ATTGTTT	37	1	240855271	CGGAGGC	1	238921894	F
Red	GAAACAC	37	14	99744403	CGTGTTT	14	98814156	R
	AACCTGT	37	Y	23566572	GAAACAC	Y	21975960	R
Red	TGGGTCT	37	16	1124349	GGGGCAC	16	1064350	F
	CTTAGGT	37	14	30649039	CGGACTT	14	29718790	F
	CAGCCAA	37	16	17499310	CGAGAAC	16	17406811	F
	CCTTTATT	37	3	109404367	CTATAAG	3	110887057	R
	GCCAATG	37	7	126885001	CTCGGCT	7	126672237	R
	GGAAAAA	37	3	48310897	TGTGTGC	3	48285901	R
	CAGTTTA	37	4	185329364	CGGTCCT	4	185566358	R
Grn	TTAGTAG	37	16	55364843	GCGAGGT	16	53922344	F
	ATACTTC	37	7	158854447	TTACTCA	7	158547208	R
	CAGCCCA	37	6	29527870	CGAGAAT	6	29635849	R
Red	CTCGGCT	37	X	152677200	CCGAGCC	X	152330394	R

	GTGAGTA	37	2	204731519	CGGACTG	2	204439764	F
	AGCCATA	37	10	85985331	CTGTGTG	10	85975311	F
	CCCCCCA	37	2	121846490	CGGCTGT	2	121562960	F
	GCAGGTC	37	2	2295969	CGCCCGC	2	2274976	R
	TTTCAAT	37	15	96869132	GGGTGTT	15	94670136	R
	GCCCTCA	37	7	27146430	TCTCAGG	7	27112955	F
	CTGCCAT	37	6	29427519	CGGCACC	6	29535498	R
	CAGAGGC	37	14	105555223	GGTGCCC	14	104626268	F
	CTGCCAC	37	3	49697458	GCATACA	3	49672462	R
	CCCTCCC	37	7	14031822	CGTAGTA	7	13998347	R
	ACACGCT	37	12	31499320	GTTAAGG	12	31390587	R
	GAGAGAC	37	12	378771	ATTGTCC	12	249032	F
	TCCAAAC	37	16	86327786	CGGGTAT	16	84885287	F
	CTATCTC	37	6	31323261	CGGGATC	6	31431240	R
	AGGACAC	37	11	126944154	TGCCAGC	11	126449364	F
	GAAGCGT	37	5	168719	CGAGAA	5	221719	F
	GCGCCTG	37	14	93153553	CACCTGC	14	92223306	F
	ATTCTGA	37	1	215923004	GCTCCTC	1	213989627	F
	GGCTCAG	37	17	75378036	CGGGGTA	17	72889631	F
	GCAGTTG	37	5	107896573	CGAGATC	5	107924472	R
Red	GCGCCCC	37	10	135498991	CGGAGCC	10	135348981	F
	GAGCAAT	37	18	9704392	CGAAACT	18	9694392	F
	CTTCTTA	37	14	104436161	CGCCCCA	14	103505914	R
	ACCCCCA	37	11	44597119	GTACCCA	11	44553695	F
	CAGTGCA	37	10	32701586	CGCTTTA	10	32741592	F
	TCTAACC	37	16	83982669	CCTTTTG	16	82540170	R
Red	AACCCGC	37	12	131171031	TATCAGC	12	129736984	F
	GATATGG	37	7	138803256	CGGGGGC	7	138453796	F
	TGATTAA	37	16	9828141	ATGAAAC	16	9735642	R
	ATCTAAA	37	10	135343193	AATGAGC	10	135193183	R
	GAGTATA	37	11	12098045	CGACAGA	11	12054621	F
	GTCATGT	37	5	156722426	CGGGTCC	5	156655004	F
Red	CTCATTG	37	11	11642011	GGGTCTG	11	11598587	F
	ATAACTA	37	12	64383297	CGGCATA	12	62669564	R
	GGCTTGA	37	16	84520021	CGCCTGA	16	83077522	F
	CATGGTG	37	14	100233454	CGGAAAC	14	99303207	F
	CAGGTCT	37	7	158533877	CTGCTGT	7	158226638	F
	GAGGTCA	37	6	43818920	TTTCCTC	6	43926898	R
Grn	ACGAAGA	37	17	37308828	CGCCCCA	17	34562354	R
	GGCCGGC	37	11	65810869	CAGGATC	11	65567445	R
Grn	CGGCCCG	37	11	5960015	CAGCTGC	11	5916591	R
	GGTTACT	37	9	44401998	CGGGGTT	9	44341994	R
Red	GGCCAGA	37	8	145728507	AGGCCTG	8	145699315	R

	TTTGTGA	37	15	94346066	CGGCAGC	15	92147070	F
Red	GTGGTTT	37	5	178450646	AGAGAAC	5	178383252	F
	TTAGATG	37	10	7839613	GCTTAAT	10	7879619	R
	CTACCAT	37	14	21467273	CGGATAC	14	20537113	R
Grn	GGGCCAC	37	17	79495519	TTCGTCG	17	77110114	F
Red	AACCATA	37	19	55644229	CGGTAGC	19	60336041	R
Red	AAAAAG	37	5	72705952	CGCCCAG	5	72741708	F
Red	GGCAGC	37	10	26681244	CGCGAAT	10	26721250	F
	CTGTTCA	37	10	49742271	CGTTGGG	10	49412277	F
Grn	CCTATCT	37	20	32856898	AGGAGC	20	32320559	F
	GTGGGGC	37	7	150067712	TAGGGAA	7	149698645	F
	GGAGCCC	37	16	90143788	CGCTGAT	16	88671289	R
	AACTTCT	37	15	70250464	TCCCAGG	15	68037518	F
	AATGTAA	37	14	82546712	TGCTGGA	14	81616465	F
	GCAGCCC	37	17	16570473	CGCAGCC	17	16511198	R
	CTCTATG	37	11	130482015	GCCCTGG	11	129987225	R
Red	TTGTGGT	37	17	79961614	CGCAGCC	17	77554903	F
	TATCCTA	37	13	26776254	CGGTTCT	13	25674254	R
	TCATCCA	37	3	141560204	TATTCTT	3	143042894	R
	CTCCTGC	37	6	167789539	GGTGGCC	6	167709529	R
Grn	GACTGCC	37	6	156983263	GGCCACC	6	157024955	R
	TGTGTGT	37	4	1874366	GAGCCAC	4	1844164	F
	CAGACAC	37	3	69058876	AATACTC	3	69141566	F
	GGCACGT	37	8	103751006	CGCTGAG	8	103820182	R
Red	GGCCCTA	37	6	28558006	TCCTTTC	6	28665985	F
	TGTGTAG	37	17	48276347	TTTTTTT	17	45631346	F
	CTTATCA	37	2	102117488	CGCAATG	2	101483920	F
	CCCTGTC	37	12	130968528	CTAGATG	12	129534481	R
	AGGCTGC	37	14	50527872	CGGGGGC	14	49597622	R
Red	GAGACGC	37	19	21106043	TGGGAAC	19	20897883	R
	CCCTTTG	37	8	98361938	AGCTACA	8	98431114	R
	TGTGCGT	37	19	58867669	CGCCCAC	19	63559481	R
	TCAGAAT	37	10	112794609	TTGATAA	10	112784599	R
Grn	GCCACCG	37	14	104552397	CCCACGC	14	103622150	R
Red	CGCGCAC	37	16	66436664	GAGCGTC	16	64994165	R
	CCAACCT	37	17	80535367	CAGGGCT	17	78128656	F
	AATGGTA	37	2	170142388	ACCTATG	2	169850634	F
Red	ACCTCCG	37	1	2121349	TCTCTGC	1	2111209	R
	CCATTGT	37	22	23489041	CGGTCCC	22	21819041	R
	AAGGGGC	37	4	183601649	GACTGGC	4	183838643	R
Red	CCAGAAT	37	14	75590896	TCTCATT	14	74660649	R
Red	ACGCAAC	37	19	3478662	CGGGCTT	19	3429662	R
Red	ACCGCAC	37	19	2250901	TCGGACC	19	2201901	F

	TCATGCT	37	13	111522755	CGCTGGT	13	110320756	F
	AGAACCC	37	17	43170343	CGGACTC	17	40525869	R
	AGGAGTC	37	17	113233	CGTGCTG	17	113233	R
	AGCGAGC	37	11	67141686	TGGGAGC	11	66898262	R
Grn	GCGCGCC	37	12	48357394	CGGCACC	12	46643661	R
	AAGATGA	37	4	4137166	CCCCCCA	4	4188067	R
	AAATCAA	37	2	225875689	CGAAGGC	2	225583933	F
	GGGGAGA	37	17	5019761	CGCCCCT	17	4960485	R
Red	GGAAGGC	37	19	18889003	CGGATTG	19	18750003	R
	TTCTAAG	37	4	164092065	CGGTTGA	4	164311515	R
	GTCACAG	37	6	33039481	CGTAGGT	6	33147459	F
Red	GCCCCGC	37	X	37706736	GGAAGGC	X	37591680	R
Red	TGCAGTC	37	7	76145672	GGAGCGC	7	75983608	F
	ATTGTTT	37	14	29250912	CGCTGGC	14	28320663	R
	ACTCTGG	37	12	10456885	CGGTGCA	12	10348152	R
	CCAGTGA	37	Y	9528418	CGACACC	Y	10138418	F
	GGCTGTG	37	6	32553920	TTTTGCA	6	32661898	R
Grn	CCCATAA	37	2	242693323	CGCAGCA	2	242341996	R
Red	CCTCTCA	37	10	124893766	CGCCTAA	10	124883756	R
Grn	GTCCCAG	37	1	2266933	CGGCGAC	1	2256793	F
	TCTTCTC	37	X	48748398	AACAACC	X	48633342	R
	GCTGCTG	37	16	5092012	CGGTGAC	16	5032013	R
	TTTAAGG	37	3	57032141	AAAGTTA	3	57007181	R
	AAATGAC	37	3	63428587	TTTATTT	3	63403627	R
	TTTCACT	37	11	93586725	AACCATT	11	93226373	F
	TGAAAAA	37	Y	6136711	CGGGGAA	Y	6196711	F
	ATGCATT	37	10	86056416	CGGAAAC	10	86046396	R
	GCCTGGA	37	12	54384744	CGGCCAC	12	52671011	R
	AACTCAC	37	6	25701717	GTGTGCT	6	25809696	R
	CTTTAGG	37	3	16225307	AGAGAAT	3	16200311	F
	CAGCATC	37	18	49865270	AGTTTCC	18	48119268	R
	CCTTTCA	37	6	6001380	CGCCCCA	6	5946379	R
	TAATCAG	37	X	100663101	CGCCCTA	X	100549757	F
	TCACCTT	37	6	32712979	CGGTCCC	6	32820957	F
	GTGAAAA	37	16	86743939	CGGGGGC	16	85301440	R
	TCAGAGT	37	10	77863526	CTGCCTC	10	77533532	R
	ATGCCCA	37	17	32581035	CGAGAGA	17	29605148	F
	CTCGGAA	37	10	729916	CGGCGTC	10	719916	R
Red	AACGTTC	37	18	77292063	CGGCCAA	18	75393051	F
Red	GACAGCA	37	8	47529280	GCGGCGC	8	47648445	R
	CAGGCAA	37	7	64314295	TCTCCAG	7	63951730	R
Red	CGAGTGC	37	16	86795490	GTCAGGC	16	85352991	R
Red	CCGGCCC	37	16	88706426	CTGAACG	16	87233927	F

	TGGAGAA	37	6	122115942	GTCACAG	6	122157641	R
Red	GAAACCT	37	17	80255419	GAGAAGA	17	77848708	R
	AGACAAA	37	2	101369330	CGTGGTT	2	100735762	R
Red	TGCCAGC	37	8	72917350	CGCGCTT	8	73079904	F
Red	CGATTCG	37	11	66326798	CGCTCTC	11	66083374	R
Red	TGGATCC	37	16	66600478	ACGCCAA	16	65157979	R
	GGTAGGC	37	16	869560	GCTTATC	16	809561	R
	GGAAGAT	37	3	23170838	CGCTGAC	3	23145842	R
	TACTGAT	37	3	149192609	CGGGGC	3	150675299	R
Grn	TGTCTGG	37	12	132845481	GGAAAG	12	131355554	R
Grn	TTGTTT	37	17	38708465	CGCTCCG	17	35961991	F
	GATTAGG	37	7	5937190	TAGAGG	7	5903716	R
	GGCATCC	37	8	36641571	CGGAGT	8	36760729	R
	AGAACGA	37	6	168918703	CGGTTCA	6	168661552	R
	TGTCGCC	37	2	80101372	CCTTGGC	2	79954880	F
	GGGACT	37	17	74868670	CGGGCTC	17	72380265	R
	AGGGAAA	37	16	66413050	CGGGTAA	16	64970551	F
	CACCTTG	37	5	149493258	CCCTTCA	5	149473451	F
	TGTTAGC	37	3	129205070	ATCATAT	3	130687760	R
	GCTGTCA	37	4	1309416	CGCCCCA	4	1299416	F
	CGCTGTT	37	17	57120	TGGAAAT	17	57120	R
	GGTTCAT	37	3	131637172	AGTTCAG	3	133119862	R
	TGAGCTT	37	8	118186764	GGCAAC	8	118255945	R
	GGTTCAG	37	17	1553415	CAAGTG	17	1500165	R
Red	GGGCCA	37	6	30039027	TGGAAG	6	30147006	R
Grn	GCCCCAC	37	5	33938213	CGGGGG	5	33973970	F
	TGAGCAC	37	15	101262162	CGACTCT	15	99079685	F
Red	GACGAAT	37	6	106434354	ACACAG	6	106541047	F
	TGAGGCC	37	16	88989069	CGCCTGT	16	87516570	F
	TGTATGC	37	5	140711852	GATCCTT	5	140692036	R
	GTATTTC	37	3	159886981	CGCTGAG	3	161369675	F
	CTGGTGT	37	16	25005762	CGGGTTC	16	24913263	F
Red	CGGGCG	37	5	2915123	GAATCCG	5	2968123	R
Grn	GCAGCCA	37	17	17109570	GTCCCGG	17	17050295	F
Red	AGGTAG	37	16	88472944	CGGGTCC	16	87000445	R
	AGGCCCT	37	10	72647652	TCTTGCC	10	72317658	R
	ATATATT	37	12	54073597	CTTTTCC	12	52359864	R
Grn	TCTGCCC	37	7	43288757	CGGAGC	7	43255282	F
	TCGCGG	37	6	42695153	CGGCTGG	6	42803131	F
Red	AGTTCTT	37	Y	21729069	CGGCCTC	Y	20188457	R
	CAATTTC	37	10	33710900	ATTCCCA	10	33750906	F
	GTTTTAT	37	19	56696870	CGAGGA	19	61388682	F
Red	CCCCAAC	37	1	150948030	CGAATA	1	149214654	R

	GAGGGA	37	10	1517218	CCTGTGA	10	1507218	R
	CAGCAGA	37	5	31197518	CGGACAC	5	31233275	R
	CCCTTTT	37	8	22960397	CGGGGGA	8	23016342	R
Red	GGTCACC	37	21	46921982	TCCTTCT	21	45746410	F
Red	CGCGGTG	37	13	111286999	CGGCTCC	13	110085000	F
	GCAACTC	37	3	195273304	CGGGGAC	3	196754593	R
	CACCAGC	37	11	67568593	CGGTAGA	11	67325169	R
Red	CCCCCTC	37	5	141660565	CGGTAGC	5	141640749	F
	TTGTATT	37	3	150093970	TGGATTG	3	151576660	R
Grn	CCAGGTC	37	7	72848703	CGCGCCC	7	72486639	F
	ATTAGAT	37	3	149685395	AAGTCAC	3	151168085	R
Red	TCCCCGC	37	6	13860661	CGCTGTT	6	13968640	F
	ATGAACT	37	6	41885417	TCACAGG	6	41993395	R
Red	CCCTCCT	37	8	97158015	TCAGCTC	8	97227191	R
Red	TGGCCCC	37	1	33235324	TCCACCT	1	33007911	R
	TGGCCCT	37	1	201665422	CGCCCGA	1	199932045	R
	TGCTCAC	37	8	19029020	ACTAGAC	8	19073300	R
	TCCTCCA	37	1	19581542	CGAGCTA	1	19454129	R
Red	CCCGGCC	37	16	81520589	CGGCGCT	16	80078090	R
	AATAGGC	37	2	192402991	TACTTGA	2	192111236	R
	GTTTAAG	37	8	119504312	CGCAATG	8	119573493	F
	GCTCAGG	37	16	49518536	GGACTGC	16	48076037	F
	AATCCCT	37	3	56896467	CCCTGTT	3	56871507	F
	TGTTCGC	37	7	137671793	CGGCTCC	7	137322333	F
Grn	AGGGAGC	37	6	32634362	CGGATCC	6	32742340	R
	GGAGGTC	37	16	2630397	GCCTGGG	16	2570398	R
	TGTCTTA	37	2	214992482	CATTAAG	2	214700727	F
	TAAGTTT	37	11	13282917	GGATATT	11	13239493	F
	CTTTACC	37	6	29911004	TCATTTT	6	30018983	R
Red	GGGAGGC	37	6	169825927	CGCTGCC	6	169567852	R
Red	AGTGCCA	37	11	66885240	GATGTGT	11	66641816	R
	CCCGGGC	37	6	33036504	GACAACC	6	33144482	F
	TTCATTA	37	2	103089678	CGGCTTC	2	102456110	R
Red	CGATCTC	37	7	44614305	CGCACCA	7	44580830	F
Red	AGGGGTT	37	1	19384827	CGGGGTC	1	19257414	R
Red	CCCACCA	37	4	165898825	CGGGGCA	4	166118275	R
Grn	GCAGACC	37	10	65801432	CGCCGTG	10	65471438	F
	TCCATAC	37	10	31026101	CGTGCAC	10	31066107	F
	CAGCCAC	37	13	112836631	ACAGGAC	13	111884632	F
Red	CAGCTCG	37	7	64035417	CAGTCCC	7	63672852	R
Red	TAGCAGT	37	17	21226409	ACTGCCA	17	21167002	F
	TGTTTTA	37	4	129292585	CTTTATT	4	129512035	F
	TCCCACA	37	7	150822006	CGTTGCA	7	150452939	F

	AGACATC	37	6	155739835	CGCCTGC	6	155781527	R
Grn	TTTCAGC	37	22	50721120	AGCCTTC	22	49063247	F
	CCGTTTC	37	8	9009352	GCTCTGT	8	9046762	F
	TTCTGAT	37	21	31709690	AGGCTGA	21	30631561	R
	GCGCATC	37	6	30707585	AAACCGT	6	30815564	F
Grn	CGTGGGA	37	13	24882296	CGGAATC	13	23780296	R
	TCAACTG	37	8	134401000	GTGGCCA	8	134470182	F
	TATGGTA	37	10	60147807	CATAACT	10	59817813	F
Red	TGCTGTT	37	10	11088146	CGGCACC	10	11128152	F
Grn	GAGAAGT	37	7	105596483	TAGTTCC	7	105383719	F
Red	GCAGCGT	37	6	42695625	CGCCCCG	6	42803603	F
Grn	TCGGGGC	37	6	29911095	CGCCCGT	6	30019074	R
Red	GCGTAGA	37	16	28634766	GTTGCTC	16	28542267	R
	ACTTTGT	37	12	76706337	CGGTCAC	12	75230468	F
Red	CGGAATC	37	5	140579470	GGCGGGC	5	140559654	R
Red	ACGACTA	37	6	31650760	TTTGCGA	6	31758739	R
	GAACAGC	37	12	312595	CGCCGGC	12	182856	R
Red	AGGGAGA	37	Y	6114255	ACCGCCC	Y	6174255	R
	CACGTCA	37	20	62402415	GCCAGCT	20	61872859	F
	GGGGGGC	37	5	1246291	CGTCAGG	5	1299291	F
Grn	AGAGCGA	37	2	232348602	CGCCCCG	2	232056846	R
	CAAGCTG	37	16	58704495	CGCCAGA	16	57261996	R
	GGGTGAC	37	7	76030355	TGGTGTG	7	75868291	F
	AATTCAA	37	8	119107030	AACCCTT	8	119176211	R
	GAGGAGC	37	8	1905131	CATCTCT	8	1892538	R
	GTCCCTT	37	20	31668448	AGCATTA	20	31132109	R
	GGTCACA	37	4	94759825	CGGGAAA	4	94978848	R
	TCCTGAA	37	18	74964030	CGGTGCC	18	73093018	R
	GCCACCA	37	19	37466940	CGGAGAT	19	42158780	R
Red	CCCACAC	37	7	158075388	TGTCTGG	7	157768149	F
	CGAAACA	37	14	104663241	GCACTTG	14	103732994	R
	GTGCTTA	37	11	36055687	TATCTCT	11	36012263	R
	AGGAGAC	37	13	26622819	CTTTGAG	13	25520819	R
	AATTTTC	37	20	18566614	CGGAGCC	20	18514614	R
	CATTCTC	37	4	155253864	CGGGGAT	4	155473314	F
Red	GGGCGGC	37	X	50213977	CGCTAGG	X	50230717	R
	TCAGTAG	37	7	1075592	CGGCATG	7	1042118	R
	GGATGGC	37	7	151565731	CGTGATC	7	151196664	R
	TTCCAGC	37	11	107583406	TACTGCT	11	107088616	F
	ATTTCCC	37	20	62957648	CGGACAT	20	62428092	F
	CTTATCG	37	6	170405014	CGGCCTG	6	170246939	R
Red	TCGAGCA	37	4	4228644	GCTGGTT	4	4279545	F
	TGCACTG	37	6	32489750	CCTGACG	6	32597728	F

Grn	CCGCTCC	37	11	118842484	CGCCTGT	11	118347694	F
	TTACCGC	37	10	44501010	CGCTTTG	10	43821016	R
Red	GGCAAAA	37	6	101846805	GCTAGCA	6	101953526	R
Red	GAGAGGA	37	17	1954986	CGGCCCC	17	1901736	R
	GACAAGC	37	12	132869069	CGAGGGC	12	131379142	F
	GAGTGAA	37	1	77711859	CGAGTGA	1	77484447	F
	GCCTGGC	37	11	14004854	TGCCTGC	11	13961430	R
	ACTGTGA	37	11	26743425	CGTGTAC	11	26700001	F
	ATGTGAA	37	16	1021780	ACAGTTT	16	961781	F
Grn	AGAATCA	37	21	45360804	CGGGGTT	21	44185232	R
	TCTCCAA	37	8	37005558	GTTATTG	8	37124716	F
	TGGGCGC	37	1	7023864	CGCCCCT	1	6946451	F
	TGTGCCT	37	2	3753297	CGGTCTG	2	3731172	R
Red	CGCTCTC	37	3	47205656	CGCAGGC	3	47180660	F
	TCTGTGG	37	16	86029348	CGCCCAG	16	84586849	R
	AAAAGT	37	5	40841590	GAAATCC	5	40877347	R
Grn	GGCGGCC	37	X	103411244	CGCCCCG	X	103297900	R
	CCACTTC	37	7	139761087	TGTGCCC	7	139407556	F
	GAAGTGA	37	8	3269952	CGTTCAG	8	3257360	F
	GCTTGAC	37	17	32612684	CGGGGGT	17	29636797	R
	AACTTAA	37	11	122051193	CGTGGAA	11	121556403	F
	CCAATAA	37	6	31976720	CGGCCTG	6	32084698	F
Red	TGCGTGA	37	8	80783997	CGGGGAT	8	80946552	R
	GGGGGCC	37	3	184280712	TTGTTTA	3	185763406	R
Grn	TCCCGGA	37	5	140530467	TGCTAGA	5	140510651	R
	CAACCCC	37	X	20134557	CGGGGAC	X	20044478	F
	AAACAAC	37	13	28912746	CGGTCTG	13	27810746	F
	TACGTTC	37	7	134017084	TGGCAGC	7	133667624	R
	GCGCGCA	37	20	3653555	CGGGGAC	20	3601555	F
	TCCGGAA	37	6	29648468	CGCCTGG	6	29756447	F
	GGGAGAC	37	2	131722957	CGGGCAC	2	131439427	R
	GCTTCGC	37	X	153096786	CGGACAC	X	152749980	F
	ACTCAGG	37	7	55100608	CGCTGGA	7	55068102	F
	GGTTGGA	37	16	83967808	CGGCCCC	16	82525309	F
	CTGGAAC	37	11	77299960	CGCGCTC	11	76977608	F
	GACCAGC	37	Y	21666309	TTGTCCA	Y	20125697	R
	TATCTGA	37	20	4795381	CGGGGAA	20	4743381	F
Red	TCTTCTC	37	16	2903246	AGGAGCC	16	2843247	R
	GGGCTTT	37	1	6561043	TTTAAAT	1	6483630	F
Red	ACGCAGT	37	1	1886501	GGACAGC	1	1876361	R
	GGCCTCA	37	7	75780412	TTGGTCA	7	75618348	R
	TGGGTTG	37	21	34444104	TGGGTCC	21	33365974	R
	AACCCAT	37	7	17822217	CTGTCTA	7	17788742	R

	CTCATAG	37	6	40324498	TTTTCCT	6	40432476	R
	TTTCCAG	37	7	2078981	AGCAGTC	7	2045507	F
	AATTTTA	37	8	37820326	CTAGGGC	8	37939483	R
	GAAGAAC	37	11	3174092	AAAGTAA	11	3130668	R
	TCAAGCC	37	1	25069938	CGGGCAT	1	24942525	F
Red	TCCTTGT	37	X	117633362	CGCGCCG	X	117517390	F
Red	CGGGGCT	37	4	174422191	AAAGTGC	4	174658766	R
	TTGTTTA	37	6	9139720	AAAACTC	6	9084719	F
Red	CTGAGAA	37	X	118986703	CGCCCTC	X	118870731	F
	GTTGGAG	37	6	31082631	CGAGACT	6	31190610	F
Red	GACGCTG	37	12	132682698	CGGCGCC	12	131248651	F
Red	ACCGCGT	37	2	242950311	CGCACTG	2	242598984	R
	GGCCCCT	37	17	72860652	CGGCCCA	17	70372247	R
Red	ACGGGCC	37	22	18985691	GACAGAC	22	17365691	R
Red	GTTCATA	37	2	100902129	TCCTGTC	2	100268561	R
	ACACATC	37	17	77300674	CGAAGAA	17	74812269	R
	GGGCATC	37	20	61456784	CGGACAC	20	60927229	R
Red	AACGGGC	37	4	942005	CGAGCCT	4	932005	R
Red	TCAGCGC	37	10	43846376	AGATGGA	10	43166382	F
Red	CCAGGCC	37	16	90148775	CGGCCGC	16	88676276	R
	GGTAGAC	37	2	201003360	CGCTTGA	2	200711605	R
	CTGAAGC	37	4	15429515	CCAAAGA	4	15038613	F
	TATTTGA	37	14	95078636	CGGACTG	14	94148389	R
Grn	CAGCCCC	37	2	241896910	CGCGTGC	2	241545583	R
	GAAAAAA	37	12	54383639	AAAAATT	12	52669906	R
Red	CTCGGGA	37	12	11700489	TGGGACT	12	11591756	F
	AGCGGCT	37	4	7436239	CGGAGCA	4	7487140	F
	ACTTGGA	37	18	24131379	AGCAGTT	18	22385377	R
Grn	AGTGGCC	37	16	3230726	TAGCGGC	16	3170727	F
	GCTCATA	37	X	39436753	GCAACAC	X	39321697	R
	TTCACCA	37	2	113942204	AAAGTCC	2	113658675	F
	GCTGGTC	37	9	68809732	AGGGTGC	9	68199552	R
	AGAAACC	37	Y	21726406	CGGCTAC	Y	20185794	F
	TCAGCCA	37	19	21265364	GGGTCCA	19	21057204	F
	AAAATAC	37	11	30344200	CGAGTAA	11	30300776	R
	TTCTGTT	37	17	74260776	ATCTGGG	17	71772371	R
	GTAGAAT	37	6	101846791	CTGGCAA	6	101953512	R
	CCCGGGA	37	1	41350292	TTGGTGG	1	41122879	F
Red	CCACACG	37	6	30039206	CTTCTGG	6	30147185	F
	GTCCCAG	37	11	64594467	TCCTCTG	11	64351043	F
Red	CCCGTGG	37	11	34852392	CGGGCAC	11	34808968	R
Red	TCAGTGT	37	16	86653215	CGTCGGA	16	85210716	R
	AGCCCCT	37	2	233282380	CGCTGTC	2	232990624	R

	GACATCC	37	13	113535686	CGGGTTG	13	112583687	R
Red	CGCCTTT	37	18	11147385	CGTGAGT	18	11137385	R
	ACTCACC	37	6	30782234	CGGTGAC	6	30890213	R
	GAGGTTC	37	16	7138889	AACCTCT	16	7078890	R
Red	TTGGGCC	37	7	157225062	CGGAGA	7	156917823	F
Red	GCCGTCT	37	X	139593371	CGCGGC	X	139421037	F
	GAGCAA	37	16	31888794	CGAGATC	16	31796295	F
	CCCTTCT	37	21	34773372	GTATAAA	21	33695242	R
	GTCCGTC	37	11	2722119	CGGGGA	11	2678695	F
	GAAAAC	37	6	32713188	TGGAATT	6	32821166	R
Red	AGAAGG	37	16	67313019	CGCGTGG	16	65870520	F
	TCAATCC	37	7	158804287	CGCCTCT	7	158497048	R
	ACCAGTG	37	3	119279147	CGGCTCA	3	120761837	R
Red	CGTCCCT	37	X	102000758	ATAGCAA	X	101887414	R
	AGTAGA	37	20	56179171	GTTTCAC	20	55612577	R
	GGACAG	37	4	57528377	CGCTTAC	4	57223134	F
	TCGGATC	37	10	101088672	CGGCTGG	10	101078662	F
	ACGCTTA	37	6	5404958	AAACCCA	6	5349957	F
Red	TGTTTAG	37	22	45704914	CCTTGTG	22	44083578	F
Red	TGTGTGT	37	6	29796985	CGGAGGT	6	29904964	F
Red	GCTAAGA	37	Y	22917937	AACAGC	Y	21327325	F
Red	ATCCAGG	37	17	39537455	CGGAGCA	17	36790981	R
	AGTCCTC	37	2	101966951	TCACCCT	2	101333383	R
Grn	CGCCGGC	37	X	153284899	AGCCGTG	X	152938093	R
	GTTGACT	37	13	50985639	CGCACA	13	49883640	R
Red	GTAGCTG	37	16	1087129	CGGCTGG	16	1027130	R
Red	AGGCTGA	37	16	888938	CGCGCG	16	828939	R
Red	CCACACG	37	13	113630878	CTGGGCT	13	112678879	R
Red	GGCCGGC	37	16	1493759	GCTGGA	16	1433760	F
	GTGCTGC	37	1	212643521	CGCCCCA	1	210710144	F
	GACCAGC	37	1	1227138	GGCCTCC	1	1217001	F
	CTCTGTA	37	3	59735420	CGAAGA	3	59710460	F
	AACAACT	37	2	242988706	AACAGTC	2	242637379	R
	AGGCCCC	37	20	62225388	CGACCTG	20	61695832	F
	AGCGATC	37	1	63249213	TCATTTT	1	63021801	F
	AGGCTCA	37	19	2058455	CGGAGCA	19	2009455	F
	GTCATCT	37	3	30349908	GTAATAA	3	30324912	R
Red	GTAGTCT	37	16	2051739	TGGCCGG	16	1991740	F
	GGGTGGA	37	11	60608291	CGGCCAT	11	60364867	R
Red	GTGGTGA	37	3	113956240	CGGGAG	3	115438930	R
Red	GGGGGCT	37	2	46049176	ACTGAGC	2	45902680	R
	GGGCATA	37	12	8403616	ATATATA	12	8294883	R
	ACACAGA	37	X	99891793	TACCCTC	X	99778449	F

Red	CTGCCCG	37		16	1128698	CGGCCA		16	1068699	F
	CACAGCC	37		6	36409495	CGAGGG		6	36517473	F
	TGACTCA	37		11	128080305	CGGCTTA		11	127585515	R
	GTACATC	37		2	242490217	CGCGCCC		2	242138890	R
	AAAGGA	37		2	202330990	CGTTCAC		2	202039235	F
	AACTATC	37		4	83384006	TTCCTTT		4	83603030	R
	CAGTCCA	37		4	38330015	CGCCTAT		4	38006410	R
	CAGGCCC	37		1	38180356	TCTGTAA		1	37952943	F
	ACCAGAT	37		5	136478693	GGCAATC		5	136506592	F
	AAGCTGC	37		5	19766434	TCTTACT		5	19802191	R
	GTGTGTC	37		3	11178683	GGTTAGG		3	11153683	F
	GACAGGC	37		18	5456880	CGAGAAC		18	5446880	F
	GCGGCAC	37		16	81740096	GGCCAGT		16	80297597	R
Grn	CAGGTGA	37		11	7110148	CGCGCCC		11	7066724	F
	TGGTGGT	37		20	62559021	GGATAA		20	62029465	F
	TCCTTCC	37		16	57541087	TGGGGAC		16	56098588	R
	GGGTGTG	37		19	7937329	AGGGGGT		19	7843329	R
	GGCTGAC	37		7	1000336	CGGGTGT		7	966862	F
Grn	ATGCCCG	37		13	112997365	CCAAGGT		13	112045366	R
	CCAGGAC	37		10	52434647	TACCTTC		10	52104653	R
	GTGAAAC	37		11	130283454	ATTCACT		11	129788664	F
Red	TTTCTCT	37		2	240174613	CGCACCA		2	239839550	F
	CAAAAAC	37		19	53107200	CGTCCAA		19	57799012	R
	GCTCAGG	37		6	33052354	AGGTTTC		6	33160332	F
	GGACCCT	37		7	4855406	CGCCCCA		7	4821932	F
	GGCTGGC	37		2	97573176	GGATGGC		2	96936903	F
	ACCCAGC	37		18	77278806	CGGGTGC		18	75379794	R
Red	GCTCAGA	37		5	140053350	CGGGAGC		5	140033534	R
	GAGTTTT	37		6	29860039	CTGCTCC		6	29968018	F
	GCAGACT	37		16	31439106	CTTCACA		16	31346607	R
Grn	AGACGCT	37	X		152864830	CCAGGGC	X		152518024	F
	GGGTGGT	37		1	234635574	CGGGCCA		1	232702197	F
Red	CACGTGA	37		17	35969640	CGCCCCA		17	33043753	R
Red	CTCCTGG	37		16	88990232	CGGCATT		16	87517733	R
	TGCCTTT	37		1	217113226	CGTTGGA		1	215179849	R
	TTCTCCA	37		20	259925	TGGATGG		20	207925	R
	CAGCTTC	37		1	53661448	CTGCTTA		1	53434036	R
	ACCCGGC	37		16	857576	CGGCCGT		16	797577	F
	AAAAAC	37		1	15631449	TGAGCGC		1	15504036	R
Grn	CACTCCT	37		2	11009092	CGGGAC		2	10926543	F
Red	TACACGT	37		11	93277161	CGGACCA		11	92916809	F
	GAATAAC	37		12	125225316	TTCACCC		12	123791269	F
Red	CTGAGAC	37		1	89990868	CGGCGCC		1	89763456	R

	CCACCTT	37	11	71150247	CGCCGTC	11	70827895	R
	GAAGGA	37	12	53490352	CGCCCAT	12	51776619	R
	AGCTCAC	37	8	1789169	CGCTCCA	8	1776576	R
Red	GGGGGG	37	18	47825363	GCGACAC	18	46079361	R
	TTAACAA	37	20	44352696	CGGTGGT	20	43786110	R
	TGCCCCT	37	4	7301176	GTGCTAA	4	7352077	R
	TGATTAG	37	13	44811779	TTAGTCA	13	43709779	F
	AGTCACC	37	17	79068856	CGGGGCT	17	76683451	F
Red	CGTGGGC	37	19	46387962	CGGCCCC	19	51079802	R
	GGATGCC	37	5	2643172	CGTTCCC	5	2696172	R
	CTTTTCT	37	3	170040557	CGGGGTC	3	171523251	F
Red	CAGAACT	37	19	57109049	CGAGGGT	19	61800861	R
	GGAGCAT	37	Y	9368165	CGGCAGT	Y	9978165	F
Red	CTAGGCA	37	11	18477299	CGTGCGC	11	18433875	F
Grn	GCTGCCT	37	11	133109552	CGCGGTG	11	132614762	F
	AGACTCG	37	2	794763	CGCCTCG	2	784763	R
	TCAGTGA	37	7	51539323	CCTGGGC	7	51506817	R
	ACTGTTA	37	11	10716164	CGGGAAC	11	10672740	F
	TCTCGGT	37	6	901264	AACGTGT	6	846264	F
	TCACGCC	37	8	144158344	CGGGGTT	8	144229719	F
	CTCAGCC	37	5	31379132	GAGTCAC	5	31414889	R
Red	ATTTCTA	37	11	32354742	ACTGTAC	11	32311318	F
Grn	GCCTTTG	37	12	54376127	CGGGCCT	12	52662394	R
	GTGGTGG	37	3	23818150	AGGGCTC	3	23793154	R
	TTGAAAA	37	2	80179759	CACAAAA	2	80033270	F
Red	ACATGTT	37	12	6898647	GAGACAC	12	6768908	F
	GAGGGAC	37	Y	21240004	AACTTCA	Y	19699392	F
Red	ACCGGAC	37	X	16964684	GACGGGC	X	16874605	R
Red	CCTGCCT	37	12	132972807	GATGTTT	12	131482880	F
Grn	TCACAGG	37	17	9806770	AGTTCTA	17	9747495	F
Red	ATGCAAC	37	2	36782386	CGAAAGC	2	36635890	R
Red	CCACATG	37	1	8442507	CGCATGC	1	8365094	R
Grn	AATAAAT	37	19	56688423	CGGCCAC	19	61380235	R
Grn	CCACCTC	37	12	8025394	GCGAAGC	12	7916661	F
	GGCTTCT	37	22	45135965	TTTGCTG	22	43514629	R
Grn	GTGCAGC	37	X	53349902	CGGGTAC	X	53366627	F
Grn	ATGCGCT	37	1	206897270	TTCTCTT	1	204963893	F
	CCTCTGG	37	19	15312129	CGTCCTG	19	15173129	F
Red	GTCAAAC	37	19	613111	AGGGGCA	19	564111	R
Red	CGAGAGC	37	16	87873837	GCGGGTC	16	86431338	F
	GGAGCAA	37	6	46293571	ACATAAC	6	46401530	F
	GACCAAC	37	17	30488883	ATTCAGG	17	27512996	R
	CCAGCAC	37	18	77292443	ATGTGAA	18	75393431	F

	TGGCCTT	37	5	174174566	TGAGAAC	5	174107172	R
	CATCTAA	37	19	45457306	CTATGTT	19	50149146	F
	AGTAAGT	37	4	99935464	TAGGGCT	4	100154487	R
	ATAGCTT	37	3	124232190	GAACCCC	3	125714880	F
	GGAGGCC	37	4	139531098	CCATGAG	4	139750548	F
	TTTTCTG	37	1	151967449	AATTTAG	1	150234073	R
	GGAAATC	37	6	158690902	GAAGACC	6	158610890	F
Red	GTTCTGC	37	11	70309970	CGCCAGA	11	69987618	F
	TCTAAGT	37	3	39444897	CGGCCTA	3	39419901	R
Grn	GGGCGCC	37	19	911965	CGCTCCA	19	862965	R
	CCGTCGT	37	2	10302454	TCGATTC	2	10219905	R
	GCTCCCA	37	16	56643342	CGGTCAG	16	55200843	R
	TGTGCTG	37	7	154720452	AGGGCCC	7	154351385	R
	TCATTGG	37	17	27338116	CCAGGCT	17	24362242	F
	ATCCCCG	37	2	133110927	TGTAGAG	2	132827397	R
	TGGCGCT	37	5	1594808	CGGGGAC	5	1647808	F
	ACATGGT	37	22	17672168	CGGAGAC	22	16052168	R
	CTTTTCC	37	15	95847523	GGCTGTG	15	93648527	F
Red	TTGAGTG	37	6	26598149	TGCATAG	6	26706128	R
	GGTAGTG	37	1	2373387	AGAGGCT	1	2363247	R
	TGTACCT	37	4	185021514	CGGGCCC	4	185258508	R
	TCCATAT	37	6	168363958	CGGCTAC	6	168106807	R
Red	CCGCAGC	37	14	101696494	CGCCCCC	14	100766247	F
	CGGAGCT	37	16	88385387	CCCACCA	16	86942888	R
	GAGTGCC	37	19	50861923	CGGCCAC	19	55553735	F
	CACAAGC	37	5	1462729	GCGGCTG	5	1515729	F
	ACCCCAG	37	4	7812988	GGGAGGC	4	7863888	F
Grn	TTACGTG	37	2	1827764	GTGTTGG	2	1806771	R
	AACAGAC	37	1	43389028	GTCTGTG	1	43161615	F
	TAAACAC	37	4	141923701	ATTTCTG	4	142143151	R
Red	CCGGGCC	37	20	61885236	CGTCCTG	20	61355681	R
	GGAAAT	37	4	54554571	TACAGCC	4	54249328	F
Grn	AGCAGCC	37	7	158121270	CGGGAGC	7	157814031	F
	TGCAAAA	37	3	72941472	GTTTCTC	3	73024162	R
	ACAGGAC	37	6	29972393	CGAGTGT	6	30080372	R
Red	CGGCGGC	37	3	44622596	GGGAAGC	3	44597600	F
	CAGAAAT	37	6	31087240	AAGGGCT	6	31195219	R
	AGCTAAT	37	16	77535527	GTGCATA	16	76093028	R
Grn	CGCTGGC	37	14	24780682	CGGGAAC	14	23850522	F
	TTCTCCC	37	2	66664871	CGACGAT	2	66518375	F
	AAGGAA	37	3	45241685	TCAGGGA	3	45216689	R
	ACCATCT	37	16	17898759	CGCTAGG	16	17806260	R
	TTTTTAA	37	11	49017551	CTGCTGC	11	48974127	R

	CGGCCCT	37	17	10195469	CGGATCC	17	10136194	R
	AACAAAA	37	1	153174654	CGCTTTT	1	151441278	R
	TTTCTATT	37	3	184934396	CGATGGC	3	186417090	R
	GGGCCCC	37	1	228359130	CATGTCC	1	226425753	R
Grn	CCGCCTC	37	7	32945575	CGCCCGC	7	32912100	F
	TTCCCCTT	37	6	32829025	GGCCAGA	6	32937003	F
	TCAAAGC	37	11	1455362	CGAGAAC	11	1411938	F
	GTTTCAG	37	2	113912567	AGCACAA	2	113629038	R
	AAAAAAA	37	4	16628713	CGGCTGC	4	16237811	F
	CTGGGCA	37	9	136151958	CTTTCAAT	9	135141779	F
	TGTTTTGC	37	17	39143567	CAACCTA	17	36397093	R
	TGCGCAT	37	14	93698216	GGATCTA	14	92767969	R
	CACTGCT	37	15	78133639	CGAAGTT	15	75920694	F
Red	GGCGCGA	37	14	24780734	CGTCTTCA	14	23850574	F
Red	GCTGCTG	37	14	102422152	GGCACGT	14	101491905	F
	GGGCTAA	37	5	10490335	CGAGGGC	5	10543335	R
Red	CGCGACC	37	16	2229298	CGCCCGT	16	2169299	R
	AACAGGA	37	6	31597708	GTGCCAA	6	31705687	F
	TCATGAC	37	1	1905080	CGGCCCC	1	1894940	R
	GAGCCCC	37	10	105389403	CGCCTCT	10	105379393	R
	CTGATGG	37	16	67978450	CGGCCCG	16	66535951	R
	AGCAGTC	37	16	9326393	CGGGCTT	16	9233894	F
	AACCCGC	37	16	88349881	CGCAGCT	16	86907382	F
	GACTACT	37	10	116337203	CGACTCT	10	116327193	R
	AGGCTTA	37	10	14099154	AATTAAG	10	14139160	F
	CTTAATT	37	22	50174028	CGCAGAA	22	48560032	R
Red	CAGGAAT	37	16	88821905	CCAGGCA	16	87349406	F
	ATGTATC	37	3	9850429	CCCAGGC	3	9825429	R
	TATGATA	37	17	452707	AAAGGAC	17	399457	R
	TTTCAGT	37	X	35937780	TGGTAAC	X	35847701	R
	GCCGCGC	37	14	104394621	AAGCTTC	14	103464374	R
Red	GACCAAC	37	14	102515026	GCGCACC	14	101584779	R
Grn	GCAAACA	37	11	18477303	CGCCTTCT	11	18433879	F
	TGGAGGA	37	8	15094107	CGGTGAC	8	15138478	F
	ACTCTATG	37	5	140620284	GCAGATA	5	140600468	R
	GAAGGTC	37	8	141248582	TGCCATC	8	141317764	F
Grn	GAGAAGC	37	5	180671201	AGGTGAA	5	180603807	R
	CCGCCTC	37	2	86092937	CGGGCAC	2	85946448	R
Red	CGTCCGG	37	14	102422310	CGGCTTG	14	101492063	F
	CAGGCAA	37	8	135609134	CGAGGGA	8	135678316	F
	CCAGTTG	37	21	47469104	CGGCACC	21	46293532	F
	TGCAGAA	37	14	32350324	ATGATGA	14	31420075	R
	TGTTTATA	37	9	4116989	CTGGAAC	9	4106989	F

	TATGTTA	37	7	13889871	CGCCTTC	7	13856396	F
	CTGCTTT	37	8	17979647	CGCCCAG	8	18023927	R
Grn	AGGTTTT	37	5	140214372	CCGAGAC	5	140194556	F
	GAAGCAA	37	14	89796856	CAGAATC	14	88866609	R
	TGAGCAC	37	1	108115416	CGGGCAA	1	107916939	F
Grn	CCACGCT	37	5	140627173	CGGCCCC	5	140607357	F
Red	CCGGCAC	37	5	140222653	CGCGGCA	5	140202837	R
	ACGGGTC	37	13	114309225	CCTGCCT	13	113357226	F
Red	CTCCCAG	37	14	76446087	GGCTGTG	14	75515840	F
	GTATGAG	37	1	224753137	AGTTCTG	1	222819760	R
	TGCGTGT	37	7	64894780	TGTCAAG	7	64532215	F
	AAGCCTG	37	14	101493361	CGGATTG	14	100563114	R
	TCTGTAA	37	11	60534911	TCGCCTC	11	60291487	R
	CCCCCTG	37	10	37106999	TATTAGA	10	37147005	R
Red	GCCTTCC	37	7	150020025	GGAGACC	7	149650958	R
	GCTGGAC	37	1	44569177	CGCACCT	1	44341764	F
	AAAGGAC	37	16	69660388	GTTACCT	16	68217889	R
	TCTCAAG	37	16	78027119	TCTTCTC	16	76584620	F
	GGGCGAA	37	11	2022021	CGGCCAC	11	1978597	F
	CTGAGAT	37	2	75785554	CGGCACT	2	75639062	F
	AACCAGC	37	5	1510512	CGGCACC	5	1563512	F
	ACGTATT	37	10	3178915	CTGCTCA	10	3168915	F
	GACTCAG	37	8	89270978	TACATTT	8	89340094	R
	GCAGGGA	37	2	47497026	GCCTCTT	2	47350530	R
Red	GCACACA	37	1	6085995	CAGTGTG	1	6008582	F
	GCGCCAC	37	1	246860007	CGCAGGC	1	244926630	R
	TCCCAAA	37	5	178322737	CGGCCCC	5	178255343	R
	ACCCGCA	37	7	158965466	TCAGATG	7	158658227	F
Grn	AAATTCG	37	14	99725468	CGGGGTC	14	98795221	F
	CCGGCAC	37	8	144302512	CGGGCAT	8	144373887	F
	TGTCAAA	37	2	1658233	AGTTCCT	2	1637240	F
Red	GCCTGAA	37	13	24269867	AGGGGCC	13	23167867	F
	CCAACCG	37	15	78287690	CGGTTCT	15	76074745	R
Red	AATCTGC	37	5	140174841	CGCCCGC	5	140155025	R
	AACGAAT	37	5	159827857	CGGGCTG	5	159760435	F
	ATAATAA	37	16	24266347	CGGCATA	16	24173848	R
	CGGGGTT	37	1	2139235	TGCAGGA	1	2129095	R
Red	CAGCTGG	37	X	30671305	CAGAGGC	X	30581226	F
Red	ACTCTTC	37	10	129794994	CGCAGGC	10	129684984	F
Red	GACGTCC	37	2	1788153	CGCCCCG	2	1767160	F
Grn	GTGACTT	37	6	25882402	CGCCACC	6	25990381	R
Grn	AGGATTT	37	7	64043012	ACGTTCG	7	63680447	F
Red	GTGGGAT	37	18	29304111	CGCAGCC	18	27558109	R

	GCAGGCC	37	8	144966879	TGGAGAC	8	145038867	F
Red	TCCTCCC	37	7	44104860	ACGGACC	7	44071385	F
Red	GTGGCCC	37	4	14451768	ACTATCG	4	14060866	R
	CAACATG	37	3	15311183	CGCCACT	3	15286187	F
Grn	TCGGGCG	37	8	22547688	TGGCGTC	8	22603633	F
	AGGGGGT	37	19	18385672	GGGCCAC	19	18246672	R
	TTAGGGG	37	11	85601106	CGGTGGC	11	85278754	R
	AATTGGA	37	3	174092757	CTTCACT	3	175575451	R
	ACAAACC	37	1	88298973	CGGCCCC	1	88071561	F
Grn	GTTCCCG	37	17	75315527	AGAGAGC	17	72827122	F
Red	CCACGAA	37	17	80970159	GCAGTTC	17	78563448	F
Grn	AGCCGTA	37	1	35586588	CGCGGGA	1	35359175	F
	ATTCATA	37	1	160769081	ACTACCT	1	159035705	R
Red	CAGTCCG	37	12	52258163	CGCCCGT	12	50544430	F
	AAATCTT	37	7	51538921	AACGTTT	7	51506415	R
	TCGCACG	37	12	7070679	CGCCCTC	12	6940940	R
Grn	GCGTTCC	37	16	3345463	CGGCTGT	16	3285464	R
Red	TTACTCA	37	15	96887959	CGACCCT	15	94688963	F
	GGGGCTC	37	1	1142932	AACGTGA	1	1132795	R
	GGCAACA	37	5	141743488	CTCCATA	5	141723672	F
	CCTGGAC	37	16	85747424	AGCCAAC	16	84304925	R
	TAGCTGG	37	1	231820076	CGGGGGC	1	229886699	R
	CAAACCC	37	1	145412774	CTAAGCA	1	144124131	R
Red	CCAGGGA	37	1	53970693	CAGGGCC	1	53743281	F
	GTGGCGC	37	18	501137	AAGGTGC	18	491137	R
	TGAAACA	37	17	80969525	GTGATGA	17	78562814	R
Red	GCCGGCC	37	1	12609308	CGCCCGC	1	12531895	F
	ATTCCCT	37	X	48957691	CGTTGGA	X	48844635	F
	CACTCAG	37	2	85890281	CGCCTCT	2	85743792	R
	CCGTCCC	37	11	18727949	AAGGCTC	11	18684525	F
	GAGAGGA	37	6	30039548	TTTTGAG	6	30147527	F
	CACCTTG	37	17	57918682	CGACTGG	17	55273464	R
	CCCACTG	37	14	33409812	CCTTTGT	14	32479563	F
	TCCAGAC	37	6	14917345	CAGACAA	6	15025324	F
Grn	CCGCTCC	37	1	148854315	TCAGAGC	1	147120939	R
Grn	GCACAGC	37	4	137316569	ACCCGGC	4	137536019	R
	AATCTGG	37	12	94699141	CGACACA	12	93223272	R
	CTGGCAT	37	2	151768348	AGTTTAC	2	151476594	F
Red	GTCCCCT	37	11	64081430	CGAGTAC	11	63838006	F
Red	AGCCGCA	37	16	1187722	CGCACTT	16	1127723	F
	ACGAGCT	37	2	238794837	CACAGCT	2	238459576	R
	AGAGCCC	37	7	158342600	CGTGACC	7	158035361	F
Grn	CAGCTCC	37	16	88497007	CGGCGCC	16	87024508	F

Red	AGGTACC	37	5	140215806	TTGACGC	5	140195990	R
	GTGGCCG	37	10	90712739	CAGTTGT	10	90702719	F
	ACCTTTG	37	15	27035245	GTGGGTT	15	24586338	F
	CTCTGTG	37	1	2336575	CGTCAAG	1	2326435	R
	AGACTGT	37	10	30276523	TCCTTGA	10	30316529	R
Grn	TCTTAGG	37	13	100583872	GAATTCA	13	99381873	R
Grn	CGCTCTG	37	7	63652720	AACCCTC	7	63290155	F
Red	GTTCCGA	37	8	61627281	AGTTACG	8	61789835	F
	TCCAGGG	37	11	130596374	GACTCAT	11	130101584	R
Red	CTAGGAC	37	16	86466427	AGGGAAC	16	85023928	R
	ATCCTCT	37	10	28971331	CGGAGTC	10	29011337	F
	CCTTCTC	37	10	12438782	CGGGGAC	10	12478788	R
Red	TGAGTTA	37	7	47493388	CGGGACT	7	47459913	R
	TGAAGTG	37	12	133304604	GGACCCT	12	131814677	R
	TGAATGT	37	5	36657993	CGGTCAG	5	36693750	R
Grn	ACGCAAC	37	6	170732353	GCCGCAC	6	170574278	R
Red	AGATGAC	37	2	3322283	CGGGATC	2	3301290	F
	ATTGAGA	37	18	42255459	GTTGAGA	18	40509457	F
	GGGCTCC	37	6	161100122	ACCTACC	6	161020112	R
	AATTTGT	37	22	38032768	CGGGGGT	22	36362714	R
	TCCTGGA	37	12	2750053	CGTCCAC	12	2620314	F
	TCAGATA	37	8	127990758	CGGAATC	8	128059940	F
	TAGGAGC	37	11	60701918	CGGCCCC	11	60458494	R
	TGGCAGC	37	16	55794031	CGCTTCC	16	54351532	F
	AATCTGG	37	5	149493034	CATGTGC	5	149473227	F
	GTGGTGA	37	6	139447669	ACAGCTA	6	139489362	R
	GAGCAAA	37	3	30667873	GCCTATC	3	30642877	R
	GTATTCC	37	3	63047382	CGTCCCA	3	63022422	F
Red	CCTCATC	37	6	32976018	CGGACCC	6	33083996	R
	TTCCAGG	37	X	19904780	GACCCTG	X	19814701	R
Red	TTTGCGG	37	12	46411898	CTGGAGT	12	44698165	R
	AAAAACA	37	2	65528222	CGGCGGC	2	65381726	F
	TTGCCAG	37	12	75785089	GAGGACC	12	74071356	R
	ACATTGC	37	17	73316721	CGTTTCC	17	70828316	R
	CAGGACC	37	16	28948179	CGGCCCT	16	28855680	F
	GCGAGCA	37	2	796476	GCAGCTG	2	786476	R
Grn	GATGGGA	37	1	109826064	CGCCCCG	1	109627587	F
	GTGGCAC	37	11	129246718	CGAGGGT	11	128751928	R
Red	CCCCGGG	37	19	1852127	TGTCACT	19	1803127	R
	CCTGTCT	37	15	31764211	GCTGCTG	15	29551503	R
	CTCTTGC	37	7	12151221	GATCTGG	7	12117746	R
	CTGTTGC	37	6	170478434	CGGGAAT	6	170320359	R
	AGACATC	37	6	128977386	CGGAGAC	6	129019079	R

	CCTTGAG	37		16	11012292	GCGAGTT		16	10919793	F
Red	GGCGGGC	37		1	32741518	CGATCCT		1	32514105	R
	TCCCCAG	37		15	48874903	AGACTGC		15	46662195	R
Red	TCCGTAG	37	X		40440191	CGCTTCC	X		40325135	R
Red	TCGAAGC	37		6	30039408	GGGCCGT		6	30147387	R
	TCCCGTG	37		6	31088208	CGGCCTC		6	31196187	F
	TCCCTCG	37		13	112927331	CTCTCCT		13	111975332	R
	GCATCTA	37		7	94953653	CGAGCCC		7	94791589	R
	CTCCCGC	37		4	141391254	CGGGGAT		4	141610704	R
	CTTACTT	37		6	30113978	TTCTGGA		6	30221957	R
	AGGCTCT	37		16	69478081	AAATTAG		16	68035582	R
	TGGATGG	37		10	14504379	CGGAGTA		10	14544385	R
Red	GCAGGGC	37		4	1398139	GGGTCGC		4	1388139	F
	GGATATT	37		4	20195367	AAAGTCT		4	19804465	R
	GAAGCCA	37		8	16908905	AGAAATA		8	16953276	F
	GCTCTGA	37		16	4506231	TGGGTGG		16	4446232	R
	CTGTGAG	37		3	14446645	GCCCCAT		3	14421649	R
	GGGTCCT	37		3	48256968	CGAGTTC		3	48231972	F
	TCATCCT	37		5	53927032	CGGCTGT		5	53962789	R
	CCCACCT	37		18	11948154	GGGTTTT		18	11938154	F
	TGAGAGA	37		3	170806983	CGAGCTG		3	172289677	F
Red	GAATATA	37		6	31650735	AACGAAA		6	31758714	R
	TGTGTCA	37		14	74704714	CGGCCTT		14	73774467	F
	GAGCCCT	37		6	66804631	GAGACTC		6	66861352	R
	CTATCTG	37		8	119152014	CGGGGTC		8	119221195	R
Grn	CGCGATC	37	X		77395088	TCTCCGC	X		77281744	F
	AATCATG	37		11	29207078	CACTGTG		11	29163654	R
	CAGCTGA	37		12	124831017	GGTGATG		12	123396970	R
Red	GTGACCC	37		17	79466438	CGTCCAG		17	77081033	R
	GTGGAAC	37		13	21680693	CGCAGCA		13	20578693	F
Red	GTTTGAC	37		17	693388	AACTTCT		17	640138	R
	ACAGAGT	37		7	47560215	CTGCCTC		7	47526740	F
Red	GTCCCTT	37		2	97505464	CGCGTTC		2	96869191	F
Red	CAGCAGC	37		5	180257795	GCAAATC		5	180190401	F
Red	AAGCAAC	37		17	34817706	CGGGATT		17	31891819	R
	AGATAAT	37		17	53573969	CGTCATC		17	50928968	R
	TCACTTC	37		18	34325827	GTCCAGC		18	32579825	F
	CGCAGGC	37		10	134672797	CGGCCCT		10	134522787	R
	AAGATTC	37		13	33825496	CTCTGAG		13	32723496	R
	TCAATTC	37		1	245843929	CGGCAGA		1	243910552	R
	TGGACGC	37		10	131665884	CGGAACA		10	131555874	R
Red	GGCCTTC	37		14	24780167	CGTGTGC		14	23850007	F
	CACAAAC	37		10	132364391	AATGAGA		10	132254381	F

Red	CCCTGCA	37	16	922132	CGGCAAC	16	862133	R
Red	GGGGCAC	37	X	18443723	CGAAACC	X	18353644	R
	AACATGT	37	7	134833299	CGATGCA	7	134483839	F
	GGTCCTT	37	19	54254388	TTGTTGG	19	58946200	F
Red	TATGATC	37	7	1332973	GCCCCCA	7	1299499	R
Red	CCTTTCC	37	21	47054539	CGCCGCA	21	45878967	R
Grn	CATTATT	37	2	71018354	TCCATTC	2	70871862	R
Red	GCCCTGT	37	20	43935283	CGTGCGC	20	43368697	R
	TAGAAAC	37	7	51539514	CGCTGCT	7	51507008	R
	CGAAATC	37	11	122727440	CGGCAGC	11	122232650	R
Red	CAACTCG	37	16	70794856	CGTGCAC	16	69352357	R
	CTATTAT	37	6	32451079	CGTTACA	6	32559057	F
	TGATACT	37	11	134585270	CGGAAA	11	134090480	F
	CAGTTTA	37	6	152126180	AAGGTAT	6	152167873	R
	GCAAGTC	37	1	2265881	CGGAGAC	1	2255741	F
Red	CTGGCTC	37	1	221055545	CTGCAGG	1	219122168	F
	TAATGCG	37	1	11917550	CGGTGAA	1	11840137	R
	TGCATGA	37	3	123838429	TGCCATT	3	125321119	R
	TCCCGTT	37	16	55365146	AAAAGTC	16	53922647	R
	AACAGCC	37	1	19210017	CGGGCCC	1	19082604	F
	GAGAAGC	37	16	28943019	CGGTCTC	16	28850520	F
Red	CCGAGGC	37	6	142409756	AAAGGAC	6	142451449	F
	GTCGGCT	37	5	415885	CGGGGTC	5	468885	R
Grn	ACACAAC	37	7	158533890	CAGCGCC	7	158226651	F
	GAGCGCA	37	Y	7142752	GAGTGCT	Y	7202752	F
	TTCTTGC	37	5	14342307	GGCCGGC	5	14395307	R
	TACCGCT	37	2	139660277	CGCAAGC	2	139376747	R
Red	TAGTTGA	37	6	152126080	TTTTAAA	6	152167773	F
	TCTGCTC	37	2	171680715	TTCACAA	2	171388961	F
	GAGTGTT	37	5	134490074	TGACTTC	5	134517973	F
Red	TGGTCGG	37	16	89036057	GCAAGAT	16	87563558	F
Red	GCTCAGT	37	10	133961825	CGTGCTT	10	133811815	R
	CCTGGTT	37	19	21860793	GTTCCTG	19	21652633	R
	AGGCATC	37	10	5004250	TACATAA	10	4994250	R
	TGTACTT	37	22	42537241	TCATGGG	22	40867185	R
	GCCCTCT	37	10	135040139	TTGCTTG	10	134890129	F
Grn	TCCCGTG	37	12	110906223	CCAAGCT	12	109390606	F
	GAAAGG	37	4	4587217	CGTGTAC	4	4638118	F
	GCTCTGT	37	12	7948517	ACTTAAA	12	7839784	F
	TGCCCAG	37	17	32909375	AAGAGCC	17	29933488	R
Grn	GCGGGCC	37	16	15489794	GCCGAGA	16	15397295	F
	AGTCCAC	37	5	1420305	TTCCAAC	5	1473305	R
	GCAGAGT	37	11	125552186	CGGGGGT	11	125057396	R

	AGCCGAC	37	17	5019840	CGCCCGC	17	4960564	R
	GCCATGT	37	9	140356830	AGAGGAT	9	139476651	F
	TTGGAGT	37	7	42896801	TTTTTGC	7	42863326	R
Red	CTCCCGG	37	X	105066526	CGGGGCA	X	104953182	F
Red	CTATGAT	37	16	80966860	CCGGGCT	16	79524361	R
	TTTCCTA	37	12	66050928	CGGTGAT	12	64337195	R
Red	GGAATTC	37	X	17755642	CGCGAGA	X	17665563	R
	ATGGCGT	37	1	31393915	GACTCTG	1	31166502	R
	TTAAAGG	37	4	146097432	CGGTACA	4	146316882	R
Grn	AGCCGCC	37	4	719908	CGCACCC	4	709908	R
	CAAAGTC	37	7	150485638	CGGCATC	7	150116571	R
	TCACCTT	37	5	33788976	TTCCCAT	5	33824733	R
	GGCCCGC	37	5	13986034	GTGCCAA	5	14039034	R
Red	GGGCCTT	37	4	147164858	CTCTGCT	4	147384308	F
	AATGAAT	37	2	71983542	TCTAGTT	2	71837050	F
Red	GATTTCC	37	20	61877875	CTGAATT	20	61348320	F
Grn	CCTGAGG	37	17	80899280	CAGAAGC	17	78492569	F
	TTCCACT	37	1	115397409	GAAATAC	1	115198932	R
Red	GAGCCAC	37	18	77246369	TTCTCTG	18	75347357	F
Red	GGCGCTC	37	16	88496476	CGTCGAT	16	87023977	R
Red	TGCAGGC	37	5	1868357	CGCGCTT	5	1921357	F
Grn	GGCTGAC	37	Y	22917087	AGGAACA	Y	21326475	R
	GTCATCT	37	5	42840698	CCAAGCC	5	42876455	R
	ACAGTCT	37	5	179588838	CGCTGGG	5	179521444	F
	GGCCAAC	37	5	52598132	AGAGTAC	5	52633889	F
	TTGATGA	37	7	94538894	GCTACAC	7	94376830	F
	CAAACAA	37	Y	6263841	CGCAAAC	Y	6323841	F
	ATTTCTC	37	X	101915091	ACCGGAA	X	101801747	R
	CTGGCTT	37	8	23712364	AACTGGC	8	23768309	R
	TGCTGGC	37	8	144702879	CCGTGTC	8	144774022	R
	GGTAGAC	37	11	118842413	GGATTGA	11	118347623	F
Red	GGCCTAA	37	3	105542204	CGCCCTT	3	107024894	R
	CATTCCA	37	6	901310	CGTGTTA	6	846310	R
	TAGGGGC	37	6	29942706	CGGGAGC	6	30050685	F
Grn	GGAGGTC	37	5	180028818	GGACGAC	5	179961424	R
	CATTAGC	37	13	99201496	CGATGTT	13	97999497	R
	TGGAACA	37	6	30114011	AGATCAC	6	30221990	F
Red	AGGACAA	37	1	9779309	CGCCTCC	1	9701896	R
	TGAAACC	37	17	8699116	TTTACTA	17	8639841	R
	GATCAAC	37	5	172216309	CGGGGCC	5	172148915	R
Red	GGCAGGC	37	5	71146876	CGCGACC	5	71182632	R
	GGTTCTC	37	5	140536320	CGAGGTC	5	140516504	F
	GGTTACT	37	7	30855293	AATTTGA	7	30821818	R

Red	TAGCATT	37	1	115397374	CGGGAA	1	115198897	F
Grn	TGCCGAG	37	10	121771388	AGCTCCG	10	121761378	R
	CCCGCCT	37	4	187810446	CCTGCCA	4	188047440	F
	GACTTTT	37	7	11568529	CGCTGGT	7	11535054	R
	AGGTAA	37	19	16302087	CGCTCTG	19	16163087	F
	TGAGATT	37	3	3073276	CGGGGGC	3	3048276	R
	GTCGTTC	37	19	4552673	CGGGGGC	19	4503673	F
	ACCTGTG	37	5	172347685	AGTGAAC	5	172280291	F
	GTAAGTA	37	5	25393894	CTGTGGG	5	25429651	R
	CCAGCCA	37	20	1914231	ACAGAA	20	1862231	F
Red	TGAAGAC	37	17	75315108	CTGTCTT	17	72826703	R
	TCAGAAC	37	12	312592	CGGGCCC	12	182853	R
	AATTCCA	37	2	19849829	CGGGATA	2	19713310	F
	CACCTGT	37	17	20687481	CAGCTAC	17	20628073	R
	AAAGGG	37	4	121569769	CGAGTAC	4	121789219	R
	GCCGAGC	37	7	3134592	CTGCTGG	7	3101118	R
	ATTAGGA	37	12	116814302	CGAGGTA	12	115298685	R
	ATAGGGT	37	12	28346883	GGACAA	12	28238150	F
	TGGGCAC	37	13	114161463	CGGGAG	13	113209464	R
	ATCTCCC	37	7	148977647	ACTGTGG	7	148608580	R
	GGCACTG	37	15	67417607	CGGGTGC	15	65204661	R
	AGTATTA	37	12	52108375	AAAGAAT	12	50394642	R
Red	CATCTTTC	37	6	32546614	CGGGAGC	6	32654592	F
	GCCGTAT	37	1	2107669	CGTGGCC	1	2097529	R
	TATCAGG	37	2	221529390	AGTCTGA	2	221237634	R
Red	ATGGGA	37	16	5482346	CGATGAC	16	5422347	R
Red	TCTGGGG	37	1	41303570	CGGGGAC	1	41076157	R
	AGATTGT	37	17	74073876	CGGCTGG	17	71585471	R
	ATGAATA	37	12	54414427	AGACTCA	12	52700694	R
	CGCGGAC	37	5	33938225	CGACCTG	5	33973982	F
Red	CGGTGAC	37	16	90114301	GCGGGGC	16	88641802	R
	GCTGTTC	37	2	232055508	ACCCAGT	2	231763752	F
	ATCATAG	37	6	32823566	CGGAAGC	6	32931544	R
	CCCCTAC	37	2	1480789	CAAGGTC	2	1459796	F
Red	GCCCCTC	37	16	88534585	CGCACCC	16	87062086	F
Red	GAGGGA	37	2	172953134	CGGCCCA	2	172661380	F
	CAGACAT	37	6	155568918	CATTTTG	6	155610610	R
	GCTAAGC	37	Y	15451782	AGTGGAC	Y	13961176	F
	ATGCCAT	37	4	69435601	AATTGGT	4	69118196	F
	GCAGGGC	37	10	27639156	CGCCACA	10	27679162	R
	TGAGCGC	37	8	119208486	CGCAAGC	8	119277667	R
Red	CGTGCTG	37	8	144809621	CGCGCCT	8	144881609	R
	TGGGTCA	37	21	46847898	TCCCTGC	21	45672326	R

Grn	CAGGGCC	37	8	142112622	TTCCCCA	8	142181804	R
Grn	TCATTGC	37	6	6614719	AGTGGGC	6	6559718	F
	TGGTTAT	37	13	77540409	CGGGTAT	13	76438410	F
	GGATACC	37	4	69435250	CGCTGGC	4	69117845	R
	CCTCTGG	37	11	69357823	TAGACCC	11	69067004	F
	GGCATGT	37	16	25598190	CTGCCGT	16	25505691	F
	AATGCAC	37	20	35198387	CACATAA	20	34631801	R
	CAGTGGC	37	6	30720311	CCTAACT	6	30828290	F
	ATGAGAC	37	6	32547019	CAATTTA	6	32654997	F
	GGCAGTC	37	7	111382084	TGAGACC	7	111169320	F
	CGCGGGC	37	11	316247	AAAAGGC	11	306247	R
	GGATGAC	37	3	15311021	CGGAGAC	3	15286025	F
	TTCTCGT	37	18	44557819	CCGATTC	18	42811817	F
	AACATTT	37	6	33038032	GCACTTA	6	33146010	R
	CCGGCGC	37	8	144659831	CCTGGTG	8	144730974	F
	GTGGCAC	37	4	162110754	CCTTCCG	4	162330204	F
	TTTTGGA	37	17	75084281	CGTGAAC	17	72595876	R
	TATTTTTC	37	1	201531514	CGGAAAT	1	199798137	R
Red	GGGCAAC	37	16	28270611	TGAGAAC	16	28178112	R
	GTTTTCT	37	4	90675036	CGGAGTT	4	90894059	R
	TTGTTAT	37	7	130005993	CGGGTGC	7	129793229	R
	GCGGGGC	37	3	71354056	CACACTC	3	71436746	R
	GCTCCGC	37	6	29911334	CGGGGCC	6	30019313	F
Grn	GACGCGC	37	6	29648901	GGACCGC	6	29756880	R
Red	ATTTCTTC	37	3	133502702	CGTCCAG	3	134985392	F
	ACCCCTT	37	12	54385436	CGCCCCC	12	52671703	R
Grn	TGGAGAC	37	14	102959357	GAAAGGC	14	102029110	R
	TGCAGCG	37	15	98196234	CGCCACC	15	95997238	R
	CCTTTATC	37	19	16606621	TCTTTATC	19	16467621	R
Grn	ATTCAAT	37	16	54315634	CCCAGTT	16	52873135	F
	ACATCTG	37	13	97909235	TTTCCGA	13	96707236	F
Red	TGCTGCT	37	16	2848577	GGGCTGC	16	2788578	R
	CGCCTGC	37	17	79961769	GGGAGTC	17	77555058	F
	TATCCAC	37	21	32255313	CGACACA	21	31177184	F
Red	AGGTCTC	37	7	96652222	CGGGGCC	7	96490158	F
	TGCTGAG	37	17	19620263	GACAGGC	17	19560855	R
	GTGTTGG	37	15	40731325	ACCTCCC	15	38518617	F
	CAGATTA	37	1	245951603	CAGAAAC	1	244018226	F
	CTCCGCA	37	17	78029642	CTACTCT	17	75644237	F
Grn	CATAATG	37	1	248753499	AATATAT	1	246820122	R
	CTGTGTG	37	7	131340667	CGGGAGC	7	130991207	R
	CACACTT	37	1	53595480	CCCTTGT	1	53368068	F
Red	CTGTGAG	37	1	248855364	AGAGGAC	1	246921987	F

	ATTTCCA	37	1	2981840	CGGGTAC	1	2971700	R
	TAGCAAA	37	7	102583144	CGGGTAC	7	102370380	R
	CTGACAT	37	14	31607371	TCAAATG	14	30677122	R
	GAACTGT	37	16	893139	CGGGCTC	16	833140	R
	CACTCTT	37	1	222790218	CGGGGGA	1	220856841	R
	AAGGGTT	37	16	55521135	CTGCATT	16	54078636	R
	GTGGTGT	37	6	139482238	GCTGAAC	6	139523931	F
	GTAAGCT	37	1	171807195	CGCGGTC	1	170073818	F
Grn	CTTCTTA	37	1	167393634	GCGTGCA	1	165660258	R
	TGTGATC	37	3	48335857	TCTTTGC	3	48310861	F
Grn	TCCTTGC	37	16	3242737	CGGCCCG	16	3182738	R
	ATCTTCT	37	11	101300838	CTACTTC	11	100806048	R
	AAGCCCC	37	12	125509502	CGCAGGC	12	124075455	R
	CTCACAG	37	Y	8150875	CGGTGGC	Y	8210875	F
	AGCGCCC	37	1	40599011	TTGGGGA	1	40371598	F
Red	ATCGTAC	37	16	12667646	CGGGAAA	16	12575147	R
	TGGGACC	37	16	58028859	CGGTGCT	16	56586360	R
	CTCATTG	37	16	16951653	TCAGTGA	16	16859154	R
Red	CCCGTCA	37	8	2078112	CGCTATA	8	2065519	F
	AAGGCCA	37	13	98605770	TAGCTCC	13	97403771	R
	CAAGCCC	37	19	18902527	CGGGTCT	19	18763527	F
	AATTGGA	37	6	26457353	CCAGACT	6	26565332	R
	AGACGTC	37	19	50862004	GGATCCA	19	55553816	R
Grn	AGTCAAC	37	3	61235829	GCTCTAC	3	61210869	R
	TAACCGC	37	1	2121449	GAATCCC	1	2111309	F
Red	TGTCTGT	37	17	56247036	CGTGGGT	17	53602035	F
	TCACTGG	37	7	11999601	CGTGAGT	7	11966126	F
	ATGACTG	37	16	19268548	TCATCCA	16	19176049	F
	CAACGTC	37	5	140530606	CGGCTCT	5	140510790	F
	ATGTTTG	37	4	15444984	CGCCACA	4	15054082	R
	TCGTGCC	37	22	24384573	GTGTCTG	22	22714573	F
Red	AACAAAC	37	4	151503501	CGACCCC	4	151722951	F
Grn	GCCGGTG	37	6	30079280	TGAGCAC	6	30187259	R
Grn	TAGAGAA	37	4	941054	CGCGGCC	4	931054	F
Red	TTGGGTG	37	1	16349079	AGCACTG	1	16221666	R
	GGTGACT	37	17	81047721	TTTGTAA	17	78641010	R
	GGGAGCT	37	8	982243	CCTTCCA	8	969650	R
	AGCAGGC	37	5	404713	CGGTTTG	5	457713	F
	TTGTTAA	37	5	112483149	TTCACCG	5	112511048	R
Red	TTTGTTT	37	19	47636543	CGGCTCA	19	52328383	F
Red	GACTCGG	37	2	864706	CGTGAGA	2	854706	R
	GACCTCC	37	7	128032651	CGGGCCC	7	127819887	R
Red	GGCCCGC	37	19	45905890	TGCTGTA	19	50597730	R

	TCCCAAA	37	1	182858007	CGGCAGT	1	181124630	R
	AAATTCT	37	14	23568017	CGGGCCT	14	22637857	R
	TACAGGC	37	Y	9237650	CATTCCA	Y	9297650	R
	GGCCCCC	37	1	32864238	CACTCTG	1	32636825	R
	TTCCATG	37	7	151290088	CCAGTAA	7	150921021	F
	ATGCAAA	37	11	76998832	CGGGTGA	11	76676480	F
Grn	CAACTTC	37	19	853054	GTCGGCC	19	804054	R
	GATGTGG	37	5	150689593	GCCAGAT	5	150669786	R
	TAGTTAC	37	8	28576644	CGGTTTT	8	28632563	F
Grn	CACCAGA	37	15	45492927	TGGCCGA	15	43280219	R
	GGCAGGA	37	16	27437900	GTGCACG	16	27345401	F
	GTGCAGC	37	15	86038622	CTCCAGA	15	83839626	R
	GATCTGG	37	2	241585355	CGACAGA	2	241234028	F
Grn	CCTGCAC	37	17	74878420	ACAAAAC	17	72390015	F
	GAGGCCC	37	11	65246590	CGGCCAC	11	65003166	F
Red	GACGCTG	37	13	112997541	TAGGCCC	13	112045542	R
	AGGGAGC	37	16	56710807	ACGGAAC	16	55268308	F
Red	TCTATGT	37	15	101266461	TCACGAG	15	99083984	F
	AGGGACT	37	10	13259274	TCTGCGT	10	13299280	R
	AAACCTT	37	4	3392274	AAAGCAC	4	3362072	R
	AGCTTGA	37	16	79692354	ATAGTAC	16	78249855	R
	ACTGCCT	37	6	4133029	GCTTCAT	6	4078028	R
	AAGCCAC	37	21	35320596	CGGCGCC	21	34242466	F
	GTGTTAA	37	12	68814447	TTTATCA	12	67100714	F
	GCTCAAG	37	6	150357289	CGGGTTG	6	150398982	F
Red	GGAGGAC	37	15	78632144	CGCAACC	15	76419199	R
Red	TGGCCCC	37	17	77086388	TACTGTT	17	74597983	R
	GCCCCGA	37	X	10126881	TGTCTAC	X	10086881	F
Red	GAGCAGA	37	16	89225495	CAGGGTC	16	87752996	F
Red	AAGCTTC	37	3	170077111	CGCACCC	3	171559805	R
	TGTTCAA	37	6	80787529	GCATGTA	6	80844248	R
	CTTAACC	37	7	158809128	CAAATCA	7	158501889	R
Red	CGGATGC	37	11	67383691	ATGGGGC	11	67140267	R
Red	ACAGCTT	37	17	56565641	CGCCGGC	17	53920640	F
Red	AGCAGCC	37	11	61322922	CGCCCGC	11	61079498	R
	CAGTATC	37	5	98111529	TCTTTAA	5	98139429	F
	TGCTTTA	37	10	134334241	CGGAAAA	10	134184231	R
Red	ACCCAAA	37	6	42672105	CAGCCTC	6	42780083	F
	AACGGCC	37	3	87036080	AATGCCT	3	87118770	R
	ACCTCAG	37	6	31780239	CCCATCT	6	31888218	F
	TTGTGAA	37	3	149191167	CGTGCTT	3	150673857	F
	ACTGCCA	37	5	112294315	TACACAG	5	112322214	F
Grn	ATGCTCT	37	19	310296	AGGGAGC	19	261296	F

	TCTGCCG	37	9	22005563	GCCTAAG	9	21995563	R
	ACTCTCA	37	7	105134734	ATAGTTT	7	104921970	F
	CCTGGTA	37	16	67605701	GCAAAA	16	66163202	F
	GGAGCCT	37	4	708242	ACGCCGT	4	698242	F
Red	ATTTCAG	37	16	858205	AACCAAC	16	798206	R
	AATCCAG	37	6	29981250	GGGCGCC	6	30089229	F
	TTTTCCA	37	11	34296462	AGCCAGC	11	34253038	R
Red	AGGCAAC	37	7	158155932	CGTGGCC	7	157848693	R
	GGCCGCC	37	13	109793152	CGCCCCT	13	108591153	F
	CTTTCTC	37	7	72868821	CGGCCTC	7	72506757	F
	TTTCTGC	37	12	102137391	CAAATAA	12	100661522	F
	TTGATTT	37	10	90013989	AGTCATA	10	90003969	F
	CATGATT	37	15	93978246	TGAGCCA	15	91779250	R
Grn	TGCCGCG	37	5	1594733	GCACGGC	5	1647733	R
Grn	GTTTTGA	37	7	18794174	ATGAATT	7	18760699	F
	GGCTGCT	37	19	2583601	CGCTCAG	19	2534601	F
	TTGGGAT	37	16	15858790	AGATATA	16	15766291	R
Red	GCCAATT	37	22	42394659	CGCCCCG	22	40724605	F
	TGACTTC	37	6	1684468	CGCCCCA	6	1629467	R
Red	GTGAAGA	37	3	133502540	CCTGGAG	3	134985230	F
	AACATCA	37	5	13745921	CTATTCT	5	13798921	R
	ACATGAT	37	2	112456811	CTCCACG	2	112173282	F
	GAGGCAC	37	6	165902024	ACTTGCA	6	165822014	R
	TCTGGGA	37	19	3135146	GTCTCTT	19	3086146	R
	CGTGTTA	37	3	8813493	CGGGAGC	3	8788493	R
	GAAGCTC	37	1	240078452	CGCAGTC	1	238145075	F
	ACAATGC	37	6	29829406	CGGCAAA	6	29937385	F
	TACCTCG	37	7	95026248	TGCTGCC	7	94864184	R
	TCGAAGC	37	1	156627572	TCTTGTG	1	154894196	R
Red	ATGCAGC	37	X	30671302	AGGGCG	X	30581223	F
	AGTGGTA	37	3	122684038	TGTCCAG	3	124166728	R
	AGCATAT	37	10	5588169	CGGGTTC	10	5578169	F
	GATAGGC	37	11	78131601	GTGGTCT	11	77809249	F
	GGCAGGC	37	16	88977278	GACAGTC	16	87504779	R
Red	GGGGCTC	37	6	30039130	CTGCGTA	6	30147109	F
	AGATCTG	37	5	168591808	GTCTCAA	5	168524386	R
Red	TCGCGGG	37	10	135273341	CGCCACG	10	135123331	F
	ATCAGGA	37	8	7079106	GTTGAAG	8	7066516	F
	TCGCGGC	37	6	1555572	CGCACCC	6	1500571	F
	TTTCTGA	37	4	77743172	CAGGCAC	4	77962196	F
	GCGTGGA	37	19	58868256	AGGTGCT	19	63560068	R
	GCAACCC	37	10	82295502	CGCAACA	10	82285482	R
	CTTGAAA	37	5	3959743	CGGTGAC	5	4012743	F

	TGCAGGC	37	17	738869	ACGCTTC	17	685619	R
	GGTCTAG	37	21	46075092	CGGCCAC	21	44899520	R
	GCGTGTA	37	7	157874020	GGTTCTC	7	157566781	F
Grn	CGCGTGC	37	6	32064206	CGGCCCC	6	32172184	F
	CTTGGCA	37	19	52218453	CGGCTGC	19	56910265	F
	GCTCCCT	37	3	111730545	CGGCTGG	3	113213235	R
	AGTATGT	37	Y	15015995	TTTCATT	Y	13525389	R
	CTTGGGA	37	5	35771584	CGAGTAC	5	35807341	F
	CGGGGTC	37	18	75886680	CGTGTGC	18	73987668	R
	CCTCTTG	37	1	25246922	AGCGTGT	1	25119509	F
Red	CCCATAG	37	7	117854304	GACGAGC	7	117641540	F
Grn	GGTTTCG	37	11	17249958	CGGCCCT	11	17206534	R
	ATTTTCT	37	7	30387954	CATTGGC	7	30354479	R
	GAACCAA	37	20	62330618	TCAGGGT	20	61801062	F
Grn	CGGGAGC	37	16	3345604	CGGCCCC	16	3285605	R
	CTCCATC	37	11	102048882	TGGTCTC	11	101554092	F
	GCACTGC	37	16	967350	CGCCCAC	16	907351	R
	AACCAAC	37	7	1245797	CGGGGCC	7	1212323	R
	AACACTC	37	2	110969853	AGAGCCC	2	110327142	R
Red	CTTGGCC	37	11	2193041	CGGAGCC	11	2149617	R
Red	GCGAAAC	37	6	31371073	CGCGACC	6	31479052	R
Red	GCGCCGG	37	X	8751402	CGCTTAC	X	8711402	F
Red	AGAAAAA	37	5	180593235	CGCGGAA	5	180525841	F
	ATATTTG	37	11	119806225	CGCTGGC	11	119311435	F
	ACCCAGC	37	5	41869963	CGCCCCC	5	41905720	R
	AGGAGTT	37	Y	15866447	GACTTCT	Y	14375841	F
	TCGCTAG	37	16	2007559	TGAAGCC	16	1947560	F
	TCTATCC	37	8	12549925	TACCCCT	8	12594296	R
Red	ACTCCGT	37	8	103540839	CGCGTGC	8	103610015	R
	TCGGCTC	37	13	28562900	GTTATAT	13	27460900	R
Red	CCGACGT	37	8	10555466	CGCCTTC	8	10592876	R
	ACTGGGA	37	13	113242997	TGCACTG	13	112290998	F
	TGGATTC	37	8	109235928	CGTAGGC	8	109305104	R
	TCAAGGC	37	7	105969911	CGTGGTT	7	105757147	R
Red	AGGAAGC	37	19	49249123	CGGCGCC	19	53940935	F
Red	CGCAGTC	37	2	54087178	CGCCTGC	2	53940682	F
	CTGTCTC	37	17	20687698	GGTATTT	17	20628290	F
	GCGGCAC	37	19	13112808	CAGCTGG	19	12973808	F
Grn	TTTCGCA	37	19	345312	CGCGTTC	19	296312	R
	GTGTTAG	37	10	6364079	TAAATTG	10	6404085	R
	GCAGCTA	37	2	128569178	TTGGTCG	2	128285648	F
	GCCTCAG	37	2	219181531	CGGAACT	2	218889775	R
	GTGGCCT	37	1	239979505	GAATCAC	1	238046128	F

	TGAGACT	37	16	31538718	ACATTTT	16	31446219	F
Red	GCGGCAC	37	X	53123489	CGCCCCG	X	53140214	R
	CCTTTAA	37	12	96188933	CGCCCAT	12	94713064	R
Red	TTGGCCC	37	7	65971372	CGCCGCA	7	65608807	F
Grn	CGCGCGC	37	19	57630524	TCCCCGG	19	62322336	F
Grn	CACACAC	37	6	169326603	CACAAGC	6	169068528	R
	TGGGGCA	37	Y	9214483	CGGGGCC	Y	9274483	R
	AATAATA	37	2	192446259	TATGCCT	2	192154504	F
	CACACGT	37	3	48694454	GCAGGGC	3	48669458	F
Red	GCAGCAC	37	4	141500606	CGCGGGC	4	141720056	F
Red	CCGTGTG	37	1	2425888	CGAGCAT	1	2415748	R
Red	CGGCAAC	37	6	116886276	TGTGAGC	6	116992969	R
	CGTGGGC	37	20	170641	GTTGTGT	20	118641	R
	TGTCTAT	37	3	153778467	CGCATAC	3	155261157	F
	GAGACAT	37	4	185381476	CGGGAAC	4	185618470	F
	AGCCTTA	37	4	53757661	CGAGGTC	4	53452418	F
	AGCCACC	37	Y	2708972	GTACTGC	Y	2768972	F
	TGGAGAC	37	19	5993794	CGGGACA	19	5944794	R
Red	GCAGCGA	37	19	38281047	CGCAAGC	19	42972887	R
	GGGCCAC	37	17	48266593	CGCTGTC	17	45621592	F
	CTTCCTT	37	19	46526489	GCTGGGC	19	51218329	R
	CACAGGT	37	6	134299594	CGTGCAA	6	134341287	R
	TCCTCAC	37	7	6653510	CGCAAGC	7	6620035	F
	GGGACAT	37	19	46526333	GAAGCAA	19	51218173	F
	CCGCAGC	37	13	112630296	CGGCCAC	13	111678297	R
	TGCACGT	37	17	81014091	CCATAGC	17	78607380	R
	TGTGACT	37	3	58319343	CGGGGCT	3	58294383	R
	TTCCAGC	37	10	3509758	CGCACTT	10	3499758	F
Grn	TCCCATC	37	16	88989212	TGCTGCC	16	87516713	F
Red	TCCTTCA	37	17	44898785	CGCAGGA	17	42253784	F
	AGTCTTT	37	17	13297839	GTACATG	17	13238564	R
Red	GCAGCGC	37	19	38886789	CGGCCTG	19	43578629	F
	GCTTAGA	37	11	132992485	CACATTC	11	132497695	R
Grn	AGAGACC	37	4	132896736	CTCTGTC	4	133116186	F
	AGGAAAA	37	11	95433344	AACTAAT	11	95072992	R
Grn	GTGAAGC	37	2	716366	CGGCAGT	2	706366	R
	CTACGCC	37	20	55043694	GAGTCAC	20	54477101	F
	GGGCTAC	37	5	85577255	CGCAGCT	5	85613011	R
	TGCCTGC	37	7	18329916	CGACTTT	7	18296441	R
Red	GATTCCT	37	12	1974122	CGGTCCT	12	1844383	R
	CAGGGCC	37	5	66462471	CCTTCCT	5	66498227	F
	GGAACCC	37	5	135416529	GGGTACT	5	135444428	F
	GCGAGGA	37	11	128321880	CGCCCAA	11	127827090	F

	TTACCTA	37	11	28650063	CGCCCCC	11	28606639	F
	AATTACC	37	5	34452378	CGGTGGT	5	34488135	R
Red	CGCTGCC	37	6	3293098	CGTGCTC	6	3238097	R
	AAAGGTC	37	11	1892392	CGGAGGA	11	1848968	F
Red	AGCCAGA	37	6	31275881	GCATCTG	6	31383860	R
Grn	CGGCTGT	37	12	2031417	TCAAGCT	12	1901678	F
	ACCCGAC	37	6	37521698	CGTATCT	6	37629676	R
Red	TTTTCCTC	37	5	51426	CGGCTCT	5	104426	F
Grn	CGTGAAT	37	7	51539583	TGGACGC	7	51507077	R
Red	CAGTGGC	37	4	41880319	CGCCAGC	4	41575076	R
Red	CAGCGCC	37	5	1594579	CGCCTCC	5	1647579	F
Red	TCGGCCG	37	6	42694995	AGACCAT	6	42802973	F
	AACGATA	37	2	27713044	CGATGAA	2	27566548	R
Red	TGCGAGC	37	7	156336675	AATCTCA	7	156029436	F
	TTGACCT	37	X	151999825	CGCAAGC	X	151750481	R
	GAACTGT	37	17	55110904	CGAGCAC	17	52465903	R
Red	CCCTGAC	37	19	55888156	CGGCCCC	19	60579968	R
Red	CTGGGCT	37	16	88053104	CGCCCTG	16	86610605	R
Red	CAGGGGC	37	6	2515318	CGGACGC	6	2460317	R
	TTGGTAC	37	2	86289505	ATTTGAA	2	86143016	R
Red	CGGGGCC	37	17	20744547	CGCACCC	17	20685139	F
Red	GCGGCAC	37	5	13810279	GTTCGTG	5	13863279	F
Red	TGCAAAC	37	22	18531447	CGTGCCG	22	16911447	F
	CGGAAGA	37	Y	22738029	CGGTTGA	Y	21147417	F
Grn	GAGGGTA	37	4	108641437	AGGAGGC	4	108860886	R
Red	TGCCCCT	37	3	11178745	ACTCCCA	3	11153745	R
Red	CTCTCTT	37	7	96652481	CGTAGGA	7	96490417	F
	CAGATGA	37	8	40235245	CGCCAAA	8	40354402	F
Red	ACTGGCT	37	6	156983304	CGTCCCA	6	157024996	F
Red	GGCGGAC	37	19	19748461	GAGCCTG	19	19609461	R
	TCTTTCT	37	8	33211598	ACCAAAC	8	33331140	F
	ACTGCAC	37	3	139060370	CGGAAAA	3	140543060	F
	AGCCACT	37	21	30517941	AAAGTAA	21	29439812	R
	TGCTTTT	37	10	45474339	TTCCCAG	10	44794345	R
	ATATTTC	37	3	99824269	ACTCAGT	3	101306959	R
	TAAGGAA	37	1	149979253	GTTAACT	1	148245877	R
Grn	GGGGCCA	37	5	346238	CGCAGGC	5	399238	R
	TGCAGCT	37	17	66573573	ATCTCCC	17	64085168	R
Grn	ACTTCTT	37	13	112062652	CGGCGGA	13	110860653	R
	CGCCACG	37	1	33772997	AGAAGTA	1	33545584	F
Red	AAGCATC	37	6	169689892	CGGCTTT	6	169431817	R
	AAAGTTC	37	12	109596187	CGATGAC	12	108080570	F
Red	TCTGGCC	37	17	77111749	CGGCATC	17	74623344	R

	CTCCTAT	37	13	21680560	CGTGCCG	13	20578560	F
	AGCAGTC	37	5	2388038	CGGCTGC	5	2441038	F
Grn	CGGGACC	37	1	41350183	CGCTGCT	1	41122770	F
	TGTCTTG	37	2	95788279	GGGTAGC	2	95152006	R
Grn	CGCCGCA	37	19	51607432	CGGGCCA	19	56299244	F
	TATTAAT	37	1	161572679	CGCATTC	1	159839303	R
Grn	GGGGCTC	37	3	10149979	CTGAACT	3	10124979	R
	GAAGTGA	37	5	168894603	GCTCCAG	5	168827181	R
	GGTTCCA	37	3	8631797	CGGCAGC	3	8606797	F
	TTTTCCA	37	10	85955302	CGGAAAC	10	85945282	F
	GGGACCT	37	15	89958944	CGTGGGC	15	87759948	F
	ATAATTA	37	6	114515500	CGAACTG	6	114622193	F
	AGAGAA	37	17	13941263	TCAGTGA	17	13881988	R
	TCTGCTA	37	17	8263420	CGCCAAA	17	8204145	F
	CTCATTT	37	16	7917211	TAGGCTG	16	7857212	R
	ATTAGTA	37	8	126649807	GCATTCT	8	126718989	F
Red	CCTGGTC	37	5	415575	CGGCCCC	5	468575	R
Red	GCAGTGA	37	11	2584917	TAATCTT	11	2541493	F
	ATGTTAA	37	1	7462176	CGTCAAA	1	7384763	R
Red	GCAGCTG	37	16	420230	CGCCAGC	16	360231	R
	CTAATGC	37	13	31455173	CGGAGAC	13	30353173	F
Red	GACACCG	37	17	80297325	CGGCCAC	17	77890614	F
	GTGTGTG	37	1	1111095	CGCAGGC	1	1100958	R
	CAGGCAC	37	7	27211117	CGCCAAC	7	27177642	F
	TGCACTG	37	5	106801945	CGGCTCA	5	106829844	F
	GGGTCCA	37	1	248100614	CTGCCCT	1	246167237	F
	ATACAAG	37	11	132946455	CGCCGCT	11	132451665	R
	GTCTCCA	37	5	87661076	CGGGTAC	5	87696832	R
	CCCAACA	37	17	7960424	TCCTTGA	17	7901149	R
	AGAAGG	37	2	77235218	TAAACCA	2	77088726	R
	TGCTGTG	37	6	32634009	GGAGAA	6	32741987	R
	GTGCTGA	37	11	3535099	CGTCTTC	11	3491675	F
	AAGACA	37	6	40323935	TATTGTT	6	40431913	R
	GTCAACT	37	10	133036065	GAACACC	10	132926055	F
	AATCTCT	37	3	168308798	CGGCCTT	3	169791492	R
	AGTATGA	37	2	183321813	CGTGTAC	2	183030058	R
	AACAGAC	37	5	140589751	CCAGCAC	5	140569935	F
	CATGATG	37	4	183062576	TTGAGGC	4	183299570	F
	AAAATAA	37	7	126866923	TCACATC	7	126654159	R
	GCAAAAC	37	19	2525459	ACTATGT	19	2476459	F
Red	TCCCGCC	37	X	118987153	GACAGAC	X	118871181	F
	AAACAG	37	6	130747460	GCCCACT	6	130789153	R
	GCCTGGC	37	3	11010256	CGCCCTG	3	10985256	F

	AAACGA	37	X	70752659	CGGATA	X	70669384	R
	TATATGG	37	1	95167783	TACTGTT	1	94940371	R
	CACTTAG	37	3	8704494	TGTCATT	3	8679494	R
	TCAGTCC	37	20	44657115	CGCTGGG	20	44090522	F
Grn	AAACAG	37	7	158110068	CAGGAA	7	157802829	R
	GCCCCCA	37	16	34404054	CGCCAA	16	34261555	F
	GCTCAGT	37	20	52199594	CGAGGC	20	51633001	R
	CAAATGT	37	7	84177905	CCTACCA	7	84015841	F
	TGTCCTG	37	5	103849273	CGGGCA	5	103877172	F
Red	AGCAGG	37	16	85202191	ACTGTCC	16	83759692	R
	GGAGGC	37	8	1365175	CGGGGA	8	1352582	R
	AACTTTG	37	8	95113521	CGTGTGA	8	95182697	F
	TGATGAC	37	6	32610735	CGCCATC	6	32718713	F
	TATATTA	37	3	44802549	CGGAGG	3	44777553	R
	CAAGGA	37	12	115117551	CCAGGG	12	113601934	F
Grn	ACAGGC	37	16	1709722	ACGGCA	16	1649723	F
Grn	TCCTCGG	37	16	4462122	CGGGGT	16	4402123	R
	AACAAG	37	2	12147206	GCAGAA	2	12064657	R
	CCTCTGG	37	16	3142911	CGGCAG	16	3082912	F
Grn	TGCCACG	37	1	228246780	TCGGGCA	1	226313403	R
	TTTCCAT	37	5	1245902	TCCAAGT	5	1298902	R
	AATGGAC	37	16	10837135	CGGGAC	16	10744636	F
	AGTCCTG	37	17	13927712	TTACCAG	17	13868437	F
	TTGAACC	37	10	61596106	CGTCTGT	10	61266112	R
	GCATTT	37	12	123757860	CGGTGAC	12	122323813	R
Grn	CACACA	37	5	346247	ATGAATT	5	399247	F
	GCTGTCT	37	15	96890598	CGCCCCT	15	94691602	R
Red	AGAAAA	37	16	936993	CTTCTTA	16	876994	R
	AGAGGA	37	8	48675911	CGCATTG	8	48838464	R
Grn	TCAGTCC	37	8	48676054	GACCCA	8	48838607	R
	GTTTGGT	37	5	43487508	CGGGAA	5	43523265	F
	TCTGTAA	37	3	164659583	TGAAACT	3	166142277	F
	CCAACA	37	12	69769552	AACCCCG	12	68055819	R
Grn	TAGGTGC	37	20	2361461	CAGGAT	20	2309461	R
	CAAAATA	37	1	79594960	CGTGCTG	1	79367548	F
Red	TACCTTG	37	16	31439393	CGGGCCA	16	31346894	R
	CTTCTGC	37	X	119133700	TCCCTCT	X	119017728	F
	GAGCTTT	37	4	40675171	CGTGGGT	4	40369928	F
Red	GATGGTT	37	8	103750904	CGGGCG	8	103820080	R
Red	GGTGGA	37	5	140625848	CGCCAAT	5	140606032	F
	GAGGCC	37	11	95962058	CGCGTGA	11	95601706	R
	GAGTGTT	37	1	221070193	TGGTAAA	1	219136816	F
	CCTGGCC	37	16	10922178	CGGGGA	16	10829679	R

	TGGCTAA	37	X	138525808	CTCCAAA	X	138353474	F
	CCGGGAA	37	1	17004834	CGCCTCT	1	16877421	F
	AACCTAC	37	12	14926986	TAGTACG	12	14818253	R
	GCTGTCT	37	13	111989685	TCCTATA	13	110787686	F
	AAGTATC	37	20	61455862	GCCAGGT	20	60926307	R
	GTAGTCT	37	1	211926526	TAGGAGC	1	209993149	R
	TGCCTAA	37	8	1914991	CCGGAAC	8	1902398	R
	GCACACA	37	20	55665224	CGCAGGA	20	55098631	F
Red	AGGCCAC	37	6	106434429	CGGTCCG	6	106541122	R
Red	GCGCTTC	37	6	29856353	CGAGGAC	6	29964332	F
	ACACAAC	37	14	100016312	TGCCCGT	14	99086065	R
	AGATCCT	37	15	90963532	CGGTAAC	15	88764536	F
	GAAGGGC	37	1	25734099	TGTTTGT	1	25606686	F
	AGAGATC	37	6	52217264	GTTTCAC	6	52325223	F
	CCTCTCT	37	12	19167591	CGTGGCA	12	19058858	F
	AGCACGC	37	16	49518414	GCCCTTC	16	48075915	R
Grn	TGTGTGT	37	1	94560697	CGCAAGT	1	94333285	R
Red	CCTCGTT	37	19	384251	CGGGCGC	19	335251	F
	CCCATCA	37	11	5279386	CGCACAC	11	5235962	F
	GGTGGGA	37	17	695428	GGACCTG	17	642178	F
	CACTTAT	37	6	128530306	CAAGTTT	6	128571999	R
	TACTTTG	37	2	230664097	CTTGGCC	2	230372341	R
	AGTTTGC	37	14	52347968	CAGCACA	14	51417718	R
	GGAGTCT	37	14	73075591	CGCATGC	14	72145344	R
Red	AGCACCG	37	17	1546403	CGCCCCG	17	1493153	F
	TCTCTTC	37	1	147806668	CGGGTTT	1	146273292	R
	GATTCAT	37	7	98438683	GGCATTC	7	98276619	F
Grn	GCTGATC	37	6	30039403	GCTTGGG	6	30147382	R
	CAAGCCT	37	12	124585152	CGGCCAT	12	123151105	F
Red	CGGAGCC	37	19	51190179	CGCGCCC	19	55881991	R
	CCTAGAC	37	X	148556545	CGTGATG	X	148364449	F
	GAACCAA	37	3	184528162	GCTAAGC	3	186010856	F
Red	CAGCGCT	37	6	28698008	CGAGAGC	6	28805987	R
	AGAGCAC	37	7	101208183	CGCCCCC	7	100994903	R
Red	TGGCTGC	37	6	29692035	CGGCAAC	6	29800014	F
	CCAACAT	37	7	57324701	CGCCATT	7	57328643	R
	CCTGGGG	37	14	69430369	AACTCAT	14	68500122	F
	AATGGAC	37	17	30770961	CGCCCAT	17	27795074	R
	AGTCAAT	37	6	32632000	AGGTACC	6	32739978	R
	CTGGATT	37	12	46009735	TGCATAC	12	44296002	R
Red	GAGCTGA	37	6	106434131	CGCAACC	6	106540824	R
	TGGGCCC	37	12	113535362	GTGGAAC	12	112019745	R
Red	CCGTCGA	37	2	176936436	CGCCGCC	2	176644682	R

	CGGGGCA	37	X	14048281	AAAAGTT	X	13958202	F
	TTCCACG	37	10	126686762	GCTGGGA	10	126676752	F
Red	CGCTCGC	37	14	73958573	GACAGAC	14	73028326	F
	TTCATGA	37	11	70266139	CCAACTT	11	69943787	R
	CTGCGCA	37	19	21265421	CGCCGCT	19	21057261	R
Red	CCGCGTG	37	16	85242446	CGCCAAC	16	83799947	R
	CTGGTCT	37	14	61933059	CGCCATA	14	61002812	R
Red	AGAGCAC	37	7	96650096	CTAATAG	7	96488032	R
	CATATTT	37	1	94587905	CGGTCCC	1	94360493	F
Red	GAACAGC	37	2	231715028	CGTTGGG	2	231423272	R
Grn	GGCAGTC	37	1	242220475	ACCGGAT	1	240287098	R
	AAATTAC	37	1	209877970	CGGGTAC	1	207944593	F
	GGGTTGA	37	10	127560294	TAAAGCT	10	127550284	F
	CCCCACA	37	6	30772293	CGCCACT	6	30880272	F
	GAGTAGA	37	6	28483411	CCTTGCA	6	28591390	R
	TGCTCTC	37	17	53847116	GCTAGAC	17	51202115	R
Red	AAGCCTG	37	7	156309358	ACTGCGA	7	156002119	F
	TCTAATA	37	6	101306732	CGTATTT	6	101413453	R
	GACTGTT	37	17	29645782	AGTAGAT	17	26669908	F
	ACAACTC	37	2	216593517	AGAACAA	2	216301762	R
	ACCTGAT	37	2	7342228	CGGGGAC	2	7259679	R
	TCCTGGC	37	Y	20501241	CGGGTCA	Y	18960629	F
	AGAACAT	37	2	224564400	ACACCAT	2	224272644	F
	CAAGAAT	37	6	32607224	CGAAGGC	6	32715202	R
	ATCCTTT	37	16	11603344	CGAGTGA	16	11510845	F
	TCATCCT	37	16	11267859	TTGCATG	16	11175360	R
Red	ATTGTCT	37	1	16490791	AGACTAC	1	16363378	F
	ATTTTTC	37	3	49538552	AGAGCAT	3	49513556	R
	CTAGCAC	37	21	47716443	CGCCCTG	21	46540871	R
	GAGTCAC	37	12	113215623	CAGCACA	12	111700006	R
	AGCGGTC	37	9	123605666	CTTCGTC	9	122645487	F
	GCATAGT	37	15	85552114	TGCCTGG	15	83353118	F
	AGGTGCA	37	16	89167018	CGTGGCC	16	87694519	R
	CGGGGCC	37	8	128427306	CGGGGGC	8	128496488	R
	CCGGGCA	37	5	499552	CGGCACC	5	552552	F
	TAAATAG	37	4	184256627	CGGGAAA	4	184493621	F
Red	CACACCA	37	16	78539954	CGGATTG	16	77097455	F
	CCCTGGG	37	4	187581093	CGCTGGG	4	187818087	F
Red	GCTTGTT	37	17	72565887	CTCGTCT	17	70077482	R
	GCAAAGT	37	15	98514710	ACTCCCA	15	96315714	F
	CAATGAT	37	6	82459960	TGAATGT	6	82516679	F
	GAGAGGT	37	3	47388736	CGGATCT	3	47363740	R
Red	GGTCTTT	37	19	3191030	GCAACTC	19	3142030	R

	CTTTCCT	37	2	36825704	CGGTACC	2	36679208	R
	CGGGTCG	37	2	71944165	GCTATAT	2	71797673	R
	CTAGCAC	37	16	47882395	CGCATAT	16	46439896	R
Red	CCGGGAC	37	17	78935269	AGCCTGG	17	76549864	R
	TGGAATT	37	16	87712353	CGTTGGA	16	86269854	R
	CTGTGAA	37	5	150169781	CGGGGCT	5	150149974	R
Grn	GGCGGCC	37	19	39056084	TGGGGTC	19	43747924	F
	TTGACGT	37	6	33092130	CGGGATC	6	33200108	R
	TGCCCGC	37	17	78735324	GAAATG	17	76349919	F
	TGAATCT	37	6	149097976	CGGATCC	6	149139669	R
	ATCCTTG	37	2	181337276	ATGTTTT	2	181045521	R
	TCTTTGT	37	8	97747124	GGCTCTA	8	97816300	R
	GAGATG	37	8	55060709	CGGCTAC	8	55223262	F
	AATGCTC	37	5	143397012	ATCCATG	5	143377205	F
Red	CCACCAT	37	10	100175082	CGGGAGT	10	100165072	F
	CAGCCAA	37	2	241776193	CGGGCTA	2	241424866	R
	GGGAGG	37	12	2339614	TCAGGTT	12	2209875	F
	AAGCCTT	37	12	4699232	CGAGAA	12	4569493	F
	TCATAAT	37	11	18414888	TCATACT	11	18371464	F
	GCCTGGG	37	16	72096944	CGGGAA	16	70654445	F
	GGTGCCC	37	17	37024020	AGGTGG	17	34277546	F
Red	TATTTGG	37	6	33288332	TCTTCCC	6	33396310	F
Red	GGTCTCC	37	X	149530886	CGCTGGC	X	149281544	F
	ATGTTCC	37	13	22458760	GATGCTA	13	21356760	R
	ATGTTCT	37	3	64725835	AGGTTAG	3	64700875	F
	TTTTGGG	37	3	71545533	ATGGCTG	3	71628223	F
	AGGAGA	37	3	64670013	CGGGCG	3	64645053	F
Red	ACTTTAT	37	7	155817478	CGGGAAT	7	155510239	R
Red	TCTTCTG	37	22	18985632	GGGCAAC	22	17365632	R
Grn	TTTGCTT	37	4	154605468	CGTACCT	4	154824918	F
	CACGCAC	37	7	123459295	CGTGTTC	7	123246531	F
Red	AAGTGAC	37	7	229695	CGGCACC	7	324778	R
	CAGTGTA	37	11	114165661	ATTGACA	11	113670871	R
	AGTTGTG	37	18	77134251	TGGTAAA	18	75235239	R
Grn	ACGCGAC	37	17	38024394	AAAAGTT	17	35277920	R
Red	AGCGGGT	37	7	158790006	CGCTTCC	7	158482767	F
	TGGCGTT	37	16	85242503	CGGCAAA	16	83800004	R
	GAGGACT	37	16	48157560	GGAAAAT	16	46715061	F
	ACCCAAA	37	20	62225654	CGCCCTG	20	61696098	R
	CGAGGAA	37	12	131030259	CGCCGTG	12	129596212	F
	TTTGATG	37	5	89352028	CAGGACA	5	89387784	F
	AACCACC	37	1	72190606	CGAGCCT	1	71963194	R
	CCATCAA	37	X	9755283	CTCGGGT	X	9715283	F

Grn	TCGGATC	37	X	56590113	CGGCCTA	X	56606838	F
	CAGAGTA	37	5	178455197	CGCAGCC	5	178387803	R
	CCACTTC	37	1	153521909	GAGTCAC	1	151788533	F
	CAGAGTT	37	7	157628140	CGGGTTC	7	157320901	R
	GAAGCAC	37	5	175241829	CGGCTGT	5	175174435	R
	AGAGAGC	37	16	85196350	CGAGTCC	16	83753851	R
	GCCTGTG	37	13	112630399	GGGAGAC	13	111678400	R
	ATTTTCA	37	5	146716604	TTTACAA	5	146696797	F
	TACCATT	37	6	17866039	CGGACAC	6	17974018	F
Grn	GGAGACC	37	16	12618726	CGGCCCA	16	12526227	R
Grn	GAGGCTC	37	7	2962240	GGCGAGC	7	2928766	R
	ACAAGAA	37	8	102550720	CGCCAGA	8	102619896	R
	CATAAAA	37	11	193112	GACTCAC	11	183112	F
	GGCTGCT	37	21	45336903	CGGGCTC	21	44161331	R
	AGGAGGT	37	12	125223650	TCATGCC	12	123789603	F
	CAGCTGC	37	4	1047097	GCTGCAT	4	1037097	F
	GCCGTTT	37	X	133118344	CGGACAA	X	132946010	R
	AGTCAGT	37	6	3473380	TAAAAAC	6	3418379	R
	TCATCAG	37	4	183935060	ACAGAGC	4	184172054	R
	ATCCCCT	37	11	107583377	CGTGGAT	11	107088587	F
	ATGGGAC	37	20	32857151	CGAGCAC	20	32320812	R
Red	GACCAGC	37	21	45336673	CGCACAC	21	44161101	F
	GTCACTC	37	19	24269890	TCAGCCT	19	24061730	R
	CCCATGA	37	15	25442386	ATGGACT	15	22993479	F
	GCCTCAG	37	15	92058845	CGGAGGT	15	89859849	R
	ACCATAA	37	15	60644157	CGGTGAC	15	58431449	F
Grn	CCCCTCA	37	16	3016378	CGGCCCC	16	2956379	F
	GTGAGTC	37	15	33571230	CGGCTTC	15	31358522	R
Grn	TTAACAC	37	4	183062729	TTAATAC	4	183299723	F
	TGGTGGG	37	10	102111107	CGGGCAA	10	102101097	R
	TACTACC	37	4	183063534	CGGGCTG	4	183300528	F
	TACTACG	37	6	168815615	CGCCAGC	6	168558464	R
	GCTTGGA	37	14	50490901	GCTGCTC	14	49560651	F
Grn	TCCTGCA	37	1	211652688	TTAGACG	1	209719311	F
	TCCTGTT	37	3	159590447	GTAGTCT	3	161073141	F
	GGAAGGC	37	1	39212920	CCGTGGC	1	38985507	R
	TTCTGTG	37	2	71723690	TGGGCAC	2	71577198	R
	ATATTGA	37	Y	2823782	AAAAAAT	Y	2883782	F
	TCTTGAC	37	5	131561058	TTGGGAG	5	131588957	F
Red	CTGCGGG	37	12	124907162	CGGCTGC	12	123473115	R
	GCATATT	37	14	63121958	CGCATAT	14	62191711	R
	TGGAATT	37	2	108745580	CGGCTCT	2	108112012	R
	GTAGGGC	37	1	35586503	CGCCTGG	1	35359090	R

	TGGCAG	37	3	48466751	CGCCTGC	3	48441755	R
	TGGAATT	37	7	22764397	CGCAAG	7	22730922	F
	GAGGAG	37	1	230250326	GGTGGCA	1	228316949	F
	AAAATGA	37	20	24929822	CGCCCCT	20	24877822	F
	AGCATCT	37	10	131930596	CGATTGG	10	131820586	R
Red	GGCATTA	37	Y	15016590	TTACTTC	Y	13525984	F
	CCAGATA	37	6	4610575	TTAGCCT	6	4555574	R
	GACTGTA	37	3	124861521	CGGCATG	3	126344211	F
	TCCAAAC	37	5	135329478	CGCTGGT	5	135357377	R
	AGGCTGT	37	4	6665095	TTGGGAC	4	6715996	R
	TAGTATA	37	7	157913147	ACCATGA	7	157605908	R
Red	TGGGTGT	37	12	95943114	CGCCCTT	12	94467245	R
	GAGACA	37	15	89595811	CCCAATC	15	87396815	F
	GGGGCG	37	4	2366831	GCTGAA	4	2336629	R
Grn	GGGCTAC	37	20	57463991	TCACCGA	20	56897386	R
	AGTCTTC	37	13	103532304	CTTCCGG	13	102330305	R
Red	GTAAAG	37	1	24968182	AGTCAA	1	24840769	R
Grn	TATCAGG	37	6	28584076	CGCGGC	6	28692055	F
	AATATTC	37	5	10226648	ACAGATA	5	10279648	R
	TGGCACA	37	17	75315244	CGGGTTT	17	72826839	F
	TTTTCAA	37	5	77808947	CGGGTGA	5	77844703	F
	GGGAGA	37	15	102025217	CCAGGAT	15	99842740	R
	TGATCCG	37	12	111620313	TCAGAGC	12	110104696	R
	GCCCAA	37	16	87248612	CGCCTTG	16	85806113	F
	ATTTATA	37	10	65460017	GCCAGCC	10	65130023	F
Grn	ACCCACA	37	2	1886105	GCTGACT	2	1865112	F
	GATTATT	37	4	90481402	TTCTAGT	4	90700425	F
Red	TACAATA	37	13	112063695	CGCGGCA	13	110861696	R
Red	CGCACG	37	8	145728526	CGGCCCC	8	145699334	R
	TGCACTC	37	16	4017270	CAAGCA	16	3957271	F
	TTACACA	37	X	7892382	CGGTTCT	X	7852382	R
	AACAAT	37	2	118614378	GGGCAG	2	118330848	F
Red	CTATCGC	37	10	82296072	CGGTCCT	10	82286052	F
Red	TTGTGGC	37	2	112898400	CGGCGA	2	112614871	F
	TGACAG	37	15	24346942	AGGGCG	15	21898035	R
	GCATTTG	37	1	44300942	CGGTCGC	1	44073529	R
	CTTTGGT	37	14	76289228	TAGGGAA	14	75358981	F
	TGGCCTC	37	10	131529435	GAGCTCT	10	131419425	R
Grn	TGACCCC	37	11	8931473	AGCGTGT	11	8888049	R
	CTGTGTG	37	14	32926900	GGCGCTG	14	31996651	R
Red	CGCCGCC	37	X	30907439	AGCTTGC	X	30817360	F
	ACTCCTT	37	2	65085243	CGGGAAA	2	64938747	R
Grn	GCTGAG	37	1	207669922	ACCCGG	1	205736545	R

Red	GAGGCCT	37	7	1952561	CGGCCGC	7	1919087	F
Red	CCCAACC	37	21	15352983	CGCCGCT	21	14274854	F
	GAGCCAC	37	16	1939295	CGGTGGC	16	1879296	F
	TATTCAA	37	4	16255438	CGGTGAC	4	15864536	R
Red	CCCCACG	37	7	36194394	CGGAGA	7	36160919	F
	ATCAACA	37	10	91453851	TCAAGGT	10	91443831	R
	CCCTTCC	37	12	53822143	CCTTCAT	12	52108410	F
	AAGAGAC	37	10	729846	ACTGGAC	10	719846	F
Red	GGTTGCG	37	2	48844971	CGCAGTG	2	48698475	R
	TTCCTTC	37	Y	8681688	CGGTGAT	Y	8741688	R
	TTGTAAA	37	2	114036953	GGAGGG	2	113753423	R
	TGGGTAT	37	7	27475596	AAGTGA	7	27442121	F
	ACGCAGC	37	4	152148822	TTTAAAT	4	152368272	R
	CCTCTCC	37	8	142139187	CGGGGCC	8	142208369	R
Grn	ATGTTCC	37	Y	21729144	CCAATCG	Y	20188532	F
	AACTCTC	37	2	100908637	CGCCCTG	2	100275069	F
Red	GGCCTGG	37	12	107348855	CGCGGAT	12	105872985	R
	TCTCCTC	37	7	25991722	CGGGCAC	7	25958247	F
	CAGCACC	37	10	121837310	CGGGAAT	10	121827300	R
	CAAATAA	37	8	16637442	AATTATA	8	16681813	F
	CTGGATC	37	11	118869922	CGAAGA	11	118375132	F
	CAGCCGA	37	8	12458558	CGGAGTT	8	12502929	F
	CCCAACT	37	1	2844356	AGTGGAT	1	2834216	R
	CAACCAC	37	14	25591076	CGGGAGC	14	24660916	F
	CCTTCCT	37	11	68550390	TGACTCC	11	68306966	R
	TGCTTTT	37	12	18845488	CGAGAGT	12	18736755	F
	ATCTGAA	37	10	107733752	CGGGGAC	10	107723742	R
Grn	GACAAA	37	12	3563899	AATAGGC	12	3434160	F
	CATACTC	37	12	19925091	TAATACA	12	19816358	R
	CAGCACC	37	6	32526414	CGCAGGC	6	32634392	R
	AGTGGG	37	4	79052724	GCACAA	4	79271748	F
	GTGAGCC	37	17	20203992	TCCTGGG	17	20144584	R
Red	CTGGGAC	37	16	88472541	GGGCGGT	16	87000042	F
	CTCCTGG	37	3	12197630	GCATGGC	3	12172630	R
	GGTCGGT	37	1	113067124	CCCGTAT	1	112868647	F
	TGACGTA	37	6	31635971	CGCATTT	6	31743950	R
	GGGAGAC	37	1	111740345	AGTTGTA	1	111541868	R
	CTGCCAC	37	7	624424	GGCTGGC	7	590950	F
	TCACTGT	37	14	69134577	CTGCCTT	14	68204330	F
Grn	ATGAAAT	37	13	111935412	GGCAGAC	13	110733413	F
Grn	CGCCCAA	37	19	57630596	CGGCGCC	19	62322408	F
	GACCTCG	37	12	101603453	GGTGCCC	12	100127584	R
	AACTCCA	37	19	45187222	CGGGCCT	19	49879062	F

	GCCACAC	37	1	43473978	ATGGCCC	1	43246565	F
	TCCTGCT	37	8	53235234	AGAGAG	8	53397787	R
Red	ATCTGAA	37	22	50482250	CGGTTTT	22	48824377	R
	TCGGGGC	37	14	92303710	AGACTTC	14	91373463	F
	TGTGCCT	37	20	4721766	CGAAGG	20	4669766	R
	AAAATTC	37	5	177941617	ACTTGGT	5	177874223	R
	GGGAGTC	37	6	72004311	ACTGTGT	6	72061032	R
Red	CCCTGCC	37	1	228756711	CGGCCCG	1	226823334	R
	GTCAGGA	37	15	57825722	AGGATGA	15	55613014	F
	TCAGTTC	37	15	42302705	CGGTGAC	15	40089997	F
	AGCTGAC	37	3	171002363	CGGCAGC	3	172485057	R
	TGCGCCT	37	7	138349158	GTTAGGC	7	137999698	F
Red	CACCGGA	37	14	24780691	CGGCCTT	14	23850531	F
	CAGCAGC	37	8	2034467	AAATTGG	8	2021874	R
Red	CACAGAC	37	5	126409007	GCCGCGT	5	126436906	F
	CCATGGT	37	16	88052956	CGAAGAT	16	86610457	F
	CCGTGGC	37	14	92303685	CGCCAAC	14	91373438	F
Grn	CAATGGC	37	5	25190672	CGGCCAA	5	25226429	F
Grn	AGAGCTT	37	5	140215762	GCGGTCT	5	140195946	R
	CTCTGGG	37	8	23775498	TATTTGA	8	23831443	R
Red	GGGGTCT	37	Y	2802975	CGCCTCT	Y	2862975	R
	TTGTGAA	37	7	26183581	TATCTCC	7	26150106	F
Red	TTATATG	37	7	48129814	AGTCACC	7	48096339	F
	TCATAAA	37	6	32607174	CGGGGCT	6	32715152	F
	ATCTAGC	37	1	60171660	CGGCCAC	1	59944248	F
	GGTTGTT	37	12	47618577	GGGATGT	12	45904844	R
	TATTAAA	37	2	168673805	CGTATAA	2	168382051	F
	CACGGAA	37	16	89647782	AACCAGC	16	88175283	F
	CTCACAC	37	12	6585594	CTTTTTC	12	6455855	R
	GAGAAGA	37	16	88497293	CGGGGTT	16	87024794	R
	GTGGACC	37	1	244920686	CGGTGCA	1	242987309	R
	AAGGACT	37	1	88026790	ATAATGC	1	87799378	R
Red	TCCGTGG	37	13	102105129	CGGTGAA	13	100903130	F
	CCCGAGC	37	17	1096705	CAGTATT	17	1043455	R
	TGGGACA	37	4	83542146	GTGATGC	4	83761170	R
Red	GGATCGC	37	Y	20508275	AGCCCTT	Y	18967663	F
	TGTCTTT	37	8	39770525	TACTCAC	8	39889682	R
	GGTTGGA	37	2	235766844	TCACAGA	2	235431583	F
Red	CGCCGCC	37	X	20009123	GGTCCCG	X	19919044	F
	GGAATTC	37	2	125183768	CGCATCC	2	124900238	F
	ATCATTA	37	13	33455187	TGGCTGA	13	32353187	R
	AGTGAAT	37	3	271185	CGCATTC	3	246185	R
Grn	GGCGCGT	37	X	30327615	CGCCCCC	X	30237536	R

Red	TTGCTGG	37	10	1772472	CGGATCT	10	1762472	R
	CTTTCTG	37	14	105620358	ACTTGGG	14	104691403	R
	CCTGGAC	37	4	187884368	CCTCAGC	4	188121362	F
Red	CCCACCT	37	X	70474613	GGTCCCG	X	70391338	R
	AGTCATC	37	11	102576374	CGGAAA	11	102081584	R
	ACAGGC	37	7	134354803	CGCCAGC	7	134005343	R
	CCTCATC	37	6	29815787	ACTGGAC	6	29923766	R
	CCACTTC	37	12	27996771	CGGCAAT	12	27888038	F
Red	AGTGCAC	37	1	32535981	CGAGGAT	1	32308568	R
Red	CCAGCCC	37	12	31272114	CGCGGAC	12	31163381	R
	TCCCTGA	37	2	232507774	CCAGTCA	2	232216018	R
	GCACAGC	37	3	127441767	CGTCTTA	3	128924457	R
	GGGGAGC	37	2	120063914	CGCCTCG	2	119780384	R
Red	GTGGCCT	37	20	60745245	CCACCGT	20	60178640	F
	CGAAGAC	37	7	95026181	ACTCATC	7	94864117	R
	CAAACAC	37	8	54628500	CGCCTCA	8	54791053	R
Red	CAACGGC	37	11	128321749	ACGCGAC	11	127826959	R
	GGCTGGA	37	3	140987789	AGGGGTC	3	142470479	F
	TAGGCCC	37	1	206848389	TAACCAC	1	204915012	R
	CTGAAAA	37	Y	2655977	AATTTGA	Y	2715977	R
Red	TCTTGGC	37	16	28756008	CGAGCAA	16	28663509	F
	AAAAGCA	37	8	57802622	AGCTCAG	8	57965176	F
Red	CGCTTCC	37	X	40440170	TACGTCC	X	40325114	R
	GGGCCGC	37	5	33937673	GCAGTTC	5	33973430	R
	GCACCGT	37	8	125617225	CCATAGT	8	125686406	F
	AGTGGCC	37	22	46481248	CGCCCAG	22	44859912	F
	CTTTGCT	37	11	27303972	CGGAAAC	11	27260548	F
	CTGGACT	37	19	12377156	CGCGACA	19	12238156	F
	GGTGTCC	37	19	45033565	GCACCTG	19	49725405	F
	GAGAAGA	37	9	45733081	CCAAACC	9	45623077	F
	ATGCCTC	37	6	32558175	CGGAGAC	6	32666153	F
	GTATGAG	37	1	56046489	TTTCCCT	1	55819077	R
	TCCAAGA	37	7	148517345	GTGAGAC	7	148148278	R
	GGGTTCC	37	6	31239320	CGGCCCG	6	31347299	R
	TTGCCAT	37	15	22921426	ATCTGTG	15	20472867	R
	TAGCTAC	37	6	164614646	GAGTTTA	6	164534636	R
	AATGGTG	37	11	110890228	CGGCTGG	11	110395438	F
	CAGAGGC	37	8	68418480	CTGTGGA	8	68581034	F
	ACTGTGA	37	6	56200769	GTCTGTT	6	56308728	F
Red	GCCGGCC	37	6	4079350	GTGGGAC	6	4024349	R
	GGATTCC	37	16	28889110	CGCTCTA	16	28796611	R
Red	ATGGGAC	37	1	115397857	CGCCCTA	1	115199380	R
	TTATCTT	37	12	131320160	ATAGCTA	12	129886113	R

	AGAAAA	37	21	27010696	ATAAGCT	21	25932567	R
	AACAGCT	37	X	154293850	CGAGAGT	X	153947044	F
	GGATTAC	37	7	92459517	AATGACT	7	92297453	F
	GTTCCAT	37	6	167524238	CGGCAGT	6	167444228	R
	CAGCTCT	37	13	112241077	GAGGGA	13	111039078	R
	TCTTTTT	37	7	124307584	CGATGA	7	124094820	F
Red	AAACTCG	37	11	133658113	CGAAAC	11	133163323	R
	AAAGAC	37	7	132617821	ACTCAGA	7	132268361	F
	TGGCTGA	37	1	161168957	AAGCAC	1	159435581	R
	TGAGCCA	37	11	61728829	CCTGGCT	11	61485405	R
Red	GCAGGA	37	X	149861761	CGCCCAG	X	149612419	R
	TCCCTCT	37	1	152299041	CCTGTAT	1	150565665	R
Red	GGTGCG	37	14	103593520	CGCCCAG	14	102663273	R
Red	ACGTGG	37	1	207997020	CGGGACT	1	206063643	F
	TGGGCTG	37	14	104782902	CGCTTCC	14	103853947	R
	CTCCGGC	37	10	102107251	TGGGAA	10	102097241	F
	CCGCTTG	37	7	65971211	CTTCACC	7	65608646	R
	CTGTCAG	37	5	133839271	CGCAGA	5	133867170	R
	TTTAGAA	37	6	3293720	TTGAAGA	6	3238719	F
	GCCTGGT	37	1	1190541	TGCCTGT	1	1180404	R
Grn	GGGCAG	37	11	1858572	CGGCAC	11	1815148	F
Red	GGGCCC	37	1	6526309	CAGGTCT	1	6448896	F
	TTAGACA	37	14	104315223	TACACTC	14	103384976	F
Grn	GGATGA	37	14	101535442	GAAGGG	14	100605195	F
	TCCCTCC	37	14	21175838	CGTCTTT	14	20245678	F
	AGTCATC	37	2	235160451	CGCTTGA	2	234825190	R
	AGCACTT	37	5	140619567	GAATAA	5	140599751	R
Red	GTCTACA	37	2	20871195	CGGCCCT	2	20734676	R
	GCCATGC	37	12	115355126	CGCCCAC	12	113839509	R
	TTCTTGG	37	1	7023625	ATGCCTC	1	6946212	R
	ATTAAGC	37	1	3286322	CGGGAA	1	3276182	F
	GGATGA	37	2	121669723	ACAGGC	2	121386193	R
	TTTTAAT	37	2	122187299	CGTGGG	2	121903769	R
	GAAGTG	37	13	45288461	CTTCTGG	13	44186461	R
Red	TCCCTGG	37	6	30039442	CCAGTTG	6	30147421	R
	GGGTTCG	37	16	67918754	TGGCTGA	16	66476255	F
	GCCACCC	37	1	233249267	CTGCATC	1	231315890	R
Grn	TGCCTGG	37	12	7781093	CGCCCAC	12	7672360	F
	TGAGTGG	37	3	14514657	TCTGGCT	3	14489661	R
	GATGCAC	37	13	36048892	TCACCAG	13	34946892	R
	CTGGTCA	37	X	106750120	GGGGCTC	X	106636776	R
	TTAATGA	37	5	140709986	TCCTCCT	5	140690170	F
	CACGGA	37	20	61290162	CCTGACT	20	60760607	F

Red	AACCGAC	37	19	56215426	CGGAGAC	19	60907238	F
	AGTGGGT	37	8	81963379	TCCATCC	8	82125934	R
Grn	CCGCGGC	37	7	51539190	CGCCAAC	7	51506684	R
	TTGTCTC	37	11	128321662	GACCAGC	11	127826872	R
Red	CAGTCAC	37	7	158280480	CGAAGCC	7	157973241	F
Grn	CCCTCGT	37	4	2366555	CGCCCAC	4	2336353	R
	ACACTCT	37	7	48319696	TGGCTTC	7	48290242	R
Grn	TTTCCTG	37	15	39006617	TCTCCTT	15	36793909	R
Red	TCGCTGC	37	13	50252564	AGGGGGC	13	49150565	R
	TGGGGCT	37	4	69435593	CGCTGCT	4	69118188	F
	ACCATAG	37	15	81122346	GGTCAGA	15	78909401	F
Red	CTGCCTC	37	6	32552453	CGCAGCC	6	32660431	F
Red	GGGGGCC	37	12	2339439	GGCGCGT	12	2209700	R
	TTATGGG	37	10	111728983	AGCACAC	10	111718973	F
	GAGAGTC	37	2	47053771	TCCACTC	2	46907275	R
Red	CTCGCGC	37	X	45710949	CGCCCGC	X	45595893	F
	CTTTTTC	37	15	94943926	CCCTCCC	15	92744930	R
Red	AAGCGGT	37	12	54384666	GTTCTTC	12	52670933	R
	TCCACAC	37	13	43360920	TCCCACT	13	42258920	F
	ATACCCA	37	3	119348585	GCTTTCC	3	120831275	R
	GAAGAG	37	X	101906537	CGCACCC	X	101793193	R
Red	ACTTTGG	37	6	160023927	CGCCCGC	6	159943917	F
Grn	CACTGCG	37	6	31937437	CGGCTAC	6	32045416	F
Grn	TTTAAAA	37	19	48077006	CGGCAGC	19	52768818	R
	ATGGAAA	37	3	134512480	GCCAGAC	3	135995170	R
Grn	CCGCCCT	37	19	50962411	CGGGGCC	19	55654223	R
	GCTGGAC	37	2	20871002	CGAGCCC	2	20734483	F
Red	GGACACC	37	17	35300645	GGATCCA	17	32374758	R
Red	TGTCTAA	37	6	31698089	CGCCCAT	6	31806068	F
	CCAGGGA	37	6	30496072	AACCACC	6	30604051	R
	ATTTCTC	37	8	143666890	GGAGTCA	8	143663892	F
	TACATCC	37	8	18432000	TGGGTCC	8	18476280	R
	GTAAGTA	37	13	41227982	CAGTACT	13	40125982	R
	GTGAACA	37	6	24936965	CGTGTGC	6	25044944	F
	GGCGGCA	37	17	76676243	CGCGCCT	17	74187838	R
	CATAGCC	37	1	95163986	CGGGGCT	1	94936574	F
	GGAAAAT	37	4	119989952	CGCCACT	4	120209400	R
	GGCGGTG	37	1	39981410	GGGGGCT	1	39753997	R
	TAATAAG	37	7	12735409	CGGGTTT	7	12701934	F
	TTCAGGA	37	13	112630569	AAATTTA	13	111678570	R
	TGGGCAT	37	2	3675155	CGGTCTG	2	3653030	F
	CTCTGTT	37	7	135433639	CGCCCCA	7	135084179	R
	CGTTTCC	37	22	22055412	CGCACAT	22	20385412	F

	GGCCAGC	37	7	150824021	GGATGTG	7	150454954	R
Red	CCCACCA	37	3	10149963	GCCCGGC	3	10124963	R
	ATGGAAA	37	13	112984976	GACTTCT	13	112032977	R
	GGCATGT	37	11	60680515	CGGAGCT	11	60437091	R
	AAGAGGA	37	7	158050299	CCCAGGC	7	157743060	F
	CTTGTGA	37	12	110888857	CGGTATG	12	109373240	F
	TAGAGAT	37	14	73927547	CGCCAAC	14	72997300	F
	CCGAATC	37	14	76819370	GAGAAAC	14	75889123	F
Red	ATCTTCG	37	19	55038290	TCGCGAG	19	59730102	F
	TTCAGAA	37	2	18063316	CGGAGTA	2	17926797	R
	GAGGACC	37	7	47990680	GTGTGCT	7	47957205	R
	TTTTTTC	37	17	45335202	CGTCCAA	17	42690201	R
Red	GGGAAGC	37	7	158109694	CGTCCTT	7	157802455	F
	TCATCTT	37	1	92101219	CGCCCCT	1	91873807	R
	CCCTGCT	37	1	2023794	CGGACTC	1	2013654	R
Red	GTGGGGC	37	15	96903559	CGGAAAA	15	94704563	R
	CACATAT	37	14	81405846	CGGCTTG	14	80475599	R
	CGCTTGC	37	7	87556005	CAACAGC	7	87393941	R
	TGTGTAT	37	6	26351915	AAGGAGC	6	26459894	F
	AAACACA	37	14	76445988	ATGTCTG	14	75515741	F
	GAATCAC	37	13	48011758	CGTAAAC	13	46909759	F
Red	TTGGCCC	37	12	54376019	GGCAGGC	12	52662286	R
	AGTTTCC	37	10	116444356	GACTCTG	10	116434346	R
Grn	GCCTCAA	37	7	102096976	CCTCCCA	7	101883981	R
	ATGCTCT	37	13	114829496	TGTTTTCT	13	113847598	R
	AGGTGCA	37	2	177016837	CGGGCTG	2	176725083	R
	GTGGCTA	37	5	140603270	GTCAGCA	5	140583454	F
Red	GCTCCCT	37	4	190906077	CGCACAC	4	191143071	F
	CTGGACG	37	2	9437253	AAGGGCT	2	9354704	R
	GAGAAAC	37	1	234667461	CGCGGTG	1	232734084	R
Grn	CACGCCG	37	5	126409211	CGCCGGC	5	126437110	F
	ATATTCC	37	1	153014310	TCTTTGA	1	151280934	R
Red	CTGCAGT	37	19	289902	GAAACGC	19	240902	F
	AGCCAAT	37	4	168824531	TCATTTC	4	169061106	R
Red	TGTCAAT	37	2	198174542	CGCCGCA	2	197882787	R
	CTCTCCC	37	17	80970892	TAGCAAC	17	78564181	F
	CTTTCTT	37	15	40269214	TGTTGGG	15	38056506	F
	ATATTTA	37	7	141630634	TGTTGTT	7	141277103	F
	CGGCCCT	37	17	139511	GGCAACA	17	139511	F
Red	GGACGAC	37	17	18553663	CGCCCGG	17	18494388	F
Grn	GCCGGGT	37	12	131303194	CGCCGCC	12	129869147	R
Grn	GAGGTGC	37	1	32741454	AATGGAT	1	32514041	F
	GCGGGGC	37	X	9432900	TGGTAGG	X	9392900	R

	AGTGTCT	37	6	47665926	CGGGACA	6	47773885	R
	GTAGCCT	37	20	828445	TGTGACC	20	776445	F
Red	GCCTCCT	37	2	119599189	CGCCCCC	2	119315659	F
	TTCTCTT	37	2	235732349	CTTTGCC	2	235397088	R
	GAAAGCT	37	7	4242962	CGCAGAC	7	4209488	F
	CCTGGCA	37	10	135342218	CGGCGAT	10	135192208	F
	ACTCAGC	37	19	46526483	TCTCTGG	19	51218323	R
	AATGAGC	37	2	101398178	CGGCCCC	2	100764610	F
	GTGAGAA	37	6	41383225	CGGGCAA	6	41491203	F
	CTGTGCT	37	6	31937470	CGGCCAC	6	32045449	F
	AAAGAGC	37	5	96314976	CGGGAAC	5	96340732	R
	TGAACCA	37	2	26624604	CGGAGCT	2	26478108	R
	GAAGATA	37	2	242620306	ACTAAAT	2	242268979	R
	CTTCTTT	37	10	5446942	TGGATAA	10	5436942	F
	CACTCAG	37	8	101174067	CGCTTAC	8	101243243	F
	CTCGCCC	37	12	54377225	TTATCCA	12	52663492	F
	GCCAGGC	37	7	56242407	CGGGCCA	7	56209901	R
	CACAAAC	37	4	152147390	CGCCTGA	4	152366840	F
	AAAGTAA	37	3	106447444	CGTCTGT	3	107930134	R
Red	CGTGCGG	37	11	75139736	CGACCAC	11	74817384	F
	TTGCAGT	37	12	125271306	CGTGAGC	12	123837259	R
Grn	AGTGAGC	37	X	148713660	CGCCGCC	X	148521467	F
	GGGGGAC	37	10	134974555	GATGACT	10	134824545	R
	TCTCCTT	37	5	146253830	CGGGATC	5	146234023	R
Red	GGCGGAC	37	6	30039476	CAGGCGC	6	30147455	R
Red	CATGGCG	37	17	77478569	GTGGGGC	17	74990164	R
Red	GGCCACC	37	5	177434438	CGCCCTT	5	177367044	R
	AGCTGCA	37	5	36243704	CGCAAAA	5	36279461	R
	ACCTACC	37	10	50890136	TCACCTC	10	50560142	R
	CAAGACA	37	10	122262397	CGGGAGA	10	122252387	R
	TCTATTA	37	12	99118507	TATTCAT	12	97642638	R
Red	CGAATAA	37	12	115134886	CGGCTTA	12	113619269	F
Grn	TGCTTGC	37	6	21761486	AGCGCGA	6	21869465	R
	TACCCTG	37	1	1555396	TCGGGGA	1	1545259	F
	TGGGTTG	37	2	86423274	CGCCCTG	2	86276785	R
	ACTCATC	37	7	47539511	TGGCTCA	7	47506036	R
	CCACCCT	37	9	79792074	GATGAGC	9	78981894	R
Grn	TCCTGGG	37	6	30079102	CGCCCGG	6	30187081	F
	GACTCTG	37	22	21479855	CGTGCCA	22	19809855	F
	AGTAACC	37	1	6521490	CGGCGCC	1	6444077	R
	TGTGATA	37	15	52018762	CAGACCC	15	49806054	R
	CTGTATC	37	2	9319526	CGCCCTT	2	9236977	F
Red	GGGTACC	37	3	75704824	GAGGCCC	3	75787514	R

	CATTATT	37	10	99278449	CGACAAC	10	99268439	R
	TTCCTAA	37	6	32629920	CTGCTGG	6	32737898	F
	TGCCTTT	37	10	129144210	CGGCACA	10	129034200	F
	CCTACGC	37	Y	16637142	CGGGAA	Y	15146536	R
	TAAACAA	37	6	109450463	AAAAAA	6	109557156	R
Red	GTGGCGC	37	1	32741152	CGCTTCC	1	32513739	F
Red	CTGATAG	37	X	48858587	CGCGAGC	X	48743531	F
	TATGCTT	37	6	32522872	CGCCCTC	6	32630850	F
	AATGGTT	37	3	114102615	CGTCTAG	3	115585305	F
	ACTGCTA	37	6	75589206	CGCTTCA	6	75645926	R
	CATCCGG	37	7	55412682	CGCCCTA	7	55380176	F
	CCCAGAT	37	3	49237327	CGGAGAC	3	49212331	F
Red	GCTTCTC	37	5	140590533	CGCTCAC	5	140570717	F
Red	AGGTGCC	37	X	140271314	AGGCCTC	X	140098980	R
Red	AGGCCTT	37	11	33097335	CGGACTC	11	33053911	R
	TGTCTGG	37	7	171613	AGCTCTC	7	266696	R
Grn	CAGGCGC	37	12	131303247	CGCTGGG	12	129869200	R
Red	GAATCCT	37	20	62313737	CGGATCC	20	61784181	F
	ATGTATG	37	2	86106058	CACCTCT	2	85959569	F
	CTAAGGA	37	2	12609420	CGCCTGA	2	12526871	F
	AGCTCGT	37	22	48896579	CGGCAGC	22	47275243	R
Red	CCGTTGA	37	X	70150787	CAGCTCT	X	70067512	F
	ATTTCAG	37	15	27020039	TTCTCCT	15	24571132	R
	TAATAAT	37	17	79378207	CTCTGGC	17	76992802	F
	CAGGCAA	37	3	43465503	CGCTGGG	3	43440507	R
	GCACTGG	37	6	29759078	ATACAAC	6	29867057	F
	TTTCAAG	37	11	101576844	CCCTGCC	11	101082054	F
	CTTTTTG	37	10	50536966	CCAACAA	10	50206972	R
	GAGAGGC	37	3	64670017	CCACCCC	3	64645057	F
	CTAGCAT	37	12	2353479	CGGTGTT	12	2223740	F
Red	TCCCTGG	37	8	142852219	CGGCTTG	8	142850126	F
	TTTCATA	37	17	80450903	CGCCACT	17	78044192	R
	AGGTTAC	37	6	13924544	CGGGAGC	6	14032523	F
	CTCCGGC	37	16	88053094	CGAGATC	16	86610595	R
	GAGGAGT	37	2	128453445	CGCACTC	2	128169915	F
	CCCAGAA	37	17	46652399	AGAGGAT	17	44007398	F
	TATGTCC	37	10	79622515	CGGACAC	10	79292521	F
	CTAATCT	37	14	20691777	CGCAGCT	14	19761617	F
Red	AAAAAA	37	1	185373486	AAGATTC	1	183640109	R
	AAATGAC	37	8	40925730	CGGTATT	8	41044887	F
	ACGCGTG	37	2	241581770	CGGCCCC	2	241230443	F
	CATCTGG	37	6	153066907	CGGACAC	6	153108600	R
Red	GGGTCAC	37	6	79339334	GAGCGGC	6	79396053	F

	TTTGGAA	37	11	78130236	AATCCCC	11	77807884	R
	ATAGCAC	37	6	166856074	GGCACGT	6	166776064	R
	GTGGGCC	37	11	44037829	GGGACAC	11	43994405	R
Red	CTAAATC	37	10	7859676	GGCCAA	10	7899682	F
Grn	AACGGAC	37	13	19919156	CGCGTGA	13	18817156	F
	CCTCACT	37	4	183063637	CGCCTCC	4	183300631	R
	CCTCTGT	37	10	134334283	CTTTTCC	10	134184273	R
	GCAGCTC	37	2	174024669	CGGCTGC	2	173732915	F
	TGGCCAT	37	10	30643845	ATTTGGG	10	30683851	F
Red	ATATATA	37	8	38032157	CGTGTAA	8	38151314	R
	GCAAAAT	37	5	80595275	AAATAAT	5	80631031	R
	AGAGTTG	37	12	46068618	CGCTGAA	12	44354885	F
	GGAGAA	37	7	158280771	CGGGGAC	7	157973532	F
	TTCTTGA	37	2	218114431	GAGGCCT	2	217822676	F
	GAGGAAC	37	8	27779092	ATCAGAA	8	27835011	R
	GTAATTA	37	7	131422820	GGACACA	7	131073360	F
	CAGACCA	37	17	40561514	GGATCTG	17	37815040	R
	GGGGGGT	37	15	68835517	GGCTTTG	15	66622571	R
	GAAGGCA	37	5	27038802	ACTCTCT	5	27074559	R
Red	ACAGAGT	37	5	1491579	CGCCCCC	5	1544579	R
Grn	TCAGCGC	37	1	247681781	CGCCGCA	1	245748404	F
Grn	CCACGGC	37	5	1857477	GCGACCC	5	1910477	R
	TTCAACA	37	11	67142030	GGCTTCT	11	66898606	R
	CGGGAAA	37	2	153419601	CGAGGGA	2	153127847	F
	AACATTA	37	5	101925501	TTAGAGC	5	101953400	F
Grn	TGGGACC	37	6	169825345	CGCCTCC	6	169567270	R
	AGCTTTG	37	4	83718165	CGGATGC	4	83937189	R
	AGTGAGC	37	6	1056970	CGGCCCC	6	1001970	F
Grn	CGTCTGT	37	8	39172111	CGCGAGC	8	39291268	F
	TTCAAAA	37	6	28120928	AATATCT	6	28228907	R
	CAGGACA	37	6	29690766	ATTGTCT	6	29798745	R
	AGCTTCC	37	14	71022665	CGTCCTT	14	70092418	R
	ACGTAAA	37	7	77788546	CGGGCAA	7	77626482	F
	AAATAGT	37	1	210419938	ATTTCCT	1	208486561	R
Red	CTTCTTG	37	1	161280287	CGCACAC	1	159546911	R
	ACCCAAA	37	1	230493133	CGGCTGC	1	228559756	F
	CCCCACC	37	3	46661640	CGCCAGT	3	46636644	F
	GAGTTGG	37	17	43319137	GGAGGTT	17	40674920	R
	GTGACGC	37	Y	22737663	AGTGCGC	Y	21147051	R
	TTCAACA	37	3	57015101	GCTGGCC	3	56990141	R
	TGCTCAG	37	2	238065451	GGGACCT	2	237730190	F
	ACCCACC	37	2	110907413	CGCCTGA	2	110264702	R
	TGCAAAT	37	5	140724362	CCCACCA	5	140704546	R

Red	GGGAAG	37	X	34674799	GGATGCC	X	34584720	R
Red	GACTAAT	37	12	149495	CGGCTGC	12	19756	R
Red	AGCTGCA	37	11	8679885	CGACATT	11	8636461	F
Red	AAACTCT	37	5	180085446	CGGCGCC	5	180018052	R
	TTTTGAG	37	1	113229103	CGGGGAC	1	113030626	R
	TACAATT	37	17	80969749	CGAGCTG	17	78563038	R
	ATCTCGC	37	5	180497114	AGCGAGT	5	180429720	R
	GGCTGCC	37	7	158815080	CGGAGC	7	158507841	F
Grn	CCGGCTC	37	5	178266137	CGCCCAC	5	178198743	F
	AATGGCT	37	X	77151316	TTGCTAG	X	77037972	R
Red	AGGTGG	37	4	157119935	ACACAAC	4	157339385	R
	TTTTTGC	37	13	94957721	CGGGCTG	13	93755722	R
	TCCTCTT	37	1	40236125	GGGGCTT	1	40008712	F
	CTTATGT	37	13	46202047	TCTGTTT	13	45100048	F
	GGCAGC	37	8	142161887	CTTGCTG	8	142231069	F
	ATTGAGG	37	19	41782183	CGGCCCC	19	46474023	R
	CCGGGTC	37	8	72757456	CGCATGG	8	72920010	R
	GCTGGTC	37	9	69147680	AGGGCGC	9	68437500	R
Red	TCTCGGA	37	X	114468360	TGGAACC	X	114374616	F
	GCTCACC	37	6	31689459	AAAATCT	6	31797438	F
	GGAGCCC	37	X	129114238	GAGGTGC	X	128941919	F
	AAATAAC	37	17	35161825	CGGGAC	17	32235938	R
	TTTGCCA	37	X	47077877	CGCCAGC	X	46962821	F
	AGAGGAC	37	6	32362407	CGAGGTC	6	32470385	R
Red	AGATATG	37	7	52155829	CGGATGT	7	52123323	R
Red	TACTTCT	37	17	15686309	CGGCTCC	17	15627034	R
	CTCCCAA	37	21	27010160	GGAACAC	21	25932031	R
Red	CCCTCCC	37	6	168502341	GACCCCT	6	168245190	F
Red	TGACTAA	37	1	196746875	GTAATTT	1	195013498	R
Grn	CCAGCAT	37	7	56605830	CGGCCGC	7	56573324	F
Grn	TACCAAG	37	2	220361467	CGTTTAG	2	220069711	R
Red	ACAACAC	37	7	96651983	CGGGAG	7	96489919	R
Grn	GGCCGCC	37	1	19600730	TGCTCGG	1	19473317	F
	TACATCC	37	19	51818377	TATTCAT	19	56510189	R
	TACCATT	37	5	43038611	CGCTGGA	5	43074368	F
Red	TTAGCTG	37	6	20032841	GCGATTG	6	20140820	F
Red	CCATTGG	37	6	29648590	CTGGGG	6	29756569	F
	CCTTGGC	37	8	43136445	CGGCTGG	8	43255602	F
	GATCCCT	37	13	64009677	CGCAGTG	13	62907678	R
	CCTCCCT	37	5	53751919	CGGAACC	5	53787676	F
	TCCAAAC	37	17	14139857	TTGAGGC	17	14080582	F
Red	CTTCTCG	37	15	74345103	CGCCTGA	15	72132156	F
	ATAATGA	37	6	170455498	CGGCTCG	6	170297423	R

Grn	GTGTGGA	37	21	47404268	CGCGTGA	21	46228696	R
	CCACTGG	37	15	82425284	CGTGTTG	15	80212339	R
	ACCTTCC	37	15	22923741	CGGGGAC	15	20475182	R
	TCCCTGA	37	11	103721961	TGGAGCC	11	103227171	F
	GCCCTGG	37	1	24122853	CGGGCCA	1	23995440	R
	ACTTGAG	37	15	67323243	CGCACCC	15	65110297	R
	CTTCTCT	37	8	92570895	CGATGCC	8	92640071	R
	GACCGTT	37	5	1110019	CTGTGTG	5	1163019	F
	CTTTTTCT	37	1	230220668	CGTCCAG	1	228287291	F
	CCGGCGA	37	5	2643177	CCAGGGC	5	2696177	R
Grn	TACAGGA	37	19	1851995	GGAGCCT	19	1802995	R
Red	ATGGCGC	37	7	95026073	CGCCTCA	7	94864009	R
Red	AGCTGTA	37	6	33036958	CATTGAC	6	33144936	F
	CTTTATG	37	13	110970196	CGCTATG	13	109768197	F
Red	GTGTTCG	37	10	135343248	GAGACAA	10	135193238	F
Red	CCGTACG	37	X	53449647	CGGCAAA	X	53466372	F
	GCCGCGC	37	9	139741803	CGGGCCC	9	138861624	F
	CCAGATG	37	13	27174884	CGTCTTT	13	26072884	R
Grn	TCCCAGG	37	5	138714337	CGGGGCT	5	138742236	R
	TCAACAC	37	15	32607260	CCTCATC	15	30394552	F
	GGAGCTA	37	4	154707153	GACAATT	4	154926603	F
Red	CACCCAC	37	10	670815	AACTACG	10	660815	R
	CCTGTCT	37	12	52888480	AGGTGCT	12	51174747	R
Red	ACAGCAC	37	20	62053198	CGGCCCG	20	61523642	F
Red	TGGGACC	37	9	72027409	GATCCCG	9	71217229	R
Grn	CCGCTCT	37	1	7023784	CGCGCCC	1	6946371	R
	GGTGTGT	37	7	1981254	CCTCACA	7	1947780	F
Red	CAGCGCC	37	21	36041683	CCCTTAA	21	34963553	R
	CATGAAC	37	5	142098838	GTAATAA	5	142079022	F
	AGTAGTT	37	5	180028658	GGGAGGA	5	179961264	F
	AGTGTCT	37	22	46934981	CGTGTTC	22	45313645	R
	TGGGTGG	37	1	153234342	CTTCGCC	1	151500966	F
	TACTGGG	37	7	127291444	CGCTCTC	7	127078680	R
	GGCAAAA	37	10	94250865	GGACCCC	10	94240845	R
	GATCTGT	37	5	80501337	CGGGCAT	5	80537093	F
Red	TTCTCAT	37	2	133014805	CGCTTCC	2	132731275	F
	ACAAGCC	37	2	99081350	GCAATAA	2	98447782	F
	CTCCTAC	37	5	140580769	GTAGCGA	5	140560953	F
	GCACCCA	37	8	144406532	ACTCCTG	8	144477907	R
	CCATGTG	37	2	241644188	CGTCAGT	2	241292861	F
	ACAAATC	37	12	72233249	CGCAGGC	12	70519516	R
	TCAACCC	37	22	30947032	CGGTCAG	22	29277032	R
	ACCTTGT	37	12	122851438	CGAGTAC	12	121417391	R

	TGAGCGA	37	6	5087031	TATTCTG	6	5032030	F
	AGGAAG	37	10	99356163	ATGGTGG	10	99346153	R
	AAGGGG	37	5	176099987	GTCCAGC	5	176032593	R
	AACTGAC	37	8	39172020	TATCAAT	8	39291177	R
	TCAATGA	37	1	201857591	TGTGTTC	1	200124214	R
Red	TGTGGAG	37	4	146656091	CGGCTCT	4	146875541	R
	ATCAAGT	37	3	4794020	GAGGGA	3	4769020	R
	TGGCACG	37	5	177433673	CGCTACC	5	177366279	F
Red	CTTCCGT	37	5	135415948	TTGGGAC	5	135443847	R
	TTGAATG	37	6	114661277	TGCCCAG	6	114767970	F
	CTTGTAA	37	6	127780352	CGACCAC	6	127822045	F
Grn	GGGCACT	37	17	48263189	CGCCGAC	17	45618188	R
	GACTGAC	37	X	152000347	CGGGGAT	X	151751003	R
	GCCGCAC	37	17	79011140	TGAAGGC	17	76625735	R
	CAGGGGC	37	13	25320388	CCTCTCT	13	24218388	F
	CAGGCCT	37	7	139351108	CGCCACG	7	139001648	F
Red	GTGAAGT	37	17	7960449	CTGAGCG	17	7901174	R
Red	CCCTGGC	37	11	66193993	CGCTACG	11	65950569	F
	ACTGACT	37	4	159732036	CGCTTCA	4	159951486	R
	CTTTTCA	37	3	171543413	CGGCTCA	3	173026107	R
	TACGGAC	37	3	52864694	CGACAGC	3	52839734	F
	TCCTGGG	37	6	110732115	GTTCCCA	6	110838808	R
	AAGAGCC	37	8	1327546	GGTATTT	8	1314953	F
	CACTTCC	37	12	12038352	TGAGTCA	12	11929619	R
	CATGTGG	37	11	64116250	GGTGACC	11	63872826	F
	GCTGTGC	37	20	61924423	GGTCCTT	20	61394868	R
	TGATATT	37	13	97928231	ATGGTAG	13	96726232	F
Red	AAGCCGA	37	X	100663213	CGCTTAC	X	100549869	F
	GTTTCCC	37	4	119759900	GCTTTCT	4	119979348	F
	TGGCCCC	37	22	23922551	AGCAGGC	22	22252551	F
Red	TCCTCGC	37	10	104835919	CGGCGTC	10	104825909	R
	CAAGAGC	37	1	68025026	CGGAGGA	1	67797614	R
Red	GGGTGGC	37	4	176349171	GTTCCGG	4	176586165	R
	AGGAGGC	37	10	6821048	TGCTGGG	10	6861054	F
	ATCCAGC	37	10	72191087	TCTGGGC	10	71861093	R
Red	GACAGCC	37	12	133035885	CGGCTTT	12	131545958	F
	TCTGAAA	37	5	113699683	CGCCAGC	5	113727582	F
Red	TACCTTT	37	X	129520156	CGGGGGA	X	129347837	R
Red	AAGACAC	37	X	20134346	CCAGGGC	X	20044267	F
	AAAGCCC	37	13	112820997	GGCTGCA	13	111868998	R
	AAACTCC	37	7	27703436	ACAGAAC	7	27669961	F
	CCTGCGA	37	4	736485	TGGCCAG	4	726485	R
	AGTCATA	37	7	29037910	CGGACCA	7	29004435	R

	TTGGCTT	37	1	81878937	CGGTAGC	1	81651525	R
	CTTCCTG	37	1	2885168	GAACATA	1	2875028	R
Red	AACGGAC	37	10	134420208	CGCGCCC	10	134270198	R
	AAATCCC	37	17	10634140	CGGCTCA	17	10574865	F
	CCGTTGA	37	6	32526669	TGAAAAT	6	32634647	F
	CAAGTTC	37	6	7998697	TAGGCCT	6	7943696	R
	AGGCCAC	37	X	68050216	AATGGGA	X	67966941	F
	ATATAGG	37	2	84714510	CGAGGCT	2	84568021	R
Red	TGAAACT	37	7	1622775	CCCACGG	7	1589301	F
	CTCATTC	37	10	79605162	TTTCGTG	10	79275168	F
Red	AGAATGC	37	5	140201656	CGCCCTC	5	140181840	R
	TGACTTG	37	6	116248269	TGAAGCC	6	116354962	R
	CTGATTT	37	6	32610971	CGGGTGC	6	32718949	R
	CGCGTCT	37	5	178208610	TGCTCAC	5	178141216	R
	TACCATT	37	5	36273196	CGGAAAA	5	36308953	R
	TAGAGGT	37	1	31988382	CGAGAGA	1	31760969	R
	ATAAACA	37	21	40145361	GTATGTA	21	39067231	R
Red	ACCCAAC	37	1	228659093	CGCCCAG	1	226725716	F
	AATAACC	37	17	12922839	CGCCCTC	17	12863564	R
	ACTGTTG	37	5	140098496	ACTCACT	5	140078680	R
	GAGGGGC	37	6	29910755	CGGTCAG	6	30018734	R
	TCAGGAT	37	10	134800741	CGCTGGT	10	134650731	F
	CAGTGCT	37	5	81553088	CATTACT	5	81588844	R
	AAATCAC	37	17	80970825	CGGACGT	17	78564114	F
Grn	TCGCTGA	37	X	48901162	TGAGGGC	X	48788106	F
Red	CTGGAGC	37	8	43131431	GTGGACA	8	43250588	R
	TTATACA	37	4	2402019	GGTCTGG	4	2371817	R
	GAGTGTC	37	7	158279846	CGTGGTC	7	157972607	R
	TGACAGC	37	10	129090134	CGGTAGC	10	128980124	F
Red	CGTAGGT	37	3	49940919	CGTGAAC	3	49915923	R
Grn	CACCCAT	37	12	115134956	TCGATCA	12	113619339	F
	CTATCTC	37	3	25646267	CGGTAGC	3	25621271	R
Red	AAGCCAC	37	7	150119075	GAAGCTT	7	149750008	R
	GAATCTG	37	14	100441223	CTGGCCA	14	99510976	R
	CTTCTCA	37	1	240776316	CGTCTTT	1	238842939	R
Grn	GCTCAAG	37	10	47083392	CGCTCCA	10	46503398	R
Grn	CCCACCC	37	5	176045983	CGGGCCA	5	175978589	F
	CCCTCCA	37	17	54230878	CGCCTCC	17	51585877	R
	AGAAAGA	37	X	117957616	AAATTCC	X	117841644	R
Red	ACTCTTC	37	14	101908830	CGTTCCT	14	100978583	R
	TCCAGAT	37	10	19918310	CGGAGGA	10	19958316	R
	TACAAAA	37	7	110496797	TATTTCT	7	110284033	F
	TCCACAT	37	6	154408701	CGCATGG	6	154450394	R

	CTTCAAC	37	3	101658926	CTTACTT	3	103141616	R
	GTGGGCC	37	8	134081000	TGAAGAC	8	134150182	R
	CTTGGCT	37	6	167631788	AGCTGGT	6	167551778	R
Red	CACAGAT	37	3	138152902	CGTCATT	3	139635592	R
	CCTACTT	37	7	96652153	CGCTAAC	7	96490089	F
	CAGCTCT	37	5	137785499	CGGGCAC	5	137813398	F
	CAGAGTA	37	20	23550632	CGCAATG	20	23498632	R
	CCTACCC	37	Y	2655866	TACCCTG	Y	2715866	R
	TCTGTCT	37	8	2263331	CGAGTCA	8	2250738	R
Red	GGGCATC	37	12	54384763	CGCTGCC	12	52671030	R
	AAAGGAC	37	3	70911187	CGGGGTT	3	70993877	R
	GGAAATA	37	8	122685859	CGGTTTT	8	122755040	F
Red	AGAGCTA	37	11	58598338	CGCCCTG	11	58354914	F
	GCCAGCA	37	13	68745297	TGTGCTC	13	67643298	R
	CCAGCTT	37	19	50479865	GGACACT	19	55171677	R
	GCGCTCC	37	4	176987009	GCGACCT	4	177224003	R
Red	GGGCTCT	37	4	155254326	CGGACTC	4	155473776	R
Grn	AGGGCTA	37	3	133502564	CTCCGGG	3	134985254	F
Red	GCTGTGA	37	6	79339195	ACCTGGG	6	79395914	F
	CTCCTTG	37	19	43383986	CCTTCTG	19	48075826	R
	GCAATAA	37	3	167659189	GGGTGGA	3	169141883	F
Red	TGACGGA	37	2	233216220	CGCAGCT	2	232924464	R
	TCTCAGG	37	5	53920730	GATTTGT	5	53956487	F
	TAAACAA	37	2	135970350	CGTTGCA	2	135686820	F
	ACTAGAC	37	1	23521307	AAGAAGT	1	23393894	R
	CTGTGAG	37	4	39531927	CGGGGAC	4	39208322	R
	CCGGCTA	37	12	2017093	GTTGTAC	12	1887354	R
	AGCAACC	37	2	209145835	GCTCTTA	2	208854080	R
	TTATTTT	37	7	16457583	CGCATGC	7	16424108	R
	TAACTGC	37	1	159439981	CGCAGGC	1	157706605	R
	TGCAGAA	37	19	40031368	CGGATGT	19	44723208	R
	CTCAGAA	37	4	122721721	ACTACTA	4	122941171	F
	TCTAACA	37	1	98518557	GATGGTC	1	98291145	F
	ACAGGAC	37	4	54765826	CGCAGAT	4	54460583	F
	AGCAGCT	37	6	32634316	GCACTTA	6	32742294	R
	TATAAAA	37	18	29205358	CGGGAAC	18	27459356	R
Grn	GTGAGAC	37	1	1663860	CGGCCAC	1	1653720	F
Red	GGCCTGG	37	6	32557404	AGCTCCC	6	32665382	F
	CATTTCT	37	10	121609179	CGTGATG	10	121599169	F
	AATTCCT	37	2	204674074	TCTCCTT	2	204382319	R
	GCAGCCC	37	13	112628711	CGGCGCC	13	111676712	R
	GGTTTGG	37	4	1366463	CGGGAGC	4	1356463	R
Red	GCGTTCG	37	10	729479	GGGCATT	10	719479	F

Grn	GGCTGAC	37	6	90597394	GCTGAAA	6	90654115	F
	AGTGTGT	37	14	55263199	CGGAGCT	14	54332949	F
	AGGAGGA	37	15	63758958	CGGGGGC	15	61546011	R
	AAGATCT	37	14	51187290	CGGCATA	14	50257040	R
	TGTTTGC	37	1	114717638	CGAGAAC	1	114519161	R
Red	TAGTCGT	37	X	152736032	CGCGCCC	X	152389226	F
Grn	ATTCTCT	37	7	130130189	CGGCCCT	7	129917425	F
	TACTTCA	37	2	172377981	GGACCGC	2	172086227	F
	GACCCCG	37	10	133036449	GTTCCAG	10	132926439	R
	TGCAGGT	37	6	31275791	CGAGGAA	6	31383770	F
Red	GCTGTGA	37	6	30419543	CGGTCCT	6	30527522	F
	GTCAAAC	37	2	147789639	CGAGCAA	2	147506109	F
	AACCGAC	37	13	47470350	CGCTCGG	13	46368351	F
	AGCGGCT	37	6	164092588	CGTCATG	6	164012578	F
	GAGCCCC	37	17	7381683	CGCTCCT	17	7322407	F
	AATTGTT	37	12	54068942	ACAACTT	12	52355209	R
	GTTGCTG	37	8	75880384	CGGAGCA	8	76042939	R
	ATGGTCT	37	19	13320368	CGGGACC	19	13181368	R
Red	ACGCCGC	37	X	125715154	CGGACCC	X	125542835	F
Red	AAAATAA	37	8	144850435	CGGTGCG	8	144922423	F
	CAATAAA	37	19	617195	AAAGCTC	19	568195	F
	GTGCTCA	37	15	65214588	GCTGGGC	15	63001641	F
Red	CCTGGGA	37	13	25115869	GCACATG	13	24013869	R
Red	CCAGCTT	37	17	46621709	CGCTGTT	17	43976708	F
	TGGGCTG	37	19	55417361	ACAATTG	19	60109173	R
	GCAGTTC	37	10	92079600	CGGAGTA	10	92069580	F
	AAGACAC	37	10	6014983	AAGACTC	10	6054989	F
Red	CCCCCGC	37	X	152783792	CGCCCAC	X	152436986	F
	TCATTTT	37	17	14483597	CGTGTCC	17	14424322	F
Red	CTGGCCA	37	19	613818	GTGAGCA	19	564818	F
Grn	ACTAAAC	37	7	4133290	TGGAGAT	7	4099816	R
Red	TCCTCCG	37	11	77907332	CGGGTAT	11	77584980	R
Red	CACAACC	37	2	242056226	TGCTACG	2	241704899	R
	AGGTCAC	37	6	33036934	GCTCAAC	6	33144912	F
Grn	CGGCGGC	37	6	170338591	GGGGGTC	6	170180516	F
Red	ATGCTTC	37	6	168918116	AGGAACA	6	168660965	R
	TCGGGTG	37	3	11178652	CGCTTCT	3	11153652	R
	AGTATAT	37	3	16843387	CGCTGTG	3	16818391	F
	GAAAGGC	37	11	66317822	TCAGGAC	11	66074398	R
	TATGTGA	37	17	53339697	CGGCAGT	17	50694696	F
	TGTACCC	37	1	1666808	TGGGCGA	1	1656668	R
	CAGGTTG	37	11	33474484	CGCAGGA	11	33431060	R
	AGATACA	37	10	5936426	CCTGAAG	10	5976432	F

	AAGGGAC	37	11	77033664	GGACCTT	11	76711312	F
Red	CAGCCGC	37	15	76484473	CGACGCT	15	74271528	R
	GTTAATG	37	2	153504453	CTGCAGT	2	153212699	F
	ACTTAAG	37	2	100926650	AGGTCTG	2	100293082	F
Red	GGAGTGC	37	22	46451518	ATGACAC	22	44830182	F
	GTCCGCT	37	15	31355430	CGTCTTG	15	29142722	R
Grn	CAGGGCC	37	19	57630536	CGCCCAA	19	62322348	F
	CTCACTG	37	15	27597471	TTGGCAG	15	25271066	F
	CAAGATC	37	4	19740944	CGCCACT	4	19350042	F
	CACCAGC	37	10	4868398	CGGCTGA	10	4858398	R
Grn	GGGAAGC	37	19	49232187	ACTGCTG	19	53923999	F
	CATTTAC	37	18	56963742	TGGTTGT	18	55114722	F
	TCTTCCG	37	2	75136334	CGAGAAC	2	74989842	F
	CCCACAT	37	4	108972693	AATTGCT	4	109192142	F
	ATACAGC	37	4	174538350	CGGCATT	4	174774925	F
	TACTAGG	37	6	32728862	CGGCTCT	6	32836840	R
Red	CTGATGC	37	6	158080750	AAGACGA	6	158000738	F
	ATTTCTT	37	6	130031784	GGACAC	6	130073477	F
	GTTTCTG	37	1	205283250	CGGAAC	1	203549873	F
	CCTCTCC	37	11	103305609	CGAGACT	11	102810819	R
Red	TCTTGTC	37	6	25882481	CGGCCGC	6	25990460	F
Red	ACTCCAG	37	X	63615339	CTTTCGC	X	63532064	F
	GAAGCAC	37	6	31240814	GGCAGTC	6	31348793	F
	GAAGCAC	37	2	161887154	CGCTGCA	2	161595400	F
	GGGCATC	37	2	8530521	CGGAGG	2	8447972	R
Grn	TGGCAGC	37	19	15568511	GAAGTGC	19	15429511	R
	GTGCCTT	37	7	50109467	GTCATAG	7	50080013	R
	TCAGGAC	37	11	95824265	CGTGAAC	11	95463913	R
	TTTGTTC	37	12	58758818	CGTGGGT	12	57045085	R
Red	TCGCTTC	37	6	134436620	CGAGCTG	6	134478313	R
	AGAAGG	37	1	33608053	CGTTAGG	1	33380640	R
	CATGAGC	37	1	117233299	CGTGCAG	1	117034822	F
	GTGTACA	37	15	90755932	CGTCTGC	15	88556936	F
	CATAAAC	37	6	33037662	CGGACC	6	33145640	R
Red	ACTCGCT	37	5	140537692	TCTACCT	5	140517876	R
Red	AGGCACC	37	5	1196154	CGGCCAT	5	1249154	F
	ACTTCTT	37	3	180546915	CCAAGG	3	182029609	F
	AGGGCCC	37	5	136636409	CGGAACC	5	136664308	R
	GTCACCA	37	10	116394557	TAGTTGC	10	116384547	R
	CAGAGA	37	1	146548032	CTTTCAG	1	145014656	R
Grn	GCCCAGC	37	15	101912471	CGCTCCC	15	99729994	R
	TCAGTTC	37	1	25698385	CGTGGTG	1	25570972	F
Red	TGCATTC	37	1	3659656	CGGCGGC	1	3649516	R

	ACCCATA	37	5	141900671	CGGCCCC	5	141880855	R
Red	GGGAGA	37	X	48755596	CGCAACT	X	48640540	R
Red	AATTAGT	37	5	140090300	CGCCCCT	5	140070484	R
	GATGTTC	37	10	1083304	GCCCTAT	10	1073304	F
Red	ACAGAA	37	6	2515337	GCACGCT	6	2460336	R
	CTTCACT	37	14	105830606	CGGGCTG	14	104901651	R
Grn	CTATTGT	37	1	168198488	TTTGAT	1	166465112	R
	CAGGAA	37	21	19191096	CCTGCAC	21	18112967	R
	TCCAGAG	37	17	39094308	CGGGCA	17	36347834	R
	CAAACG	37	7	158342394	CGCTCCA	7	158035155	F
	CTCGCCA	37	17	19627822	CGCCTGC	17	19568414	R
Red	GCAGTAT	37	1	17004764	TCAGCGT	1	16877351	R
Red	GGCGGG	37	8	56685709	AGCCTGC	8	56848263	R
	CGCTCCC	37	5	98112437	CAGGTA	5	98140337	F
	GGTGCTC	37	2	148394181	CGGCAAT	2	148110651	R
	ATTCAGG	37	2	30669597	CGAGAC	2	30523101	F
Red	CGCCGCC	37	1	158147629	CGCGCA	1	156414253	F
Red	CGGGGC	37	3	49236860	CGCCCCG	3	49211864	R
Red	CACACA	37	X	153151235	CGCCCCC	X	152804429	F
	TTTGCTT	37	17	10602001	CGGAAC	17	10542726	F
Red	TTTTTTT	37	19	45724963	CGGTGTG	19	50416803	F
	AAAAAA	37	1	23474871	AGAAGA	1	23347458	R
Red	CGTGCTG	37	15	34782820	CGCCGCC	15	32570112	F
	TCTTAGC	37	12	43253257	TGATAAA	12	41539524	F
	ATAATCG	37	17	57743594	CTGAAG	17	55098376	R
	TGGAGTG	37	10	133810178	CGGGCCT	10	133660168	F
	GTGGTGC	37	10	134411480	CGGGCTG	10	134261470	F
Red	AAATGCA	37	2	240898385	CGTGAGA	2	240547058	F
	TAAGACA	37	10	75913585	CGCTAAA	10	75583591	R
	CAGACA	37	2	28022223	CGCTGAA	2	27875727	F
	ATAAAAC	37	5	16614241	CGGAGA	5	16667241	R
Grn	CAGGCTC	37	X	153084761	CCTCTCT	X	152737955	F
	CTGGGGC	37	17	17875168	CGAGTCC	17	17815893	R
	GTTTAAC	37	6	166260964	CATGCTT	6	166180954	F
	ACAGCTG	37	17	2886453	CTCACAG	17	2833203	R
	GAACTAC	37	2	177016167	CGTGTAA	2	176724413	R
Grn	GAACTTT	37	7	155333337	TTTCGCA	7	155026098	R
	AAAAGA	37	12	55640113	CGAGGG	12	53926380	F
	ATCCTCC	37	11	116664039	GGCTCAT	11	116169249	R
Red	GCAGAA	37	5	1219873	GGTCACA	5	1272873	R
	ATGGAAT	37	7	94034808	CGGTATT	7	93872744	R
	CTCCATG	37	2	241644240	AGTCAG	2	241292913	R
	GGTGTCT	37	18	11151764	GGTTAGT	18	11141764	R

	TAAGGGA	37	2	72788795	CGTCTTT	2	72642303	R
	CCGTTTC	37	13	112985499	GCCTTGG	13	112033500	F
	GGAGGGA	37	7	1080836	CGGAGCC	7	1047362	R
	AGCCTCC	37	13	114965839	CGCCTGC	13	113983941	F
Grn	CCGCCCG	37	11	77299805	CGCCCGG	11	76977453	F
	TTTTTCAA	37	1	192520335	CATCTGA	1	190786958	F
	AAGTGGT	37	17	78765948	AAGTTCT	17	76380543	F
	CGGTGAG	37	17	80255510	GCCCTTC	17	77848799	F
	TCTGTGC	37	13	113652368	CGGGGCC	13	112700369	R
	AGCCTTG	37	5	86687001	CGAGATA	5	86722757	R
	GTCTGGC	37	6	131520996	AATAACC	6	131562689	F
	CAGCAAA	37	6	30103459	GGGTGCC	6	30211438	F
	ATAGCCT	37	8	8667411	CTACTTC	8	8704821	R
	TGTGTTT	37	X	125954246	CGGAAGA	X	125781927	F
	TGGATAG	37	8	55180538	CGCCTGC	8	55343091	F
	AGCGCCC	37	1	4844027	CGGGCCA	1	4743887	R
Grn	CCACGGC	37	2	97778927	CGCTGGC	2	97142654	F
Red	GCGGGCC	37	6	30039435	CGCCGCC	6	30147414	R
	AGAACAA	37	12	121345228	CTTGGCT	12	119829611	F
	GCTCCTG	37	10	105408599	AGCTTCC	10	105398589	F
	GGAGCCC	37	4	1496981	CGGGACC	4	1466309	R
Red	ACCATTT	37	18	12255318	CTTGAAG	18	12245318	R
	ACCTTGC	37	5	75918112	CGCTCTT	5	75953868	R
	CTTGTAA	37	17	35302352	CGGCTTT	17	32376465	F
	GCGGTGC	37	9	139607421	GACTTCG	9	138727242	F
	CGTCGCT	37	13	111281384	CGGCAAC	13	110079385	R
Red	TCTGGGC	37	21	46851112	GGCAGGC	21	45675540	R
	CACTTCA	37	6	422935	GCCTGAA	6	367935	R
	GTCCCCA	37	12	2017510	AAGTGGA	12	1887771	F
	ATGAACA	37	12	113229989	CGCTAAG	12	111714372	R
Grn	CTTGGAT	37	17	19883602	AGACACA	17	19824194	F
	TTGATGT	37	4	74921425	ATAAATC	4	75140289	F
	GTGCTTC	37	4	157897045	TAAAAAA	4	158116495	R
Red	GAGTTGA	37	2	90016302	AGAAGGC	2	89653603	R
	TGGAAGA	37	17	32581466	CCTGTCC	17	29605579	F
Red	CTGTGAT	37	1	3504125	GTTTGCA	1	3493985	R
	CAAAGTC	37	8	1312875	CGCAAGC	8	1300282	R
	TCACTTG	37	8	131685278	CGGGAAC	8	131754460	R
	GACTATG	37	12	132853388	CGGTAGA	12	131363461	R
	GGTCAGA	37	3	127468611	AACACAC	3	128951301	R
	AGAAATT	37	3	145969718	CGGGAGA	3	147452408	F
Red	AGATGCC	37	6	30039010	CGGCCGC	6	30146989	R
	GTATCTA	37	7	138229989	CGCCAGC	7	137880529	R

Red	CAAGGCC	37	1	27676205	CGACCGC	1	27548792	F
	TACAAAA	37	6	33585071	CGCATTT	6	33693049	R
	GGTGCTC	37	22	18531077	CGGGTGT	22	16911077	F
Red	GGACTGC	37	1	19600719	CGCCGCC	1	19473306	F
	GTTTTGA	37	5	146864669	CGATTGC	5	146844862	F
	TATTTAC	37	1	115398123	TCCCAGG	1	115199646	F
Red	CAACCTA	37	2	108157524	CTCGCAC	2	107523956	R
	CATGGAC	37	14	22370643	CGGATGA	14	21440483	R
	TTCAAGG	37	10	77228852	AGCACCA	10	76898858	F
	TGAAAGC	37	8	100649114	CATTAAC	8	100718290	F
	AAACCCC	37	8	61626646	CAGACTC	8	61789200	R
	GCTACAG	37	5	72683866	CGAGGTA	5	72719622	R
Red	GCTGCGA	37	8	54935605	GACCTGA	8	55098158	R
	TTTGTTG	37	15	89640878	CGCATTC	15	87441882	F
	CCTAGAT	37	8	89281994	TCCAGCT	8	89351110	R
	AAAGGA	37	6	29981404	CGTGGCT	6	30089383	R
	ATCCCGT	37	11	46389249	GGAGTCA	11	46345825	R
	TTTTGTC	37	6	33033176	CGGGCTT	6	33141154	R
Red	GCCTTGC	37	17	75385278	CCTCGCA	17	72896873	R
	ATATTAA	37	6	33042551	CGAGGA	6	33150529	F
	ACATGGA	37	6	32549283	CGGTCCC	6	32657261	F
Red	CCCTAAT	37	12	128752246	GCGGGGC	12	127318199	F
Red	GGGCGTC	37	10	44185097	CGGCACC	10	43505103	R
	AATAGGA	37	5	80493	GGGGCAC	5	133493	R
	GCCTGAT	37	14	26862142	CGGCTAA	14	25931982	F
Grn	AGCAGCA	37	17	629613	CGGAGTC	17	576363	F
Red	CATTAGT	37	5	140097950	CGCCCCT	5	140078134	R
	GTAGGAA	37	6	109812795	CGCTCTC	6	109919488	F
Red	GTAGCGA	37	22	32599516	GCGGGTT	22	30929516	F
Red	AGAGAAC	37	6	4403020	CGGATGC	6	4348019	F
Red	TCGGCCA	37	6	109611667	AGAAGAC	6	109718360	R
Red	CGCCTGG	37	6	28558070	TTTCCCG	6	28666049	F
	GCTCATT	37	1	92002689	CGGTCTC	1	91775277	R
	GAAATGC	37	7	158820418	ATTTGCT	7	158513179	R
Grn	GGAGGCA	37	5	130344188	CGGGCCC	5	130372087	R
	AGGCAAC	37	5	71475303	CGGGCCA	5	71511059	R
	TAAAGTT	37	7	19759345	CACTTGA	7	19725870	R
Grn	TGGGGCC	37	5	179588551	CATCGCC	5	179521157	R
	TTGCTTG	37	13	50975679	AGCTTCA	13	49873680	F
	TGCCAGG	37	8	1915076	TTCATGG	8	1902483	F
	GTCTCCA	37	7	158084782	CGGGCTG	7	157777543	R
	TCACTGT	37	3	131756545	TGGTGTT	3	133239235	R
	AAGTTTC	37	5	17395952	CGTGGTA	5	17448952	R

	CACCTCA	37	7	69058543	ATCCTGG	7	68696479	R
	AGTTAAC	37	12	94376970	CGTGGTG	12	92901101	F
	TTAGATA	37	11	76998821	CTTATTA	11	76676469	F
Grn	ATAACTG	37	11	93063662	CGGCTCC	11	92703310	R
	GGACCTG	37	14	51411481	GGAGGCT	14	50481231	R
	GGTTCTT	37	6	32609094	GGCCAGA	6	32717072	F
	CCTAGCC	37	3	42725643	CTATTAT	3	42700647	F
	CCCACTC	37	12	126465510	TTCCTAT	12	125031463	R
	GATGCAA	37	5	140086190	CCCAGTC	5	140066374	F
	TCCTTCC	37	7	116909621	CGTAGCA	7	116696857	F
Red	CACTCAC	37	6	31324916	CAGGTCT	6	31432895	R
	GTCACAG	37	5	171831028	CGGCAGC	5	171763633	R
Red	TGCGCTT	37	5	147699892	ATGGGCT	5	147680085	R
Red	GCAGCGC	37	3	160170242	GAGGAAC	3	161652936	F
	GATGAGA	37	7	107574783	GAGGAAC	7	107362019	R
	TGGGAAA	37	12	109248326	AGGGCAC	12	107772455	F
	GTGACCA	37	11	67141961	CGGACCA	11	66898537	F
	GTAAAAA	37	6	28092048	GTGACTT	6	28200027	F
	TGCCTTA	37	11	57195382	ATCTAAT	11	56951958	F
	CCAGGAA	37	6	32633114	CGGGCTG	6	32741092	F
Red	GGCCTCC	37	3	10149882	CCCTATC	3	10124882	R
	CCAAGAC	37	1	206677719	TAACATT	1	204744342	F
	TGCAGAC	37	11	10339086	CCCTCTA	11	10295662	F
	GTGCTGG	37	1	85584420	GAAGTGA	1	85357008	R
Red	GGCGGGA	37	1	234350834	CTGCAGC	1	232417457	R
	GCAAGAC	37	3	43927675	CGTCTGC	3	43902679	R
	ACTTGAG	37	11	19078052	GCTGCAT	11	19034628	R
	AATCAAC	37	1	5526684	AGTGGGC	1	5449271	R
	AACCCAC	37	15	22947765	CGGTAGA	15	20499206	R
	CAGCGGT	37	1	24373210	CGGTCAG	1	24245797	R
	AGACAGA	37	6	32520916	CGACTCA	6	32628894	F
Red	GGTGATC	37	12	115137528	TCTGGTA	12	113621911	F
	GACTCTC	37	1	92203667	CGGGAAC	1	91976255	R
Red	TAGGGCC	37	6	101846797	AAACCTT	6	101953518	R
	CTAGCCC	37	1	16345368	TCTAGAA	1	16217955	R
	TTTATGG	37	14	70827109	CGCTTTT	14	69896862	F
	ACAGTGC	37	6	114053961	GCCTTTT	6	114160654	F
Red	GTCCCGT	37	1	182921688	GACGAAT	1	181188311	R
	GGGGAAT	37	12	124810173	TGAGGCC	12	123376126	F
	ATGAGGT	37	1	36689477	CAGGCTC	1	36462064	F
Red	GCAAATC	37	7	2768988	CGTGGTC	7	2735514	F
Red	GCCGCAC	37	2	233251770	CCTCGTT	2	232960014	R
	TGAGCGC	37	6	42695332	CGGCCCA	6	42803310	F

	AAGCCAA	37	14	65078521	CGGCATA	14	64148274	F
	ACCCAAT	37	11	122047028	CGTTGCT	11	121552238	F
Grn	TCACTGA	37	13	23755059	GGATGAA	13	22653059	F
	CCTATTT	37	15	77481069	GACCTGC	15	75268124	F
Grn	GCAGTG	37	1	1362340	GGCCGCT	1	1352203	F
	CATTGCC	37	6	30043924	CGGCCCC	6	30151903	R
	GGGAAT	37	8	41258634	CGCTTGC	8	41377791	R
	CATTTGG	37	11	69245569	TTCCAGC	11	68954750	R
	AGGAGA	37	6	153405859	TTGGCCA	6	153447552	F
	GCATTTT	37	17	39151857	CGCTATT	17	36405383	F
	CCTCTAT	37	2	238647857	CGCCAG	2	238312596	R
Red	CGGCCCA	37	6	30039202	CGGCCG	6	30147181	F
	GTGACCT	37	13	30061917	CGGCACA	13	28959917	F
	GCATATG	37	1	2705849	CATGTCC	1	2695709	R
Grn	TGGGCCG	37	4	4860190	CGGGGT	4	4911091	R
	AGCCTTT	37	7	158541253	GAGCTAT	7	158234014	F
	GAGGGTA	37	17	48136824	GAAGCC	17	45491823	R
	CAGCCTG	37	2	240020028	AGGGCCT	2	239684965	R
	ACTCATT	37	6	152640475	CGTTAGT	6	152682168	R
	AGACTGT	37	17	6495080	CGTTTCC	17	6435804	R
Red	CCTGACT	37	14	93106414	CGCAGTC	14	92176167	R
	CTGTCAC	37	1	27524410	TGTGTAA	1	27396997	F
	CCTCTGT	37	1	204556835	ATTGTGC	1	202823458	R
	TGTGATT	37	4	123090679	CGGTAG	4	123310129	F
	CTTGCCG	37	13	36049673	GGAGTG	13	34947673	R
	CTCTTTC	37	8	130713856	CGCCCCC	8	130783038	F
Red	AATGACA	37	14	101908752	GCTGCAC	14	100978505	F
	GTTTTAC	37	15	86062960	GAACCA	15	83863964	F
	GCGTGGT	37	2	239999466	CGCAGC	2	239664403	R
	GAGAGT	37	22	36960499	TCTCCTT	22	35290445	R
	GTAGCTT	37	11	96076288	TTCCTTT	11	95715936	R
	CCCGCAG	37	4	39772940	GTGAGCA	4	39449335	R
Red	GTCCTAG	37	2	121412005	CCGCTGC	2	121128475	F
Grn	TGGTTGT	37	2	879510	CCCGTTC	2	869510	R
	GGTATCA	37	7	155492281	CTTTCAC	7	155185042	F
	TACCTGT	37	1	225838196	ACTGACA	1	223904819	R
	CAGGGT	37	5	71713491	CGGGAAT	5	71749247	F
	TTTCAGC	37	6	140364611	CGGTGAT	6	140406304	F
	GGCGCC	37	2	232395300	TTGTGAG	2	232103544	F
	ACGACTG	37	10	135341528	CGGCGTT	10	135191518	R
	ATGATGT	37	10	63388439	CCAGCAA	10	63058445	F
	CCCATTG	37	4	146018723	CGGCAGA	4	146238173	F
	ACAATAA	37	11	48509778	CGGGAAA	11	48466354	F

	GAATGGC	37	1	217313824	CGACTCC	1	215380447	F
Grn	AGAAAGA	37	8	1899406	CGGTCAG	8	1886813	F
	ATTGAAC	37	6	55965977	CGACTGA	6	56073936	F
Red	CTCCGAC	37	12	125223502	CCCCGAC	12	123789455	R
Grn	AAATGGT	37	7	79084196	CGGAGCT	7	78922132	R
	ACCACAC	37	3	27575278	ACCACTC	3	27550282	F
	CCCGGGC	37	6	4661470	CGGTCCA	6	4606469	F
	TTTTTGCA	37	10	7670827	CGCTACA	10	7710833	R
	AAACGTC	37	17	146670	GGATGCT	17	146670	F
	TATAGCT	37	6	30856386	CGGCCCA	6	30964365	F
	AGCCCAA	37	6	32634276	CGGGAGA	6	32742254	F
Red	AGACGCC	37	2	54087189	GGCCGGC	2	53940693	F
Red	CTGCGTC	37	2	198650987	CGCGCCC	2	198359232	R
	CATTTCT	37	1	230241764	CGGTCTT	1	228308387	F
	CCTGGTG	37	4	47035074	ACAAATT	4	46729831	F
	GTGCTGG	37	Y	27210334	CGTCACC	Y	25619722	F
	CTGCAAG	37	12	10336861	CGGTAAT	12	10228128	F
	AACACTT	37	5	177505451	CGGCCCC	5	177438057	F
	TCCCAGA	37	X	53350895	CGGGAGC	X	53367620	F
	TAGCAGC	37	1	27899025	CGTCCGT	1	27771612	F
Grn	GCTCAGT	37	19	40375973	CGGGACC	19	45067813	F
	CCCCCCT	37	6	30419135	CGGGTCC	6	30527114	F
	ATATATT	37	12	76414534	CGTTGGC	12	74700801	R
	CAGGAGC	37	18	60646614	CATAGTG	18	58797594	F
Grn	AAGCCAC	37	13	25212556	GTGCAGC	13	24110556	F
	TAGCTCA	37	1	8480963	CGGAGTC	1	8403550	F
Red	GGCGCGC	37	6	30039432	CCTGGTG	6	30147411	R
	ATTTTTT	37	9	116133216	CACACAA	9	115173037	R
	TTAACAT	37	2	191365138	AAAGTCC	2	191073383	F
	TTTCATCA	37	6	3592887	CGAAACA	6	3537886	R
	CCATGGC	37	13	111287117	GAAGGCT	13	110085118	R
	CAGCAAT	37	19	50550359	CTGTAGC	19	55242171	R
	CTTGGGG	37	3	11596003	CGGTCCC	3	11571003	F
	GTGTGGA	37	9	101869277	CGGTGTG	9	100909098	R
	CATAAAT	37	17	3814718	TTCCCAC	17	3761467	R
Red	GGGAGCA	37	1	991708	CGCCAGA	1	981571	R
	TACTAAG	37	9	37780478	CGGTACA	9	37770478	R
Grn	GCCACAC	37	6	887704	GGCGGAC	6	832704	R
Red	TCAGAAC	37	10	43846281	GTTGAGA	10	43166287	F
	CGTGGCA	37	9	2234921	TCCTCAC	9	2224921	R
	GGAAAAC	37	10	3823758	CGGGCCT	10	3813758	R
	TTTGGTG	37	9	99615182	CGAGGGA	9	98655003	F
Red	CTAGGCT	37	10	27702309	CGGCAGC	10	27742315	R

	GCAGCTC	37	1	62499140	CGGGAAT	1	62271728	R
	GGAGTCG	37	17	57116416	CATGGAC	17	54471198	R
	AGCCCCG	37	4	1046988	GTTCCTT	4	1036988	R
	GCTCCTA	37	2	20638399	GGTTCTG	2	20501880	R
	AATGGTT	37	9	131081198	ATTTTTC	9	130121019	R
	CACGGAT	37	9	16442831	GCCTATG	9	16432831	R
	AGCCAGT	37	1	5137221	TTGATGC	1	5037081	R
Red	AGGCTTC	37	17	21191452	CGGCTGG	17	21132045	R
	TATACAT	37	1	217004524	CGTGTCT	1	215071147	F
	TTGGTGC	37	9	92681430	TGTGGCT	9	91721250	R
Red	AGCTCGC	37	1	152161927	CGCTCCG	1	150428551	R
	CAAATAC	37	2	176997504	CGCTCAA	2	176705750	F
	TCTGCGG	37	13	29914200	GCCAAGT	13	28812200	R
	TATGCCA	37	22	32650997	CATAAAT	22	30980997	F
	TGGCTAG	37	19	55417390	CGCCTCT	19	60109202	R
Red	GGCGTGT	37	10	135273122	GGGGCAC	10	135123112	F
	CAAGGA	37	11	3117181	ATTTGAT	11	3073757	F
	GCAGGCT	37	9	140330627	CGCCCCC	9	139450448	R
	ACCAAGA	37	7	158098282	CGCCTTG	7	157791043	R
	ATTAACT	37	17	76607622	ATCCATT	17	74119217	F
	CTGTCTG	37	10	135269787	AGGTGGA	10	135119777	R
	TGAGGTA	37	5	112825132	CGGGCAC	5	112853031	F
	CAATAAA	37	13	102108074	CGCAGTC	13	100906075	F
Red	CCTACAT	37	9	32426330	CCTCCCA	9	32416330	F
	AGCTTGT	37	6	112688607	CGGTAGC	6	112795300	R
	ATTCAGC	37	1	209997303	GTATTGT	1	208063926	R
	TTTTCCA	37	2	243017952	CGGCACC	2	242666625	F
	GCTGAAG	37	14	62004353	TCTCAGA	14	61074106	R
	GGTTAGG	37	9	136822302	CGGGCCT	9	135812123	F
	TGAGTTC	37	1	42954129	CCACCTT	1	42726716	F
	ACAGTTC	37	15	45449437	CGCATAT	15	43236729	R
	ACATGGT	37	19	4033718	AGCAAGA	19	3984718	R
Red	GCCCCTC	37	7	72813978	CGGGGAA	7	72451914	F
	CAGCCCC	37	8	22925391	CGCAGCT	8	22981336	R
	CACAGAC	37	4	57824450	AGAGTTG	4	57519207	F
	TACAGGC	37	5	135415781	TATTGCC	5	135443680	F
	CAGGGTC	37	5	172324773	ATGTGAG	5	172257379	R
Red	GCCCCTC	37	9	132016282	CGCAGCC	9	131056103	F
Red	GGTGACT	37	2	875437	CGCCCCT	2	865437	F
	GTCTCCT	37	15	42186830	CGGGCCA	15	39974122	R
Red	AACAGAA	37	11	132582488	TGAACCT	11	132087698	F
Red	TGCTTGG	37	9	137662926	CGCAGCC	9	136802747	F
Red	ACCAATC	37	9	127534760	CGCATCC	9	126574581	F

	TCTCTTT	37	17	63926873	AGTGCTT	17	61357335	R
Red	GGAGGA	37	19	33572088	CGGGCC	19	38263928	R
	CTCTTAA	37	17	68070495	CGGTGGC	17	65582090	R
	ATCAGTA	37	12	59281920	AAAAAT	12	57568187	R
	AGGATG	37	20	37054900	AGCCCA	20	36488314	R
Grn	TATAAGG	37	12	54380956	GCATGCG	12	52667223	F
	TAACAAA	37	6	32843055	ATTAATT	6	32951033	F
	AAAAAG	37	8	72755052	GAATGCT	8	72917606	F
	TGAGACC	37	X	69509727	TCCGCTT	X	69426452	F
	TCTTTCC	37	11	13987766	CGGCAA	11	13944342	F
	GAGAGG	37	9	6932042	TCTCATA	9	6922042	F
	GCCTCCT	37	9	101264699	CTCTGAA	9	100304520	R
	GAAGAC	37	9	119475712	CGGGCCT	9	118515533	R
	GCATTTG	37	2	33359356	TATTAAG	2	33212860	F
	CATCTCA	37	10	129197384	CTTAATC	10	129087374	F
	TCCACCA	37	6	33035284	AAAAGC	6	33143262	R
Grn	GGAGCA	37	11	2176877	TGAGCTG	11	2133453	R
	GCCCGCC	37	19	5335254	CGGACG	19	5286254	F
	TCCACCC	37	12	54387530	ACAAGG	12	52673797	R
Grn	CCATTGC	37	9	135114066	CGCCGTG	9	134103887	F
	CTAAGGT	37	9	136152547	CGCCCAG	9	135142368	F
	TTATTT	37	10	1511173	CGGGGC	10	1501173	R
	AAACATT	37	14	81879247	CGGGCG	14	80949000	F
	TGCAGCT	37	5	11851713	CATTAAC	5	11904713	R
	ACATACA	37	17	48211226	CGGCCA	17	45566225	R
	GACTTTT	37	1	147144052	GTGATTC	1	145610676	R
	CCAATAA	37	6	31587680	GGCTAG	6	31695659	F
	TCTGTGG	37	11	27016671	TATCCTT	11	26973247	F
	CAGTGCA	37	13	111522651	GCATGA	13	110320652	F
Red	GGCTCTG	37	X	30671314	CGCGCC	X	30581235	F
	TGGGATT	37	2	86251199	CGCTGTG	2	86104710	R
Red	TTCACAG	37	6	85824168	CGCCGCT	6	85880887	R
	GATTCCT	37	14	84720664	CACTACT	14	83790417	F
Red	GCCATTG	37	12	121147668	TTGGGAC	12	119632051	R
Red	GGAGAC	37	9	100000033	CGAGCTC	9	99039854	R
Red	TCAGTTC	37	9	15371248	CGGAGG	9	15361248	F
	TACAGAA	37	9	18825658	AGAAATC	9	18815658	F
	ACCCTTT	37	5	142001033	TGGTCTG	5	141981217	R
	GTGCCAA	37	9	135879019	CGCCCAG	9	134868840	R
	CTGGCTT	37	19	8953473	CGAGAA	19	8814473	F
	GACAAA	37	6	1387836	CGCTCAG	6	1332835	F
Red	GGCCCGC	37	19	52954722	CTGGGTG	19	57646534	F
Red	TCGAGGA	37	8	144810657	CGAGCG	8	144882645	R

	CCAACTT	37	9	36989127	GAGCTCA	9	36979127	F
	CAGATTT	37	11	93754223	CGGCTCA	11	93393871	F
	CCCTGCT	37	7	2289888	CGTCAGG	7	2256414	F
Grn	ACTCAGG	37	15	24506388	CGCGCTT	15	22057481	R
Red	GAGACCT	37	14	75722495	CGCAGAC	14	74792248	R
	GGGGTCC	37	9	138591683	GTTCCCA	9	137731504	R
	TATCAAG	37	9	38477418	CGGGAA	9	38467418	F
	CCTTTCA	37	9	139635449	CGCCCAC	9	138755270	F
Grn	TCGTGCG	37	2	24583121	GGGTGAA	2	24436625	F
	CAGCAGT	37	9	138586311	TGAGCTC	9	137726132	F
Grn	GCGGGTC	37	17	4901063	CGAGCGC	17	4841787	F
Grn	TAAAGTC	37	19	15982569	CGGCACC	19	15843569	R
	CTCAAGC	37	14	105576362	CGCCCAG	14	104647407	F
Red	GTCCACG	37	5	76250527	CGGGTCA	5	76286283	R
	ACACCAC	37	6	32609783	CGGGAGA	6	32717761	R
	TTTTCAC	37	2	43618836	CGATGCT	2	43472340	F
	TGTTGTT	37	9	126816959	CGGCTGT	9	125856780	R
	GAATTCA	37	3	98848062	TCTGTGA	3	100330752	R
	GGGGACT	37	7	75829463	TTCCTGG	7	75667399	R
	TAGCGAT	37	10	28030033	CGAGAAC	10	28070039	R
	AATCCTG	37	Y	24453658	CGGCGCC	Y	22863046	F
	TATTATT	37	9	36100589	CGGAGGC	9	36090589	R
	CAATTCA	37	2	101124858	CGCTGAT	2	100491290	R
	GCCTCTC	37	9	34953950	CGACAAC	9	34943950	F
Red	CAGTAGA	37	X	8751330	CGGACCC	X	8711330	R
	ACATCCA	37	12	115118806	CGGGGTC	12	113603189	F
	TCCCAGC	37	19	16989699	TCGGGTG	19	16850699	F
	GATAACT	37	9	72735830	TGTATGC	9	71925650	F
Grn	AGTCTGT	37	12	9555480	TTTCCCC	12	9446747	R
Red	TGACTGT	37	9	38488083	CGGGCAC	9	38478083	F
	CTTTTTA	37	15	24675297	CCAACAA	15	22226390	F
	TTAAAAG	37	6	30045936	CGGCTGT	6	30153915	F
	GCAGTAC	37	9	140356757	TCAGGCG	9	139476578	F
	TTAGACT	37	10	101421142	CGATATT	10	101411132	F
	AAAAATA	37	7	55638724	CGCATGA	7	55606218	R
Red	GTCTTCA	37	6	169092843	ATCTCTT	6	168834768	R
	AATTGAT	37	10	95848649	CGCAAGC	10	95838639	F
Red	TGATTTT	37	9	115835616	CGCCGGC	9	114875437	R
Grn	CACCCTC	37	17	77704250	CGTGGTG	17	75318845	F
	GCTATTT	37	19	58951672	TCCTTCT	19	63643484	F
	GTGATAC	37	12	95840895	TTTAATT	12	94365026	F
	AGCCTTA	37	6	52454298	TCCAACA	6	52562257	R
Red	GTCGGGC	37	17	47502298	GGAGTAC	17	44857297	R

	CAGGACA	37	9	84228185	GTTGTCT	9	83418005	F
	ATACCTG	37	1	1549699	CGGACTT	1	1539562	F
	TTTCCAA	37	9	77282233	TTGCGAA	9	76472053	R
Red	AGAATGT	37	12	130824015	CGCCGTG	12	129389968	R
Grn	AAGGAAC	37	11	5959945	CTTCTGA	11	5916521	R
	ACCCAAA	37	5	141485167	CGGTGGA	5	141465351	R
	GACCCAT	37	6	32549849	CGGCATG	6	32657827	F
	CGTCTTG	37	5	172970	AAATTCA	5	225970	F
	GTGCACC	37	X	152908309	CGCACCA	X	152561503	F
	TTTCTGC	37	11	35644854	GACAGTA	11	35601430	R
Red	CTGCGCA	37	6	30039380	CGCCCGC	6	30147359	R
Red	CGGGGGC	37	9	34810228	GACCGGC	9	34800228	R
	AGGGAGC	37	1	154194049	CGCACAC	1	152460673	R
Red	GCACAGC	37	1	1168432	CGACCCG	1	1158295	F
Grn	GAAACAC	37	11	10750890	TTCCCAT	11	10707466	F
	CCAATCC	37	9	84646696	AGAGTGA	9	83836516	R
	GATGTTA	37	5	39800321	CGGGGAA	5	39836078	F
	AAACATT	37	1	6063654	CGTTTCC	1	5986241	R
	CGTGGGC	37	1	179777372	CTCAGGC	1	178043995	R
	CCTTGGT	37	9	27575280	CGTCTAA	9	27565280	F
Red	CCCCGCC	37	X	153236838	CGCCCAG	X	152890032	F
Red	CACCCAT	37	15	65143918	CGCTGAA	15	62930971	R
	AGAGAGT	37	4	87959251	TGCATTG	4	88178275	R
	CGTTTGT	37	12	10096112	CAGCCAA	12	9987379	F
	CGTACAC	37	9	94533180	CGGCCGA	9	93573001	F
	GTTGTAG	37	5	32445523	CGTTCTA	5	32481280	F
	TTCCGGC	37	19	10928696	GATATGA	19	10789696	R
	TCTTTGT	37	7	127526253	ATCTTCT	7	127313489	F
Grn	ATGGGAA	37	9	137662888	AGCGCCC	9	136802709	F
	GAAAGCA	37	5	74344416	AGGATTT	5	74380172	F
	AGAGCTT	37	14	59183596	GCTGGTG	14	58253349	F
	TTTATTT	37	9	99776416	GAAAGAT	9	98816237	R
Red	GGAGACC	37	X	153210107	CGGGACC	X	152863301	R
	CAAGTTG	37	7	127222520	CTTGGGT	7	127009756	R
	GATGAAT	37	6	119862526	AAATGCT	6	119904225	F
	ACCACTC	37	17	10220829	CGGGAAA	17	10161554	F
	AACTGAA	37	17	57187728	CGGTAGT	17	54542510	R
Grn	GCCCTGG	37	9	134699541	GTGTTTT	9	133689362	R
	CTCTTTG	37	7	154719422	CGACAGC	7	154350355	F
Red	ATACTGA	37	9	117134861	CGCTCCA	9	116174682	F
	AGGTCGC	37	X	53350200	GAGCTGA	X	53366925	F
Red	GCATAGA	37	19	46526321	CGGGCGC	19	51218161	R
	CTGTTCC	37	9	93983210	CGCGAGT	9	93023031	R

Grn	CCTCGGC	37	2	131046122	CGCCGTT	2	130762592	R
	CGAACCC	37	10	104535020	CGGCCTG	10	104525010	R
	GCGCAAC	37	6	29911265	CGCACGT	6	30019244	R
	ATTTCCC	37	9	826657	GAGTGGT	9	816657	F
Grn	GGGGCAC	37	9	139943146	CCCGTCG	9	139062967	R
	AATGCCA	37	10	46010523	CAAACTG	10	45330529	R
	GAGGCGA	37	1	211909305	TGTCTCA	1	209975928	F
	TGTATAA	37	4	127811266	CGGAAGT	4	128030716	F
	AATCACG	37	4	169645874	CGATCAG	4	169882449	F
	CCAGCTG	37	8	134271505	TGGAGGC	8	134340687	R
	AACCAAC	37	6	32312351	GCTCAAT	6	32420329	R
	ATCCTGA	37	6	31439497	GATGTGG	6	31547476	R
Grn	GAGGTGC	37	19	853145	GGGAGGC	19	804145	R
	TGACCCT	37	3	185676640	CGCAGGC	3	187159334	R
	GCTGCCG	37	2	241860995	TTAGTAA	2	241509668	R
	ATTCAGC	37	9	115771599	AGCCAAA	9	114811420	R
	CTGGGGT	37	9	132598917	CGTAAGC	9	131638738	R
Red	CCTTAGG	37	19	18054643	GGGACCC	19	17915643	F
	GAGACCT	37	9	139406352	CGGCTGT	9	138526173	R
	TCAACAG	37	5	140579303	AAATCCT	5	140559487	R
	GCAAGGT	37	13	109439124	TGGTTAC	13	108237125	R
	TATAACC	37	9	110231817	GTTTATT	9	109271638	F
	TGTGACT	37	9	133838188	CGGAGAC	9	132828009	F
Red	CAGCCCG	37	6	32552515	CGCTTTA	6	32660493	F
Red	TGGAGGA	37	7	231526	CGCCAGC	7	326609	R
	GGCTGCC	37	6	127796989	TGCCCAG	6	127838682	R
	GCTCCGG	37	21	44782497	AAGGCCT	21	43606925	F
Red	ATTAGTC	37	9	130454671	CGGAACC	9	129494492	F
	TTTTTAG	37	9	35848330	CGAAAGA	9	35838330	R
	GATACAA	37	14	91820590	CGCAGAA	14	90890343	F
	CACCACA	37	11	1682006	ACATTCA	11	1638582	F
Red	GACCCGC	37	13	23412409	CGCTACC	13	22310409	R
	TCCGGAG	37	19	6425737	CGACCCC	19	6376737	F
	CTAACCT	37	11	67141628	AGACAAA	11	66898204	F
	CCGCCAC	37	9	32979252	CGGAGCA	9	32969252	R
	AGCTAAC	37	13	21889774	GGCAAAT	13	20787774	R
	GGAGTGA	37	6	47666329	CGGCTTC	6	47774288	F
	CGGGGAC	37	X	9433597	CGCTCCA	X	9393597	F
Red	GCACCAT	37	19	50733985	GCAGCGA	19	55425797	F
Red	TGACAAC	37	12	8717487	CGCTCAA	12	8608754	F
	TGAGACC	37	19	8619925	GGCCAAC	19	8525925	R
Red	AAGGCCT	37	X	77154916	CGCGAGA	X	77041572	F
Red	GCGCCTG	37	19	14607017	CGCAGCC	19	14468017	F

	GCTAACT	37	2	134391847	GGTGATT	2	134108317	R
	AGCAAA	37	5	121499498	CGCTGTG	5	121527397	R
	TTGGGAG	37	18	6283067	CGTCACT	18	6273067	R
	TTTTGCT	37	9	100502742	CCTCCTA	9	99542563	F
	TTTGACC	37	Y	14652924	AAGTTAC	Y	13162934	R
	AAAATG	37	14	52708188	AGCCTGC	14	51777938	R
	TCTTGTT	37	Y	19678535	CGGGTCA	Y	18187929	R
	TCTTTTC	37	9	28596895	TATAGCC	9	28586895	F
	AACCCAC	37	6	83893273	CGGACTG	6	83949992	R
	TCTCAAA	37	9	132937709	CGGGAG	9	131977530	R
	ACAAAGC	37	2	206585563	CGGCCTG	2	206293808	F
	GGAATCT	37	9	138749560	CGGCCTC	9	137889381	R
Red	CTGGGCG	37	14	104574715	CGAGGGC	14	103644468	R
	TGAGGAT	37	11	70424559	CGCACAC	11	70102207	F
	AGCCCCC	37	7	155191709	CGAGAAC	7	154884470	F
	CTTCCCA	37	21	43835592	CTCTAAA	21	42708661	R
	TTATACG	37	7	75269642	CGGCAGC	7	75107578	F
	AGTGGCC	37	9	82286351	ACTGTGA	9	81476171	R
	TGCCGTA	37	4	7374582	CGGGAGT	4	7425483	R
	AATTTGG	37	12	20003184	CGCTATG	12	19894451	F
	GATGCGT	37	2	97651611	CGGGCAC	2	97015338	F
	CTCAACC	37	7	42896343	TTCCCAG	7	42862868	F
	AGTTCCT	37	12	30878975	CTGAGTC	12	30770242	R
	TTTTAGC	37	15	77436852	TTGACTC	15	75223907	F
	CCAGGG	37	11	65342283	CGGTCTT	11	65098859	F
Red	GGTAGAC	37	19	46417639	GCTGGCC	19	51109479	R
	TGCTGAG	37	17	80849463	CGGGAGT	17	78442752	F
	CAGAAA	37	4	174723167	ATAGTTT	4	174959742	F
	TCTCAAA	37	14	67983484	CGTGTTC	14	67053237	F
Grn	TGACCTT	37	4	183063397	CTAGTGA	4	183300391	F
	CTCGCCT	37	6	170190660	GTGGGGT	6	169932585	R
	TGAAGCT	37	11	114166636	CGGGATC	11	113671846	F
	CCTCTGG	37	11	66738758	GAGCCTG	11	66495334	R
Red	GCTCTTT	37	8	38508585	CGGTGTT	8	38627742	F
Red	AGCTCTC	37	14	24439157	CGCAACC	14	23508997	F
Red	CCGCAGC	37	7	27146445	GGAAGCT	7	27112970	F
	TGGGCTG	37	16	857981	CGCCAGT	16	797982	R
	CCCGGAC	37	2	113190197	CTGTATC	2	112906668	F
	ACAGATT	37	7	137013465	CGCAGGC	7	136664005	F
	CTCTTCT	37	11	103677503	CGGGGCT	11	103182713	R
	CACCTGT	37	1	22328026	AACAGGT	1	22200613	F
	TGGGGCT	37	12	46005115	TGGGGCT	12	44291382	R
	CTTTAGA	37	11	6378691	CGGGGCT	11	6335267	F

	GACCCAC	37	7	48124921	GGGTTTC	7	48091446	R
	AGGAATC	37	19	15248535	CGCAGCT	19	15109535	R
	TTTCACT	37	2	137077233	CTCCTGC	2	136793703	F
	AGTGGCA	37	13	110132672	CGGGAAC	13	108930673	F
	CCTTTTG	37	2	33226136	CGCTGAC	2	33079640	F
Red	CGCGAGT	37	19	12995624	CGGACGC	19	12856624	R
Red	CCTTCCC	37	13	111935521	CGCAGAC	13	110733522	F
	GAGTCTG	37	2	238410067	GGTTACC	2	238074806	R
Grn	TTCCTGC	37	6	74064434	ACGTTCC	6	74121155	R
	TTTTACA	37	9	32455910	GTTACAG	9	32445910	F
	TATACTG	37	19	55669189	TCCTGTG	19	60361001	F
	CCAAGCC	37	2	227662014	CGGTCAC	2	227370258	R
Red	CTGTCTT	37	6	31164848	CCCCAGG	6	31272827	F
	TGATTGT	37	9	128512035	TCAGAAT	9	127551856	F
	AATCTGC	37	14	68665820	GAATTCT	14	67735573	R
	GCATGGA	37	10	18995362	CGGCACC	10	19035368	R
	CCTCCCA	37	9	91361323	ATACAAA	9	90551143	F
	GCTCCAC	37	9	136134067	CGGCCCA	9	135123888	R
	AATGACT	37	6	33032830	TCTCCCC	6	33140808	R
Grn	CTCATGA	37	19	51330469	CGGGTAA	19	56022281	R
	TGTCTGG	37	9	114812406	TTGTCAT	9	113852227	R
	TCTGGAT	37	10	3568949	CGCCATC	10	3558949	R
	ACCAGGC	37	6	32574199	TTCCGAT	6	32682177	F
	CAGAAAC	37	6	168436353	AATCAGC	6	168179202	R
Red	GATTTTCT	37	9	115851947	CGCCGGC	9	114891768	R
Red	GGGTCAC	37	8	216788	ACCTGCG	8	206788	R
	TGACCCA	37	19	22800693	CCTGGGT	19	22592533	R
	TATTCTT	37	6	32628305	CTACTGC	6	32736283	F
	GTCTAGA	37	7	63498313	CGGGGAC	7	63135748	F
	CATATTC	37	20	34700675	CGGTGGC	20	34164089	R
Grn	GGCTGTG	37	3	138763899	CGGCCCG	3	140246589	R
Grn	GTGTCCA	37	22	21025079	CGCTGGC	22	19355079	R
	CTTCAGC	37	9	111230512	CATGGTG	9	110270333	R
	ATCGTGG	37	7	75779857	CGGCCCG	7	75617793	F
Grn	TACTTGG	37	14	104696094	CGATCAA	14	103765847	F
	GGACTTG	37	17	12631363	CGAAGGC	17	12572088	R
	TCTCCAC	37	17	77922738	GGAGCAC	17	75537333	F
	CTCATGC	37	X	70318366	TTGCTCC	X	70235091	F
	AAAGAGA	37	13	27927490	CTTTGCA	13	26825490	R
	CCAGGCT	37	19	58665643	TGAGTGC	19	63357455	F
	CCCAATT	37	5	126408756	TCAACAT	5	126436655	R
	CGAGGCC	37	9	839557	GGCGCCT	9	829557	F
	GGCTTGT	37	21	46890997	TGGGTGT	21	45715425	R

Grn	CGTCCCC	37		13	111465457	CGCCCTC		13	110263458	F
	ACATCAC	37		6	31509244	CTTGACT		6	31617223	F
	GGCTTAG	37		1	28417750	AGTGTGC		1	28290337	F
	CGCAGGC	37		2	193393	ACTAACG		2	183393	F
	TGTTTCC	37		5	150051778	CGGCGGC		5	150031971	R
Red	TACCCAC	37		13	23412250	CGGCTAA		13	22310250	R
	TCCATCC	37		7	50570049	ACTGTGA		7	50537543	R
	GGCTCTA	37		18	77836355	GGGATGT		18	75937343	R
	CGGGGCT	37		6	43964296	CGTTTCT		6	44072274	R
Red	GACTGCC	37		2	131009681	CGGCCCT		2	130726151	F
	AACTAAA	37		2	225798831	CGATCAC		2	225507075	R
	GGGCTGA	37		6	37425031	TCATTTG		6	37533009	F
	CAACTTG	37		2	198666752	CGAGCAC		2	198374997	R
Red	ACGCCCG	37		9	126794772	AGTTCAG		9	125834593	R
	ATTCCAC	37		9	120160335	TAAAGAT		9	119200156	F
	CATCGCT	37		12	70002985	GTAACTG		12	68289252	F
	CCTTGCG	37		7	157260817	GTTAGTT		7	156953578	F
	TGGAAAC	37		12	115107540	CGGGCTT		12	113591923	R
Red	CCTGGGA	37		9	93799278	CGGGGCC		9	92839099	R
	TGCATCA	37		9	2817906	CGCTGGA		9	2807906	R
	GGAATTT	37		6	141301409	GCTCCCA		6	141343102	R
	ATCACAG	37		4	99352003	CGGAATT		4	99571026	R
	AAGAAA	37		9	123257038	ACTAGGT		9	122296859	R
	GAAGAG	37		11	120678447	CGGAGCT		11	120183657	F
	CCCATCG	37	Y		15817372	CGGAGTC	Y		14326766	F
	CTGGATC	37	Y		23757241	CGGGAAT	Y		22166629	F
	GTCTTCA	37		9	89149587	CGGGAGT		9	88339407	F
	AGAGATT	37		8	8506370	GGATTCA		8	8543780	R
	CCCAATG	37		9	134484581	CGTCCTC		9	133474402	R
	TCGTCTG	37		4	132896579	CGGCTGC		4	133116029	F
	GCCTGAG	37		4	528497	CGGGGGC		4	518497	F
Red	CTCGCAG	37		6	159655392	CGCGCGC		6	159575382	F
	TGGGTTG	37		2	218295405	TCATGCT		2	218003650	F
Red	GCCCCGC	37		2	636606	CGCAGCC		2	626606	R
	CATGGTG	37		7	83097669	CGGTGTG		7	82935605	R
Grn	CACAGAC	37		7	157263638	AAGGCAC		7	156956399	R
Grn	GAGACGC	37		5	140582125	CACCACG		5	140562309	R
	CCACAAC	37		14	91017836	CGCTGAA		14	90087589	F
Grn	GCCGTCC	37		14	102973717	GCCGCGT		14	102043470	F
Red	CGTCGCC	37		2	27341893	CGCCGCC		2	27195397	F
Red	AGACAGC	37		21	35831954	CCCGGGC		21	34753824	R
	TGTTTAT	37		2	11430093	CATTTTT		2	11347544	R
	CTGGTGA	37		19	55417500	ACATCGC		19	60109312	F

	TAGCAGA	37	2	154262055	GGCTCCA	2	153970301	R
	ATGCTGA	37	2	88367362	CGCGGCA	2	88148477	R
	CCATAGC	37	9	40698808	AGTTGAT	9	40688808	F
	TAAATGG	37	9	126523663	CGCAAGC	9	125563484	F
	GTCCTCA	37	12	107348689	ACCTTCT	12	105872819	R
	TATCGGA	37	9	13280025	CGCAGGT	9	13270025	R
	TTTAGCT	37	3	10019040	CAGAGCC	3	9994040	R
	TATTTGG	37	15	31749573	TGCACAG	15	29536865	R
	GTGGGTG	37	5	1300309	ACAGCAC	5	1353309	F
Grn	AGCGGTC	37	9	96623480	CGGAGCC	9	95663301	F
	TCATGCC	37	15	84363061	GATAACA	15	82154065	R
	CCTGCCC	37	X	133507642	TAAAGGC	X	133335308	R
Red	GGAAACC	37	5	178577570	AATGTCC	5	178510176	R
	GATTTTC	37	9	93881805	GGAGTCT	9	92921626	R
Red	GGCCTCT	37	19	17571873	CGCATTA	19	17432873	F
	GACATCA	37	10	111989324	CGTGCAG	10	111979314	R
	AGGAGGC	37	1	203526848	TGTGTCT	1	201793471	R
Red	GCGGGAC	37	1	35586649	TCTCTCA	1	35359236	R
	GTATCGG	37	11	65363274	GGGCCTT	11	65119850	R
	ACATCAC	37	9	100000026	CGAAAGC	9	99039847	R
	CAAATTT	37	X	47229908	AAATCCT	X	47114852	F
	ACTGTGT	37	7	128003225	GAATGAT	7	127790461	R
	GGATGCA	37	9	136133628	CGGGAGC	9	135123449	R
	AAAGTTT	37	11	35547903	CGCAGGA	11	35504479	R
	AAAGCTG	37	9	27408242	CAATTTC	9	27398242	F
Red	CAGGAAA	37	6	32552205	TGTGGGG	6	32660183	R
	GGCATTT	37	10	126158871	CGGGCCT	10	126148861	R
	TCTCCCT	37	7	157209551	GAACTGA	7	156902312	F
	CGCACTG	37	17	76676303	TCTCAGC	17	74187898	R
	TTTCCTG	37	9	130151001	TCACGAG	9	129190822	R
	GGCGTGA	37	2	120063972	CGAACCA	2	119780442	F
Grn	CCCTACA	37	2	233246431	AGCAGCA	2	232954675	F
Grn	GTGGCCG	37	1	54151053	AGGAATC	1	53923641	F
Red	TCTGCTG	37	11	64216417	CGTGGCT	11	63972993	F
	AAATGTC	37	19	35736529	TACCCAA	19	40428369	R
	TCATAGC	37	6	31937758	CATACCA	6	32045737	R
	ATGTGGA	37	5	112405789	CGGTTAT	5	112433688	F
Grn	TACAGCG	37	1	155247706	CGGTATT	1	153514330	R
	CCTGTAG	37	19	10232899	TTCATAT	19	10093899	F
	TTCCCCA	37	12	54385526	CGCTCAG	12	52671793	F
	GGTAGTG	37	2	223784609	AAAACCT	2	223492853	F
	TGCGTCG	37	6	8776747	AATATCT	6	8721746	F
Grn	CCCTCCC	37	12	31272119	TGGCTCT	12	31163386	R

	GGAGGCT	37	7	1688174	GGTGCAC	7	1654700	F
	CGCCAGC	37	2	133014784	CGGCATG	2	132731254	F
	AGCAATC	37	11	86644657	CGGCTAT	11	86322305	F
	CCATTCT	37	19	18091245	CGCTTGG	19	17952245	R
Red	GTGGGTT	37	X	47092993	CGCCCCC	X	46977937	R
	TTGGGTT	37	10	64193068	AATGAAT	10	63863074	R
	CAGTCTT	37	12	132514956	CGCCAGT	12	131080909	R
Red	GGCCTGC	37	11	71724583	CGCACGC	11	71402231	F
Grn	GCTCCAA	37	5	1060679	CACTGGG	5	1113679	F
	TTAACTT	37	1	227689829	CGGGAGC	1	225756452	R
	TGCGTGA	37	3	128597701	TCTCTCT	3	130080391	R
Red	GTCTGTG	37	17	77127487	CGTTGGT	17	74639082	F
	AGAGAAC	37	10	96796860	CGGCAGC	10	96786850	F
	CACTCTG	37	10	129789429	CGGGATC	10	129679419	F
	GGGACTC	37	6	24724537	CGTCCTC	6	24832516	R
	TTGGGAG	37	12	115102713	GAGGTTG	12	113587096	R
	GTGAAGT	37	10	34476091	ATGGTAA	10	34516097	F
	CCCCTTG	37	22	30195299	CGGCCAC	22	28525299	F
	GAGGTGC	37	Y	17569363	GTTATAC	Y	16078757	F
	CCATCAC	37	11	43852883	CAATTGC	11	43809459	R
	TTCTAGA	37	18	12041672	CGCAGTC	18	12031672	F
	GGACGTC	37	20	43945254	CGGGGCC	20	43378668	R
	TGGGAAC	37	6	166117676	CGCAGCC	6	166037666	R
	GATCCAG	37	4	155254602	TTCAGAC	4	155474052	F
Grn	CCGCGTC	37	2	20870812	GGGCAGT	2	20734293	R
	CTGGTGT	37	6	33131893	CGGCTTT	6	33239871	F
Grn	GGGCACC	37	2	1480944	CGCGCTC	2	1459951	F
Red	TGTCATT	37	3	146262023	CGGCAAC	3	147744713	R
	CTCAAGT	37	3	128267611	CGCAAAA	3	129750301	R
	GCAAGTT	37	5	124309096	CGAGACA	5	124336995	R
	AAGCCCA	37	5	72602175	CTTGGCT	5	72637931	F
	TCCACTA	37	6	32608095	TTTGTTC	6	32716073	R
	ACTTGCC	37	2	86418754	CGCGCCT	2	86272265	R
	CCCCGTT	37	17	73055792	GGTCTGC	17	70567387	R
	GTAAGAC	37	10	103333981	TTTAATT	10	103323971	F
Red	CCCCCCT	37	20	29611903	CAGAAAC	20	28225564	R
	GTATGAA	37	7	41956427	CGCTTCA	7	41922952	F
	CTCTGCG	37	3	56717657	CGGTTTT	3	56692697	F
	CTGTCCC	37	17	75598365	TCATGTG	17	73109960	R
	AGGGTCT	37	5	78531681	CGGGTTC	5	78567437	F
	GCAGTTT	37	1	24921758	CGGTATC	1	24794345	F
	TGTGTAA	37	12	11287271	CGGGTTA	12	11178538	R
Red	GCTCGCC	37	X	30671327	CGCCCCC	X	30581248	F

	GATCATT	37	17	48275004	AGGGCAC	17	45630003	R
	CCGGGTG	37	2	54087028	GAGGCGC	2	53940532	F
	TCTTCCA	37	1	152506886	CGCCGTT	1	150773510	F
	TAAACAA	37	7	129868685	TTATGAT	7	129655921	R
Red	GTTTCGT	37	13	112927276	CCTCGTG	13	111975277	R
	AGTACAT	37	1	20235923	CGCAGAC	1	20108510	F
	CGTGTCT	37	14	102438734	CTTTGCT	14	101508487	F
	GGCTGCA	37	5	149683334	TTAAAAA	5	149663527	R
	TGTCACG	37	1	19111089	CGGCCAT	1	18983676	R
Red	ACCCTGG	37	12	6436676	CGCCGAA	12	6306937	F
	AGAGTTG	37	1	154238265	CGTGGTT	1	152504889	F
	TCCTCAG	37	4	146841701	ATTGTCC	4	147061151	F
	TTTCGTG	37	8	104032876	CGCCAAC	8	104102052	R
	GTCACCT	37	10	34151366	CGCTGGC	10	34191372	R
Red	TGCGGAC	37	2	3699353	CCCGCGA	2	3677228	F
	CTTTCCC	37	14	57021828	CGAGGGA	14	56091581	R
Red	CACATCA	37	18	30353000	CTTGGGC	18	28606998	R
	CCCAGCG	37	14	102554969	GACCGGC	14	101624722	R
	AAGACTC	37	11	65794352	CGGGAAA	11	65550928	R
	GTCACTA	37	8	28930481	CGGAGGA	8	28986400	F
Grn	TCCTGGT	37	4	7735312	CGCGGTC	4	7786212	R
	ACCACCC	37	2	131046313	CGGAGGT	2	130762783	F
	GAGAGGA	37	6	35454069	CGGGCTC	6	35562047	R
Red	GGGGCCC	37	20	43935471	CGGCTCT	20	43368885	R
Red	GGGCTGA	37	6	37616482	CGCCTTC	6	37724460	R
	GGGGAGC	37	16	88793811	CGCAGAC	16	87321312	R
Red	GGGTGTC	37	2	241562485	AGAAGGC	2	241211158	R
	AGGGAGC	37	6	31238803	CGGGAGA	6	31346782	F
Red	AGACCAC	37	10	369977	GGAGGGC	10	359977	F
	AACTTTT	37	8	122118171	GCCATGC	8	122187352	R
Grn	AAGGGCT	37	19	3595702	CGCTCCG	19	3546702	R
	CTGTCAT	37	10	128947230	GAGGATT	10	128837220	F
	TCACTAG	37	11	47256035	CGGGCAT	11	47212611	R
	TTTGCAT	37	3	115155686	CGGCTGT	3	116638376	R
Red	GGCTGCT	37	2	27373128	CGCCGCC	2	27226632	F
	AAAACTC	37	16	4525986	TGACACC	16	4465987	F
	AGTTCTT	37	7	141285961	CGGGGAC	7	140932430	R
	CTGCCCA	37	21	47530705	GATGCCC	21	46355133	F
	ACGCCGA	37	19	37794573	TCAGCTT	19	42486413	F
	CATCGCC	37	8	810491	TTTTCTG	8	800491	R
	ATCTATG	37	3	194314457	CATGCTT	3	195795746	F
	ACAGCCC	37	2	70942718	CGGCAGC	2	70796226	F
Red	CAACCTG	37	7	48129822	CGACCGC	7	48096347	F

	AATGGCT	37	19	29218262	TTGGGCT	19	33910102	F
Grn	GAGGCAC	37	2	97136729	AGTATAG	2	96500456	R
	ATTTGCC	37	3	158427635	ATTTGCT	3	159910329	R
Red	TCTTGCA	37	12	115105220	CGCTAAT	12	113589603	F
	TCATTAG	37	1	71555947	TTAAAAG	1	71328535	R
	ACCAAAC	37	1	3721781	CGCTCCG	1	3711641	R
	TTTTTCT	37	5	82771274	TCTGCTG	5	82807030	R
	GGTTCTC	37	6	49681178	CGGGTCT	6	49789137	F
	CGCAAAA	37	9	115822072	CGGGGGC	9	114861893	R
	GGGCACC	37	8	17454394	TTTCACA	8	17498671	R
	CCTGATG	37	5	72802430	CGCTGGC	5	72838186	F
Grn	TGGGTGG	37	19	50931432	CGCCGCT	19	55623244	F
	GTGCCCT	37	1	49085506	CGCTGAT	1	48858093	R
	CATGAAT	37	6	32609212	AGTGCAC	6	32717190	F
Red	CCCCACC	37	13	91827286	TTCCTTC	13	90625287	F
Red	AAGCGCC	37	17	46908359	GGGGCGC	17	44263358	R
Red	TCCATTT	37	1	152161237	ACCATGT	1	150427861	R
	CTGCATT	37	X	7137413	TGCCTAG	X	7147413	F
	AGCTGGT	37	1	2082458	TCGTGCA	1	2072318	F
	TCTCATT	37	1	223889141	AAAGGGC	1	221955764	F
	GCGAGGC	37	17	35501295	CGTAACC	17	32575408	F
	ATACGTT	37	10	126434204	CATAGCA	10	126424194	F
	CAAGGAT	37	5	140501784	GAAGCAA	5	140481968	F
	GGCGTGC	37	22	16288741	CGGATGC	22	14668741	F
	CGGAATC	37	6	152464791	CGGGGCC	6	152506484	R
	CAAAAAC	37	11	129310863	GTTGCTG	11	128816073	R
	CACCTTC	37	Y	22737505	CTGAGGC	Y	21146893	F
Red	AAGGGTA	37	1	149680232	CGGGTCT	1	147946856	F
Grn	GGAAATC	37	3	13974467	GAGAGAA	3	13949468	R
Red	CTAATTT	37	7	130130203	GAGAGAC	7	129917439	F
Grn	TTCAATG	37	13	112547653	TCACGAG	13	111595654	F
Grn	ACCGAGT	37	11	1892307	TGCATGT	11	1848883	R
	GATGCTT	37	2	160758480	TATCTTT	2	160466726	R
	ACAAACT	37	3	14160960	CGACTTT	3	14135961	R
Red	AGGCCAC	37	10	3169259	CTCCGGC	10	3159259	F
	GGGGCAC	37	1	247511364	CGCCCCA	1	245577987	R
Red	TCGGATA	37	4	4860061	GTGAGCC	4	4910962	F
	AACTGGC	37	19	30365441	CGGCCAC	19	35057281	F
Red	TCTGCTT	37	4	167448796	CGGAACA	4	167668246	F
	CTGGTGC	37	4	940614	GGCTACA	4	930614	R
	CAAACCC	37	5	140166589	GCAAGGT	5	140146773	R
Red	GCCTCCC	37	19	51330265	CGCCTGA	19	56022077	R
	AGCCGCC	37	3	10150083	CGCCCCC	3	10125083	F

Red	CGACTCC	37	5	140256817	GCAGCGC	5	140237001	R
	GGATCGC	37	17	76503526	CATTAGG	17	74015121	R
	GAACCAC	37	1	16060610	CGGGCAC	1	15933197	R
	TGTTGCC	37	2	33359281	ATCTCCT	2	33212785	F
Red	TTCTGCC	37	2	66805086	CGCCTTT	2	66658590	F
	CATCTGT	37	6	33051749	CGGGATT	6	33159727	F
Grn	CAGCTCC	37	3	48694534	CGCCGAC	3	48669538	F
Red	AGGAACT	37	5	6755386	CGCGAAC	5	6808386	R
	AAAACAC	37	16	28550619	CGGCCAC	16	28458120	F
Grn	CCCGCAG	37	6	160023626	TCAGTCA	6	159943616	F
	ATCCCAG	37	15	40272006	CGGGACC	15	38059298	F
	AAGCGGT	37	19	21265264	GTGGCTG	19	21057104	R
Red	GAGTCCC	37	19	50249737	CGATGCC	19	54941549	F
Grn	AAACCCA	37	5	123679203	CGCTGCG	5	123707102	R
	TGAAATA	37	19	18888799	CGCCAGC	19	18749799	R
Red	CTTCCTC	37	17	19883474	AGCGGGC	17	19824066	F
	ATGCCTC	37	6	1841153	CGCCCTC	6	1786152	R
	CTGCTCC	37	1	46858748	CGGTGGC	1	46631335	R
	CACTTTT	37	6	85821320	TCACTGC	6	85878039	F
	TGCCAGG	37	1	55909399	CGGCAGC	1	55681987	R
Grn	CTTTAAC	37	1	6526051	CGGAAAC	1	6448638	R
	CTGAGGT	37	4	152096590	CGGCTGC	4	152316040	F
Red	TGAAAGA	37	19	18344520	CGCGGAC	19	18205520	R
Red	CTCCCCG	37	6	35479628	CGCGAGC	6	35587606	F
	TGCTGAC	37	5	7540955	CGGACCA	5	7593955	R
Red	TCTGCCG	37	X	73642618	CGCCCGC	X	73559343	R
Grn	AGCAAAC	37	20	43935462	CGCGGGT	20	43368876	R
	TGTGGAC	37	10	134109919	CGGGTAC	10	133959909	R
	ACATCCC	37	3	111853297	CGGGTGC	3	113335987	R
	ACCAGGC	37	12	68405565	GTAGGCT	12	66691832	F
Red	CTAGATA	37	17	80627638	CGCTCAA	17	78220927	R
Red	CCCAGTC	37	8	8770972	TATTTCT	8	8808382	R
Red	AGCCTAG	37	12	8025582	CGGGAGC	12	7916849	F
Red	CCCCGAC	37	22	24384393	TGCCCCA	22	22714393	R
	AACTCTT	37	7	14031941	CGCTACA	7	13998466	F
Grn	ATGTCAG	37	10	29214117	GCTGCTT	10	29254123	F
	GCAACGA	37	6	171036378	ACTGGTG	6	170878303	F
	CTGGGCG	37	12	125346253	CGGCCCC	12	123912206	F
	GATTTCT	37	7	158069943	CGCACAC	7	157762704	R
	CCTACAT	37	10	237794	CGGTGGC	10	227794	R
Red	CGGCAAC	37	17	76897139	TCACACG	17	74408734	F
	CCTCAAT	37	17	15176491	CCAATCT	17	15117216	R
	CCGTTTG	37	17	80557543	GATGTGA	17	78150832	F

	GGAATCC	37	2	1166311	AAAGATC	2	1156311	R
	GCTGAAA	37	3	151309377	CGATCTA	3	152792067	F
	TTGTTAC	37	6	160182438	CGCTCCC	6	160102428	F
	CGCCCAG	37	6	39040812	CCAGTGG	6	39148790	R
Red	TCTCATC	37	12	114162813	CGCCGAT	12	112647196	F
	CACACTA	37	8	1310764	GGTCTAG	8	1298171	R
	TGCTTCT	37	2	180427325	AATCATA	2	180135570	R
	GTTGTCT	37	15	79973958	GCAAGCC	15	77761013	R
	GCAGATC	37	7	157730196	AGCTACT	7	157422957	R
	TTAGCCG	37	3	50648891	GGACCTC	3	50623895	F
Red	AGGTGGC	37	Y	21239461	GAGGACC	Y	19698849	R
Red	GTCCTCC	37	10	88702795	CGCGGCC	10	88692775	F
	AATTCCT	37	3	24203479	CGCCCAG	3	24178483	F
	CATGAAA	37	3	143567492	TTTCATA	3	145050182	R
Red	AGGGACC	37	12	131057032	TGGACAC	12	129622985	R
Red	GGAACTC	37	5	140535810	CGAGCTG	5	140515994	R
	GCTGCGG	37	14	24780551	CGCCATC	14	23850391	F
	TTGTGCC	37	6	149356915	GGTCAAT	6	149398608	F
	ATACTGA	37	7	107205253	TAACAGC	7	106992489	R
	CGAGGTC	37	X	21674175	CGCCCAG	X	21584096	F
Red	GGAGCAC	37	5	140475049	CGGCACC	5	140455233	F
	GTATGAC	37	11	74654369	CTTTTCT	11	74332017	R
	ACCAGCC	37	11	59209777	CGCGACT	11	58966353	R
	GACCCCA	37	1	207996459	CGCAGTC	1	206063082	R
	CAAGCCT	37	12	87232821	CGCTTAA	12	85756952	R
	AACTGCG	37	1	95010070	CGGTAAA	1	94782658	R
	CGCATGA	37	19	43769725	CGATCCT	19	48461565	F
	CGGCTTT	37	2	31806275	CGTGGGC	2	31659779	F
Grn	ACTCTCC	37	19	4724679	GGAAAAA	19	4675679	R
	GCACTGC	37	5	126409310	TAGTTTG	5	126437209	F
Red	TGTCCCC	37	10	135105487	CGGGAGA	10	134955477	F
Red	TATTGAG	37	12	54392884	CCCAAAA	12	52679151	F
Red	ACCAGGC	37	6	74064047	CGCCCCC	6	74120768	F
	ACTCAGA	37	11	112028288	CAGCACC	11	111533498	F
	TTTTGCC	37	14	69341905	CCTGTAA	14	68411658	R
	CAAAACC	37	7	64450926	TTTAAGT	7	64088361	F
Red	AAGGCCC	37	3	194901357	CGGCGGT	3	196382646	F
Red	TCTCTCG	37	17	48270097	GGGACCC	17	45625096	R
	GCACACA	37	14	103687580	CACCAGC	14	102757333	F
	TATGACA	37	7	12247070	GTGGACC	7	12213595	F
Red	GACAGAT	37	7	8029589	TCTATGT	7	7996114	F
	GTGTCTC	37	1	221057561	TCCTTGT	1	219124184	F
Red	TAAAAGC	37	X	153218916	CGGTGCC	X	152872110	R

	AAGATTT	37	1	65889855	CAACCTT	1	65662443	R
Grn	GCAGGG	37	21	44574022	CGGGCCA	21	43447091	R
	CACGAGT	37	17	4124222	TTTTCTG	17	4070971	F
	GGGATTC	37	10	133657199	CTAGGGC	10	133507189	R
	ACAAGG	37	22	18832673	CGGATGA	22	17212673	F
Grn	GGTTTCC	37	10	2543763	CGCGGTT	10	2533763	F
Grn	CCTCTGT	37	20	61447369	GGCTGAC	20	60917814	R
	TGTCCCT	37	13	19919208	CGGCTCT	13	18817208	R
	CTTTGCA	37	14	101539455	GAAGCAT	14	100609208	F
	CTGGGCT	37	2	101086893	TCTGGTT	2	100453325	F
	TACACCG	37	8	123706630	GAAGCAT	8	123775811	R
Red	TCCAGGG	37	12	129554566	CGGCCTC	12	128120519	R
	ACGCAAA	37	8	144661051	CCTTCAT	8	144732194	F
	CGTGCTG	37	2	238224257	CACACAC	2	237888996	F
	GTGACAC	37	1	11922765	CGACTGC	1	11845352	R
Grn	AGCTCGA	37	2	99771531	CACGAGC	2	99137963	R
	ACGATTA	37	5	140588139	CGCAATA	5	140568323	F
	ATTTTGT	37	19	54183186	TCAAACA	19	58874998	F
	TAATATT	37	7	12411370	CTTTGTG	7	12377895	R
	CTAGACC	37	7	563891	CGTGGCC	7	530417	F
	GCCGCTG	37	6	32551949	CGGCCCG	6	32659927	F
	CTTGTCT	37	7	30430591	CGCAAGA	7	30397116	F
	CAGGCCC	37	3	61235985	AAGGTTC	3	61211025	F
Grn	CGTGCGC	37	7	2019874	CCCGCTG	7	1986400	R
Red	GCCCCTA	37	6	33041218	AGGAGCT	6	33149196	F
	CTTCCAC	37	11	35551852	CGGCTGT	11	35508428	F
Red	ACAATTA	37	6	29692475	CGCGGTC	6	29800454	F
	GTCTGTG	37	1	111733668	CGGCTTC	1	111535191	F
Red	TGGACGA	37	5	1867978	CGCAGAA	5	1920978	F
	TCCTTAG	37	5	150005953	CGAAGGC	5	149986146	F
	ACCTGGT	37	1	17309539	CGCAGAC	1	17182126	R
	TGTCTAA	37	2	1166067	CGGGCTG	2	1156067	R
	TATCTTT	37	5	41087721	AGTCATA	5	41123478	F
	GAGCCCC	37	13	45563400	GAGACTC	13	44461400	R
	TGGAGAT	37	10	80270722	CGAGTAA	10	79940728	F
Red	CGGGGTA	37	7	27224343	CGACCAC	7	27190868	R
	TTAGCAA	37	4	48137323	TCCCTGC	4	47832080	F
	CCGCCAA	37	8	131025902	CATGAAT	8	131095084	R
	ACAGCCA	37	10	3179703	CGCTTGC	10	3169703	R
Red	ACCTGCG	37	6	31238908	CGTGCCC	6	31346887	F
Red	CGAGTCC	37	10	82295864	GCCGCGC	10	82285844	F
	AGAAAGA	37	12	54448769	CGCTGTG	12	52735036	F
	CCTGATC	37	2	30669759	CGCGAAC	2	30523263	R

	CATCACA	37	2	43323957	GTCTGTG	2	43177461	R
	AGGTCCT	37	13	113030673	TCCACAG	13	112078674	R
	GCCCGGA	37	6	29895116	TCCAGGT	6	30003095	F
	TGTTGAG	37	11	44881786	CGCCTCC	11	44838362	F
Grn	TGGCAGA	37	6	33037413	TGAATAC	6	33145391	F
Grn	AGCATGT	37	Y	9747821	CGGCTGC	Y	10357821	R
Grn	TTCTGAC	37	X	78622682	CGCAGCC	X	78509338	F
Red	CAGATGA	37	1	1226929	AGCCCAC	1	1216792	R
	GGGGCTT	37	11	17498952	CGCTGTA	11	17455528	R
	GCTCTCT	37	5	1795014	CGAGGCT	5	1848014	F
Red	GAACCGC	37	19	50931515	CGGCGAC	19	55623327	F
	ATGGAGA	37	6	101993140	TGAGAGA	6	102099833	F
	CAGTGGA	37	5	76429218	GCTTGGA	5	76464974	R
	TCCGCGG	37	5	140457609	CGGCCCT	5	140437793	F
Red	GCCCCTG	37	1	106623593	CGGGCTC	1	106425116	F
	GTCCCCG	37	7	45808275	CGCCTCA	7	45774800	R
	GGACAGA	37	2	103239842	GAGTTTT	2	102606274	R
Grn	TATCCGG	37	X	151806528	ACTACTG	X	151557184	F
	CCTGGCT	37	22	49447845	CGGGGTA	22	47833849	R
	ATACCAC	37	17	39217766	TTCTGTG	17	36471292	R
	GCAATGA	37	4	7769884	CGGGGCC	4	7820784	F
	GGGCCTG	37	8	38782090	GCGCTGG	8	38901247	R
	CAGGACA	37	3	30714671	CGCAGTG	3	30689675	F
	CCAACAC	37	3	46718979	TAGGGGC	3	46693983	F
	CGGGCCC	37	22	51135736	CCTAGTG	22	49482602	F
	TGAGTAG	37	18	64271469	CGAGCGT	18	62422449	R
	GAAGCCC	37	X	149530190	CGCCCAA	X	149280848	R
	CAACTCA	37	12	131171530	CGCAGCC	12	129737483	F
Red	ACCCAGC	37	12	8717467	GGCAACC	12	8608734	F
	TCATACA	37	3	99988576	ATCAGCA	3	101471266	F
	AGCTCGG	37	6	32634481	CAGTGCT	6	32742459	F
	TTGTCTC	37	5	4866318	CGTGGAA	5	4919318	R
	AGGACGC	37	7	152600816	CGGGAAT	7	152231749	R
	TTAAACC	37	7	37484562	CGTCGTC	7	37451087	F
Red	TACCCTG	37	18	77292134	TGCTGCA	18	75393122	F
	TACACCA	37	3	141022255	TTAATCT	3	142504945	R
	GCCAGAA	37	Y	7569967	CGTTGAG	Y	7629967	F
	TGGACGC	37	7	2100357	CGGCCTT	7	2066883	F
Red	GGAGCCA	37	12	133014399	TGTGGGT	12	131524472	R
Red	AGTGATT	37	19	15833777	GATCCCG	19	15694777	R
	CCAGCTG	37	11	494944	CAACCAC	11	484944	F
	AGGTTGC	37	19	4638503	CGCCCTG	19	4589503	R
	GACCCCA	37	7	76129360	CCTTGTC	7	75967296	R

	GTTGGGC	37	19	38345819	TGCTTTT	19	43037659	F
	ATTACTC	37	4	54392970	TCTCTTG	4	54087727	R
Red	CTCGCCT	37	14	101366368	CAAACTT	14	100436121	F
Grn	CGGTCCC	37	13	25506235	GGGACGC	13	24404235	R
	CAGAAAT	37	16	85832091	CGGGAAC	16	84389592	F
	AGTTGTT	37	11	18617206	TTAAAGA	11	18573782	R
Grn	GTCGGGC	37	15	45403733	CCAACCA	15	43191025	F
	TCCCACC	37	4	124572578	CTAGAAT	4	124792028	R
Grn	GCCGCCG	37	1	247802935	CTCGCAG	1	245869558	R
	GGACTCT	37	1	147801025	CGTCCCA	1	146267649	R
	CATCGTT	37	2	231734413	CAGCCAA	2	231442657	F
	GGGCCAT	37	2	242887344	CGCATGA	2	242536017	R
	TGGGAGA	37	21	46850665	CGGGCCA	21	45675093	R
	CCAGCCA	37	5	16785399	ATCTTCC	5	16838399	R
	TACCTCT	37	6	31913250	CGGGTCT	6	32021229	F
	CTTCAAG	37	15	23692512	CAGTTGC	15	21243605	F
	CGCTCTC	37	15	40583422	GGGGCAC	15	38370714	R
	GAATTGT	37	2	52656979	CGGAATC	2	52510483	F
	TAGTATC	37	7	104945248	TACAGGA	7	104732484	R
	AGGAAAT	37	11	61450294	GGGTCAC	11	61206870	R
Red	AACCTGA	37	X	43741557	GGATCGA	X	43626501	F
	TGACCTA	37	7	123713651	CGGGAGT	7	123500887	R
Red	AGCCCTG	37	6	30039376	CGCGCCC	6	30147355	R
	TACTAAC	37	12	106361273	CGCTCTG	12	104885403	F
Red	AGGTTAA	37	12	122265088	GGGGCAC	12	120749471	R
	AACAAAA	37	7	126984590	CGCAGAT	7	126771826	R
	GACAAAA	37	5	141625843	GAAACAA	5	141606027	F
	GGATATA	37	10	20210338	CGAGGAA	10	20250344	R
	GAGTTAA	37	1	214650225	TATAAAT	1	212716848	R
	ATTGTTA	37	4	78852682	CCTCCTG	4	79071706	F
	TTAATTG	37	2	69586350	GTAAGTA	2	69439854	F
	TGTTGAA	37	7	126698829	CAGATAA	7	126486065	F
	AGATCAT	37	5	17381798	GCCACAT	5	17434798	F
	CCAATCA	37	11	58208367	AATCTCT	11	57964943	R
	TAGTTAT	37	5	140556888	TGGATTT	5	140537072	R
	ACAGCAC	37	4	2431872	CGGACAC	4	2401670	F
	AGTAGCA	37	10	27909711	CGGTACA	10	27949717	F
	GCGAGAC	37	14	103687675	GTGGATG	14	102757428	R
	AAAGAAC	37	17	68984117	TCCTCAA	17	66495712	F
	GTTGGAG	37	8	113655436	CGGCTGC	8	113724612	F
	GAAGGGT	37	6	30421089	CCAGGAC	6	30529068	R
	TAGCCTG	37	17	80040611	CACAGGA	17	77633900	R
Grn	CAAGGAT	37	1	19600454	CGGACTG	1	19473041	R

	AAGCAG	37	5	141879669	TATTCTC	5	141859853	F
	GGGAATC	37	6	30079192	AGGGCGC	6	30187171	R
	TTCTTTT	37	4	157682848	CGTGCCT	4	157902298	R
	AAAAGA	37	2	150845309	CTCTCTT	2	150553555	F
	TTTACTC	37	21	46763239	GTTTGTT	21	45587667	F
	TACTTTC	37	4	15895695	CAGCCAT	4	15504793	F
	CGGCGAC	37	21	46812511	TTTGTAG	21	45636939	F
	ACAGAA	37	4	71382958	CGCAAGC	4	71417547	R
	CTGAGCA	37	1	221335745	CGGCTCT	1	219402368	F
	TGGGAAC	37	8	119097956	CCACATG	8	119167137	R
	ACATGTA	37	6	30122432	CCTACGT	6	30230411	R
	CCCTGTT	37	11	70336800	GAGATGT	11	70014448	R
	TTCGAAA	37	4	1192053	AGCAGCC	4	1182053	R
	TAGGGCT	37	13	27516202	ACACCTG	13	26414202	F
	CCTTGAA	37	10	118380345	GGCAGG	10	118370335	F
Red	CTCTTCT	37	6	29526376	CGGCAGT	6	29634355	R
Red	TCCCAGG	37	2	239997987	CGAGGA	2	239662924	R
	AGTGATG	37	1	243050875	CGAAAAC	1	241117498	R
	ACCCAGC	37	19	55669872	CGGGGCT	19	60361684	F
	CTGAAAT	37	3	111852325	CTGTGGC	3	113335015	F
	GGCCGGC	37	6	101846707	CGTCAGA	6	101953428	F
	TAAAAGC	37	1	205579533	CGACCAT	1	203846156	R
	GTATTT	37	5	163786073	CGGCAAC	5	163718651	R
	CAGTGAT	37	19	52146598	GCATGTG	19	56838410	R
	AAACAG	37	18	40696164	CTATGTT	18	38950162	F
	AGGGAGC	37	7	38361199	CGCCCAC	7	38327724	F
	AAATTCT	37	14	64905375	CGCTGGG	14	63975128	R
	CCTGAGT	37	5	10513925	CGGGTGC	5	10566925	R
	GTCAAAT	37	12	130084035	CGGATTA	12	128649988	R
	CCCACGG	37	1	26074002	GACCTGG	1	25946589	F
Red	TGGAAGC	37	4	13300500	ATACAGT	4	12909598	F
	AATGAA	37	14	94179847	GCTTGCA	14	93249600	R
	CTGGAAA	37	18	76498163	CGGATGC	18	74599151	R
	GCACCAC	37	10	94350577	TCTATTT	10	94340557	F
	GAGGAA	37	1	117487269	TGTGGTT	1	117288792	R
	CACGTAC	37	22	18531028	GCACCTT	22	16911028	F
	CTGTGGA	37	2	240567630	GCCCTGC	2	240232567	F
	TACGAAT	37	6	135172385	CGGTAGA	6	135214078	F
	TTTCTTT	37	14	50862509	CGGGTCA	14	49932259	R
	CTTAAAT	37	2	168244895	CGCTTTG	2	167953141	R
	CCTGGGG	37	5	308268	CGGCCTG	5	361268	F
Red	TGGAGTC	37	11	133900846	GCCGGCT	11	133406056	R
	ATAAAAC	37	6	35109722	ACTCGAA	6	35217700	F

	GCCACAC	37	11	61716821	CAGAGCT	11	61473397	F
Grn	TGGGGAC	37	10	129947807	CCTGACT	10	129837797	F
Red	TGTGAAG	37	5	178488100	AAATACT	5	178420706	R
	TTGGGGG	37	1	9224376	CGGCCCC	1	9146963	R
	AGAGACC	37	12	27627468	GAGAATC	12	27518735	F
	GAATTCC	37	15	34339800	CGGGAGC	15	32127092	F
Grn	CTGGCTG	37	11	126310323	CGGGCGC	11	125815533	R
	CCCGCCT	37	1	201123745	CCCTTCC	1	199390368	F
	GGCACAA	37	1	11207707	CGGATCT	1	11130294	F
Red	TCACGGC	37	15	40268777	CATGAGA	15	38056069	R
	CCTCCTT	37	10	51589507	CGTCCAC	10	51259513	R
Red	CAACCAC	37	22	32750777	CGCCACG	22	31080777	F
Grn	GGTGGGT	37	5	140176361	GCACGTG	5	140156545	R
	TCCCACC	37	17	53684393	CGGATGA	17	51039392	R
Red	GGACTTG	37	21	45198592	CAAGGGA	21	44023020	R
Red	GCTCATT	37	3	194573365	CGGACCC	3	196054654	R
Grn	GCACAGA	37	1	9341141	CGGGTCT	1	9263728	R
	TGGGCAC	37	5	179759	GCCATGA	5	232759	R
Red	AACGAGC	37	8	103750821	TGGGTGC	8	103819997	R
	TCACCAG	37	6	116381609	CGGGACT	6	116488302	R
	TCTGTCC	37	18	10032765	CGGAGAC	18	10022765	R
	CATCCAA	37	16	12059019	ATGAACT	16	11966520	F
Red	CGAGCCC	37	7	23245900	ACGCAGT	7	23212425	R
	GGGGGCT	37	17	79609161	GAGATAT	17	77219566	F
	GGGGAGC	37	6	1555389	CGAATCT	6	1500388	R
Red	GCGAGTC	37	18	76674571	CGCGGCT	18	74775559	F
	GAGGAAC	37	8	140926709	AAGGCGC	8	140995891	R
	GGGAGAC	37	10	48828106	CGCCGCT	10	48448112	F
	CTATCAA	37	6	147235033	CGCAGAC	6	147276726	F
Red	GTGTGGT	37	14	104625420	TGCAGAC	14	103695173	R
Red	AGGAGGA	37	7	12151356	CGCCCTG	7	12117881	R
Red	GGAGATC	37	10	135379215	CGCGCCT	10	135229205	R
	ACCCACT	37	13	107028903	CGGTGAC	13	105826904	R
	GGAGGAA	37	5	112882744	CGTGAAA	5	112910643	R
Red	TCGGCTC	37	6	42099392	TGGCCAA	6	42207370	R
	TCTTTTTT	37	2	20001490	TTTAACT	2	19864971	F
	CGGGGGC	37	5	140188119	TTCGCTG	5	140168303	R
	AACAGCC	37	5	75698461	CGCAAGC	5	75734217	R
Grn	CGAGTTC	37	10	131350999	ACTTCGG	10	131240989	R
	TGGTTTT	37	11	131934835	AACATAC	11	131440045	F
	GTACCGA	37	18	57634307	TGCATGC	18	55785287	F
	CGTCTCC	37	5	140710509	TAGGATG	5	140690693	R
	TTAAAAA	37	3	129132966	GGGTCTC	3	130615656	F

Red	TAAATCT	37	18	76751616	CGGCCAC	18	74852604	F
	CAGCGAT	37	8	8131077	CGCCCAG	8	8168487	R
	TATTCAA	37	6	126000798	CGCCAGC	6	126042497	F
	TGTGACC	37	12	122297080	CGGCTCC	12	120781463	F
Red	CACGCTT	37	20	25281332	AATGCTC	20	25229332	F
Red	CGGGGAA	37	4	77997182	CGGCTCC	4	78216206	F
Grn	CCACTTT	37	11	61159649	TCGCGTG	11	60916225	R
Red	CCACCGA	37	6	22356972	AGGGAGA	6	22464951	F
Red	CGGGCCC	37	14	102422355	GTGCCGA	14	101492108	F
	AAAGCAT	37	2	33295138	CGCTGAG	2	33148642	R
	TGCTAAG	37	8	10657514	CGGCTCT	8	10694924	R
	TCAGGAT	37	3	159493194	ATGACCC	3	160975888	F
	GCCTTCC	37	6	32633102	ATCCCTC	6	32741080	F
	TTAGTAC	37	15	49012706	CCATATT	15	46799998	F
	CGCTCTG	37	16	10346074	CAGCCGC	16	10253575	F
	AATGCTC	37	3	138739900	AGAGGCC	3	140222590	F
	GCACTTT	37	1	233248845	AATTACA	1	231315468	R
Grn	GAACTGT	37	16	55794595	TTCCAGG	16	54352096	R
	ATGTATT	37	5	55289001	CGGGGAA	5	55324758	F
	CACAACC	37	12	55248207	CCAATCA	12	53534474	F
Red	CGCTGGG	37	11	14927549	CGTGCGG	11	14884125	R
Red	ATTGATC	37	12	114204091	ATATTAA	12	112688474	F
	CACATTT	37	5	110899314	CGGTCTA	5	110927213	R
	AAGGTTT	37	10	3164740	CGCCACC	10	3154740	R
Red	CACATCA	37	15	100821466	CCGGCTC	15	98638989	R
	GGGGTCA	37	1	59986591	CGGTTCT	1	59759179	R
Red	AAACAAA	37	1	91300215	CGCGTGG	1	91072803	R
	GTTGAAG	37	14	95973710	CGGCTGG	14	95043463	R
	TTTCAGT	37	12	115118777	GAAAGTC	12	113603160	R
	GCACACC	37	14	105344761	CTGGGCG	14	104415806	R
	GAGCAGA	37	3	133502952	GGACTCC	3	134985642	F
	ATGACCT	37	3	98534089	AGGTTTC	3	100016779	F
	AATCAAA	37	7	41743001	ATGTCTC	7	41709526	R
Grn	GTGGTGG	37	2	172967431	GAAAGAC	2	172675677	F
	ATATCTT	37	16	51360402	CGGGATT	16	49917903	F
Red	GGCTCTG	37	10	129947858	CGACCCC	10	129837848	F
Red	AGGGCAC	37	2	10302391	CGCCCGT	2	10219842	F
	TTCCATT	37	14	22279816	CGTGATC	14	21349656	R
Red	CGCGCTT	37	17	40192112	CGCGCAC	17	37445638	F
Red	AAGGGGC	37	20	34190258	AGGGGTA	20	33653672	R
	CTGCAGT	37	16	3317428	CGTTGCC	16	3257429	F
	GACCCCA	37	10	13544863	CGGGGTC	10	13584869	R
	AATATAT	37	10	47964834	CGAGAAC	10	47484840	R

	GTGCTGG	37	11	94307971	CAGGCAT	11	93947619	R
Grn	TTCCCAC	37	20	32856846	CGCCCTG	20	32320507	F
	TTGGTAA	37	5	73234433	CGAGCAC	5	73270189	R
Red	ACCCAAT	37	3	170626822	CGCGAGT	3	172109516	R
	CCTGGCC	37	5	71475356	CCCAGTG	5	71511112	R
	GAGGAT	37	7	76145632	GAGTGCA	7	75983568	F
	CCACAGC	37	6	157264715	AATTGTA	6	157306407	R
Red	GCGCTCC	37	15	95870262	AGGAGGC	15	93671266	R
	GAAATTA	37	17	818890	CCAGCCC	17	765640	F
	GTGAGGA	37	12	106460704	CGGGGCC	12	104984834	F
	CAGATCC	37	7	44229319	CGGGATC	7	44195844	R
	GGTCTTT	37	16	50896074	CGCATAA	16	49453575	R
	AAATCAC	37	8	20080666	GTCACTA	8	20124946	R
	CGTTCGC	37	6	32120955	TACAAGC	6	32228933	F
	TTTTACC	37	6	111659754	CGGTGAA	6	111766447	F
	AATTTGC	37	1	235292369	CGCGTTA	1	233358992	F
	GCCGGGA	37	11	7928236	CGGGGAC	11	7884812	F
	TTGAGGT	37	6	29868207	GTAGTCT	6	29976186	R
	AAATCCC	37	5	55460876	AGGCAAA	5	55496633	R
	GAGATGA	37	6	33158020	ACTCTGA	6	33265998	F
	AACCGCA	37	6	32552152	TCCGTCC	6	32660130	R
Grn	CGGAGAC	37	17	48263159	GCCCTGC	17	45618158	R
	CAATGTA	37	17	79787551	CGAGGGT	17	77380840	R
	AGGGTTA	37	3	129147846	CGGGGCA	3	130630536	R
	CTCGCAG	37	12	54383678	CGTCTAT	12	52669945	R
	TCATGCA	37	6	34524698	CCTTTGG	6	34632676	F
	TAAAATG	37	3	24782112	AAGTGAA	3	24757116	F
	CAACAGT	37	12	27901072	GGAGAAC	12	27792339	F
	CACTGTC	37	6	29922522	AAGATTG	6	30030501	F
	GGATCCT	37	5	43802496	ACATGCT	5	43838253	F
Red	AATCAGT	37	17	79652024	CGCCTTT	17	77262429	R
Grn	GGGAGGA	37	12	115813214	GGGGCTC	12	114297597	R
	TCGCTAC	37	1	21023132	GGTGACC	1	20895719	R
	AAGGGCT	37	13	113660298	TCACGGA	13	112708299	F
	TTGTACT	37	5	2642995	TGTGAAG	5	2695995	R
Grn	AGCAGCT	37	6	28983079	GCAGGTT	6	29091058	F
	TGTTGGG	37	3	185476452	TGTTAGC	3	186959146	R
	CTCTACC	37	9	115851255	ATCCTCC	9	114891076	F
	CGCGGAC	37	7	129410227	CAGGATC	7	129197463	F
	TTTGACG	37	8	61197710	CCTTGAA	8	61360264	F
Red	AGAACAC	37	6	30038998	CGACCTG	6	30146977	R
Grn	CCGCCCT	37	5	140553150	GCATTCT	5	140533334	R
	ACCAACC	37	1	85755348	CGCCTCA	1	85527936	F

Red	CCCAGGC	37	12	54389477	CGCTCCG	12	52675744	R
Grn	TTATGGT	37	14	93698053	CGCCGAT	14	92767806	R
Red	AGGGGTC	37	7	51081446	AGCGGTC	7	51048940	R
Red	AGGTTCT	37	3	10149918	GGCCGCC	3	10124918	F
	AGGTCTT	37	3	53380856	CGGAAA	3	53355896	R
	GGGCCGT	37	5	135416594	CGGGGTT	5	135444493	F
	CGTATCA	37	12	15039560	CCTGCCA	12	14930827	F
Grn	TGGGTGG	37	7	1577003	CGGTGAC	7	1543529	R
Red	CGTCGCC	37	5	140529775	CGACCCT	5	140509959	R
	GACAAGC	37	11	71010448	TTTAAGC	11	70688096	R
	CGCGTGT	37	10	134420036	TGCTGGG	10	134270026	R
Red	GCCGACC	37	7	157867015	TCTGCTG	7	157559776	R
	GCCTCTC	37	13	113585948	CGCTCGT	13	112633949	R
Red	AGGATTC	37	X	19141251	GATGGTT	X	19051172	R
Red	CCCAGGC	37	11	65685316	CCAGCTT	11	65441892	R
	AAGGCTC	37	11	121699840	CGTGGAC	11	121205050	F
	GTCTGTT	37	1	7432614	CTGATCA	1	7355201	R
	TTGCGTT	37	12	122012243	CACCCAG	12	120496626	R
	CACCTCC	37	6	29701563	CGCTGTA	6	29809542	R
	TTCCAAC	37	6	108145930	AGTTTTC	6	108252623	R
	ACATTAA	37	5	166711687	CGTCTGA	5	166644265	F
	GCGTTAT	37	6	4352453	CGGGGGC	6	4297452	F
	CTAAATG	37	5	57073212	CGGGGGC	5	57108969	R
	TGAGAGC	37	10	114116449	CGGGGAA	10	114106439	R
Grn	GCCTTTT	37	13	100218136	CGGCACC	13	99016137	R
	AAAAAGC	37	18	33485594	TCCTCAT	18	31739592	F
	TCCTCCA	37	11	63529520	CCCTACT	11	63286096	F
	TGTCATC	37	11	86643955	TCCCTCT	11	86321603	R
	AGTTTAT	37	13	99974673	GGCTCTT	13	98772674	F
	CAGAGGA	37	4	128791896	AAGAAGA	4	129011346	F
Red	GGCTCTT	37	10	135259860	CGCGCCC	10	135109850	F
	TGTAGTG	37	16	81518253	CGGGTCT	16	80075754	R
	ATCTATA	37	14	22361282	CACAAGC	14	21431122	F
Red	CAGGGAC	37	7	55517132	GTAGTGC	7	55484626	F
	ATTGTTT	37	12	107350911	TTGAAAC	12	105875041	R
	CCCCCGT	37	10	3509710	GGGGCAC	10	3499710	R
	CCTCTGC	37	11	1048635	CGGAAAC	11	1038635	R
Red	GCACTTT	37	2	568198	AACAGCC	2	558198	F
	AGCTGGA	37	11	73577813	TCACCTT	11	73255461	R
Grn	CGCAGGT	37	12	124968359	CGGCTCT	12	123534312	F
Red	CGTTGTG	37	15	45493438	AGCAACC	15	43280730	R
Red	CTCGAGC	37	21	37442385	CGCAGGT	21	36364255	F
	AAAGGGA	37	3	109735618	CGGAACT	3	111218308	F

	GCTGCAG	37	6	30228431	CGGGCTG	6	30336410	F
Red	TCCTAAA	37	12	125149524	CGATGGC	12	123715477	F
	CATACCT	37	16	75149501	CGTGGGA	16	73707002	F
	GTCAGAT	37	1	222544693	CGGTCAC	1	220611316	F
	CGTTGTA	37	13	84453665	CATTGTG	13	83351666	R
	TGGAAA	37	11	68776397	AGAGCAC	11	68532973	F
	TGTGTGT	37	8	11994639	GTGTGCC	8	12032048	F
	CGCTGCA	37	6	29911366	CGGGCTG	6	30019345	F
Red	CAATCAT	37	19	17905626	GCTAGGC	19	17766626	F
	TATCTCA	37	12	9885998	CGCCAGA	12	9777265	R
Red	GGCACCC	37	16	31551613	GGGGACT	16	31459114	R
	TGCAGTT	37	6	4370460	CGACCTT	6	4315459	F
	AGAGAG	37	16	3334273	CGGGGGC	16	3274274	R
	GCCGGGC	37	8	1792758	CGGCTCC	8	1780165	R
	CTTCTCT	37	2	242101289	AGAAGA	2	241749962	R
	AGCCAAC	37	8	97803770	CGGTGAC	8	97872946	R
Red	GCAGTCG	37	17	80866063	CGCAGCC	17	78459352	R
	CCTCAGC	37	16	2749792	CGGGCCA	16	2689793	R
Red	TACATCA	37	17	113262	CGCGTCA	17	113262	R
Red	GGGCTGC	37	7	1787831	GTCTGAG	7	1754357	R
	TGAATTC	37	3	18877557	CGCTGAT	3	18852561	R
Red	CCTGTAA	37	22	37493863	CGGTGGC	22	35823809	R
	CCCTTTC	37	3	151178760	CGAGCCC	3	152661450	R
	GCACCAC	37	17	48273001	CGGGGCC	17	45628000	F
Red	GGGGAGC	37	21	44105474	CGCGGGC	21	42978543	F
	ATGTTTG	37	7	133974228	TACACAG	7	133624768	R
	ACTGCCT	37	14	102975405	TTTAACT	14	102045158	F
Red	TAGAGCT	37	11	67141792	AGGCGCT	11	66898368	R
	AGGATGA	37	3	192577951	CGGCCAT	3	194060645	R
Grn	AGCCCCA	37	17	46507777	GAAGGAT	17	43862776	R
	GTAGAAT	37	16	73102243	AATCCAT	16	71659744	F
	TTCACGC	37	X	40036466	CTCCTCC	X	39921410	R
Red	GAACTGC	37	15	27111572	TAGGACC	15	24662665	R
	GATAATC	37	11	66104993	GCCGAAC	11	65861569	F
	CTTCATT	37	8	91681699	ATAGCTT	8	91750875	F
Red	CCACCCT	37	X	48776486	TTTCAAG	X	48661430	R
Red	ATGCTAA	37	11	36383991	CGCCCAC	11	36340567	R
	GCCCCTG	37	17	79524882	CCTGTTG	17	77135326	F
	AGCTCCC	37	17	52981853	GATTGTT	17	50336852	F
	GAGCAAC	37	17	78725375	TGAGATG	17	76339970	F
	GGTTCAC	37	19	6362787	GTGAGCC	19	6313787	F
	CTGCCTG	37	8	1843398	CGGAGTC	8	1830805	R
Red	GAGTTAG	37	19	52206691	CGGAGAT	19	56898503	R

Red	GTGCCTG	37	6	761284	CGCCCAG	6	706284	F
	GACTTTC	37	6	112005207	CGGGAT	6	112111900	R
	ATTTGAG	37	2	116601613	CGTGTCT	2	116318083	F
	AAATAGA	37	3	42306150	TAATCCA	3	42281154	F
Red	CGGAGAC	37	19	49200180	CGGCCCC	19	53891992	R
	CAAGCAC	37	10	65682643	CCATTCA	10	65352649	R
	GCTGATA	37	11	75210723	CGGGAAA	11	74888371	F
Red	ACTGCAC	37	2	161504834	CGCGGCC	2	161213080	F
	CCATCTC	37	13	36050158	CGGAAAC	13	34948158	F
	CCTCCAA	37	7	82136223	CGGGCAT	7	81974159	F
	TAGAAAC	37	12	54377550	CCTTGGA	12	52663817	F
	AAAAAAA	37	1	224698362	ACCTGCC	1	222764985	F
	ACCTGGG	37	2	11728079	CCACCTC	2	11645530	R
Grn	GTGGACC	37	20	42788699	CGCAGCC	20	42222113	R
	ATTCTAA	37	18	722818	AAAAAAT	18	712818	R
	ACAGCTC	37	7	51539678	AAGTTCA	7	51507172	R
	AAAAGCT	37	19	58952249	CGCCAAA	19	63644061	F
	CCCCTGG	37	3	11178593	CGGGTGA	3	11153593	F
Grn	AGTGACC	37	20	2731371	TAGCCTC	20	2679371	R
	CCATCAC	37	3	66475150	CGATGGT	3	66557840	F
	GCAGGCC	37	3	193988639	CGGGGTT	3	195471333	F
Grn	GATATTG	37	10	729226	AGAAGGC	10	719226	R
	CTGGCAT	37	1	218575437	CGAGAGT	1	216642060	R
	ACTTCAC	37	3	75834271	AAAGAGA	3	75916961	R
	CCTGTGT	37	4	7373065	TGGATCG	4	7423966	R
	GCAAGAT	37	15	25490008	CCCACCA	15	23041101	R
	GAGTTCT	37	11	1001560	TTTTCAG	11	991560	R
	TAAAATC	37	5	140588424	CGCAGTT	5	140568608	R
	GCACGCC	37	14	77041277	CGCTGCA	14	76111030	R
Red	GACTTTA	37	5	14380323	AGCAGAA	5	14433323	R
	GGCCGGC	37	12	103352694	GCCGAGC	12	101876824	F
Red	CTTGATG	37	6	28557765	CGCTCAC	6	28665744	F
	CATTGCT	37	1	19291857	CGGCAGT	1	19164444	F
	GCGAGCA	37	2	238647755	CGCACGC	2	238312494	R
	AAATATA	37	11	128568943	TTACTGA	11	128074153	R
	TGGCATT	37	3	159852976	ATTCAAT	3	161335670	R
	GGGCGTC	37	11	58944103	CGGCAGT	11	58700679	F
	ATATATT	37	8	69348660	CGATACT	8	69511214	R
Red	CCCGCAG	37	5	140731399	CGAGCTC	5	140711583	F
	AGAACCC	37	12	75785295	CGGACAC	12	74071562	F
	ACACACA	37	7	158152141	CGGGGGC	7	157844902	F
Red	CAAAGGC	37	5	25190850	GTCCTGG	5	25226607	R
	AGCCTGC	37	5	149493243	TCTCATT	5	149473436	F

	CGTCTGC	37	13	113624866	CGGAAAA	13	112672867	R
	TAGAGAC	37	4	177262070	CGTGATA	4	177499064	F
	GCCTGAA	37	10	93044533	GTCTTAA	10	93034513	R
Grn	AAAGGCC	37	12	115103351	CGCCTGC	12	113587734	R
	CTCAGCC	37	11	11642133	CGGGTGA	11	11598709	R
	GTGGGTC	37	3	115524190	CGGAAGA	3	117006880	R
Red	GACTGGT	37	4	110524473	CGGCTCC	4	110743922	F
	GAAGGTT	37	6	135072384	CGGCCCA	6	135114077	R
Red	AAGAGCA	37	1	149294708	CGCCTCA	1	147561332	R
Red	GCCATTC	37	6	31238788	TCAAGGC	6	31346767	R
	GGCCGGC	37	19	3655825	TAGGAGT	19	3606825	F
	CAGCCCG	37	2	241562085	CGCCACC	2	241210758	R
	TTTGTGA	37	10	80312528	CGGGCCC	10	79982534	F
Red	GGGTCCA	37	7	112032599	ATCACTC	7	111819835	F
Red	GAGCCGC	37	X	30907432	TTGCCAA	X	30817353	F
	AAACACT	37	17	25773641	CGGCTTC	17	22797768	F
	TTGAAAA	37	1	243877447	ACACAGT	1	241944070	R
Red	AGCAGCT	37	2	162197875	AGAACTC	2	161906121	F
	TTCTACC	37	6	106546824	ACTCAAA	6	106653517	R
	AAAAACT	37	2	69812277	CGAGGAT	2	69665781	F
	CAAGGCA	37	15	83949772	CGGCAAC	15	81740776	F
Red	TTGAGAA	37	X	48660379	CGCCTCC	X	48545323	R
	GCTCACA	37	4	2305734	GGCGGGA	4	2275532	R
	GCCATCA	37	2	1886127	TAAAGAA	2	1865134	F
	GCCACAT	37	8	13209750	CCTTTAC	8	13254121	F
	CAGTTGA	37	8	41393714	AGGTTGT	8	41512871	R
	TTGGCTT	37	11	77271314	CGTGGCT	11	76948962	F
Red	GGTCCCC	37	11	400385	CGGGCTG	11	390385	F
	TGGTTAC	37	6	27521041	TATTTAC	6	27629020	R
	TGTGATT	37	1	169599754	GTGCCCA	1	167866378	R
	GTTGAAG	37	11	119023062	TAAACCA	11	118528272	R
	GTATGAC	37	2	178109973	CATCTCA	2	177818219	R
Red	GGCCGGC	37	1	205818956	GTGCGTG	1	204085579	R
	TCTTATC	37	1	31282519	AAGATAA	1	31055106	F
	ACCTCAT	37	2	97004840	CGCCCAG	2	96368567	F
	TGTGCTT	37	2	121442251	ACATTTT	2	121158721	F
	TCCCGTG	37	11	132107476	CTCCGTC	11	131612686	F
	CGCCCAC	37	X	73834683	CGCAAAT	X	73751408	R
	TCTTTTTA	37	8	37005572	CCGATGC	8	37124730	F
	ATCCATT	37	7	152345227	AAGAAAT	7	151976160	R
	ACAGAAC	37	10	130279674	CGCAGGT	10	130169664	F
	GGGGAGC	37	22	49840886	CCACCCC	22	48226890	R
	TATGGTT	37	2	17982866	CGGGACC	2	17846347	R

Red	CAAGTTG	37	X	129244725	AGAGATC	X	129072406	R
	GACACTC	37	4	189359992	CGACAGC	4	189596986	R
Red	GAGGCTC	37	X	2886295	TGGAAGA	X	2896295	R
	ACAAATT	37	7	141536997	CGAGAAT	7	141183466	R
	CCACAGC	37	1	42248998	GGCTGGC	1	42021585	R
	CCAAGAA	37	7	34911385	CGGGACA	7	34877910	R
	TTCCCCT	37	6	27791827	CGCCAAC	6	27899806	F
	CGAAGCC	37	17	22193895	TCTCTGT	17	22118022	F
	CACAGTG	37	13	52701588	ACTCAGC	13	51599589	F
Red	GCTGGAC	37	15	35086890	GGGTCCC	15	32874182	R
	ACATTTT	37	2	47604176	CGCGTTA	2	47457680	F
	ATGAGCC	37	2	36815511	GCCCAGC	2	36669015	R
	CCACCCA	37	6	31275875	CGGCTCA	6	31383854	R
Grn	AGATCAT	37	5	139088815	CGCGCCC	5	139068999	R
	GAATCAC	37	11	133917375	CGGCCCT	11	133422585	R
	CCTTTTT	37	4	114366508	CGGATCA	4	114585957	F
	TGGGGTC	37	6	4358810	CGGCCAC	6	4303809	R
	TTCGTAC	37	4	152597659	AAACAGC	4	152817109	F
	GGCTACT	37	6	55761410	ACCTGAG	6	55869369	F
	TGAGTAA	37	1	24921731	CGGGTAT	1	24794318	F
Red	ACGAGGC	37	17	32964596	CAGCGGC	17	29988709	F
Grn	GGCGCCT	37	2	24397845	TTTCCCG	2	24251349	R
	AGCCAGC	37	12	31272112	CCACCTC	12	31163379	R
	CTGCCAG	37	6	33050124	CGGGCCT	6	33158102	R
	AATCACG	37	13	29132547	TCCTTAT	13	28030547	F
	CATTGCA	37	8	857079	CGTTTGC	8	847079	R
	CCATAGA	37	7	24561256	CGAGCCT	7	24527781	F
	GCCAGCA	37	8	54557599	TCCTCTA	8	54720152	F
	CTGGCGC	37	5	80257322	CGGGGCT	5	80293078	F
	CCCCTCC	37	7	94953956	CGGTCAG	7	94791892	F
	TCAAGTT	37	2	80459300	CGATGTT	2	80312811	R
	ATGCTCT	37	22	17680561	ATCGCCA	22	16060561	R
	CAAAGCA	37	11	2847019	TCATTCA	11	2803595	R
Red	CACACAC	37	7	158050952	GGGCTGC	7	157743713	F
	ATTTTCT	37	10	128846231	AGGGAAA	10	128736221	F
	ATAACTA	37	5	86709409	CGAATAC	5	86745165	R
	TTTGCAG	37	2	189834269	CGCCTGA	2	189542514	F
Red	ATGAGGA	37	17	38183730	ATGTCAA	17	35437256	R
Grn	CCGCACG	37	X	100306958	GGGAGGC	X	100193614	F
	GTCCTTA	37	6	166259938	GAAATCC	6	166179928	R
	GACTGCG	37	5	140052701	AAGGGGC	5	140032885	R
	ACAGTCC	37	7	786861	CGCATCC	7	753387	F
	TGATCAG	37	6	32186244	CGGGACT	6	32294222	R

	TGCGTTG	37	1	1998716	GTGCAGC	1	1988576	R
	AGGCTCT	37	6	32725332	CGGTAAC	6	32833310	F
	TTTACAG	37	10	42673902	CGCTATC	10	41993908	F
	GGCCAAC	37	6	32485396	GAGCTGA	6	32593374	R
	CGAGGGC	37	14	56233068	CATCTCT	14	55302821	R
	CCAGTAC	37	15	34726650	GTTCCAC	15	32513942	R
	ATGACTG	37	2	197940256	CGAACGT	2	197648501	F
	TGAGAGT	37	6	149336332	ATTTTCT	6	149378025	F
	GACGACA	37	20	60745058	CGGCCCC	20	60178453	R
	CTCTTAC	37	5	135384080	CGGCAAA	5	135411979	R
	ACCATGA	37	2	114715532	TAAAGGA	2	114432002	R
	TGCTCAC	37	3	109537321	CGCATGT	3	111020011	F
	ACTTCAG	37	11	122060265	CGCAGCC	11	121565475	R
	CCAAGGT	37	7	2764129	GCCTGGA	7	2730655	R
	CCCCCCA	37	5	108820864	CGCCATC	5	108848763	R
Red	AGCGATC	37	5	110406107	TAGGAAC	5	110434006	R
	ATAAACC	37	7	76221076	AGCTGTG	7	76059012	F
	GAAGAAC	37	5	31796726	CGGAAGC	5	31832483	F
	GTTGTCA	37	1	79350918	CGGCACT	1	79123506	R
	GGTGACA	37	17	61514690	CGGCCCA	17	58868422	F
	ACATGCC	37	6	32608879	CGCACAC	6	32716857	F
Red	ACCTTTG	37	2	114259669	TTTGCTA	2	113976139	F
	AAGCCTA	37	11	126507786	CATGCTC	11	126012996	F
	TCCCAGC	37	7	149964288	CGGCTTC	7	149595221	R
	TCTGAAG	37	10	35464474	TCCAAGC	10	35504480	F
	GGATGCT	37	11	26743403	AACTTTT	11	26699979	F
Red	TGCTTAC	37	1	91300231	CTGGCTG	1	91072819	R
Red	CAGGAAC	37	7	64403162	CGGCTCC	7	64040597	F
Red	GAAGCCA	37	1	40105667	AGGCAGC	1	39878254	F
Red	GCAGCCC	37	5	140188392	CCACGAC	5	140168576	R
	CCAACTT	37	3	114566265	ATGCCTC	3	116048955	R
	TTTAAAG	37	1	92208474	AACATTA	1	91981062	R
	GACCCAT	37	1	64287452	TTAAGTC	1	64060040	F
	TCAGAAC	37	3	160936577	GTAGGCT	3	162419271	R
	TGATTAG	37	8	2082244	CTTCCGA	8	2069651	F
	TTCTTTT	37	8	129552914	TAAGCCT	8	129622096	F
Red	TTACCGC	37	3	123103936	CGGCACC	3	124586626	F
	GGTAGCA	37	10	28970998	CTTATCA	10	29011004	R
	CCCGTGG	37	2	232507842	CGTGTTC	2	232216086	R
	GGTCAGA	37	11	130476866	CGGGGAC	11	129982076	R
	GTTTTAT	37	5	67466813	CGTAAAA	5	67502569	R
	CAGGAGC	37	19	48049039	CGCCCCC	19	52740851	R
	GTTTCTT	37	1	174933574	CGTCATT	1	173200197	R

	AGCATTG	37	15	53100108	CGGCTCC	15	50887400	R
	TTATTTA	37	2	207873436	ACCATGG	2	207581681	F
Grn	CGACTCG	37	6	170452270	GATGGAA	6	170294195	R
	CCCCACC	37	2	778668	CGACGTT	2	768668	R
Red	ACACCTG	37	13	24902500	GGTGCGT	13	23800500	F
Grn	GACACCC	37	5	140502918	GAAAACC	5	140483102	R
	GATAACT	37	10	7896363	CGGCTCG	10	7936369	R
	GCCGGGC	37	7	43288771	CGGCCCG	7	43255296	F
	TTTTTAA	37	3	44802566	AAAGCAT	3	44777570	R
Red	CACGAAA	37	6	27483069	AGGGGAC	6	27591048	F
	AGGCAAC	37	7	133247477	TTGTAAG	7	132898017	F
	TGGGAAA	37	6	144417471	GAATGAC	6	144459164	R
	GGCAGAC	37	4	3371566	CGGGATC	4	3341364	R
	CCTTTTC	37	6	148914562	GTTTGGG	6	148956255	R
	TGTTCCT	37	17	67536299	ATTTGCA	17	65047894	R
Red	CCAAGTG	37	6	166259959	CACGCAA	6	166179949	R
	GCCACCA	37	2	218707806	CGATTCA	2	218416051	R
Grn	GGGAACC	37	2	241689985	GCTGCCA	2	241338658	F
Grn	GGCCAGA	37	2	48647546	CGCCTGG	2	48501050	F
	TTCTCAT	37	6	14037614	CGGGTTG	6	14145593	R
	GACCGAT	37	5	1594843	CGGGGCT	5	1647843	R
	CGATAAG	37	5	71475111	CGGGGAA	5	71510867	F
Red	ATTATGC	37	3	192289245	TTCAGCG	3	193771939	R
Grn	GCGCCCC	37	7	151411526	GCCTAGG	7	151042459	R
Red	TCAGGAA	37	17	77245327	CGGTGGC	17	74756922	R
Grn	GGTCCCT	37	3	42947565	TTGCTCT	3	42922569	F
	AGGTGGC	37	7	143130320	CGCTACC	7	142840442	R
	CAGAAAC	37	11	70266172	TGCTAAA	11	69943820	R
	CTCACAC	37	3	122712138	CGGCTGT	3	124194828	F
Grn	CCTACTC	37	X	46618639	CGCAGGA	X	46503583	F
	AAAGCGC	37	13	111281037	CGGGAAC	13	110079038	F
	CAAGCCT	37	3	124601778	CGGAAGC	3	126084468	F
Red	TCTGGTG	37	13	112985463	CGGACAC	13	112033464	R
	AAATATG	37	3	29456667	CGAGGGC	3	29431671	R
	TTTCTCC	37	22	45806309	CGCCCAG	22	44184973	R
	GCACGGC	37	13	80510936	CGCTGTA	13	79408937	R
Red	CAGTGAC	37	4	14858290	CGGAGAC	4	14467388	F
	TTAAAAT	37	2	121274655	TACTTTC	2	120991125	R
	TGGAAAC	37	6	152126337	CCTAGAA	6	152168030	R
	CTATGGT	37	11	102401523	CGAGGCT	11	101906733	R
	ACCATAC	37	13	40108007	CGGGTTC	13	39006007	R
	GAGATCC	37	6	26124704	AGCAGTT	6	26232683	F
Red	ACTACCC	37	19	10077935	ACCTACA	19	9938935	R

Red	CCCATGA	37	7	151423659	CTCTGTC	7	151054592	R
Grn	GACTGCA	37	X	70315718	TGTTTTG	X	70232443	F
	CTCACAG	37	10	118931160	TCTTATT	10	118921150	R
Red	ATTTGGA	37	10	31108190	ATGTGAC	10	31148196	F
	AGAAAA	37	5	140552505	CGGTTCG	5	140532689	R
Grn	CCCCCAA	37	17	79122455	CGGCACA	17	76737050	F
	CTAACGC	37	6	143224179	CGGTTTA	6	143265872	R
	CACACCT	37	13	92426491	CGGGCAA	13	91224492	R
	TCAGAGC	37	Y	22917782	GGACTTT	Y	21327170	F
	TGCTCTT	37	1	17308158	TTGTCAG	1	17180745	R
	TTCCATT	37	2	30669863	CGGAGGT	2	30523367	R
Red	GGGCTCG	37	4	798611	CGGCCTC	4	788611	R
	GACTCCT	37	5	71541917	GCCAAAT	5	71577673	F
Red	CAGCTCT	37	19	18888081	CGTTGAG	19	18749081	F
	GACATAT	37	8	26481696	TTTCTTT	8	26537613	R
	ATTTCCA	37	7	18653918	TCTTGCA	7	18620443	R
	GTCTGAA	37	6	33083457	CGGCAGC	6	33191435	R
	TCTTTAA	37	4	124534980	CGTGCAA	4	124754430	F
	CATGATG	37	4	3853774	GCAGGGC	4	3823572	R
Red	CTGGAAA	37	X	46306513	CGCCACG	X	46191457	F
	GCGTGCC	37	19	22700869	CCTGCGG	19	22492709	R
	GGGCAAT	37	4	83766494	CTTTGCA	4	83985518	F
Red	CCGCGGC	37	5	140554081	CGACAAC	5	140534265	F
Grn	TTTCTTC	37	X	20285083	CGCCCGC	X	20195004	F
	TGATTTC	37	3	171759519	CGGGCAC	3	173242213	R
	GCCCTTG	37	7	158106772	GGCACTG	7	157799533	F
Red	CGCTCTG	37	19	55417496	CGCCCGG	19	60109308	F
	CAACTGT	37	7	63491010	CGCCACA	7	63128445	F
	ACCCCAA	37	16	20364284	TGACATT	16	20271785	R
	AGCTTGC	37	Y	15863901	ATACGCA	Y	14373295	R
	TTCCACT	37	7	158377440	CGGCTCA	7	158070201	F
	CCCGGTG	37	8	3086479	GCTTGAG	8	3073886	R
	CCATGTG	37	1	103343469	CGCTGCA	1	103116057	R
Grn	GCGGAGC	37	1	207842917	TGCTGGC	1	205909540	R
	AGTTTTC	37	13	100394412	CGGCTTC	13	99192413	R
	CATTCCA	37	6	32577714	CGGTCAC	6	32685692	F
	CGTCACG	37	12	123259751	TTCCTTA	12	121825704	R
Red	AAACGAA	37	Y	9340946	CGAAGAC	Y	9950946	F
	AAGCTAC	37	2	13863069	AGACATC	2	13780520	R
	GGCATTG	37	1	12120304	CGCTGGC	1	12042891	R
	GCTCAAA	37	21	46077562	TTATTGC	21	44901990	R
	TTGTGTC	37	4	18580125	CGAAACT	4	18189223	F
	AGAGGAA	37	6	32822857	TCTAACT	6	32930835	R

	CCATGGG	37	10	132944904	CGCCCGT	10	132834894	F
Grn	GTTGTTC	37	17	77922775	TGTCCGG	17	75537370	R
	TTGCCCT	37	5	78281827	TTAGTGT	5	78317583	F
	GTCAGCT	37	5	126408806	GGCTCCC	5	126436705	R
	CACTTGC	37	4	9476719	GTCCACA	4	9085817	F
	CCCCAAG	37	1	221055964	CGGAGA	1	219122587	F
	TTCAGAA	37	12	106215054	AGCAGTA	12	104739184	R
	CTAAACC	37	4	106137048	CGGCCTG	4	106356497	F
	TGGGGA	37	1	221058805	TGATGCC	1	219125428	R
	GCGACCT	37	7	2728288	CTTCCCG	7	2694814	R
	GTGGGCC	37	2	233216150	TTGGCCC	2	232924394	R
	GTTTAAC	37	16	85879145	CGCTGAA	16	84436646	F
	AATTTTC	37	15	90115219	CGGGAGC	15	87916223	R
	GTTACCA	37	3	152215049	CGGGCA	3	153697739	F
	GGGCGCC	37	19	2900938	CAGCTGA	19	2851938	F
	CTACTAA	37	15	57277634	TGAGTCA	15	55064926	R
	TGGCCAT	37	12	50641260	CGCCTGA	12	48927527	F
	GTAAAAC	37	1	176521193	CGTACAG	1	174787816	R
	TGTGTTA	37	1	55117812	ACAGCA	1	54890400	F
	CGACCAC	37	10	15600165	TTTCTTT	10	15640171	F
	CCGCCTG	37	1	110230473	GTCCCAG	1	110031996	F
	TTCATAC	37	10	88395453	CGGGGA	10	88385433	F
Red	TGGAGCA	37	17	78935070	CCTGGAG	17	76549665	R
	TCGTATA	37	15	45493416	CGGCATT	15	43280708	F
Grn	CGTCTTT	37	17	25290204	AAAGGCC	17	22314331	F
Grn	AGAGACC	37	2	98928898	CCTTCCA	2	98295330	R
	GCCTTCT	37	8	61863697	CGGGCCA	8	62026251	R
Red	CGGATGT	37	7	70200532	CGGAAG	7	69838468	R
Red	GTAGGGC	37	6	30038712	CATTTTC	6	30146691	F
Grn	GAGAGAC	37	4	58060773	CGGGCCA	4	57755530	R
	ATGAAG	37	2	216982485	TTTGGTG	2	216690730	R
Red	AGGAATC	37	1	203876248	AATGTCT	1	202142871	F
	GAGCTAA	37	1	119960007	CATCAAA	1	119761530	R
	TGGCTCT	37	10	80952606	CAGGGCC	10	80622612	F
Grn	TTAGCCC	37	6	90597340	TGGCAGC	6	90654061	R
Red	GATTCAA	37	19	38040009	CGCCCAT	19	42731849	R
	CCAGCGC	37	5	9547468	CAGCCAC	5	9600468	R
	TGTGGAA	37	10	124319733	CGGAGAC	10	124309723	R
	TATCAAC	37	5	131892242	CGCACAT	5	131920141	F
	TGGAACA	37	10	121146289	CGAGAAC	10	121136279	R
	TTCTTAC	37	5	8621127	CGACATG	5	8674127	R
Red	GAGCGG	37	X	19002577	AGGGAC	X	18912498	F
	TCAGCCA	37	2	168674479	GGCAAAC	2	168382725	F

	TCTTTCA	37	20	3202228	CGCCAGC	20	3150228	R
Red	GACCCCC	37	1	228756789	CGCCTTT	1	226823412	R
	ACAAGCT	37	7	15601624	CTGTACT	7	15568149	F
Red	AGGGCGA	37	5	140230326	CGACCAA	5	140210510	R
	TCCCTAT	37	18	30349476	CGCAAAC	18	28603474	R
	ATATGTT	37	Y	2807288	CGGCAAA	Y	2867288	R
	GGAAGGA	37	2	202817042	CGGTCCC	2	202525287	R
Red	AGAGGCT	37	4	140201433	GATGGTG	4	140420883	F
	TCTTGGC	37	6	29981274	TGGTTAA	6	30089253	R
	CCAGTCT	37	22	46459890	GAGCTAA	22	44838554	R
	AATTCCA	37	3	10202595	CGGCTGC	3	10177595	R
Red	CGTCACA	37	19	58566643	TGAAGGC	19	63258455	F
Red	CTCCCTG	37	7	96655798	GCGGTCT	7	96493734	R
	ATAAACT	37	4	1202898	CGGCTCT	4	1192898	F
	GGTTCTG	37	1	115397597	GGAGCCA	1	115199120	R
	CTGGGCT	37	19	56269246	CGTTCAA	19	60961058	F
	TGGAGAC	37	11	61281763	CGGGGCT	11	61038339	F
	TTAGCCC	37	3	55232663	CGGCTTC	3	55207703	R
Grn	AGCGGGC	37	14	101175970	CGCCCCG	14	100245723	F
	AGGCCTA	37	4	184060895	CGGGTGA	4	184297889	R
Grn	GAGGGGA	37	5	2205553	GACGCCC	5	2258553	R
	GTCATGT	37	11	115062924	CGAACAT	11	114568134	F
	ACCTCCA	37	14	86088124	ACCAAAT	14	85157877	R
Grn	TCCAGCT	37	5	4942469	AGGGCAC	5	4995469	F
	CATTAAT	37	11	67142001	CGAGGCA	11	66898577	R
	GGTAAGA	37	17	4487109	GCTGGAC	17	4433858	F
	GAGAAAC	37	2	205333978	ACCCATG	2	205042223	R
	GCCAGTC	37	11	93754390	TTTCTCG	11	93394038	R
	AAAGGAC	37	6	32498493	CAACTGT	6	32606471	F
	CTGGAGC	37	Y	16636984	CGGGGGC	Y	15146378	F
	AGTACAC	37	6	46288667	ACTATTT	6	46396626	F
	ATAAGCC	37	6	43894639	AGGCATC	6	44002617	F
Red	GGCGGCC	37	11	9113184	CGGCCCC	11	9069760	F
Red	GGACAGA	37	15	74244249	GCAGGGA	15	72031302	F
	AAGGTAC	37	3	74003742	ACATTTC	3	74086432	F
Red	GGGCGGA	37	3	49941408	CGCCCAT	3	49916412	F
	CAGAGTT	37	7	65334477	CGCCACA	7	64971912	R
	GCGTGTT	37	6	166260572	TCAGAAC	6	166180562	R
	CTTCTGC	37	1	56163457	CACAGTA	1	55936045	R
	CATAACA	37	X	43515245	GGCAGCT	X	43400189	F
	GCAGAGC	37	15	48034358	CGATGTC	15	45821650	F
Red	TGCGAGC	37	20	2633340	CGCGTCG	20	2581340	R
	AGAGAAA	37	12	125205034	CGGATGA	12	123770987	F

	TCCAGGC	37	Y	7177888	GCATCTT	Y	7237888	F
	TTTGTCC	37	8	131080137	TGATACC	8	131149319	F
	AGAATTG	37	2	161214856	CAATCAG	2	160923102	R
	GAACTCC	37	10	3179821	GGTGGAC	10	3169821	R
Red	GCCTTCG	37	1	92952533	TTTCCGG	1	92725121	R
Red	GGATGTG	37	10	24755438	CGGGGA	10	24795444	F
	ACTAATT	37	10	48905601	CGGTTGT	10	48525607	R
	GGCTGCG	37	5	175626484	CGGCTCC	5	175559090	R
Red	CAAGTAT	37	10	94334836	CGAAGAC	10	94324816	F
	TGGCCTA	37	2	237620848	CATCAGA	2	237285587	F
Grn	TGAGCTC	37	17	80159595	CAACCTT	17	77752884	F
Grn	TGTCAGA	37	6	170732253	AGGTTTC	6	170574178	R
	CTGCCAA	37	13	30607830	CGTCCTT	13	29505830	R
	GCACGGC	37	10	134827324	CGGGCCC	10	134677314	R
Grn	TGCTTCC	37	12	11700321	CGGCAGC	12	11591588	F
	TAAGACT	37	7	113011963	CGTCACC	7	112799199	R
	ATTATCC	37	5	151476553	GGGAATT	5	151456746	F
	TGCTGCC	37	1	22645936	AGGCCAC	1	22518523	R
	TCTAGCC	37	10	63167726	CGCTATG	10	62837732	F
	CTTCACT	37	14	96563269	CGGTACT	14	95633022	F
Grn	GGCGGTC	37	X	108780378	CGGGGCC	X	108667034	F
	CTAGCCC	37	12	3563268	CGGAGGC	12	3433529	F
	GACAGGC	37	17	39204922	CGGCCCC	17	36458448	R
Red	CTGCGGA	37	17	41477468	CGGACA	17	38832994	F
	CCACCCC	37	7	92533866	TGAGTCA	7	92371802	R
	ATCCAAC	37	10	6183575	ATAACTC	10	6223581	F
	TGCTCTT	37	1	11783294	GCCAACT	1	11705881	R
	ACCTGGC	37	11	76414904	GTGAGGC	11	76092552	R
Red	AGCCCGC	37	6	90597356	CGCACAC	6	90654077	F
	GGAGGAC	37	4	6902932	GGCCCCT	4	6953833	F
	TCCCCAA	37	1	223904225	CGGCAG	1	221970848	F
	AATAAA	37	19	57633694	CGCCTGG	19	62325506	R
	GCAATTC	37	3	13420961	CGGCTAT	3	13395961	F
	TAAATAT	37	8	122651271	CGCCAGA	8	122720452	F
	AATTTCA	37	5	60960963	CGCTAGT	5	60996720	R
	CAGAAAT	37	6	170055332	GGCAAGC	6	169797257	F
Grn	ACTGGGT	37	10	123909456	CGCGGAC	10	123899446	F
Red	GTGATTA	37	6	30079139	GTCTTAG	6	30187118	F
	GACTGAC	37	13	24247649	CGGCATT	13	23145649	F
	TGAGCTC	37	8	126698738	CGGGTTG	8	126767920	R
	TAAGGTA	37	19	54210518	CTGCAGT	19	58902330	F
	GAGAGG	37	1	29190137	CGGGGCT	1	29062724	F
	CCTCCTG	37	19	8574557	GCTTCCT	19	8480557	R

	CCTGGGG	37	2	238795355	GGCAGTT	2	238460094	F
Red	CCGCCCC	37	19	51829984	TGTGTGT	19	56521796	R
	CAAAACC	37	14	52733216	CGATGCC	14	51802966	R
Red	AATCTCC	37	5	53813164	TTTGCA	5	53848921	F
Red	GACACCC	37	X	152736387	CGCCAGC	X	152389581	R
	TCACCCC	37	1	202129566	TGGGGAC	1	200396189	R
	CCAGAAC	37	1	223747670	CGAGGTT	1	221814293	F
	GACAACA	37	7	3801491	CACACTG	7	3768017	F
	CTCGGTG	37	1	115398073	GTGGTAC	1	115199596	F
Red	GCAAAGT	37	14	105830631	AGAGCAC	14	104901676	R
	GACAATC	37	10	24633303	AGACATT	10	24673309	F
	CCCTTGT	37	11	63828569	GACTGAA	11	63585145	F
	TAATTAG	37	4	115484805	CGGGAGT	4	115704254	F
	TCCACCA	37	14	77371470	GATCTTT	14	76441223	R
	AAACCAT	37	5	140579296	CGCGTTC	5	140559480	F
	GAGACGC	37	10	88023185	CGGTTCC	10	88013165	F
	GACAAGC	37	7	42760642	CGGACAT	7	42727167	R
	TGAACAC	37	6	32490421	TAGTGAT	6	32598399	R
	TCGTTCC	37	4	37245254	GTCCACG	4	36921649	F
	CTGTGTA	37	4	15376215	TAAGTAA	4	14985313	F
	AGAGGTC	37	17	9677572	AAGTAGC	17	9618297	R
Red	CTGCAGT	37	8	1497307	CGCCACC	8	1484714	F
	CCCACGT	37	10	2564642	TCGCCTG	10	2554642	F
	CTGTTGT	37	12	21594328	CTTTAAA	12	21485595	R
	CAGGAGC	37	18	12035841	CGGGGCC	18	12025841	F
	GAATTCT	37	13	32480222	CTGTTCT	13	31378222	R
	GTGGTGT	37	13	41593519	CGCCCAT	13	40491519	F
	ACAGCCC	37	19	42211171	ACAGAGA	19	46903011	F
Grn	GCCCCCC	37	11	67141747	CGCCTCG	11	66898323	R
	GGCCACA	37	14	20482899	GCAAATT	14	19552739	R
	TAACCAC	37	5	75376460	AAAAAAC	5	75412216	F
	ACCTTCT	37	14	21156471	CGGATGC	14	20226311	R
	AGTCAAC	37	7	44203304	CGAGCAC	7	44169829	R
	GCTGCTA	37	14	75083495	CGGCAGA	14	74153248	F
	GCCACTG	37	4	85411336	CAGCCTG	4	85630360	F
Red	TTTCTCT	37	7	149322992	AGCGTGG	7	148953925	R
	CCGCGAT	37	10	651119	AAGGAAC	10	641119	F
	GTGAGGC	37	10	729956	CGGGCCC	10	719956	F
	CTGGGAA	37	19	46286198	CGGGAGC	19	50978038	R
	GAGTCTG	37	8	62052594	CGGACCC	8	62215148	F
	CCCGGGA	37	4	1496880	CGGCTCC	4	1466208	F
	AATCAGT	37	19	44330665	CGCAAAC	19	49022505	F
	TTCTGAT	37	5	41763261	CGGTCTC	5	41799018	F

	GCCGGCC	37	16	28634844	CGGAGGC	16	28542345	F
	GCCGAAT	37	14	103839038	ATCCTCC	14	102908791	R
Red	GGTTTTA	37	12	54405379	CGGAGAA	12	52691646	F
	AAACACA	37	2	122259959	CTGCATT	2	121976429	F
	TGGCCTC	37	11	63435428	CGTCTCC	11	63192004	F
Red	TTCTATC	37	6	149151596	TGTGGCA	6	149193289	F
	ACTTGGT	37	18	35063285	TGTGTTT	18	33317283	R
	GGTCGCG	37	9	140356475	CCTCCTG	9	139476296	F
Red	ACTCGCA	37	1	148855262	CGCCGCC	1	147121886	R
	TGGCAGC	37	4	154155288	TTCTGCC	4	154374738	F
	TCCCTCC	37	19	2791705	CGCTGGG	19	2742705	R
	CCCATGC	37	14	76015669	TGAACTC	14	75085422	F
	TTTACCA	37	14	70317582	GGTTTAC	14	69387335	R
Red	GCTGGGC	37	6	30652399	GGGGGCA	6	30760378	R
Red	TCATCAC	37	2	24397810	TTCCGTT	2	24251314	R
	CTCCTGA	37	5	142623446	CTGTGCT	5	142603639	R
	AGAAAAA	37	11	55111658	CGCCTAT	11	54868234	R
	CATTCTG	37	13	39458059	AGATTTA	13	38356059	R
	TTCTGAA	37	11	26951784	CGAAGAC	11	26908360	F
Red	GACCCTT	37	4	132645884	GAGGACC	4	132865334	F
	TTCGAAG	37	3	129827549	GACCCAC	3	131310239	R
	CCGCGGC	37	6	29911087	GGCCAGC	6	30019066	R
	GTTATTA	37	6	29945409	CGGCTTA	6	30053388	F
	CTGCTTC	37	2	2295901	GCAGGAA	2	2274908	F
	TCCTGGC	37	8	41583523	CGGGACA	8	41702680	F
	CTGTGTG	37	17	48275324	CGCCAGC	17	45630323	F
	TGATTCC	37	10	82112873	CGGCTCT	10	82102853	R
	GGACGGC	37	3	10150065	CCTGGAC	3	10125065	F
	GTGTTCA	37	X	62780753	CGCCACG	X	62697478	F
	CCCCACT	37	19	44200812	CGGGAAC	19	48892652	F
Red	CCGGCCG	37	6	4079528	CGGGGCC	6	4024527	F
	GGGGTTG	37	1	26737262	CGGTGGC	1	26609849	R
Red	TCCCCTC	37	5	5887068	GTGTTGC	5	5940068	F
	GCATTCA	37	10	130831384	CGGTGAC	10	130721374	R
	AGAGTGA	37	10	133909949	CGGCTCC	10	133759939	R
Grn	CTTCCGA	37	2	99438903	AGGTTTC	2	98805335	R
	TATTTCC	37	5	140557227	GCCCAAA	5	140537411	R
	AACGAAC	37	4	37668528	TCCAATT	4	37344923	R
	AAAGGGC	37	2	233217476	CGCCCAG	2	232925720	F
	GAGCTAA	37	5	135416331	CGTCACT	5	135444230	R
Red	CACCCTC	37	X	40439984	CGCCCTA	X	40324928	F
	AAAATAC	37	14	35629311	CCCTTAA	14	34699062	R
	CTCACTC	37	19	39060314	CGGGCAC	19	43752154	R

	CCTTAGG	37	6	32301513	CGCAGAC	6	32409491	R
Grn	GCCCTGC	37	10	118387207	GTCAGGT	10	118377197	F
	GCCCAGT	37	3	139253838	CGGATTT	3	140736528	F
Red	CCTGGCC	37	18	72837627	CGGCCAC	18	70966615	F
	GGAGATC	37	14	50474530	GCACATC	14	49544280	R
Red	GGCTCCC	37	5	126409061	CGCTGTG	5	126436960	R
	TATCTTT	37	17	33390808	GCAAGAT	17	30414921	R
	AGAAGGC	37	15	64736348	CGGTAGT	15	62523401	F
	CACCATG	37	6	33035286	CGCGAAA	6	33143264	R
Grn	ACCCTCC	37	5	180048155	CGCCCAG	5	179980761	R
	GCCACCA	37	4	75608133	CGAAGGC	4	75827157	F
Grn	GGGCTTG	37	19	57630710	GAGTTGT	19	62322522	R
	ACAGCCA	37	5	34792020	CGTCATT	5	34827777	F
	CATTAAA	37	2	174719603	CGGGACC	2	174427849	R
	AGGATTC	37	6	36409367	CGCAAGC	6	36517345	F
Grn	GCTAAGC	37	5	110229987	TGCGATG	5	110257886	F
	AGCACCT	37	10	112261994	CGAGGTT	10	112251984	R
	CCTCTCC	37	1	20095795	ACTCTCT	1	19968382	R
Red	CCCCGCT	37	X	25025364	GCAGGCT	X	24935285	R
	GAACTGA	37	2	208572165	CGAGAAC	2	208280410	R
	ACTCCTC	37	22	18268631	CAGCCTG	22	16648631	F
	AGTGATT	37	15	91807630	GTCAGGT	15	89608634	R
Red	AGTGCGC	37	8	48676000	CTCGGCC	8	48838553	F
	GGAGTAC	37	11	5248426	CGGCTGT	11	5205002	R
	ACCTCCA	37	6	116381957	TGCTTTC	6	116488650	R
Red	GACCCGC	37	5	669397	CGGGCTC	5	722397	R
	CCGCAAC	37	X	55516224	CTGGCTG	X	55532949	F
	GGTGGTG	37	19	6710827	ATGCCAG	19	6661827	F
	CTTTGGT	37	2	154143768	CGCCGAC	2	153852014	F
	ATTTCTT	37	12	54385517	CGCCCTG	12	52671784	F
	AAACTAT	37	2	113594611	ATTTTGC	2	113311082	R
	TGTTTAT	37	5	80260554	CGATTGC	5	80296310	F
	GCGCAAA	37	12	59311232	CGCCAAC	12	57597499	R
Red	CGATCTG	37	6	100895050	GCTCTCT	6	101001771	F
	CCTGGGG	37	11	69830436	CGGAGAA	11	69508084	F
	CCCATCT	37	5	167831317	CGGAGCA	5	167763895	F
Grn	AGGCGGT	37	7	76145562	ATGCCAC	7	75983498	R
	AGCAGCC	37	5	135416613	CGGGGGC	5	135444512	F
	CCAGGGC	37	1	227963164	CGGCACA	1	226029787	R
Red	TATATGA	37	19	36265700	CGAGAAA	19	40957540	R
	AGAGAGA	37	10	30721971	ATTTCCC	10	30761977	F
	GAACCGA	37	3	18464935	TGCAAAC	3	18439939	R
Grn	ACCTTAA	37	5	164064	ACTTTTA	5	217064	R

	CCTGTGT	37	6	32489555	CGCGCCA	6	32597533	R
	CCTCGCT	37	5	141783822	CGCCTCA	5	141764006	R
	CAAAACC	37	17	59937758	CACATGA	17	57292540	R
	CTTTCAA	37	5	78281819	CGCTTGT	5	78317575	F
	CGCAGAC	37	6	15300007	CTCATTT	6	15407986	R
	CTCATGG	37	19	55417436	CGCTCTG	19	60109248	F
	GAGCAGA	37	13	97794052	TTCCATC	13	96592053	F
	AACCCCA	37	12	133177075	CAGGGTC	12	131687148	F
	ACTTGAT	37	7	143746594	TCTAGGA	7	143377527	R
Grn	GCGGGCC	37	6	31276434	TCCGGGA	6	31384413	R
	TTCATCC	37	11	123048161	GAATCAC	11	122553371	R
	CTGCCCC	37	10	82189478	TCCACTG	10	82179458	F
	TAGTTTC	37	6	168815477	TCCCACA	6	168558326	F
	TCTTAGC	37	2	227288863	CGCACGT	2	226997107	R
	GGAATGC	37	15	74343476	CGGGTCT	15	72130529	R
Red	GGGCGCC	37	19	33623072	CGAGATC	19	38314912	F
	TGAGATC	37	17	72192970	CGCCCTC	17	69704565	F
	AATTTAA	37	17	21727476	CGCCCAC	17	21651603	R
Grn	TCGTGCA	37	12	133378609	ATGGGGC	12	131888682	R
	TGTCCCT	37	11	46942432	CGGTTCA	11	46899008	F
	GGAGCCA	37	11	57792403	CGGTGTG	11	57548979	F
	TGTATTA	37	4	41258374	TGGTAGA	4	40953131	F
	GCGGAGA	37	2	242989856	CGGGGAA	2	242638529	F
	ACTGTGT	37	10	93624759	ACAAACA	10	93614739	F
Red	GGGCCCA	37	4	170696239	CAAAGAC	4	170932814	F
Grn	CGGCGTC	37	14	105830859	TGCGCGG	14	104901904	R
	CGTTAAC	37	2	10517323	TAATGAA	2	10434774	R
	TTAAAAG	37	5	135342478	CGTCCAG	5	135370377	R
Red	GGGATGC	37	2	175594943	CGGGCTG	2	175303189	F
	GGGTGGC	37	6	30039151	CGGCCCC	6	30147130	F
	TGCTGAG	37	1	85426586	CGGAATA	1	85199174	F
	TCAGTTT	37	13	84454283	GCTGTCC	13	83352284	F
	GGGGTCC	37	1	110230456	CGGTTTA	1	110031979	F
Grn	CCGGGGA	37	7	153749736	CGGAGGA	7	153380669	R
Red	GCAGGAC	37	10	1517083	GAGGAGC	10	1507083	R
	CCAAGCA	37	14	99858181	CGGTGGC	14	98927934	F
	ATCTGAA	37	17	32895602	CTCTAGG	17	29919715	F
	TGGGAAA	37	1	86077581	CGCTGTC	1	85850169	F
	GAGCTAC	37	13	97794113	CCTGGGT	13	96592114	F
	CACAAAC	37	11	78131895	GGTTCTA	11	77809543	R
	TGAATAT	37	10	126086354	CCATTAC	10	126076344	R
	TTCCTGC	37	10	135342936	GTAGAGC	10	135192926	F
Red	GGGAAGC	37	X	48660440	GAGGCCC	X	48545384	R

	GTTGCAA	37	12	132263618	GAGAACT	12	130829571	R
	CGGCTGG	37	3	14602840	CGAGGCC	3	14577844	R
	TCAAAAT	37	3	197272328	GCTGGTT	3	198756725	F
	AAGGTTG	37	10	34817409	CGCAGCT	10	34857415	R
	AGTCAGC	37	17	76794560	CGGAACT	17	74306155	R
	GCTCCAG	37	17	42980188	CGGCAAC	17	40335714	F
	GTCCTGG	37	13	113677628	CGGCACC	13	112725629	R
	TTTCACT	37	11	6744048	TTGACAC	11	6700624	R
	ATGCATG	37	5	176784448	AGCCTGT	5	176717054	R
	TTGCTGA	37	13	37702050	CGGAGGT	13	36600050	F
	GGGGTCC	37	6	29911091	AGGTTCT	6	30019070	R
Red	GCCAAAC	37	6	30038922	GTTGGAG	6	30146901	R
Red	CGGGTCA	37	17	46619923	GGCCGGT	17	43974922	F
	GTCTTGG	37	12	49662405	TTTCTAG	12	47948672	R
Red	GGTCTTA	37	7	1099421	GCGGGTC	7	1065947	R
	TCCTTTC	37	2	45581335	AACATGC	2	45434839	F
	TTTTAAA	37	6	106536036	CGCCGTT	6	106642729	R
	CAACGTG	37	4	190123606	CGCCACC	4	190360600	F
	CAGATGT	37	2	158723291	CAGTTTC	2	158431537	R
Red	CCACGGC	37	1	1190137	CGCGGAC	1	1180000	F
	TCCCTCA	37	15	38361362	CACAAAA	15	36148654	R
Red	ACAAATC	37	10	6274873	GAACCGA	10	6314879	F
	GAGACCC	37	6	170054730	TCTCACT	6	169796655	F
	CATTGAA	37	6	46623767	CACAGAA	6	46731726	F
Grn	CCGCCGC	37	7	64043193	CGCGCGC	7	63680628	F
Red	CCCCCGC	37	17	61926700	GGTGTAG	17	59280432	R
	CATAAAC	37	8	39844956	CGCAGGA	8	39964113	R
	AAGTGGT	37	2	169346613	CGGGACA	2	169054859	R
Red	GCAACGC	37	X	133678716	CGCGTCC	X	133506382	F
Grn	AATTAAT	37	3	101406347	GAATGTT	3	102889037	F
	GGTTCCG	37	6	30421114	CAAGGAT	6	30529093	F
Red	CGTCCAC	37	11	65769518	GGGAACT	11	65526094	F
Red	CTCCCCT	37	6	1555311	ATGCTTT	6	1500310	F
Grn	CCTGTGT	37	17	77922865	CGCCACA	17	75537460	R
Red	AGATGGA	37	17	48858746	CGTCAGA	17	46213745	F
	CATATTA	37	3	142854187	ATAGAGA	3	144336877	F
	CAGTTGC	37	11	75130069	TCTGGCA	11	74807717	F
	AGGTCCC	37	2	242869012	TCTGGGC	2	242517685	F
	GCTTAAT	37	2	173902435	CGGCGCC	2	173610681	R
Grn	AGGTGGA	37	20	56725873	CGGCGAA	20	56159279	F
	CCAAATA	37	13	95652307	AAACACC	13	94450308	R
Grn	CCTGGCG	37	6	33860869	GCAGCGC	6	33968847	F
	CACCGTT	37	12	133382933	CGCTGTA	12	131893006	F

Red	CAACACA	37	7	944607	CGCAGCT	7	911133	R
	CATGCCA	37	6	30850581	CTGGGGT	6	30958560	R
	CAGCAGC	37	6	30955358	CGCCTCA	6	31063337	R
Grn	GGGGTTG	37	20	59542589	CGCCCTC	20	58975984	R
	TATCCCT	37	15	30264290	CGGTGGT	15	28051582	F
Red	GGGCGGT	37	7	150020108	CGGGAGC	7	149651041	F
	CCAATCC	37	2	233216865	TCAACAG	2	232925109	R
	CACACAA	37	2	10340837	TTGTGAA	2	10258288	F
Grn	TTCCCCA	37	12	114395548	CCGCTCT	12	112879931	R
	AACGCCC	37	17	38708638	CGGCTTG	17	35962164	F
	CAGGGTC	37	12	125223540	GAGAAGC	12	123789493	R
Red	GCGTATC	37	6	110721138	AACGGAC	6	110827831	R
Red	ACAAGA	37	8	120429518	CGGACAC	8	120498699	F
Red	GAGGGGC	37	10	135246701	CGCCCCA	10	135096691	F
Red	CGGCTAA	37	21	36041605	TCCTTGA	21	34963475	F
	CTGAAGA	37	13	100470738	CGGACAC	13	99268739	F
	AGCAGAT	37	2	127951364	CGCCTTT	2	127667834	F
Grn	TAGTGGC	37	6	28322086	CGCCTGC	6	28430065	F
	TTGTCAC	37	19	20576478	CGTTGGA	19	20368318	F
Red	CTGCAGG	37	13	111111172	CTGGGGA	13	109909173	R
	CCTAGGC	37	12	7129898	AATGGTA	12	7000159	F
	AGACTTA	37	19	13276344	CGGAAGT	19	13137344	R
	TGGTATT	37	7	73476337	CGCTCCC	7	73114273	F
Red	AAAGGTC	37	10	134953542	GGCTCCG	10	134803532	F
	TCTGATG	37	6	32141882	CGCCAGT	6	32249860	R
	TTGGCGT	37	7	76624761	CGCCCGT	7	76462697	F
	GGAAATT	37	20	4795444	CGGGGGC	20	4743444	F
	CTAGGGA	37	1	161569954	CGATGGC	1	159836578	R
	CCTAGTC	37	Y	16636990	TCCCAGG	Y	15146384	F
	GACGCCC	37	10	110671988	AGTCAGT	10	110661978	F
Red	AGTGCAA	37	10	29747315	CGCACGC	10	29787321	R
Grn	GAGGAGC	37	17	7790048	TGCCAAG	17	7730773	F
	CGTGTTC	37	X	9434519	CGAGTCA	X	9394519	F
	TCTGGCT	37	7	140135515	CGCCCTA	7	139781984	R
Red	TGCTTCC	37	1	41303922	CGCCCCC	1	41076509	F
Grn	GGCTGTG	37	2	24625812	CGGAGTC	2	24479316	R
	TAGTTGG	37	2	161209326	ACCCTCA	2	160917572	R
	TTATAGA	37	13	27769437	CGCACAC	13	26667437	R
	TGTAGCA	37	12	6162821	CGCCCAG	12	6033082	F
	TCCACTG	37	6	16962712	CGGATGC	6	17070691	R
	AGCTCTT	37	6	54200888	CGGGAAT	6	54308847	R
	GAGCCGC	37	5	502074	TGTTGTT	5	555074	F
	AGCCAGC	37	12	67040901	CGGGAGT	12	65327168	R

Red	TGGACTA	37	19	37569299	CGCTCCC	19	42261139	F
	GACCATG	37	17	7820248	CGTGATG	17	7760973	F
	ATGAAC	37	2	46542361	CGGGTTG	2	46395865	R
	TTCCCCT	37	11	19463903	TTATGTA	11	19420479	F
	GAGGAG	37	17	46560683	CGGTGGA	17	43915682	F
	GCAAGA	37	2	88771031	AGGACCA	2	88552146	R
	AAAACA	37	6	52288804	CACAGAA	6	52396763	R
	GATGAC	37	12	131369535	CGGCATG	12	129935488	R
	GTGCATA	37	12	113516445	CGGGGAA	12	112000828	F
	GCAACC	37	10	123731471	CGGATAC	10	123721461	F
	ACTCCAG	37	1	42420460	CGGACTA	1	42193047	R
Red	TATTTAG	37	8	6664522	GGAGAA	8	6651932	F
Red	CTCAGTG	37	1	248791716	CGGGCTC	1	246858339	R
	AAGGAA	37	6	31529897	CTCTTTG	6	31637876	F
	TGCCCAG	37	15	79722028	CGCGAAT	15	77509083	R
	AGAATG	37	1	219634786	CGGCAA	1	217701409	R
	GGCAGA	37	18	77292410	CGCCAG	18	75393398	F
	GACTTAG	37	10	72138124	CGCCCGG	10	71808130	R
	CTCCTCT	37	19	55309528	CGGGGAA	19	60001340	F
Red	GCCACCA	37	X	150067114	CGGGCG	X	149817772	R
Red	CTACGGG	37	19	36485356	CAGTTAC	19	41177196	F
	TGCGCCT	37	10	4868333	ATGGCTG	10	4858333	F
Red	ATTCCCC	37	X	105855052	CGGACGA	X	105741708	F
	GTGCTCT	37	4	104123084	CGGGCCA	4	104342533	F
	CCCAGAT	37	8	129165545	CGGCTCG	8	129234727	R
	TTGTGGT	37	5	34687565	TCCTCCA	5	34723322	F
Red	CCGCCAT	37	4	967324	CGCCGCT	4	957324	F
	ACACACA	37	1	13877579	AAAATTT	1	13750166	R
	GAAGAA	37	10	115388944	CGGGCC	10	115378934	F
	GGGGCT	37	19	17219073	CACGTTT	19	17080073	F
	GCAAACA	37	4	79077191	ATTCTTT	4	79296215	R
Red	TGTGTTC	37	5	95295965	CGGAAG	5	95321721	R
Red	GCGTGG	37	20	61919450	CGGGAC	20	61389895	R
	GCGGGCT	37	7	98889946	CGCCGTG	7	98727882	F
Red	CGCGAG	37	3	126194923	TGGGCTG	3	127677613	R
Red	CGGGCTG	37	17	17628656	CGCAGGA	17	17569381	R
	TTTTCTCT	37	11	12785773	GGTTTAT	11	12742349	R
	CTACAAT	37	15	96891476	CGCACAT	15	94692480	R
	TGCACTC	37	2	237551858	GTTTCCC	2	237216597	R
	TCTCCAT	37	15	68564546	AGCTGG	15	66351600	R
	GCAGCCT	37	10	135341870	CACCCCT	10	135191860	F
	CCAAATG	37	14	99613263	CGCCTTG	14	98683016	R
	GGCTGCT	37	1	41828130	CGGGGG	1	41600717	R

Grn	AGGACA	37	6	39271655	CCGGATT	6	39379633	R
Grn	CAGCAC	37	18	77172117	CGCGTGA	18	75273105	R
	GAATCTC	37	9	22005288	AGAGAG	9	21995288	F
	GAAGAG	37	4	119990940	CGAGGC	4	120210388	F
Grn	CAAATTT	37	11	123940566	CGGGAA	11	123445776	F
Red	CGCCGCA	37	X	73513453	CGCTAAG	X	73430178	F
	TCCTCAT	37	2	218925608	AAGTTCA	2	218633853	F
	GGGAGA	37	15	76016056	CGGGTGA	15	73803111	R
Red	CCAGCCC	37	1	248300479	GCCTTCT	1	246367102	F
	TGGACAA	37	2	158301839	ACTCCCT	2	158010085	F
Grn	TTTGCAG	37	2	177016490	GCTCACC	2	176724736	F
	AGTGCCG	37	X	83757504	CGTCACG	X	83644160	R
	AATCCAG	37	6	32493994	CGGCTGG	6	32601972	R
	GCTGCTG	37	4	141391053	GAGGGT	4	141610503	R
Red	AGGGCT	37	22	49717457	AGAGGA	22	48103461	R
Red	GAAAGA	37	X	134555711	CGTGCCC	X	134383377	R
Red	CCGGTCA	37	22	25160075	GGTTGAA	22	23490075	F
	CTAAGAA	37	3	112876728	GTAATGA	3	114359418	R
Red	GGCTACC	37	8	41583498	CGTCTGA	8	41702655	F
	GGACCA	37	14	35032169	GAAAAA	14	34101920	F
	GTTTATA	37	15	81028959	CGTGAAT	15	78816014	R
	GTTGCCA	37	5	10401195	CGGTATG	5	10454195	R
Grn	ATCGGGA	37	12	8025640	CCGTAAG	12	7916907	R
	CGGGCA	37	1	230513337	CCTGTTC	1	228579960	F
Grn	CAGGGG	37	4	57458863	GCCGCG	4	57153620	R
Red	CCGCACA	37	6	10720630	CGGTGCC	6	10828616	R
	TCTGTTG	37	14	22362410	CGGATCC	14	21432250	R
	CTTTGTG	37	6	29913343	AAGAAC	6	30021322	R
	GAAGAG	37	6	2972896	CGCCATA	6	2917895	R
	GCCAATG	37	15	79729041	TTCATTG	15	77516096	R
	ATGTTTT	37	8	100770219	GAAACC	8	100839395	R
Grn	GTTCTCA	37	2	231714995	CGCCTCC	2	231423239	R
Red	TGCGACG	37	10	135278901	TGGGACC	10	135128891	R
	AGCAGCC	37	5	139040928	GTGTGCT	5	139021112	F
	TTCTCCT	37	4	187984958	GTCAGGA	4	188221952	R
	GGCAATC	37	6	118873071	CGATGAA	6	118979764	R
	CGCCAA	37	6	29649084	CGAGCCT	6	29757063	F
	GGGTGTA	37	19	18503517	GCGGTCT	19	18364517	R
Grn	TTCTTTA	37	12	116864616	CGCCCCG	12	115348999	R
	TGGTGGC	37	5	140594406	CAGAGAT	5	140574590	F
	CCGGGTG	37	12	11700343	AAATTGA	12	11591610	F
	TACGAG	37	12	10096118	GTGCCCC	12	9987385	F
	AAGGTGA	37	14	101505898	AGAACCT	14	100575651	R

	GTTTCTC	37	14	36563446	TCTAAGT	14	35633197	R
Red	CCCATCC	37	7	94953810	AGGGTGA	7	94791746	R
	CTGCTAC	37	5	67845133	TCACTTT	5	67880889	F
	AGCATAA	37	5	74908142	GGCAGCT	5	74943898	R
	TCAGCCA	37	6	5512308	CGCCCAG	6	5457307	F
	GTGGATA	37	19	55477759	CGGAGAT	19	60169571	F
	CCGAGCA	37	15	42186945	GGACTAC	15	39974237	R
	AGCCCAC	37	6	7106952	CGCTTCG	6	7051951	R
	ACAGGCT	37	2	179923444	CGCCCCT	2	179631689	R
	CCTGTGG	37	22	25571929	CTGAGGT	22	23901929	R
	GAAGTGA	37	5	83681563	CGGTTAG	5	83717319	F
	GGTCAGC	37	7	112063079	ATGGGTC	7	111850315	R
	ATGCTGT	37	3	32400704	CGGCCCA	3	32375708	F
	GCGAGAT	37	10	6183872	CGCACTT	10	6223878	R
	CGAGCCC	37	11	2813121	TGGGGGC	11	2769697	R
	CCACCTT	37	2	74357872	TGCTTGG	2	74211380	R
	CTTTCCT	37	14	71022823	CGGCTGC	14	70092576	R
	ATGTGGC	37	12	56115029	CTTCTGC	12	54401296	R
	ACCACAC	37	5	76010598	CGGCTGA	5	76046354	F
	CCTCTCC	37	2	8144208	AAGTGTT	2	8061659	F
Grn	GTTCCAC	37	11	1712765	AGGGGTC	11	1669341	F
	GACCTGT	37	5	153039227	CCATGGT	5	153019420	F
Grn	CCCCGGG	37	X	110039080	CGCGCAC	X	109925736	R
Red	GCTCAGA	37	17	650208	CGCGACC	17	596958	R
	GGGGGGC	37	10	50829959	CGCCCCC	10	50499965	R
Red	ACTCTAG	37	4	183063459	CGGGTCG	4	183300453	F
	CCGGGAA	37	17	56283364	CGTCTTT	17	53638363	R
	ATTTTGT	37	19	10231711	CTCCCTG	19	10092711	F
	TATAAAG	37	2	145753993	CGCAAGA	2	145470463	R
	TGCTGAT	37	6	32522400	CGCTCAG	6	32630378	F
Red	GTCAGTG	37	3	194786989	GGGTGTG	3	196268278	R
Red	GCACGCT	37	12	297831	CGCACGT	12	168092	F
	CAAACAC	37	12	24974720	CGGGATC	12	24865987	F
Grn	GTGGGGA	37	8	145737513	CGGGCGC	8	145708321	R
	TTCTAAT	37	17	77906735	AAAACAT	17	75521330	R
Red	ATCAGTC	37	6	7758958	AGGCGGC	6	7703957	R
	GCAGTAC	37	12	113408421	CGGAAAA	12	111892804	F
Red	AGCACTC	37	1	201618284	CGCTCGC	1	199884907	F
Red	ACTGGCA	37	18	22006089	CGATCGC	18	20260087	F
	AGGTCTA	37	17	79045765	CTGCAGA	17	76660360	R
	TTTGGAA	37	21	36421941	CGCTGGC	21	35343811	F
Red	CCCTTCC	37	8	48675647	AACACCC	8	48838200	F
	TCACTGT	37	5	54448226	CGGATTA	5	54483983	R

	AGCTGCT	37	15	29213748	GAAAGGA	15	27001040	F
	CCTGTAG	37	17	13249936	CGCGCCA	17	13190661	F
	TTGCGGG	37	10	34344580	TGGCCCA	10	34384586	F
	GTTTTTC	37	7	134298937	CGCCACA	7	133949477	F
	CACACTT	37	1	218382922	TTTAGTC	1	216449545	R
	GTTCTAA	37	14	92301922	TCAATGG	14	91371675	R
	AGCAAAA	37	4	144208277	AGAAAAC	4	144427727	R
	ATAGATG	37	3	4762242	AGGCAGT	3	4737242	F
	AGCCCCA	37	11	64815313	CGAGGCT	11	64571889	F
	CTCCCGG	37	7	134856654	CTTCAAG	7	134507194	F
	CCTGGGC	37	7	105423113	GCTCCAT	7	105210349	R
Grn	GGGCGGC	37	X	152740227	GGGCGGC	X	152393421	R
	GCAGAAT	37	12	54383692	CGGCTAG	12	52669959	F
	GCCGAGC	37	X	150067102	GCCACCA	X	149817760	R
Grn	CCACTGA	37	15	23811369	TGCAGCC	15	21362462	F
	TTCACAA	37	11	102139781	AGCACTA	11	101644991	F
Grn	TCCTGGC	37	1	161450473	GCAGGAC	1	159717097	F
	GAAGTCT	37	X	149531880	TTCTGGG	X	149282538	R
	GTTTCAG	37	10	44494208	CTTTGAT	10	43814214	R
	GTGGCTA	37	16	31439191	GAACAGA	16	31346692	R
	GTACCCG	37	9	115841081	TGTTGCT	9	114880902	R
	GGAGGCT	37	14	94759767	CGAGAGC	14	93829520	F
Grn	CGCGCCC	37	13	25320133	GCTGCGC	13	24218133	F
	GTGGTTT	37	7	1113237	CATCACG	7	1079763	F
	ACAGTGA	37	11	108408969	CAAAGCT	11	107914179	F
	GCTTCTG	37	14	87265617	ATTCTCT	14	86335370	F
	AAAAGCT	37	2	19886939	CGTTCAA	2	19750420	F
Red	TGCCCCT	37	2	233271154	CGGGCCA	2	232979398	R
Red	CAGCGGC	37	5	140535759	GCTGCAA	5	140515943	F
	GCCTGGT	37	10	79110632	CGGTGAC	10	78780638	R
	CCAGTCA	37	21	42839625	CGGAGAA	21	41761495	F
Red	CTGAAAC	37	11	2779993	CGGGAAT	11	2736569	F
	TGTGTCA	37	17	80096661	CTTGTTC	17	77689950	R
	CCAAAAT	37	5	140246626	CGCCAAC	5	140226810	R
	CAAAACA	37	5	171870875	TACCATG	5	171803480	R
	TTATCTT	37	20	36530548	CGGCTTG	20	35963962	F
	TAATCAC	37	4	154491023	CGGGAGA	4	154710473	F
	AGTTCAC	37	14	59844444	CGGGCCC	14	58914197	F
Red	GACTCCT	37	X	144900177	CGCCGGC	X	144707869	F
	TTGAAAT	37	7	96649956	CGGAAAA	7	96487892	R
Grn	TCTTGGT	37	2	238777656	GCCCTAA	2	238442395	F
Red	GGGAGTC	37	6	142238173	CAGTGGC	6	142279866	R
Red	CTACCGC	37	14	24780404	CGCCGCC	14	23850244	F

Grn	AGCCGGC	37	X	19905497	CCGCCGA	X	19815418	R
	TAAACAC	37	7	5179884	CGGCCTC	7	5146410	R
	AGGTCCA	37	6	32549496	TGTGAGT	6	32657474	F
	GATTGCT	37	7	130875551	CGCTCCA	7	130526091	R
	GAGGAAC	37	4	154174325	CGCTCCT	4	154393775	R
	TTGGCTT	37	12	3563432	CTGAGCC	12	3433693	F
	GAAGGGT	37	14	77926864	AGGTCTG	14	76996617	F
	CCAGCTC	37	10	73770523	CGGCCAC	10	73440529	R
	AGAGAAC	37	3	123339334	GAACATC	3	124822024	F
Red	TGAGAGC	37	6	37617864	CGGGTGC	6	37725842	F
	ACGCCAC	37	14	21467375	CGCCTTC	14	20537215	R
	CGGGGCT	37	X	12993759	CGGCATC	X	12903680	R
	CCGAGTG	37	7	102574504	CGCACCA	7	102361740	F
Grn	CGCCGCG	37	8	52322009	CGTGGGC	8	52484562	R
	AGACTCC	37	14	69784107	CGGAGCT	14	68853860	R
	TCTGGCC	37	22	46481816	TCCTGGG	22	44860480	R
	TGTTTGT	37	4	107434718	CTTCTAA	4	107654167	R
	CTTTGGT	37	22	45608713	AGATCTG	22	43987377	R
	CATCTGT	37	10	96442154	AGTAAAC	10	96432144	F
Grn	CCTGCGT	37	10	135379242	CGGGCTT	10	135229232	R
	GGTCTCA	37	8	1321375	TTTGGCC	8	1308782	R
	GTGATGG	37	12	3384898	TTGGGCG	12	3255159	R
	AAGCAAC	37	11	72327160	CGCTGAG	11	72004808	F
Red	CCAGGTG	37	17	36718549	CGCATCG	17	33972075	R
	GAGGAAA	37	18	34917603	CGCTGCC	18	33171601	R
	GAATCCC	37	6	170058205	CGCTGTG	6	169800130	R
	ATAAAAC	37	6	30920086	CGAAGCT	6	31028065	F
Red	GCGCACC	37	X	17674384	CGGCCCT	X	17584305	R
	AAGTAAA	37	7	94954144	TGGCTGT	7	94792080	F
	GGAAAGA	37	11	27017005	CGGGTGT	11	26973581	R
Red	AATTCTG	37	11	119970504	TCCATAT	11	119475714	F
Red	CACTGAA	37	10	27235598	TACAAAT	10	27275604	F
Red	ATCTCTC	37	1	2928616	CGCCGAC	1	2918476	R
	AGTTATT	37	19	55416928	CGACTTG	19	60108740	F
	GTTCTGG	37	20	61731979	CGGCCCC	20	61202424	F
Grn	CGGCCCC	37	7	63642083	GGGTTCG	7	63279518	R
	ATTTTAG	37	10	64323709	GAGTCAC	10	63993715	F
	ATGACTA	37	6	134026410	CGGTGGT	6	134068103	F
	GCAGAGC	37	12	313104	CTTTCCT	12	183365	F
	AAGTGAA	37	12	11080457	TGTGATA	12	10971724	F
Grn	AATATTG	37	7	96648205	TGACCGC	7	96486141	F
	TGCCAAA	37	6	39769426	CGCCTGT	6	39877404	R
	CGTGTTC	37	10	1251771	CGTCAGC	10	1241771	R

	AATGCAC	37	3	30512797	GAAGAA	3	30487801	R
	TTATGTG	37	11	61159687	CTGGAAA	11	60916263	R
	GAATTAA	37	4	147557774	CGGGAG	4	147777224	R
	CCCCAGT	37	17	77478637	CTGCAGG	17	74990232	F
	GGAGGGT	37	18	77678514	CGACCCC	18	75779502	R
	ACTAAGA	37	12	99130587	AAATTAG	12	97654718	R
Red	TGGGGAC	37	7	158059142	CTGCTGC	7	157751903	R
	ACTATCA	37	19	49202858	CCCAGTA	19	53894670	R
Grn	CCCAGCC	37	19	41317837	TTCACGA	19	46009677	R
Red	GGAGCCT	37	15	79104481	CGGCCGT	15	76891536	F
	GAAGCCC	37	6	30039374	ACCCAGC	6	30147353	R
	ACCCGAC	37	17	8124867	CCGGGTC	17	8065592	F
Red	TTGGACG	37	15	40268687	CGCAGG	15	38055979	F
	GGTTGCA	37	14	70826997	CGTCTCA	14	69896750	F
Red	CCTGCTG	37	1	207842927	CGCCCCC	1	205909550	R
	TACGTGT	37	10	68688049	CTGGGAC	10	68358055	F
	GATTTAT	37	1	230992616	CGGTGTA	1	229059239	R
Red	TTCTCAC	37	7	149469722	GGGGCCC	7	149100655	F
	ACCCACT	37	8	37660108	CGGGACC	8	37779266	F
	TCCTTCT	37	2	133429169	CGGGGAC	2	133145639	F
	CGGCGTG	37	1	41303356	GGGCCCT	1	41075943	R
Grn	AGGCTGC	37	X	18443740	CGGCAG	X	18353661	R
Grn	TCTGCGC	37	10	4868331	GGCTGGA	10	4858331	F
	CAGTCAT	37	18	33548566	CGGCTTG	18	31802564	R
	GTCCTCA	37	1	168091000	ATCACTG	1	166357624	R
	ACCGCTA	37	19	58728728	CGGGCCT	19	63420540	F
	AGTACCC	37	1	246416688	CGGGAAC	1	244483311	R
	ATGGCAC	37	4	22239907	CGGCAGC	4	21849005	F
	GACCGCA	37	1	247457841	CGGTTAC	1	245524464	R
	GGGGGTT	37	1	156624237	CGGGAGC	1	154890861	F
	GTTCTGA	37	1	2120985	CGCATTA	1	2110845	F
	AGATGCA	37	2	64839958	CGGCCTG	2	64693462	R
Grn	CCCGGAC	37	20	25128805	ACTAAAA	20	25076805	R
	GGACTCT	37	1	244763541	CCAGCTT	1	242830164	F
Red	AGAAATC	37	2	1746207	CGGGTGA	2	1725214	R
	AACCCAC	37	2	97331035	GTTTGTT	2	96694762	R
	CAGCAAC	37	10	10403467	CGCCACT	10	10443473	R
Red	GCAGAAC	37	8	62052207	GCGCAGC	8	62214761	R
	GTCTTAG	37	2	236234204	CGGCAAC	2	235898943	F
Grn	TGGCATA	37	10	3138418	CGCGTGC	10	3128418	F
	GAAGGA	37	11	1892074	ATGGCAC	11	1848650	R
	TGATGGT	37	7	143081287	AGTCCAA	7	142791409	R
	CCTCCTC	37	1	226107899	CGCAGGC	1	224174522	F

	TGCGCAG	37	19	55038263	GGTGAAC	19	59730075	F
	TTTTTAA	37	12	124780809	CAAACCC	12	123346762	R
	CCCATTC	37	10	104512523	CCTGGCT	10	104502513	R
Red	TCAGTCT	37	12	54391631	CACTTGG	12	52677898	F
	TAGATGG	37	21	46829943	TTGGGCC	21	45654371	R
Red	CTTCCCT	37	X	71351980	CGACCTC	X	71268705	R
	CTGGGTG	37	3	115758614	GCCATTC	3	117241304	F
	AGAGGAC	37	6	31838544	CGCCCTG	6	31946523	R
	GTGCACA	37	11	132939610	GTCACCT	11	132444820	F
Red	CCGGCAC	37	X	30907117	CGCCGCA	X	30817038	F
Grn	GACCCCA	37	7	96650668	TGTCTTT	7	96488604	R
	ATTCTAT	37	19	36801408	AACAGCT	19	41493248	R
Red	CTTACAC	37	7	158122229	GGCAGGC	7	157814990	F
	AGGGATA	37	6	158136705	CGTGGCC	6	158056693	F
	TTGGCCC	37	17	40439433	CGGGTTG	17	37692959	R
Red	CGTTGGC	37	6	127796683	GCAGATC	6	127838376	F
Red	GAAGCGC	37	12	25055967	CCATGGG	12	24947234	R
	CCTCTCC	37	Y	7141681	AAACGCC	Y	7201681	R
Red	GGGCGGC	37	12	54381013	CGCCCGT	12	52667280	R
Grn	GGAACCC	37	12	54377457	CGGTCTT	12	52663724	F
	CCGTGGG	37	1	7122726	CTGTTGG	1	7045313	F
	AACCCTT	37	7	130600075	TTGAGTA	7	130250615	F
Red	TGAAGGC	37	6	166260012	CGCGGAC	6	166180002	R
	AGAGGTC	37	7	127720749	GTGAGGA	7	127507985	R
	TCCCATC	37	1	248101009	CGGCAGC	1	246167632	R
	GCCTCAG	37	1	84831593	TCTGAGG	1	84604181	R
Red	CTGAGTC	37	4	190905801	GGAACCC	4	191142795	F
Red	GCCGTTA	37	6	28584061	CGGGCGA	6	28692040	R
	AAATGGC	37	2	158687877	CTTGAAC	2	158396123	F
	CAGTTCC	37	6	47668044	CGCTGAG	6	47776003	R
	GATGGAA	37	17	9546550	CATATAC	17	9487275	R
	CTCTAAT	37	1	203372112	AGATTTC	1	201638735	R
	ATTCTGT	37	6	2773876	CGAAGAA	6	2718875	F
	CCTAACC	37	11	103403056	CGTTCCC	11	102908266	R
	AGACTTC	37	11	74323002	CGGTAGC	11	74000650	R
	TTTGAAA	37	X	11682132	ACCCGCT	X	11592053	F
	TGATGAT	37	8	142505578	CGGCTTC	8	142574760	R
	GATGTGT	37	14	100497940	CGTGGTC	14	99567693	F
	AGACAAC	37	18	13916113	AACCCTG	18	13906113	R
	CCTGGAG	37	6	31474086	AGAATCC	6	31582065	R
Red	CCGACTG	37	X	152912606	CGCCCCG	X	152565800	F
Red	GTCAGGA	37	6	170547656	TGCAAAA	6	170389581	R
	GTGGGCC	37	1	248100600	GAGACAC	1	246167223	F

	TGGCCTC	37	1	8960134	CGGAAAT	1	8882721	R
	GGCCCAC	37	8	131457460	CGCAGCT	8	131526642	F
	ATAAAAT	37	7	17316151	CGGACAA	7	17282676	F
	CCATCAA	37	7	158032352	TCTCCTC	7	157725113	R
	TCCTCAA	37	3	9976241	AAAGCTG	3	9951241	F
	GCGAGGC	37	7	158533927	CGCTGCT	7	158226688	R
	GTTTACG	37	13	100989375	CGCGCCC	13	99787376	F
	AAAAAAT	37	8	91683243	CGCATTC	8	91752419	F
	AGGTTTA	37	7	150263322	CAGAAAC	7	149894255	R
Red	CCACACT	37	7	157370486	GGTCTGG	7	157063247	R
	CAGCCCA	37	15	33586239	CGGGACA	15	31373531	R
	CAAACAT	37	15	40421005	CGCGGGC	15	38208297	R
	AGCTGCT	37	6	36076933	CGGGCCC	6	36184911	R
	AAAATTT	37	17	73316280	AAAAACT	17	70827875	R
	CTGGGGT	37	6	30039900	GGATTCC	6	30147879	F
Grn	AGCAGTT	37	X	84258823	GACAAAT	X	84145479	F
	TAGTACT	37	1	215177441	ATCAGTT	1	213244064	R
	ACCTATA	37	1	170044647	GTCACTT	1	168311271	R
	GTTTCAG	37	12	101381320	TCATTGG	12	99905451	F
	TGTGGCT	37	4	188131622	CATGCAA	4	188368616	R
	GGATTCA	37	6	36891482	CGGGCCT	6	36999460	F
Grn	TGACGGC	37	14	21191754	TCTAGGG	14	20261594	F
	TAAAATG	37	19	1070986	CGGGTCC	19	1021986	R
Red	CGTGGCG	37	2	89065319	CGGCCCC	2	88846434	R
Grn	AGCTGGT	37	15	40364740	AAAACAT	15	38152032	F
	GCTATTC	37	2	65290738	TCTGAGA	2	65144242	R
	GGCTTGG	37	15	83332087	CGGGGCA	15	81129142	F
	CGAGGCC	37	20	33292126	CGGCACA	20	32755787	R
	AACCATG	37	12	68592548	ACTGACT	12	66878815	R
Red	CCCCTGC	37	2	9235898	CCCTGCC	2	9153349	R
	TGAGTCC	37	6	33040610	TCCTCTC	6	33148588	F
	GTCTCAC	37	6	27799380	CGCCAAC	6	27907359	R
	CGCAACC	37	10	112404997	CGACCCA	10	112394987	R
Grn	ACCACTT	37	15	31355304	GTCCTTT	15	29142596	F
	TATAAAA	37	7	48124396	ATTTATC	7	48090921	F
	AGATTCC	37	12	49061475	CGGGTAA	12	47347742	F
	GCCAGCC	37	15	50170642	CGGCTTT	15	47957934	F
	CAGTACA	37	17	40936820	TTTAGAA	17	38190346	R
	AGTTGTT	37	2	28509570	TAACAGA	2	28363074	F
Red	TGGGTGT	37	X	153095300	CGCACTC	X	152748494	F
	TTAGGGC	37	17	6734940	CGGTGGC	17	6675664	F
Grn	CCCTAAG	37	17	80969547	TCCAGAA	17	78562836	R
	TGAACTC	37	19	17762314	ATCTCAC	19	17623314	F

	CGATTCA	37	1	23521332	GCAGTCC	1	23393919	R
	AATTGGC	37	1	19186260	CGGTGGC	1	19058847	R
	CTGCCCC	37	3	28944854	CGGGCCA	3	28919858	R
Red	ACATTTC	37	10	12853879	GCCTGAA	10	12893885	R
	CAGGGTC	37	X	150396221	TAAGGCC	X	150146879	R
Grn	TGGAGAC	37	1	20238347	CGGTGTG	1	20110934	R
	TTTAACC	37	17	35853648	AACCATA	17	32927761	F
	AGATGGA	37	10	95706927	CGCACTT	10	95696917	F
	CGTCCTC	37	7	5731340	CACTAGT	7	5697866	F
	TCAGGGA	37	2	242843504	ACCTGAA	2	242492177	F
	TTCCTCC	37	7	157869970	CGACCCT	7	157562731	F
Red	CCCACTG	37	5	171534017	CCGGGTT	5	171466622	F
Grn	GGAGGCT	37	2	3699334	GAGAGCC	2	3677209	F
	TTGAAAA	37	3	41460736	CGGTGTT	3	41435740	F
Grn	GCCTGGC	37	12	48336164	ACCCGGA	12	46622431	R
	ACCCCCC	37	6	42695674	CAACTCT	6	42803652	F
	AGCAATG	37	1	230566509	CGAAGAC	1	228633132	F
	CATTCCC	37	5	218153	CGGGGCT	5	271153	F
	CACACAT	37	3	55517496	CCCTGGG	3	55492536	F
	CTGTGCT	37	11	126660703	CGCCCCC	11	126165913	R
	GAGAACA	37	17	80394529	CGGACGT	17	77987818	R
	AGGAGGC	37	7	158187725	CGGCTCC	7	157880486	F
	AGCAGAC	37	17	73074561	GAGCTGA	17	70586156	F
	ATTTCCT	37	13	31422123	AATCATG	13	30320123	F
Grn	CGCCGCC	37	X	20009138	AAGGAAC	X	19919059	F
	TTATGAA	37	4	152090378	CGGTATT	4	152309828	R
	GGGAGGC	37	1	110670021	GGAAGAC	1	110471544	R
	TTAGCAT	37	1	234754601	CAATGTG	1	232821224	F
	CCTCCTC	37	5	5057500	GACATGC	5	5110500	R
	GCCGGCC	37	5	1857306	CGGCCCC	5	1910306	F
	GCTAGGC	37	8	30087400	CCACCAC	8	30206942	F
Grn	GACATAT	37	6	30419612	CGCCTGC	6	30527591	R
	GAGGCCA	37	17	76179594	CACACCA	17	73691189	F
	ATTAAGA	37	6	32414433	AAAAGTA	6	32522411	R
	CTGCTTT	37	17	46618614	AAGGGCA	17	43973613	R
Red	GGAAGTC	37	20	29611924	CGTCTGT	20	28225585	R
Red	ACGGGCC	37	4	940893	CGCATGC	4	930893	R
	TGATTGG	37	6	32709158	CGAGGTC	6	32817136	F
	CACTGAT	37	7	1055600	GGATCCT	7	1022126	F
	CCGCAGC	37	4	730453	TGTCCCC	4	720453	R
	AGTTTTT	37	17	37024042	AGCCATC	17	34277568	R
Red	TAGACAT	37	1	204452127	CGCTGTA	1	202718750	R
	TTGGTGG	37	11	71524500	CTCTGGG	11	71202148	F

Red	CGAGGAC	37	6	28584121	CGCCTTC	6	28692100	F
	CATAGGC	37	X	118827407	GGGTGTG	X	118711435	F
	GTATGAG	37	6	28322103	ACAAACA	6	28430082	R
	AGAACCC	37	8	1400221	TGTTCGC	8	1387628	F
Grn	GCTGCCG	37	11	73054121	GCCGGGC	11	72731769	R
	CTGCGTG	37	6	9399379	ATGAGCT	6	9507365	R
Red	TCCGGTC	37	7	27208285	CGCCCTC	7	27174810	F
Red	ACTGGTG	37	X	40440209	CGGGTCC	X	40325153	R
	AGCAGTC	37	2	101680441	CGCAGGA	2	101046873	F
	GGTCCTG	37	2	9705768	TTTAGGG	2	9623219	F
	CAGGTGT	37	14	100618491	CGGGCTG	14	99688244	R
Red	CCTAAAA	37	6	33041221	CGCTCCT	6	33149199	F
	CATTTGC	37	14	96284990	AAAACTC	14	95354743	R
	TTTATTT	37	4	141877033	CCTAATA	4	142096483	F
	CACATTT	37	18	44627440	CGGACAT	18	42881438	R
	GAGAAGC	37	7	129996313	CGGAAGA	7	129783549	R
	GTTCACC	37	3	195578259	CGGCCAC	3	197062656	R
	GTCTCGT	37	2	240121297	CGAATGC	2	239786234	F
	GGCAAGC	37	3	115120356	CGCGTTA	3	116603046	R
	TCATAAC	37	12	7863229	TTTTTGC	12	7754496	R
	CCAATCG	37	1	209878178	CTACAAC	1	207944801	F
Red	ACTCCGC	37	2	74875227	CCTGGCC	2	74728735	R
	TTGAACT	37	4	79258587	CGGCCAC	4	79477611	R
Grn	TTCAGCT	37	X	64754701	TCCGATT	X	64671426	F
	CCTTGCC	37	X	152774831	TCTAGGA	X	152428025	F
	ATCACAG	37	1	182002021	CATGAGA	1	180268644	F
	TCTTAGC	37	6	7787925	CGCAAAT	6	7732924	R
	GATGTAC	37	1	1227307	CGTGTGT	1	1217170	F
Red	CATCTAT	37	1	12184574	CGGCCTC	1	12107161	F
Grn	AGACAAC	37	20	52199748	CTGCTGC	20	51633155	F
	TTTAAAG	37	3	22422855	CGGAGCA	3	22397859	R
	ACATGAC	37	6	33049983	CGCAATT	6	33157961	F
Grn	CTCGCCC	37	19	52954615	TCTGCTA	19	57646427	R
	CGGCAGC	37	1	226150312	CGCTGCA	1	224216935	R
	ACTAGTT	37	8	124284393	CGAAAGA	8	124353574	R
	GGGAGAC	37	1	181290986	CGGTAAC	1	179557609	F
Red	GGGCCAA	37	8	283841	AAGACGT	8	273841	R
Grn	CACCCGC	37	1	27687232	CGCACCC	1	27559819	F
Grn	CTCACAC	37	7	63353570	CCCGGGA	7	62991005	R
	GGGCCTT	37	4	159191054	ATTTCCC	4	159410504	R
	GATTCAC	37	1	15538911	AGACTAC	1	15411498	F
Red	CGGGAGC	37	14	105400489	CGCCCGC	14	104471534	R
	TGAGAAC	37	8	38847958	TTTTAAA	8	38967115	R

Grn	CCGAGCA	37	2	795935	TTTCTGT	2	785935	F
	CAGCCTC	37	14	97832998	GTGCTAT	14	96902751	F
	AAGTCGA	37	17	182928	CGGCCAT	17	182928	F
Red	CGAGGCC	37	X	139014368	CGCCCCC	X	138842034	F
	TCATCAT	37	13	59169584	CGTGGGC	13	58067585	F
	TTCTTCT	37	2	189762162	TAAACAT	2	189470407	F
	CATAGTA	37	12	25611175	ATGTCAC	12	25502442	F
Red	GTCAGGA	37	11	20134289	CGGGCTC	11	20090865	F
	CCCTGTC	37	2	233216361	CCTGCAC	2	232924605	R
	TGGTGCT	37	12	113652889	GGTCAGT	12	112137272	F
Grn	CACGGAC	37	6	887772	CGCGGAC	6	832772	R
	AGGGAA	37	5	110105162	TGTTTGA	5	110133061	R
Grn	GGGCAGC	37	7	997617	CGCGTGG	7	964143	F
Grn	GCACTCG	37	4	1202966	CAACCGT	4	1192966	F
	TTTGTGA	37	6	2528653	TCTCATT	6	2473652	F
Red	CAGGCGT	37	3	56717625	CGGGCTT	3	56692665	F
	GGCTCTT	37	14	93502930	TGGGGTG	14	92572683	F
Red	GTTAACG	37	1	202778869	TAAGAGA	1	201045492	R
Grn	CAGCGCC	37	1	207843084	TGGGCTG	1	205909707	R
Grn	GCTGTGC	37	3	132115350	CGGGGCC	3	133598040	R
Red	GCCGCTG	37	13	102105049	AGCAGAT	13	100903050	F
	CTCACTT	37	19	7766960	GTGTCTC	19	7672960	F
	GGTAAAC	37	5	68787747	CGGGAA	5	68823503	R
Grn	TCCGCAA	37	5	118603938	CGGGCCT	5	118631837	R
	GTTAAGT	37	3	119243933	GACTATC	3	120726623	R
	CGCTGGG	37	7	64035529	CGGTAGT	7	63672964	F
	CTTTCCA	37	1	3096986	CGCGGCC	1	3086846	R
	ACCCACC	37	5	43316468	CGAGATC	5	43352225	R
Red	AGATTGA	37	19	1456157	AGCTGCT	19	1407157	R
Red	CGCGCTG	37	X	53461271	CGCTCCG	X	53477996	F
Red	TTCTGTG	37	20	59542578	GGGTTGG	20	58975973	R
Red	GGTCTCC	37	8	7537673	AGCGACC	8	7575083	R
	TCCTGTT	37	1	3208865	ACACTTG	1	3198725	R
Red	TCAGCTT	37	9	136098495	CGCTCAA	9	135088316	R
Grn	CGCCTGC	37	5	1594676	ACACCGC	5	1647676	R
	ACGGGGC	37	9	140268976	GAGATTT	9	139388797	F
	GTTCAGC	37	3	99378032	ACCACGA	3	100860722	F
	TGTAGCA	37	8	108208344	TTCCCAA	8	108277520	R
	AGGCTGT	37	8	144659627	CGGCGGT	8	144730770	F
	AGAGAA	37	5	114830673	AAAAGC	5	114858572	R
Red	CCCCTGC	37	2	26205876	CGCCAGC	2	26059380	F
	GCTTCAA	37	2	19082803	AAGAGC	2	18946284	R
	GAAAAG	37	X	21858304	CGCTCTA	X	21768225	F

Red	CATCTCG	37	3	193587490	CGCAATG	3	195070184	R
	TCAGAGT	37	4	38622735	CGTGTTT	4	38299130	R
	CCTTATT	37	1	226599374	CGGAGA	1	224665997	R
	CTCTGGC	37	9	91997686	AGCCAAC	9	91187506	R
Red	TGGGGA	37	X	139585911	CGGAACC	X	139413577	R
Red	TGGGTGA	37	14	103687728	CTTCTAA	14	102757481	R
	CTGAGCA	37	9	100881995	CGTTTTG	9	99921816	F
	GCGTGCG	37	8	72917695	CGCCAGT	8	73080249	R
Grn	TAAAACA	37	1	110752307	CGATGAA	1	110553830	R
Grn	GCTGGAC	37	19	3595778	CGCGGCC	19	3546778	F
Red	CCTCTCC	37	12	115124768	ATTGGCG	12	113609151	F
Red	GAGGGCC	37	6	30079203	CGGAAAA	6	30187182	R
	GATTTCA	37	6	143607364	CGTGGAC	6	143649057	R
	GGGGCAT	37	9	124363848	CGGAACA	9	123403669	R
	CCTGTGT	37	9	120510294	ACTTTCA	9	119550115	R
	CAGGATC	37	9	139371233	CGGAAGA	9	138491054	R
Red	AGCTGGC	37	8	1914262	CGCCCAG	8	1901669	F
	TCCGGAT	37	12	114123213	CGGCCTA	12	112607596	R
Grn	GGTTCCG	37	9	140311919	GACTTTC	9	139431740	F
	TCTGATT	37	9	115824717	CTCCCCT	9	114864538	R
	CCAGGAC	37	X	152000116	GGTGTCA	X	151750772	F
Grn	ACACTCA	37	7	144100802	CGGTCCC	7	143731735	R
	GCCACAA	37	12	75785232	TGTAAAC	12	74071499	F
	TTGGCTT	37	1	152162025	ATGACTT	1	150428649	F
	TGTGAGT	37	17	48098926	CATCTTC	17	45453925	R
	AGTTTTC	37	6	77563066	AACAAAC	6	77619785	F
	TTGCTTC	37	6	1599123	CGGGCAC	6	1544122	F
Red	GCCGTGC	37	2	237123218	TAGGAGC	2	236787957	R
	TCCCTGT	37	13	20714863	CAGCTCT	13	19612863	R
	TATTGTA	37	1	244525971	GGGCCTA	1	242592594	F
	GCTCATG	37	7	157348237	AGACCAC	7	157040998	R
Grn	CCCCTGC	37	X	102319001	TCTGCGC	X	102205657	R
	CTGCTGA	37	17	45699260	CGCCAAT	17	43054259	F
Red	TCAGGGC	37	8	131000521	CCCAGGC	8	131069703	F
Red	GGCGGGC	37	10	135171718	CGGCCCG	10	135021708	R
	CCCTTTG	37	1	22303523	CTTCTGC	1	22176110	R
Grn	ATTCCCT	37	2	105118572	CGCGCGC	2	104485004	R
	GCTGAGT	37	13	36049335	GATCGGC	13	34947335	F
	CCAGCGC	37	1	247537159	TCTATGT	1	245603782	R
	CTCTTGA	37	17	73056681	TTTTCAC	17	70568276	R
Red	ACCCTAG	37	1	149186607	CGGGGTC	1	147453231	R
	ATATAGA	37	13	52736798	CGGTGAC	13	51634799	R
	TGTTCGC	37	6	11901382	TTCTCCA	6	12009368	R

	AGCGGGT	37	11	13985911	GGGCACC	11	13942487	R
Red	AGCCCGC	37	17	80255457	CGCTCAC	17	77848746	R
Red	TCCCCGC	37	8	70623422	CGTGAAT	8	70785976	F
	GTCTTTC	37	3	11688349	GATCCGG	3	11663349	R
	TTTTTCT	37	12	6658378	CGCAAGC	12	6528639	F
	CTGTATA	37	22	18738315	CGTCGCT	22	17118315	F
Grn	TCCAGTA	37	20	23969237	CGCGGGT	20	23917237	F
	TTATTTT	37	2	222807796	CGCTTTG	2	222516040	R
	GGTGACT	37	7	37534909	TTTGAGG	7	37501434	R
	ACTTAAA	37	3	23727711	TGGAATT	3	23702715	R
	CACTTAC	37	2	113930840	CGGGGAA	2	113647311	F
Red	GGGGCTC	37	19	519609	CGCGGGA	19	470609	F
	TCCGCAG	37	1	202003813	GAGATCT	1	200270436	F
Grn	TTGGCCC	37	8	22132874	CGCGGCC	8	22188819	R
	CAAGGGA	37	3	181721674	CGGTTAG	3	183204368	F
	CTCTGAA	37	5	131268130	CTTTTGG	5	131296029	F
Red	CTCCTCC	37	13	81229358	CCCGGCG	13	80127359	R
Red	ACATACA	37	7	37487352	CGCCGCC	7	37453877	F
Red	CTGTCCG	37	7	48129992	AGCCGCT	7	48096517	R
	GTGCTGT	37	3	168268421	CGAGCTC	3	169751115	R
Red	GAGGCAA	37	6	32632338	TAAGGCA	6	32740316	R
	TACCATG	37	8	1651128	AGCCACA	8	1638535	R
	CACGTAC	37	11	45698622	AGGAGCA	11	45655198	R
	CTCACCC	37	4	38825551	CCGAAAC	4	38501946	R
	TGGCAGT	37	1	243584861	CTGCTTC	1	241651484	R
Red	TCACCTC	37	3	11610214	CGCATCC	3	11585214	F
	GTTCCGA	37	3	64547373	TGTGTCC	3	64522413	F
	GATCACT	37	12	308821	CGGGAAC	12	179082	F
	GAGCCTC	37	11	1892092	CGAGGCA	11	1848668	R
	GAGGCCT	37	5	140481267	CGGTGGC	5	140461451	R
	ATACTCT	37	22	27006498	TGAGTCA	22	25336498	R
Grn	GACAGTA	37	13	25875133	CGCCCAG	13	24773133	R
	CCTTTTC	37	7	135662562	TCCCTCT	7	135313102	R
	GTGCGGT	37	1	228475463	CGCAGTG	1	226542086	R
Red	GCTTCAG	37	5	140794993	GGCTTGA	5	140775177	R
	TGTGCTT	37	2	175629224	CGGCTCA	2	175337470	F
	TGGGACT	37	5	140503914	GTTCAAG	5	140484098	R
Red	CCGTGCG	37	13	114193150	CGGGAGC	13	113241151	R
	TCCTAAG	37	15	101936156	ACGTTAA	15	99753679	R
	GTAAGTG	37	4	96051461	AGTTCCT	4	96270484	F
	ACAGCGC	37	4	2431998	CGGACAC	4	2401796	F
	AGCCCTA	37	11	84028582	CGGCAAC	11	83706230	R
	TCTGCAT	37	17	100892	CGGACTG	17	100892	F

	TAATAAA	37	12	54421335	ACCAACA	12	52707602	R
Grn	GCGTCGG	37	19	853540	CGCGGAC	19	804540	R
	AAGACCT	37	10	839609	GAGAATC	10	829609	R
	GTGCTTG	37	2	170834853	CGCCAAC	2	170543099	R
	AATAAAC	37	2	112391213	GGGAGAT	2	112107684	F
	CCGTGCG	37	16	88706389	CGGGGCT	16	87233890	F
	AAGGAAC	37	4	88142277	CGCGCAT	4	88361301	R
	TGACTTC	37	5	82771513	ATTGCTC	5	82807269	F
	TTTGGTG	37	2	240874769	ATTTTAG	2	240523442	R
	AAAGAAC	37	12	105630720	CGGAAGC	12	104154850	F
	TCAAAGC	37	2	101508685	CGGCCAT	2	100875117	R
	GTTGGCA	37	3	23861312	CGTCCAG	3	23836316	R
	TGACCAG	37	5	14230166	CGTGCAA	5	14283166	R
	CCTGCAC	37	13	97927242	GACTATT	13	96725243	F
	GCAGTGC	37	4	119888794	CGGGTAT	4	120108242	F
	GTACTGA	37	11	20389052	CGACGTC	11	20345628	R
	CTTTTAC	37	12	177995	CCAGATC	12	48256	F
	ATATGAT	37	4	108744891	CGCAACT	4	108964340	R
Red	GGGCGCC	37	X	68835885	CGCCCCA	X	68752610	R
Red	AATGGGT	37	6	101847058	AAGCGGA	6	101953779	R
	AGACGTC	37	7	151553615	GGGAAGC	7	151184548	R
	TGGTCCT	37	8	144646939	CCGAGGC	8	144718082	F
	AGTTTGT	37	8	11663584	CAGGCTG	8	11700993	F
	TCAAGCT	37	4	6673551	AACAGAT	4	6724452	R
	TGATTTA	37	3	23710303	GGCTTCC	3	23685307	F
	AAGCCAT	37	2	1657483	CTGGCCT	2	1636490	F
Red	TGGAATC	37	1	116311395	CGCACGC	1	116112918	F
	GCCACAC	37	7	1097952	CGCACAC	7	1064478	F
	AGATAAA	37	13	30733388	TTTTCAC	13	29631388	F
	AATGGCT	37	15	86584249	AAGATGC	15	84385253	F
	AAATCCT	37	6	127785332	CGCTACA	6	127827025	R
	ATGAAAT	37	13	102276634	CGCTAAA	13	101074635	R
	AGTGAGA	37	1	240562805	CGGCTCC	1	238629428	R
Red	AGGGTCT	37	17	40835849	AGGAGGA	17	38089375	F
	GGAAACC	37	6	169978203	CGGAGCC	6	169720128	R
	GTGCTTT	37	2	236436519	CGGATAC	2	236101258	R
	GCCTCAG	37	6	32829062	GAGCTGC	6	32937040	R
	ACATCTC	37	9	123604514	CGCACAA	9	122644335	F
Red	GCGGCGC	37	5	140712459	CGGGCAT	5	140692643	R
Grn	GGAGAGC	37	7	63560711	GTGATCC	7	63198146	R
	TATATAT	37	8	97975467	CGTCACT	8	98044643	F
Red	AAGTGAA	37	11	2908036	TGTGTGC	11	2864612	F
	CGCAGTG	37	3	196048411	GCAGGAC	3	197532808	R

	TAGCCAG	37	6	36788637	CGATCCT	6	36896615	R
	AGCCAAA	37	2	239860241	AACAGCC	2	239525178	F
	AATATCT	37	6	28321301	TCCTCAG	6	28429280	F
	AGTCTTT	37	10	133796476	TGAAAGC	10	133646466	R
	AGAGACC	37	8	47751623	CGTGCTC	8	47870788	F
	CAAAGTC	37	3	13057143	AGTCAGA	3	13032143	F
	TGGACCG	37	5	140536238	CGCCCAG	5	140516422	F
	AAATGCC	37	6	136915367	CGGACCA	6	136957060	F
	GAAAGTC	37	7	34013871	CACCAGC	7	33980396	F
	CTTCTGG	37	1	201923663	CGAGGGC	1	200190286	F
	TTCAGTA	37	7	99137009	ATTTGCT	7	98974945	F
	GAGGCAC	37	4	25818940	AGTTTCT	4	25428038	R
	CTCTGAG	37	7	120657213	CGCAGAC	7	120444449	F
	GAACATT	37	1	204560985	CTTTCTG	1	202827608	R
	TCCCACG	37	17	4464294	CGGCCAC	17	4411043	R
Grn	TGCCCCA	37	6	30079265	TCTGCCG	6	30187244	R
	CCCTGAC	37	6	32549139	CCCTGTA	6	32657117	F
	CCCTGCT	37	17	77923275	CGAGAAT	17	75537870	F
	GGATCTG	37	1	9097241	AGGATGA	1	9019828	R
	CAGTCTC	37	14	53170147	CGGCTCT	14	52239897	R
	TTTGATG	37	6	1001966	TGGCCCA	6	946966	F
Grn	CGAGGCC	37	15	101593831	CGCTCCC	15	99411354	R
	TTATGCT	37	7	150381356	CGGATGC	7	150012289	R
	TTGATAC	37	14	94873879	CGGGACC	14	93943632	F
	AAAAAAT	37	11	114466093	CGGTGCA	11	113971303	R
Red	GGGAGAT	37	7	156337168	CGGCCAA	7	156029929	F
	GAGCTTG	37	3	66853898	CGGGATC	3	66936588	F
	CAAAACC	37	7	968493	GTCACGA	7	935019	F
	CCTTGTC	37	17	48268237	CGCCATC	17	45623236	F
	GGGTGTT	37	1	144989624	CATTGTT	1	143700981	F
	ACGGCAC	37	2	242805838	CGCCACT	2	242454511	R
	TGCTCCA	37	1	170344621	TGCTTGA	1	168611245	R
	GAGGCTC	37	3	71586357	TGAGTTC	3	71669047	F
	GCTGAGC	37	20	60692839	GTCACAC	20	60126234	F
	GTGGCTA	37	14	96526884	AATATTG	14	95596637	R
	GTTCAGA	37	17	33390736	TCATCTC	17	30414849	R
	GAGAACA	37	11	8931708	GGGGCAC	11	8888284	F
Grn	CAGTCCC	37	7	150026567	CGGTCCC	7	149657500	F
	AGAGGTA	37	5	77888194	CGCTCTA	5	77923950	F
	CACGCTA	37	17	19883326	GGATGAA	17	19823918	R
Grn	TTTGTAT	37	6	28447115	GCGGAGT	6	28555094	R
	CCACCTC	37	18	55289797	CTCTCCT	18	53440795	F
Red	GGAAGAA	37	19	48495301	CGCGTCG	19	53187113	F

Red	CGCAGTG	37	5	140182627	AGACTCA	5	140162811	R
	CCATTCA	37	7	1138716	CGTGACA	7	1105242	R
	CGCTGGC	37	8	10555382	GCATGGA	8	10592792	R
	ACCGGCC	37	8	135494242	CGCTCTG	8	135563424	R
Grn	GAACCGC	37	5	1594715	GTGGGAT	5	1647715	R
	GAGCTGC	37	2	36922916	AGTTACT	2	36776420	R
Red	GTCAGAC	37	15	45493106	CGGGCCT	15	43280398	R
	TCAGCGA	37	1	149162518	TTCAGGT	1	147429142	R
	TTCTCAG	37	2	879563	TTCATGA	2	869563	F
Red	GTCTAAG	37	1	200271342	GATTCGG	1	198537965	F
	TCTGATT	37	7	90879360	CGTGGGC	7	90717296	F
Grn	ATGGATC	37	19	52206258	CTGCAGA	19	56898070	F
	GCAGCCC	37	15	26487777	TCTGACC	15	24038870	F
	TTAACTC	37	2	145425418	CGTGGCA	2	145141888	F
Red	AGGGCTT	37	4	1594995	AGGCGCC	4	1564954	R
	ACAGCAC	37	17	948956	AGCATTT	17	895706	R
	GTATGTA	37	8	96805352	CGTCTGA	8	96874528	R
	GGATTAT	37	17	77351122	GGTGTTA	17	74862717	R
	CGCAGGA	37	16	20360217	CGCACAA	16	20267718	F
Grn	CTTCTGG	37	17	6411087	CGCAGGC	17	6351811	F
	ACACCTC	37	4	155312410	CGGAGAA	4	155531860	R
Red	AAGCCAC	37	6	138192658	ACTCAAC	6	138234351	R
	TTCGCTC	37	19	50861789	CGCAGCC	19	55553601	R
	ACCAGAC	37	12	41830372	CGGACAC	12	40116639	R
Red	GCACAGC	37	2	236674257	TCCTGCA	2	236338996	F
	CTGGAGA	37	8	1790861	CGGGCCT	8	1778268	R
	TTGCTAT	37	15	100121570	CGGTCTC	15	97939093	F
	TGTACAA	37	6	33037690	CGACAAA	6	33145668	F
	TACAAGA	37	2	241611931	CGACCCC	2	241260604	F
	ACATAGC	37	11	19081590	CTGGTGG	11	19038166	R
	AGAGTTT	37	15	66478674	CGGGGCA	15	64265728	R
	GGCAGAC	37	3	160168922	AGATGCC	3	161651616	R
Red	CAAGTAC	37	2	90016264	CTTGTTA	2	89653565	F
Grn	CTGCAGG	37	X	47004150	CGCGACA	X	46889094	F
	GAATTCT	37	3	63399168	CGCTTTT	3	63374208	R
	ACTTGGA	37	1	3335858	CGCACCG	1	3325718	R
	CACCTCT	37	4	6691093	CCTCCTC	4	6741994	R
	GAGGGTC	37	7	134879060	AAGGGAT	7	134529600	F
Grn	CGCCGCC	37	7	100203350	CGGCAGT	7	100041286	R
Grn	TTGCTAC	37	6	27661905	AAGCTTA	6	27769884	R
	ATAGCCA	37	7	102102804	CGGAAAC	7	101889809	R
	CCAGTCC	37	17	3499093	CGACTGA	17	3445842	R
	AAATTAC	37	17	41545935	CGAGCCA	17	38901461	F

	GGGCCTT	37	5	135270833	TGACTAA	5	135298732	F
	CACACGC	37	22	25758637	AGTGAGC	22	24088637	F
	TGATACC	37	11	130036542	AGTGAGC	11	129541752	F
	CCATCAC	37	11	48026889	CGTGGGC	11	47983465	R
	AGTCCAC	37	2	91758369	CGGCCCT	2	91122096	F
	TGCCTGT	37	13	114212078	TAAAGTG	13	113260079	R
	TTACTTC	37	3	64547310	ATTCCTC	3	64522350	R
Grn	CGGCGCA	37	6	28584138	CGCCCTA	6	28692117	F
	AGTTCAG	37	6	111907043	CGCCCAG	6	112013736	F
	TGAGGTC	37	13	59686676	CGTCACC	13	58584677	R
	AGAAGTC	37	15	90891614	TACGGAA	15	88692618	R
	TCCTCAA	37	17	68070411	CTTGGTT	17	65582006	F
Red	GCAACGC	37	6	88757358	GCACCCG	6	88814077	R
	TGGTAGG	37	11	64594647	CGCCCAC	11	64351223	R
	ATAGAAC	37	18	33078241	TTACTTT	18	31332239	R
Grn	GTTGGTG	37	5	140208954	CAGTGCC	5	140189138	R
	TGGGCCC	37	3	65334190	CATCAGA	3	65309230	F
	CACCTTT	37	4	69536319	GCTTCCA	MULTI	MULTI	R
	AGGATTT	37	6	14729030	AAGGTCA	6	14837009	F
	CTGCAGG	37	10	1405937	GGAATGC	10	1395937	F
Red	CGGTCAG	37	18	12947723	CGTCCCG	18	12937723	R
Red	CTCCGCC	37	22	42395067	CGCCACC	22	40725013	R
	GGTAAAA	37	5	140552347	ATCCTTC	5	140532531	R
Grn	GAGGAAC	37	6	1594411	CGCGCTC	6	1539410	F
Grn	CCGCGCA	37	2	233323840	GGTGGGC	2	233032084	F
	CTCTAGA	37	13	102103051	ACATAAT	13	100901052	F
	CTGGATC	37	12	65155719	AAGATTA	12	63441986	F
	GGTTGGT	37	6	33128903	CGCCGTA	6	33236881	F
	ATCGGGT	37	5	175561172	CGCCCAC	5	175493778	R
	TGTCTTC	37	11	113546261	GAAATCT	11	113051471	F
Red	GGCGCTG	37	19	15564105	ATGCTCA	19	15425105	R
	CACTGGC	37	17	76421442	CGGACTC	17	73933037	R
	CCCTCCC	37	13	99095684	ACGTGGC	13	97893685	R
Red	GTACTCT	37	17	69199815	GGACAAC	17	66711410	F
	TGGACTT	37	15	72519739	CGGTCTC	15	70306793	F
	TTCAGCT	37	8	103742123	GACCTCA	8	103811299	R
	ACACAAA	37	13	93990004	CGTTCTC	13	92788005	R
	GGATGCT	37	1	27964774	CGGCACT	1	27837361	R
	CGGGCGA	37	3	36986992	AAGTACT	3	36961996	R
	GGATTGG	37	18	76751952	ATCAATA	18	74852940	F
Red	CTCCAGA	37	17	75789365	TCAAAGC	17	73300960	R
	AGGAAGA	37	2	134326204	CGCATGT	2	134042674	R
	AGAGAAC	37	12	45751145	CGGCCAC	12	44037412	R

	ATGTCAA	37	21	46822283	CGGGTTG	21	45646711	F
	GCTTGAA	37	3	133020205	AACTCCA	3	134502895	R
	ACATTCC	37	6	16713613	CGCCATT	6	16821592	F
	GGAGGGC	37	10	21462145	CGGGTGT	10	21502151	R
	ATCTTCT	37	13	30686841	CGGTCCC	13	29584841	F
Red	CCAAGCC	37	17	76417995	CGCCGCC	17	73929590	R
	TGAGAGC	37	2	207741102	CGGGTCA	2	207449347	R
	TCCTAAC	37	2	227560785	CGGCTGG	2	227269029	R
	CGAAGGA	37	5	180670469	CGCAGCT	5	180603075	R
	AGTGACT	37	20	60645197	TGAGCTT	20	60078592	F
Red	AGTAGTC	37	17	70636625	CCAGCGC	17	68148220	F
	ACATGGA	37	11	47639458	AAATATA	11	47596034	R
	TTGCGGT	37	17	72667062	CGCAGGT	17	70178657	F
Red	TGTCTGC	37	1	159001170	CGACCGA	1	157267794	R
	GTTTTGG	37	19	39265241	CGGGGAC	19	43957081	F
	TGGGATG	37	1	46420220	CGGGTGC	1	46192807	R
Red	CACAGCA	37	19	22891978	CGCCTTA	19	22683818	F
	GCCCGGC	37	19	48048583	CGGTCCC	19	52740395	R
Grn	CTCCCAG	37	22	46287028	GCGATGC	22	44665692	F
	GGACCTC	37	7	12151481	CGCCCTG	7	12118006	F
	CCTGAAG	37	1	33909498	CGTGTTC	1	33682085	R
	TTCCCTG	37	7	2953836	CGCCGGC	7	2920362	F
Red	GCTGGGC	37	1	27481531	CGCGGCC	1	27354118	F
	GTGACTG	37	1	231964048	CGAAGCA	1	230030671	R
	TGTGGAT	37	21	32129060	CGAGTGA	21	31050931	R
	TATTTGG	37	8	17220621	TAACAAA	8	17264992	R
Red	CACTCCC	37	13	113735031	CGGCGAT	13	112783032	F
	GGGCTTT	37	7	3215287	CTGCCCA	7	3181813	R
	TATGAGC	37	13	101860408	CGAACCC	13	100658409	F
	TACCACA	37	7	157997479	CGTTGCT	7	157690240	F
	TAAAAAC	37	5	112370191	CAGCGGT	5	112398090	R
	CGCAGGC	37	1	223926325	CGTGCAC	1	221992948	F
	TCACATA	37	1	38000170	CGTGCCA	1	37772757	R
	GGTCTCT	37	6	37958953	CGTGTGC	6	38066931	F
	AAGTGTA	37	17	78253912	CGGCCAA	17	75868507	R
	CTAATTC	37	2	235422165	CCCTGCA	2	235086904	F
Grn	GTCACGT	37	15	69754698	CGGCCAC	15	67541752	F
Red	GTATGGC	37	6	29895037	CGGTCCA	6	30003016	F
	ATGAAGT	37	5	54287462	AGCCTGT	5	54323219	R
Red	GAGCGAA	37	1	149155849	CCATGAT	1	147422473	F
	AGGGCTC	37	5	6434966	CGGGGCT	5	6487966	R
	AAGGAAA	37	19	17015427	CGCTCCA	19	16876427	R
	TTCTACC	37	12	69016159	CGGAGGC	12	67302426	R

Red	GAAAAG	37	2	91777482	GCTGGTT	2	91141209	R
	GGCAAG	37	7	158110152	CGGTGTG	7	157802913	F
Grn	GCGGGG	37	7	5184014	CCAGAC	7	5150540	F
	TGCAGCA	37	6	101846779	GTAGAAT	6	101953500	R
	GAAACCT	37	3	182883005	CGCCCGG	3	184365699	R
	TTGTGCC	37	15	48732134	CTGTCCA	15	46519426	R
	GCCTCAT	37	12	9065171	ATTATTC	12	8956438	R
Red	GGGCCTC	37	19	52094375	CAGGCC	19	56786187	F
	AAGCTCT	37	19	11276529	AGGCTCT	19	11137529	F
	GGCCATG	37	5	180335743	CGGGAA	5	180268349	F
	AATGAA	37	15	78856949	CGGGTTT	15	76644004	F
Red	ACCCGCT	37	19	13409671	CCTGGAG	19	13270671	F
	AGACATT	37	9	123007424	CGGTTGA	9	122047245	F
	GACGGG	37	7	91763103	CGGGTCG	7	91601039	F
	CCTCTGA	37	7	94250352	CGGTGTG	7	94088288	F
	TTTTAGG	37	5	112810343	TTATTAT	5	112838242	F
	CCAAATC	37	2	46883368	CGCTCCC	2	46736872	R
Grn	TCCGCTA	37	20	13200929	CGCGGTG	20	13148929	F
	CTGTTCC	37	3	71439885	CAAGTAA	3	71522575	R
	TGATCAT	37	15	91912699	CTGCCCC	15	89713703	R
	CGCCGG	37	19	10172841	CGCCCCA	19	10033841	F
	AAGGAA	37	10	61900940	CGGCAAT	10	61570946	R
	TCTCACT	37	19	53092499	AAGCAA	19	57784311	R
	CTGGAAC	37	1	20307906	CGGCTTT	1	20180493	R
Red	TTAGCTG	37	1	217203173	CGCAGCT	1	215269796	F
	ATGGAA	37	11	123295944	CCAAAA	11	122801154	R
	TAGAGG	37	X	45016993	CGCTGG	X	44901937	R
	TTATTTG	37	1	80447732	ATCATTC	1	80220320	R
Red	GGAATA	37	6	32520615	CGAGGC	6	32628593	F
	TCTGCTG	37	4	141575212	AAAAAA	4	141794662	R
Red	TGTGTGT	37	10	3711048	GTGCAG	10	3701048	F
	CAGCTTT	37	7	48044273	GGTAGG	7	48010798	F
Red	CCCCGCG	37	12	115109934	CGCCATG	12	113594317	R
	TCGCCTA	37	8	134203841	TTGGAGT	8	134273023	F
	AAACCC	37	19	22990650	CGGGTAT	19	22782490	F
	TGCCAA	37	11	19876031	CGCAACA	11	19832607	F
Red	CTTCCTC	37	10	81214225	CCTTCCG	10	80884231	R
Red	TCCTCCT	37	2	233274144	GAAACG	2	232982388	R
	CATTGTT	37	5	140557256	CTGTATG	5	140537440	F
Red	GCTCTCC	37	13	39526272	CGCTGAA	13	38424272	F
Red	TTTGGGG	37	17	46608355	CCTTCCT	17	43963354	F
	AAACTCC	37	5	128795827	CGTCCAG	5	128823726	R
Grn	GCGCTCC	37	X	12156718	GCGTGG	X	12066639	R

	CCCATTT	37	1	248758128	CGTGACA	1	246824751	F
Grn	AAGTCTT	37	6	135203613	AGTAGAA	6	135245306	F
Red	TGCTATG	37	20	16552305	CGCTCTG	20	16500305	F
	ACCCGGA	37	6	1555080	TGGTAAC	6	1500079	R
	TGGCCTC	37	8	28175021	AGATGGT	8	28230940	R
	ATGCAGT	37	2	178499509	GCTGATG	2	178207755	F
	AGCAGAC	37	1	37732046	AAAATAA	1	37504633	R
	CAAGACC	37	10	120001266	TTCCGCA	10	119991256	F
	GCCTGAG	37	2	2570283	TTCATAC	2	2549290	R
	CTCAAGC	37	1	63249209	CGCCCGA	1	63021797	F
Red	AATCTCG	37	6	6737080	CTTCCGA	6	6682079	F
	CCTGTCT	37	1	246798258	CGCACCA	1	244864881	R
	ATGTGGG	37	2	61847725	CGACACC	2	61701229	R
	TCTGATA	37	21	46348691	CGTGGCT	21	45173119	R
Red	TAGACCG	37	1	228743131	CGCGGGC	1	226809754	R
Red	CGCTCTC	37	1	149186391	CCAGGCT	1	147453015	F
	CAAGGCT	37	3	137414342	CGGATCT	3	138897032	F
	CAGGAAC	37	X	30327819	AGGAGAC	X	30237740	R
Red	AGTGGTG	37	1	2254245	CGGGCTC	1	2244105	R
	AAGGGAC	37	15	53075421	GTGTGAG	15	50862713	F
	CCACTTG	37	10	28419523	ATTTTAT	10	28459529	R
	CTCCCTC	37	1	150554875	CGCCGTA	1	148821499	R
Grn	ACGCAGC	37	12	29542598	TGGGCGC	12	29433865	R
	CCCATAA	37	13	49853124	CGTGTGA	13	48751125	R
	CCATGTT	37	13	41593582	GGACCCA	13	40491582	R
Red	AGAAGGC	37	1	161410551	CGCCCTC	1	159677175	R
	TCCATGC	37	4	4993033	CGGACGC	4	5043934	F
	GGGGAAC	37	11	77532707	CGCCTCT	11	77210355	R
	TCGACAG	37	19	50931616	CGGAGCC	19	55623428	F
	TACATAT	37	6	150276311	CGTGTTT	6	150318004	R
	TGGGAGC	37	4	8633794	CGTGCTC	4	8684694	F
	CCACCCA	37	7	150020218	TATTGAA	7	149651151	R
	GTGTGGT	37	15	32206583	CGGCAGA	15	29993875	R
	GTAGGCA	37	2	135125439	ATGATGG	2	134841909	F
Grn	AGATAAC	37	12	58329936	GAACCCC	12	56616203	F
	GGGGGAC	37	13	24902376	GTGCCCA	13	23800376	R
	ATGATGT	37	20	24446527	CGGGCAC	20	24394527	F
	GAAGCCA	37	5	177612982	TACACCA	5	177545588	F
	TCTTACT	37	19	35720295	CTGGGCA	19	40412135	R
	CCACCTT	37	4	26198975	CAGTGTG	4	25808073	F
	CAAGCAA	37	6	31034042	ACCAGAC	6	31142021	R
Red	GAAACAA	37	17	981643	CGCCGCC	17	928393	F
Grn	CTGTGTT	37	14	65068635	GAAAAAT	14	64138388	F

	AGATTCG	37	12	128869988	CGAGACA	12	127435941	F
Red	AAACCCC	37	17	43037114	CGCCCGG	17	40392640	R
Grn	GAGCGCC	37	5	140503531	CGCGGAC	5	140483715	R
Red	TCATGTT	37	13	111935508	GTAGGCC	13	110733509	F
	AGTGACC	37	8	142452509	CTGGGCA	8	142521691	F
	TGCTAGC	37	1	31732891	CATCCAA	1	31505478	R
	GGAGACA	37	1	164682021	CGGAACA	1	162948645	R
	AGAAGGT	37	3	124780157	GTTGCTA	3	126262847	F
	TTAGAGA	37	7	150765472	CGGTGGT	7	150396405	R
	CACCTTC	37	6	32713827	CGAGCCT	6	32821805	F
Red	CATTGGG	37	6	29556225	GTCGAAT	6	29664204	F
Red	AAACACC	37	8	6633067	CTGGAAA	8	6620477	R
Grn	AGATCGC	37	X	47077986	AGTACTA	X	46962930	R
	TCCCTCC	37	X	56258808	CGGCCGC	X	56275533	F
	ACCATTC	37	11	2925623	GGGCTTG	11	2882199	F
	ATTGTTG	37	3	158189615	AGAAGCA	3	159672309	F
	TCCAGAC	37	11	88288530	GAATCAC	11	87928178	R
	GCTGTGC	37	15	25434030	CGGCCAA	15	22985123	R
	CAGGCGC	37	6	101847388	TCTGCCT	6	101954109	R
Red	GCCACTC	37	2	72371255	CAACGTG	2	72224763	F
	TTTGGCC	37	6	32774788	TCCACTC	6	32882766	R
Red	GCAGACT	37	5	28928346	CCAGCAC	5	28964103	F
Red	CGCGAGC	37	7	5862983	CGCCCCC	7	5829509	R
	GTTTTTCA	37	2	173647945	CGGCCGA	2	173356191	R
	CTCTCGC	37	6	33288296	CGGCTGG	6	33396274	R
Red	CCCACCT	37	5	126409198	CCGGCGT	5	126437097	F
	AGGCATT	37	11	84659234	CACCCCT	11	84336882	R
	GTCACCA	37	8	6875661	CGGCCCC	8	6863071	F
	AAACCCA	37	13	44453235	CAGTCTC	13	43351235	F
	CAGCGGC	37	22	51001387	TTCCCGA	22	49348253	F
	TTAACTA	37	3	108021293	CGGAATT	3	109503983	R
	GGTAAGC	37	5	180581761	TGAAGCT	5	180514367	F
	AATGTGT	37	4	124430271	CGGTTTA	4	124649721	R
	ATTTATG	37	6	32605704	TCATTCT	6	32713682	R
	CCTCCAC	37	6	136257948	AGGATCC	6	136299641	R
	CTTCCAT	37	10	90752569	CCCTCTA	10	90742549	R
	TTAAGCT	37	11	55606216	GTGGCCT	11	55362792	F
	AGTAAAC	37	22	31498218	AGATCCT	22	29828218	R
	TTTGTGA	37	20	19266250	TTTTTTT	20	19214250	R
	TAGTGTT	37	5	140572766	CGCTGGA	5	140552950	F
	TTGACTC	37	10	128590997	ATGGCCC	10	128580987	F
	TGTGATG	37	12	31771672	ACCTAGG	12	31662939	F
Red	GCCCAAC	37	17	56566398	CGGTATC	17	53921397	F

	AGAGGGA	37	12	15983280	CAAGTCA	12	15874547	F
	AGCTCAG	37	7	157406032	GACTTAT	7	157098793	R
	CTGGGTA	37	2	47572939	CGTTCCA	2	47426443	R
Red	AGGAGGC	37	2	150037200	CGCTGCC	2	149745446	F
Red	CGGTGCT	37	2	72371261	CGCGTAT	2	72224769	F
Grn	CGTGGCG	37	7	64043119	GAGTGGC	7	63680554	R
Red	TGGGTCT	37	3	194790434	AAGGAAC	3	196271723	R
Red	AGAGGTC	37	20	56725871	CGCGGCC	20	56159277	F
	TGTTCCT	37	19	22891847	CTGAGAT	19	22683687	R
Red	TGACCTC	37	19	4784940	CGCGCGC	19	4735940	F
Red	GGTTGTT	37	3	49756301	AGTAGAC	3	49731305	R
	TAATGTC	37	19	33719749	TCCATTA	19	38411589	R
Red	TGGAGGC	37	2	239012831	CGGGCTC	2	238677570	R
Grn	CTCGATC	37	14	56979854	GAGAAGC	14	56049607	F
Grn	CAGGCCC	37	11	2891065	TATGGGC	11	2847641	F
Grn	CAGCTTT	37	15	101862689	GAAATGC	15	99680212	R
	TAGCCTT	37	1	18700603	CGCCCCA	1	18573190	F
Grn	GACTCCA	37	14	102050627	AAATGTT	14	101120380	F
	GCCGCTA	37	14	97493395	CGGGAAC	14	96563148	R
	CTATGGG	37	5	10091925	CGAGCCC	5	10144925	R
	CCACACT	37	14	52733243	CCAATTT	14	51802993	R
	TATGGGA	37	1	244545617	CGGGAAA	1	242612240	F
	AGTCTCA	37	12	64575346	CGCATGA	12	62861613	R
	CTTCCCT	37	1	149155775	TCCTCGC	1	147422399	R
	TATGAGA	37	10	91136753	GTAATGA	10	91126733	R
	CCAAACC	37	4	190587808	CGGGGAA	4	190824802	F
	GAGAAAA	37	3	105466016	TATGCTG	3	106948706	F
Red	CCACGCA	37	7	158075705	TGAGGCC	7	157768466	F
Red	AGCCAGC	37	1	33631017	CCTGGCC	1	33403604	F
Red	GGGGGGC	37	2	95540265	GGGCCGC	2	94903992	R
	ATCCAAG	37	11	106269962	CGCACTC	11	105775172	R
Red	CATCTGG	37	7	158032496	CGCTTCC	7	157725257	F
	CTCCAGA	37	6	6543402	TTTCTTC	6	6488401	R
	GTAGGCA	37	5	140718731	CGGACTC	5	140698915	R
	AAGCAAT	37	15	25145254	GTCCTTA	15	22696347	F
	AGTACAT	37	10	28975991	CGCTGCA	10	29015997	R
	CCCTGTT	37	1	13111908	CGTGGTC	1	13034495	R
	ACCCCCG	37	7	138349443	CAAGAGA	7	137999983	F
	GCTCGGG	37	8	144635444	TCTGCCC	8	144706587	F
	ATTTTAC	37	2	172650722	CGCTTAC	2	172358968	R
	CTCACCC	37	10	134920382	GCTCAGA	10	134770372	R
	TCTAAAG	37	1	149162430	ACTACCT	1	147429054	F
Red	TGGCACC	37	1	41304105	TCTGTGC	1	41076692	F

Red	CCTCTGC	37		1	6526398	CGCGTGT		1	6448985	R
	CGGGCGC	37	X		27882053	TTAGATA	X		27791974	R
Red	CCCATCT	37		17	4440116	GGTGCAT		17	4386865	F
	GTGGAGC	37		2	175922785	CGCAGTG		2	175631031	R
	TAAAACC	37		10	132909289	GGTGCCA		10	132799279	F
Red	GACGCAC	37		2	26950956	CGGCGCC		2	26804460	F
	GCGGTGC	37		3	14615941	CTTGAGC		3	14590945	F
	ATAGACA	37		2	114033830	CGGCAAA		2	113750300	R
Red	AAACAAA	37		12	132845336	CGCCCAA		12	131355409	F
	TTATCAA	37		12	2690385	CGCAATC		12	2560646	F
	GAAATCC	37		7	157345746	GTTATGT		7	157038507	R
	TAGCTCC	37		5	166938213	TCTGATT		5	166870791	F
	GCAAGTC	37		13	114775133	CAAAGGC		13	113793235	F
	TGGACAC	37		5	174771462	ACTTCTC		5	174704068	R
Red	TGGAATG	37		1	227635558	AAAATTT		1	225702181	R
Grn	CCCCAGC	37		1	86081894	GGAACCT		1	85854482	R
	AGATTCT	37		10	3503185	AAGCCAC		10	3493185	R
	AACGTCC	37		5	177823864	TCTGCTC		5	177756470	F
Red	CCTGTGA	37		3	4344661	CGTTCTA		3	4319661	F
	GCCTGGC	37		7	1099788	CGGCCAC		7	1066314	R
Red	CGCAAAA	37		11	67383651	AGCCTCC		11	67140227	F
	TCTCATC	37		6	33037640	TGTTTTC		6	33145618	F
	CCCACTG	37		1	33793808	ATCTGTG		1	33566395	R
	GAGATGA	37		13	21728944	CGCCCCT		13	20626944	R
	CTAAGCA	37		1	232086152	AAAAATA		1	230152775	R
	CTTTCCA	37		4	95680414	CGGAGGA		4	95899437	F
	ATGACAC	37		2	176928222	TAATGCT		2	176636468	R
	GCCTAAG	37		5	157003983	TCAGCAA		5	156936561	R
Grn	CTAACCA	37	X		70752794	CGGGTTG	X		70669519	R
Grn	TCCAGAC	37		1	2885244	ACACTGT		1	2875104	R
	GGCTAAC	37		2	12674976	CACAAAA		2	12592427	R
Grn	ACCACCG	37		19	2250956	GGGCGGC		19	2201956	F
	GCTCTAT	37		14	59109856	CGTGGAC		14	58179609	R
	CAGCACA	37		2	9518751	CGCTGGG		2	9436202	F
Grn	TCCGCGC	37		2	98206733	CGCTGGC		2	97573165	R
Red	CCCGCGC	37		1	247537224	GTCCCAG		1	245603847	F
Grn	AATAGAC	37		7	47976869	TCGTCAC		7	47943394	F
	TTTTGGT	37		7	20198439	AGGAGCA		7	20164964	R
	GCAAGGT	37		4	47427537	CGATCGA		4	47122294	F
	CTCAGGG	37		2	5605864	CGGTATC		2	5523315	F
Red	GCGGAGA	37	X		25025519	TCTGCCT	X		24935440	F
Red	TCCCTCC	37		5	6633531	CCCGCAC		5	6686531	F
Red	CTCTGAG	37		6	106434169	AGATGCC		6	106540862	R

Red	TCAGCTC	37		5	140530410	GAGTTGG		5	140510594	F
	CTCTTAC	37		5	179741104	CGCTCAA		5	179673710	F
Grn	GCTTTTT	37		6	28661310	CGGGTAC		6	28769289	F
Grn	TGTCCAA	37		14	93252030	GCAACCC		14	92321783	F
	ATTCATT	37		3	188888584	CTCTCCT		3	190371278	R
	GTCTTGT	37		13	42848367	AGCTCAT		13	41746367	F
	ACTTAGT	37		1	32264315	AGGGAG		1	32036902	R
Grn	AAGGAC	37		1	18809531	GCCGAG		1	18682118	R
	GTCTGTT	37		8	23656074	CGGCTCA		8	23712019	R
	GCAGGG	37		14	102554846	CGCTTTA		14	101624599	R
	TTTCTGT	37		4	38006787	CGCATCC		4	37683182	R
	TCATCTG	37		1	44287964	CTTGAAG		1	44060551	R
	CCAAACA	37		5	147777756	CGCAATA		5	147757949	F
Red	GATAATG	37		7	158159286	CGCAGAC		7	157852047	F
Red	CTCTTCC	37		7	157406096	TTCTGGC		7	157098857	R
	GGTAAGC	37		8	22561893	CATATGT		8	22617838	F
	GCTATTC	37		17	31888899	AAGATCT		17	28913012	F
Grn	GGGGAA	37		7	154706386	CCCCCGG		7	154337319	R
Red	ACTCCTG	37		14	101539489	CTGGGG		14	100609242	F
	TCAATGT	37		6	33039606	CGGGAG		6	33147584	F
	TCACTGA	37		6	33050741	CTCCAGG		6	33158719	R
	TCTCTGC	37		6	32634344	CGGGTAC		6	32742322	R
	TCCCCTG	37		3	73620925	GCGGCTC		3	73703615	R
	CTGGCTC	37		2	109803622	CCACAGC		2	109170054	R
	AAAAGCA	37		6	148079619	GAAATAT		6	148121312	F
Red	CCCCCTG	37		10	1120539	CGGCAGC		10	1110539	R
	GATGTTG	37		2	150179794	CGAGGG		2	149888040	R
Grn	CAGCGCG	37		14	44002338	TGGGTGG		14	43072088	R
Red	CCGGCGC	37	X		125714973	GGTCGAC	X		125542654	R
	TTCCTGT	37		2	105877824	AGAGAA		2	105244256	F
	CCAAAAC	37		1	203275927	CACTGGC		1	201542550	R
	GGGTGCT	37	X		12993075	CGGGGTC	X		12902996	R
Grn	CGGGCTG	37		12	2339513	GAGCCGC		12	2209774	R
	TTCCCAG	37		2	80688129	GTTGACT		2	80541640	R
	GGCTTCG	37		10	135342560	CGCTTCA		10	135192550	F
Red	TGAGTCA	37		8	141248667	CGCGTCG		8	141317849	R
	TGCCATT	37		2	178178939	CGGCATT		2	177887185	R
	CCTGCCA	37		11	123892725	CGGTGAC		11	123397935	F
Red	CGGCCGA	37		6	74064064	CGCCCCC		6	74120785	F
	GGGCTGA	37		14	24665079	TCCTGGC		14	23734919	F
	ATAGCAC	37		2	9816010	CGGGAA		2	9733461	F
	TGGAGCA	37		2	10942687	TTCTACA		2	10860138	R
	AGTATCT	37		14	78758042	CGCAAA		14	77827795	R

	CTGTTCG	37	14	102050815	GCAGAA	14	101120568	R
	GGGATTA	37	14	106892175	AATGCAC	14	105963220	F
	ATTTTAA	37	14	80440817	TACGTGT	14	79510570	R
	AATTTAT	37	15	50140549	CGTCTCT	15	47927841	R
Red	ACAAAGC	37	4	187126114	CGTCCCA	4	187363108	F
	GAGTCTG	37	5	536783	CGCTCAG	5	589783	R
	CTCTCAC	37	14	104770790	CGGAAC	14	103841835	R
	GAAGAGC	37	6	32633163	GGGCTGA	6	32741141	R
Grn	CGCAACC	37	5	176543964	CGGCCCA	5	176476570	F
	GCTTTAA	37	2	130989361	CGCCAGC	2	130705831	R
	GGTCCTT	37	11	89655871	CGGCTGT	11	89295519	F
Grn	CCGCCAG	37	5	218452	CCCCGGT	5	271452	R
	ATCGCAG	37	7	1142861	AAGCTTT	7	1109387	F
Grn	GAGTTCC	37	5	140626788	GGGTACA	5	140606972	F
	TGGAGCT	37	7	19417585	ACAGCTA	7	19384110	F
	GCCCATG	37	3	195870009	CAGGGTC	3	197354406	R
Red	GGGAGGC	37	17	9129824	CGTGGGC	17	9070549	R
	GGGCTTC	37	17	38677884	AGTCATC	17	35931410	F
	CTGGTAG	37	10	65670534	GGGTGCA	10	65340540	R
	GCGGGC	37	8	127570482	CGGGGGC	8	127639664	F
	TGGGACC	37	5	6581849	GCTCTCA	5	6634849	R
Grn	TGAGCTC	37	20	62052997	CCACAGA	20	61523441	R
Red	GGCAGA	37	2	37617601	CGAGCGA	2	37471105	F
	GCTGGAC	37	10	133038915	CCTTCCC	10	132928905	F
	GGGAAGC	37	14	23623684	CGGTGCA	14	22693524	R
Red	CGGCTCT	37	7	5184155	CGCCGTT	7	5150681	F
	TGCCTAA	37	12	80427292	CGGCATA	12	78951423	F
	TTTGTTT	37	17	6546898	TGACTCC	17	6487622	F
	GTGAGTA	37	1	204951209	CGCTCAC	1	203217832	F
	TGATGAG	37	5	83429	CGAGGCT	5	136429	R
	GGAGAGC	37	13	51482661	CGCCTCT	13	50380662	R
	GCAGGCT	37	14	85292067	CGCTTGG	14	84361820	R
	AATTTTT	37	6	112409052	CGGGACC	6	112515745	F
	GGAGGCC	37	12	75784862	AGGCTTG	12	74071129	R
Red	CCTGATC	37	7	157102769	ATGCATC	7	156795530	F
	TGGATTG	37	12	114851495	GTGCAAA	12	113335878	R
	AAAATTG	37	12	70092840	CGGGAGT	12	68379107	R
	AGTTTGA	37	11	46879516	CGATCAG	11	46836092	R
	ACTGGAA	37	5	140530222	CTTGCAG	5	140510406	R
	TCCGTGC	37	6	157198648	CCTTGCC	6	157240340	R
Grn	AAAAACA	37	1	149298587	AAACAA	1	147565211	R
	CTCTGTT	37	2	102666444	CGGCACA	2	102032876	R
	GATTTCT	37	X	133931641	CGCAATG	X	133759307	F

Red	AGGAGTC	37	17	40706682	GTAGCGC	17	37960208	F
	TCTAGGG	37	13	111089337	TGTTCCC	13	109887338	R
	CCTCCCT	37	15	101587658	CTCTGTG	15	99405181	R
Grn	CACAGTG	37	4	967822	CGGAAAC	4	957822	R
	CCCCTCC	37	6	32828996	CGTCAGG	6	32936974	R
	TACCAAA	37	8	43101403	CGCATGC	8	43220560	R
Red	AGATCCT	37	22	25160033	AGTGTGC	22	23490033	F
	ATATGAG	37	4	11631423	TCTCCAG	4	11240521	F
Red	TGTTTAG	37	2	200775458	CGGGGCC	2	200483703	R
Red	CACCCGG	37	6	88757371	CGCCGCC	6	88814090	R
	AGGAAAT	37	1	47901632	CGTCCTC	1	47674219	R
	GCACTGC	37	3	187467427	CGAACAC	3	188950121	R
	CCGCCAG	37	3	140660432	CGCCCCT	3	142143122	R
Red	CGACTTC	37	11	118842650	CCGCCTC	11	118347860	R
	GATAAGC	37	1	180166190	AATGGGC	1	178432813	F
	CAGGGGA	37	17	37560925	GTGAGTC	17	34814451	F
	TCACTGC	37	12	131715734	CGTCAGA	12	130281687	R
Red	TGCCACG	37	2	202004875	GCCAGGC	2	201713120	R
	GCGCAAC	37	6	29895175	CGCACGT	6	30003154	R
Red	CAGCAGC	37	11	3254065	CGGTCTG	11	3210641	R
	TAGAGAA	37	10	115086103	CTATAAG	10	115076093	F
	TACTGTT	37	6	159392353	GCCAGAA	6	159312341	F
	AGTTGTC	37	11	94036363	ACCTATT	11	93676011	R
	GCCCTGC	37	7	47445681	TCCTGAT	7	47412206	R
	CCTTTCC	37	10	121346762	CTCCTGC	10	121336752	R
	ATCCGAG	37	13	32835962	GGACCTC	13	31733962	R
Grn	GGCTCAA	37	6	30039132	GGCTGCG	6	30147111	F
	CCAGCAC	37	10	134910285	CCTGGGG	10	134760275	F
	GGAGTTT	37	7	16966323	CACAGAT	7	16932848	R
Red	TGTTCAC	37	17	48270089	CGGCCTC	17	45625088	R
	TAACAGT	37	6	32409386	TTCCCAG	6	32517364	F
	GGGCGGC	37	1	839752	CGCCCTG	1	829615	R
Grn	TTCAAAG	37	6	36930021	ATGTTAG	6	37037999	R
	CCTCCAC	37	15	96890880	CGACCGC	15	94691884	R
Grn	CGGCAGT	37	17	41437982	TCTGCAG	17	38793508	R
	CTTTGCA	37	22	29225779	CGGTGAT	22	27555779	F
Red	GGGAAGA	37	6	30039006	TCCCCCA	6	30146985	R
	CTCATCA	37	4	172509909	CATCAAC	4	172746484	R
	AAATAAT	37	1	152333596	CATTTTC	1	150600220	F
	AAAAAAA	37	2	238252272	CGGAGAC	2	237917011	R
	CATCTTG	37	4	95799256	CTTAAAG	4	96018279	F
Red	ATGTCCA	37	17	39240789	CGCCCCA	17	36494315	F
	GCGTAGA	37	12	133177546	ACGGTGC	12	131687619	F

Red	CCGCTGC	37	22	30685664	TTCTGGC	22	29015664	F
	CAGCTGG	37	17	70710154	CGGCCTT	17	68221749	R
	AATTTGG	37	17	74868604	CGAGCAC	17	72380199	R
Grn	CTCCGAT	37	6	10720455	CGCCCAC	6	10828441	F
	GTAGTGG	37	15	80189782	CGAGTCG	15	77976837	F
	GGGGCCA	37	2	236409849	AGTTATT	2	236074588	R
	AGTTTTC	37	5	43411929	CCATAGA	5	43447686	R
	ATGAGAC	37	14	96722482	CGGCAAT	14	95792235	F
	CATATGT	37	6	167175937	CGGCACC	6	167095927	F
	GTGGTCA	37	6	170467487	GCAGCCA	6	170309412	R
Red	GGGGGCC	37	19	292271	AGCTGGC	19	243271	R
	GCATATA	37	12	124827315	CGGCAGC	12	123393268	R
Red	GGAGAAA	37	8	59058656	ATGAAAC	8	59221210	R
	GAGCCCG	37	1	12606996	CGAGCAC	1	12529583	F
	GGCATCT	37	10	27639136	GGGCAGC	10	27679142	R
	GACTCAG	37	1	227684434	CGGCACA	1	225751057	R
	ACATTTA	37	6	32546626	CGGTTTA	6	32654604	F
	AATCTTG	37	6	32549935	ATCAAAA	6	32657913	F
Red	AAATTAG	37	X	71401384	GTGAAAC	X	71318109	R
	ATAACCA	37	15	101206599	AGGAACT	15	99024122	R
	TCTTTCC	37	1	161368787	CGTGACT	1	159635411	F
	ATTTCTG	37	5	140479025	ACAACCT	5	140459209	R
Red	AGTTGTC	37	2	88583805	CGCCTCC	2	88364920	F
Grn	GCTATGA	37	1	228890884	TCCGAGG	1	226957507	R
Red	GAGAGGC	37	19	46996713	CGCAATC	19	51688553	R
Red	ACTGGGC	37	9	140312446	CGGCCTC	9	139432267	R
	TCCTGAC	37	1	114605704	CGCAAAA	1	114407227	R
	CCATAGG	37	12	25056083	CGCAACC	12	24947350	F
	GACCCAA	37	1	7762151	CGAGCCC	1	7684738	F
Grn	TTGGTTT	37	4	940644	AAGGTCA	4	930644	R
Red	CGGGAGC	37	7	56437746	CGGCCTC	7	56405240	R
	AAGCCAT	37	2	160058036	CGAGCAA	2	159766282	R
	CGTTGCG	37	15	20150114	TGACCTG	15	18410128	F
Red	ATGTGGC	37	17	79485043	CGGCTTC	17	77099638	F
Grn	GGCGGGA	37	X	9983205	GGGAGCC	X	9943205	R
	GAAGGAC	37	8	103750999	GTCGTGG	8	103820175	R
	GTTATTA	37	3	186928338	CGTGCTT	3	188411032	R
	TCTGGTT	37	17	80006606	CGGTGAC	17	77599895	R
	TATCCAC	37	8	107058373	TACTGTT	8	107127549	F
	GGACACA	37	5	140625794	CGGTGGC	5	140605978	F
	GCAGGTT	37	13	22560659	ACGTCTC	13	21458659	F
	CTAGGGA	37	1	115732999	GGAAATC	1	115534522	R
Red	AGCGCCC	37	X	68385233	CGCTTTT	X	68301958	F

Red	TGCCCCC	37	19	594272	CACCGAC	19	545272	R
Grn	CTCGGCC	37	X	19140934	CGGGACC	X	19050855	F
Grn	ATAAGAC	37	2	206842760	AAGCAGC	2	206551005	R
	AAGAGCC	37	19	526333	CGGACCC	19	477333	F
	CTGTGAA	37	11	65196222	TCTGAGT	11	64952798	R
	CTAAGCC	37	8	142192568	CGGTCAA	8	142261750	R
	CGTCGCC	37	Y	9194584	GAGAAAC	Y	9254584	R
	TTCTGGG	37	6	39290715	CGCCCCC	6	39398693	F
	GATGGAC	37	6	31106235	CTGAACT	6	31214214	R
Grn	TCCTCCT	37	19	37797500	AGGAGCC	19	42489340	F
	AAGAGCT	37	16	30485383	AGCTCTA	16	30392884	R
Grn	GGCGGGT	37	14	101005128	GCGGTCG	14	100074881	R
Red	ATTCTCA	37	11	11606082	CAAGGGC	11	11562658	F
Red	CGCTCTC	37	X	153095663	CGCGCCC	X	152748857	F
	TGCGGCT	37	2	88427630	GAACCTG	2	88208745	F
	CCCATCT	37	10	111912029	CGCTGGC	10	111902019	R
	TTTAGAT	37	1	39340282	CGTGATT	1	39112869	F
	TCACCGC	37	17	212481	CGGACAC	17	212481	F
	TCCAGGC	37	6	30419401	TGTGTCC	6	30527380	R
	TAATTTA	37	13	103478447	AAGAATC	13	102276448	F
	TATACTA	37	17	69357976	CATCCTA	17	66869571	F
	GCAGCCG	37	1	18808559	TGCAGCT	1	18681146	F
	AATCCCC	37	4	54357010	CTGGTGT	4	54051767	R
	AGGCTGC	37	19	40372977	AACTCCT	19	45064817	R
	AGTGCGC	37	6	32797488	CGGAGGC	6	32905466	F
	AACTCCC	37	1	63249199	CAGATTA	1	63021787	F
	GTGGCTC	37	10	6316599	CTTTTTA	10	6356605	F
	TCCACAG	37	6	170467790	CGGGAAT	6	170309715	F
	GGCTCTT	37	6	21916568	ATTGCTA	6	22024547	F
Red	CCCGGTC	37	7	1311498	CGGGCCT	7	1278024	F
	TCCCTCC	37	6	29649024	GCATGGC	6	29757003	F
	CAAATGA	37	6	30039801	CGAGGGA	6	30147780	F
Red	CCAGTCC	37	6	28584167	GGTGGCC	6	28692146	F
	ACCTCTG	37	5	167899230	GGCAGCA	5	167831808	R
	ACGTCAA	37	5	114791124	GAATGTC	5	114819023	F
	CCATACT	37	1	183116950	CTTTTTC	1	181383573	R
Red	GGCTGTA	37	7	4876057	GCAGAAC	7	4842583	R
Grn	GCTTGGG	37	4	581937	GACTTGG	4	571937	R
	AAACACT	37	5	140579644	CGAGCCT	5	140559828	F
	CAGTGCT	37	12	3019650	CGGTTTT	12	2889911	F
	GAGCTTT	37	5	179982651	AGATGAT	5	179915257	F
	TTTCCTT	37	1	200558537	CGGTTTT	1	198825160	R
Red	TCGCACC	37	X	107019430	CGCTTCG	X	106906086	F

Grn	ACAGGCT	37	7	158122151	GGAGCGT	7	157814912	F
	ACTGGTA	37	17	14989749	CGGCTCC	17	14930474	R
	CAGAGGA	37	6	33137570	CGGGGAC	6	33245548	F
	AGTCACA	37	8	48675771	TCACTGC	8	48838324	F
	ACCCTGT	37	5	78282669	CGGGGGA	5	78318425	R
	TAATGCT	37	13	106971568	GCTCTTG	13	105769569	F
Grn	ATGACTC	37	3	15311269	CGGCAGT	3	15286273	R
	GTGGGAC	37	10	123900861	AGCCAAA	10	123890851	F
	GGGGCAC	37	17	74074118	TGAGCAA	17	71585713	F
	CACCATG	37	Y	9384015	CGGTGCC	Y	9994015	R
Red	CTCCGGG	37	7	55431084	TCTCCGC	7	55398578	R
Red	ACCTGGC	37	7	2643340	CTTTACC	7	2609866	R
Grn	GCGTCCT	37	19	292131	CGCTGAT	19	243131	F
Red	GAGGCGC	37	19	17439877	GCGGAGT	19	17300877	F
	AGCCACC	37	13	24365000	CGAGAGC	13	23263000	R
	GAAGCCA	37	19	52133837	ATTTGAG	19	56825649	F
	GAGGTCT	37	7	22122872	GGGGACT	7	22089397	R
	CTGTTAC	37	19	46527410	TGTGCAC	19	51219250	R
	ACTGCAG	37	19	18761792	AGGGGCC	19	18622792	F
	GCACCAC	37	10	93998677	TACACAT	10	93988657	F
	AGTGGTA	37	10	43084809	CGGAAAA	10	42404815	R
	AAGAAGC	37	12	131258414	AAAGACC	12	129824367	F
Red	GGGGCTG	37	10	77871958	CTGGAGC	10	77541964	R
	TGATGTT	37	3	42139507	CGAAGGC	3	42114511	R
Red	GGAGGTC	37	10	12999599	CGCACCA	10	13039605	F
	TCACTCA	37	6	33041268	CGGAGAC	6	33149246	F
Red	CCCTCAG	37	6	170231220	GGATGCA	6	169973145	F
	GTAAGAC	37	1	212434331	CGCAGTA	1	210500954	R
	CCCGATT	37	6	166577958	AGAGGTT	6	166497948	R
	CACCAAC	37	12	10096152	GGTGAGC	12	9987419	F
	TGAGATC	37	1	169079632	CGAGTCA	1	167346256	R
	ACATCGA	37	12	8995965	CCGATGC	12	8887232	R
	CAAATAC	37	1	159748210	GCCACAT	1	158014834	R
	GTCAGCC	37	17	40489584	TTTCTGA	17	37743110	F
Grn	AGCTCTC	37	10	25238461	CCTCCTG	10	25278467	R
	GAGAGCC	37	11	27406919	CGGAGGT	11	27363495	R
Red	CTCCCCC	37	19	49891574	AACTGCC	19	54583386	R
	TAAATCT	37	1	184943911	CGTGATC	1	183210534	R
Grn	TCCGCTG	37	6	30038955	ATGCGGA	6	30146934	R
	CAAACCT	37	8	117457111	ATTGAAA	8	117526292	R
Grn	AGGCCGA	37	21	45842649	CGGCGCT	21	44667077	R
	TGAAAAC	37	3	47138673	CGGTGTT	3	47113677	R
	CTCGCTC	37	7	27163929	GGTAATG	7	27130454	F

	AATGTGT	37	10	131215469	CGGAGTC	10	131105459	R
	GTGAGCA	37	15	25430653	CGTGGCT	15	22981746	R
Grn	GCGGCCA	37	2	162197869	CATAAAA	2	161906115	F
	TACAAGT	37	1	161931993	CGGAGGT	1	160198617	F
Red	CCCCGGC	37	3	42947690	CGCCCCA	3	42922694	R
	GTAACCA	37	3	97591258	TCTTTGC	3	99073948	F
Red	TGTGGAC	37	12	2760969	CGCAGGC	12	2631230	F
Grn	CGGGACC	37	7	55517045	CGGCCCT	7	55484539	F
	CCAAGAA	37	11	88153520	AATGAAC	11	87793168	R
	TTGGGTC	37	17	80914695	CGGGGAC	17	78507984	R
	TAGGAAT	37	17	40808068	CGGAGTC	17	38061594	F
	TGTTAAA	37	19	5510310	CGGGGCC	19	5461310	R
	GGCCAAC	37	18	11947936	CGGTCTT	18	11937936	F
	CATCCCA	37	13	20764859	TGAATTG	13	19662859	R
	GAGACTA	37	17	76588724	GACTGCA	17	74100319	F
Red	ACTCTGC	37	10	82295723	CGGGGAC	10	82285703	F
	ATGATTT	37	21	44103949	CGGGGGA	21	42977018	R
	TTGGCAG	37	1	32177995	CGTCTTT	1	31950582	F
Red	TCTTTTC	37	19	292102	CGAGCTT	19	243102	R
	CAACCGC	37	1	155167337	CGTAGTC	1	153433961	R
Grn	GCTAGTC	37	1	179713828	CGGGCCT	1	177980451	R
	TGATTTA	37	12	115104460	CTATGCC	12	113588843	R
	GGATTTC	37	1	215196452	CGAAAGC	1	213263075	R
	ACTAGAC	37	2	172452502	CGCCAGC	2	172160748	R
	TTATTTA	37	6	32608858	GTGCACT	6	32716836	F
	ATGGTGA	37	12	98850691	CGGCCAC	12	97374822	R
Red	AGAGAGC	37	19	6710658	CGCAGGA	19	6661658	F
	CCATGCT	37	1	246592123	CGCCGAT	1	244658746	F
	AGGCTTG	37	21	46675571	GTGTGTG	21	45499999	F
	CAGCCGC	37	2	795989	AATAAGC	2	785989	F
	CCAAAGT	37	4	183006582	CGTGTGT	4	183243576	R
Grn	GCCCTCT	37	1	110230401	GCCTCCA	1	110031924	R
	CGCCTTC	37	1	207992403	GCAGAGT	1	206059026	F
Red	GCGGAGC	37	10	124578209	CGCACAC	10	124568199	R
	TGAGGAC	37	11	115571126	AGCCTCT	11	115076336	R
	ATCTTCC	37	6	28697846	TTGGGAC	6	28805825	F
	ACAGAAC	37	5	140579046	CGGAGGA	5	140559230	F
	GAGTCAC	37	8	143781340	CGTGAGT	8	143778342	R
Red	CTGTGCC	37	8	216659	GCGGAGC	8	206659	R
	GATGGTC	37	5	112824920	TGATCCA	5	112852819	R
	GGCAGGC	37	11	10715360	CGACCAC	11	10671936	R
Red	CGGGTAC	37	20	45170494	GGCAGCC	20	44603901	R
	AGGTGCC	37	1	3721846	CGGCACA	1	3711706	R

	TTCCCTC	37	7	154719693	CACAGGC	7	154350626	F
	AGGAGA	37	17	80921117	TGAGCTA	17	78514406	R
	AAGGCAC	37	1	230240631	CCCTTGC	1	228307254	R
Grn	AGCACCC	37	5	179059426	GACGGTC	5	178992032	F
	GCAGATC	37	1	222162028	CGTCTTA	1	220228651	R
	TTTCCTA	37	2	109826107	CGACTGC	2	109192539	F
Red	CACCTTC	37	13	19918951	AGTCCAG	13	18816951	F
	TCTTATT	37	12	114887657	GTTTGGT	12	113372040	R
	CCCAGCG	37	6	32633157	CGCCCTG	6	32741135	R
	GTGAACA	37	2	113379847	AAGTCAC	2	113096318	R
Grn	CGCGCTC	37	X	117480246	CGGCGGT	X	117364274	R
	TTGCTTG	37	2	26578508	GCAAGGA	2	26432012	F
Grn	CGCACCG	37	2	91937265	TAATTTC	2	91300992	F
	ATGACTT	37	8	59698273	GTAAATT	8	59860827	F
	AGTGATC	37	6	42186179	CATTATT	6	42294157	F
	CTTCCGC	37	10	130279707	GTGCCGA	10	130169697	R
	ATAAATT	37	1	17500642	GTCTCAG	1	17373229	R
Red	GTGCCCC	37	17	4437925	GGGACAC	17	4384674	R
Red	GATGAAT	37	8	81787111	CGCTCAT	8	81949666	R
Red	TGCGCTC	37	6	30039013	CGACGGC	6	30146992	R
	AGAAAAC	37	7	2802942	CGGGCTG	7	2769468	R
	CCGCGAG	37	X	102863004	CGCCCAC	X	102749660	R
	TAAAAAT	37	17	80970434	CGGGCCC	17	78563723	F
Grn	GCCGGCC	37	6	44243304	GCTGCGC	6	44351282	R
	TCCAAGA	37	7	127078268	CGGTGTG	7	126865504	F
	CGGAGCA	37	1	210013268	CGTGGTG	1	208079891	F
Red	GCCCGCG	37	6	36930062	TGGGTGT	6	37038040	R
Grn	TTGGCCT	37	1	156211892	GCTGGGC	1	154478516	R
Red	GTTATGG	37	11	48374446	CGATACT	11	48331022	F
Grn	CAGGCTG	37	5	140189548	ATAAAGC	5	140169732	R
Red	GCAAGT	37	12	116044032	CGCCAGC	12	114528415	R
	GACTCAT	37	13	38231017	CGGCTCT	13	37129017	F
	GATACAA	37	17	80735406	AGGGGCA	17	78328695	R
	TGGGTCT	37	3	134047274	AATCTCT	3	135529964	R
	CACCACC	37	2	23746926	CGGAAGA	2	23600431	R
	CCTCCTT	37	15	55513621	TTGCAAC	15	53300913	R
	GCCACGC	37	10	118387095	CGGGGCA	10	118377085	R
Red	GGGGGCC	37	11	67383802	CGGAGAC	11	67140378	R
Red	CAGGCGC	37	3	10749371	CGGCCCG	3	10724371	F
	CGGGCTC	37	8	125150452	CGCATCA	8	125219633	R
	AGGTCGT	37	6	28697819	CGGGGCT	6	28805798	F
	GGGAGTA	37	22	43168851	CGGCTCA	22	41498795	R
	ACCAAAC	37	6	28876508	CGTGGGA	6	28984487	R

	CCCAGCC	37	10	97419053	TTTTCT	10	97409043	F
Red	CTCTGGG	37	14	101175645	ATTGTCC	14	100245398	F
Grn	CACTCAC	37	7	101961796	GCTGGAC	7	101748516	F
Grn	AGGCTTC	37	4	3235319	GGCCTCG	4	3205117	F
	TTTTGTG	37	18	11818701	CGGACC	18	11808701	F
	ACAATTC	37	5	76034887	AGCAGC	5	76070643	R
	TCCTCAA	37	19	49339397	CGGAGAC	19	54031209	F
	AAGTAGC	37	1	225955869	CGGAAC	1	224022492	F
	TTTTATT	37	5	102114455	CGAAGCT	5	102142354	F
Red	CGTGGCC	37	1	2229140	CGCAGAT	1	2219000	R
Red	CTCAGAA	37	6	167589370	GCGGGTT	6	167509360	R
	TTCTCCT	37	15	71890066	TGTCCCA	15	69677120	R
	CGTCAGA	37	6	101846767	TGCAGCA	6	101953488	R
	CACTAAA	37	2	133062155	AAAGTGC	2	132778625	R
Grn	GCTGTGA	37	14	101908865	CGACAAC	14	100978618	R
	ACTATTT	37	6	32557970	CATTAAG	6	32665948	F
	TCCTTCC	37	19	937444	CGGGCA	19	888444	R
	CACCTTT	37	11	78052863	ATGATAC	11	77730511	R
	TATGAAG	37	15	33111288	CCTCAGT	15	30898580	F
	CTACTCT	37	18	74118243	CTCGTCC	18	72247231	R
	GGGCCAC	37	15	22982193	CCAATGC	15	20533634	R
Grn	CCCCGCC	37	4	163085276	CGGCCCC	4	163304726	R
Grn	AGCTGCA	37	6	37617956	GGGAAGC	6	37725934	F
	CCCGACT	37	4	7502706	GCTACAG	4	7553606	F
	AAAACTC	37	17	74260692	GTGAACA	17	71772287	F
Red	CACAGTG	37	8	108441547	CTCATAA	8	108510723	R
	ATACAAA	37	10	35893624	CGGATAT	10	35933630	F
Red	CCCCATC	37	13	112984728	CGGGGCC	13	112032729	F
	AAGTACT	37	7	158075968	CGGTTCA	7	157768729	R
	GCAATCC	37	6	112111043	CGTGTCC	6	112217736	R
Red	CACTACT	37	3	143690208	GGGGCG	3	145172898	F
	GTAGAGC	37	12	12620789	CCATGTG	12	12512056	R
Red	AGCGCTC	37	12	124929963	TGCAGCA	12	123495916	R
Grn	GGAACCC	37	12	130822603	CGCCGCC	12	129388556	R
	AGAACGC	37	6	29895260	CGCCTGT	6	30003239	F
	GTGGATT	37	13	98126969	CGGAAAT	13	96924970	R
	GAGAGAC	37	1	18684587	CGCCATG	1	18557174	F
Red	CGAAAAC	37	3	12595473	CGGCGCA	3	12570473	F
	GTCGGAC	37	3	150480910	GGGGCTT	3	151963600	F
	TGCTGAT	37	12	2017134	TGTTCAC	12	1887395	R
	GACAAAC	37	5	155901557	CTTTCTG	5	155834135	F
	TCCTGCC	37	20	17680544	CAGTCTC	20	17628544	F
	GCCCTGG	37	2	135072000	CGGGCCT	2	134788470	R

	TGGATTC	37	5	1228214	CCAAAAA	5	1281214	R
	ACCACAA	37	1	180069210	CGCGCCC	1	178335833	F
	ATACTAA	37	1	220000086	CGATGGC	1	218066709	R
Red	GGCGGCC	37	6	28853021	CGCCCCC	6	28961000	R
	TTCTGTT	37	17	32612675	TGACTTC	17	29636788	R
	AAATATC	37	11	18300953	CGGTGTA	11	18257529	R
	ACAGCTT	37	11	14431708	CGCCACA	11	14388284	F
	ATTGCAA	37	13	102686228	CGTCTCC	13	101484229	R
	TTTTTGT	37	10	72163076	CGCTGCT	10	71833082	F
	GTCCTGG	37	10	3088502	AGAGTGT	10	3078502	F
	CCAGAGC	37	18	14457820	GGAATTA	18	14447820	F
	TTTGGAC	37	15	41118060	CCATGGC	15	38905352	R
Red	CAATTTC	37	6	31785597	CGGTTTC	6	31893576	F
	GAACATC	37	5	59837426	CGGTTCT	5	59873183	R
	GGGTGTG	37	5	73188814	CGGTGGT	5	73224570	R
	AAACAGA	37	1	169072106	TCTGAAT	1	167338730	F
	GGCAGTA	37	11	10320161	GTCAGAC	11	10276737	R
	CTTGATT	37	2	58482767	CGGTGCT	2	58336271	R
Red	AGGCAGT	37	11	128812992	TTTTCAC	11	128318202	R
	TCAGGAT	37	4	24780369	CGCAGCT	4	24389467	R
	AAATTGG	37	7	65227864	CGGTGAT	7	64865299	F
	GGTGCCA	37	2	110979750	CGGTGGC	2	110337039	F
	CTTCGCG	37	11	7110561	CGGCAAC	11	7067137	F
Red	ATCCGCG	37	13	44971694	CGCGTGG	13	43869694	R
	CCACCTT	37	2	792213	CGGCAGC	2	782213	F
Grn	AAGGAGA	37	8	8679450	CGGGTCG	8	8716860	F
Red	AGACTTT	37	19	40904691	CGAGAAC	19	45596531	R
	GGCCAGC	37	1	2245221	GACCAGC	1	2235081	F
	CCTCTGC	37	1	151557485	CGGCTGC	1	149824109	R
	GCAGGTA	37	7	147732939	CGGGTGA	7	147363872	F
	CTGCCGA	37	2	88427637	CGGCCAC	2	88208752	F
	GGGCTGT	37	20	61731415	AGAGATT	20	61201860	R
	CTAAGCC	37	13	79694063	TGCACGT	13	78592064	F
Grn	CCCTGTA	37	4	115416755	GCAGATC	4	115636204	F
	CCCTGCA	37	11	56615725	CGCAGCA	11	56372301	R
Red	CAGCTGA	37	17	75522344	CGGCGCC	17	73033939	F
Red	GGGTGGC	37	8	6481608	CAGCCCC	8	6469016	R
	TCTTCCT	37	6	32297615	CGGGAAA	6	32405593	R
	CTAGGGC	37	5	415729	CGCCCCA	5	468729	R
	CGCGCGT	37	15	31355362	AAGAGCC	15	29142654	F
	GAAAACA	37	5	140515961	CGTGGAA	5	140496145	F
Grn	CCTGCGC	37	5	1594678	CGCGGCA	5	1647678	R
	CTGAGTA	37	15	67361773	CGGCAAA	15	65148827	R

	ATTATTC	37	8	8932588	CTGAATC	8	8969998	R
	CAGCACA	37	10	85321586	CGGGGCT	10	85311566	R
	GAAGGTA	37	6	32606845	AACTTTC	6	32714823	R
Red	GAACCCA	37	11	67764320	GCGGGGC	11	67520896	F
	CATCTTG	37	17	38249266	CGAGACC	17	35502792	R
	GCAGGGA	37	7	1420943	CGACTCT	7	1387469	R
Red	AGGGCCC	37	20	259898	CGGGAGC	20	207898	R
Grn	ACCTGGG	37	1	247803033	GCCAGTG	1	245869656	F
	AAAGTCC	37	10	49654342	CGCCTGG	10	49324348	F
	TTGGTGG	37	8	61785026	GAGAGGC	8	61947580	R
	CTGTTGG	37	14	89604062	CGGCCCT	14	88673815	R
Red	CCCTCGC	37	17	75238703	TTGCCGT	17	72750298	R
Grn	AGTGGGA	37	1	247802802	GGGCCTG	1	245869425	R
Red	TTGAGAA	37	1	154947060	CGGAGGC	1	153213684	F
Red	GGAAGAA	37	5	140554819	CGCGTCT	5	140535003	F
	TCAGTGC	37	7	157495282	CGGGGCC	7	157188043	F
	AAGTAGT	37	13	47326127	CGACTCA	13	46224128	R
Red	TGTCTCA	37	1	35586358	CGCGGCC	1	35358945	F
	AGTATTC	37	6	29794657	CGCACTG	6	29902636	R
	CCCCAGG	37	22	20283373	CGGCACC	22	18663373	F
	CTTCATT	37	Y	7431190	CGGTGTG	Y	7491190	R
	GAGCAGC	37	10	93100919	CGAGTCA	10	93090899	R
Red	TTCTTTCC	37	1	150335507	CGGCACC	1	148602131	R
	ATTCCAA	37	4	155254016	GCAGAGT	4	155473466	R
	TAATGCC	37	6	156954565	ATGCTTT	6	156996257	R
	GACTCAT	37	12	1391371	AGGATTC	12	1261632	F
	ATGTTCT	37	2	18158708	CGGTGGC	2	18022189	F
	TGGATTT	37	4	152147803	CGTCACA	4	152367253	F
	AATTTAT	37	12	47610734	CTTTGTG	12	45897001	F
	AAGCGTC	37	7	76109396	CTGTGTT	7	75947332	F
Grn	GCGGCAC	37	3	42727489	CGCCTGT	3	42702493	F
	GGGTCAC	37	12	25454990	CGGTGCC	12	25346257	R
Red	TGTGGCC	37	5	1650942	CGCTAAT	5	1703942	R
	CCTGACC	37	6	32522683	CGGCTCT	6	32630661	R
	TTTGGCG	37	X	47433716	CGCCAGC	X	47318660	R
	CGGATTT	37	22	18531591	CGCTATG	22	16911591	R
Red	CTTCACT	37	8	141294201	GGCAAGC	8	141363383	R
	AGCTCAG	37	7	134212463	TGAGACC	7	133863003	R
	CTGTGAG	37	11	65631880	GGATGAC	11	65388456	F
	CATAATA	37	8	25107121	TCTTTTGT	8	25163038	R
Red	TCTGCTG	37	22	49847690	GACTGGC	22	48233694	F
	AACAGAA	37	10	25162298	ACATCAC	10	25202304	F
	CTAGGTG	37	11	133771378	CGGGCAA	11	133276588	R

	GTGGAAC	37	5	113699604	CGCCTGC	5	113727503	R
	CTGAGGC	37	1	17018684	CGGGAAC	1	16891271	R
	CTACCAG	37	6	110964408	CGTCAGG	6	111071101	R
	ATCTGTG	37	11	100760935	CGAGAGC	11	100266145	R
	GGTGAAC	37	5	140517411	GGGAAA	5	140497595	R
	AAGAAA	37	1	235796187	TTAGTTC	1	233862810	F
	AGACCAT	37	6	32640493	CGGAACC	6	32748471	F
Grn	TTCTCTC	37	1	247802774	GAGGAGC	1	245869397	F
Red	CGGGGGC	37	5	140222253	TTCGCTG	5	140202437	R
	AGACTCC	37	X	70474172	CGCCGTC	X	70390897	R
	AGATTGA	37	10	102239027	CGCCAAC	10	102229017	F
	CAGTGCC	37	19	12940950	GGGGCTC	19	12801950	F
Red	TTTTCAC	37	4	40267141	TGACAAC	4	39943536	F
	CCTAAAG	37	12	113842581	CGCCAGC	12	112326964	R
	CGCAGAT	37	12	2881762	CAGGACT	12	2752023	F
Red	TGGCCTC	37	2	242713790	CGGCCAC	2	242362463	R
	CCTGGTG	37	10	3163518	CGCACTG	10	3153518	F
	CTCAGGA	37	6	158234655	CAGCAGT	6	158154643	R
	TCCATGA	37	10	112580109	CGGACAC	10	112570099	F
Grn	CCAGTGC	37	22	18531243	AGATTCC	22	16911243	R
	CCAGCAC	37	13	101315319	CAGTGGC	13	100113320	F
	AGCGCTC	37	2	128453484	CGCCCCC	2	128169954	F
	TTTTGTA	37	7	127409937	CGCTGAG	7	127197173	R
	GAAGAAC	37	6	33033484	CGGCAAT	6	33141462	F
	ACTATAT	37	10	113944114	CGCTAAG	10	113934104	F
	ACCTCAG	37	15	56531754	CGCGCCT	15	54319046	F
	TTGAATT	37	7	98976900	TCTTACC	7	98814836	F
Grn	GTGGCCG	37	2	233217079	CGCCGCT	2	232925323	R
	ACAGTTA	37	8	38578802	CGCGGAC	8	38697959	F
	CCTTCAA	37	13	110434467	GGGACAA	13	109232468	R
	CGGTGTT	37	19	468773	CCCCACA	19	419773	R
	GGGGCCC	37	11	5960081	ACCGGTT	11	5916657	R
Red	AAGGCTC	37	8	1439535	GGGAGCA	8	1426942	F
Red	ACGCAGC	37	7	158769805	AGCTCTG	7	158462566	R
Red	AGAAAAT	37	17	73286282	CGGAGAC	17	70797877	R
	ACCACTG	37	2	30887962	CAGGCAC	2	30741466	R
	TGGGCTT	37	2	196399403	GGCCTGC	2	196107648	R
Red	GAGAGGC	37	5	135416398	GAACTGA	5	135444297	F
	CCCAGAT	37	12	108078835	TGTATCT	12	106602965	F
	GAAACAC	37	10	64875536	CGGCAGT	10	64545542	R
	TCCAGGC	37	15	100517183	CGGGCCT	15	98334706	F
Red	GTTCGGG	37	10	77155376	GTGGGTG	10	76825382	F
	GCAAGTC	37	1	46649132	CGGCCCA	1	46421719	R

	CCCGTGT	37	2	9062790	CGGGTGT	2	8980241	R
Red	GTAGCCC	37	1	98510328	CGCGCTA	1	98282916	F
	CAGCTGA	37	3	30383960	AACTTTG	3	30358964	R
Red	CCCGAGA	37	11	1529608	ATGGAGC	11	1486184	R
	TCCTCCT	37	5	77178418	TCTCTTC	5	77214174	F
	AACTCAA	37	3	23496403	CTTTTCA	3	23471407	F
	GGGTGGC	37	17	80084596	CGCAAGC	17	77677885	F
	GGCTGGC	37	X	131157336	CGAGCCC	X	130985017	F
	GGGTGGC	37	5	66462293	CGGAGGC	5	66498049	F
Red	AAAGGT	37	10	133558485	CGCCCAT	10	133408475	F
	CCTATGC	37	1	31197913	TGCTAAA	1	30970500	F
	TCTGGCC	37	11	20053759	CGAGGG	11	20010335	R
Grn	GAGAGTT	37	6	31651059	TCAGAAC	6	31759038	F
	CTTCTTT	37	5	76785615	ACTAAAT	5	76821371	R
Red	GGACACC	37	18	59221601	GGGAGAC	18	57372581	F
	AGAGGTC	37	11	65683543	GCTTTTC	11	65440119	F
	TAAGGTG	37	13	114928103	CGCTTGT	13	113946205	R
Red	TCTTCTG	37	22	22987072	CGGCGCC	22	21317072	F
Grn	TCCTTGC	37	8	83353753	CGGCTCT	8	83516308	R
Red	GCATCAC	37	17	60744005	TCCACGA	17	58097737	R
	TTGGCAT	37	3	45677346	CGAAGGT	3	45652350	R
	CCCTTCT	37	5	85110900	CCTGGGA	5	85146656	R
	AGAGAA	37	5	2387924	GCAGGTC	5	2440924	R
	TTGCTAT	37	4	176486240	CGGGCAT	4	176723234	F
	GGGATAT	37	17	46970175	CGGCTCA	17	44325174	F
Red	ACCGTTG	37	22	42524984	CGGGGA	22	40854928	R
	CCACTCA	37	19	42274924	TTCACCT	19	46966764	R
	CCAAATG	37	10	105032988	CGTGTCT	10	105022978	F
	TCATTTT	37	1	212335061	CAGATAA	1	210401684	R
Grn	CGGCCTG	37	8	144810034	GGAAGCC	8	144882022	R
	ACAGATC	37	3	17680687	TGTTTTG	3	17655691	R
Red	CGGTGCT	37	1	15541349	CTAACTC	1	15413936	R
Grn	TGCAGGC	37	1	31280143	CGCGGCC	1	31052730	R
	CACAGCC	37	3	71111489	AATCCCT	3	71194179	R
	AGCCTAC	37	3	41723017	AAGGAG	3	41698021	F
	GAGCTGC	37	2	242048127	AAAGGGC	2	241696800	F
	TTTCTAA	37	2	138045743	CGCCCTT	2	137762213	F
	AAGAGC	37	3	42307519	CGCCCAG	3	42282523	F
	AAGATGC	37	6	101878898	TGTAAGT	6	101985619	R
Red	CCCTCCC	37	13	42002627	GATCGTC	13	40900627	R
	GCCATGC	37	11	74030400	CGCATGA	11	73708048	R
	CCCACAG	37	13	19960816	CGGCATC	13	18858816	R
	TGTGTGA	37	8	49502710	CGCCGCT	8	49665263	F

	GCAGGAA	37	5	112540429	CGGTTAT	5	112568328	F
Red	AATGGGC	37	4	6474782	CGCGCAA	4	6525683	F
	TTTCATG	37	13	44000493	CGTGCTG	13	42898493	F
	GAAAGGT	37	8	90986930	TTCCTTC	8	91056106	F
	CTAAGTC	37	8	112691450	CGTCGAT	8	112760626	R
	TTCTTCA	37	13	41070900	CGGCCAT	13	39968900	F
	AGGCAAC	37	19	2525384	GGGCTTA	19	2476384	F
Red	GGGCCTG	37	X	133594204	CGTGGCG	X	133421870	R
	CAGAAAC	37	3	190104266	TTCCACA	3	191586960	F
	GTCTTCT	37	4	189026860	CGAGTCA	4	189263854	F
Red	CTTGACC	37	2	48844892	CGCCCCC	2	48698396	F
	GGGCGCC	37	14	24780557	CGTGCTT	14	23850397	F
	ATACTGA	37	15	99709980	TGGATTC	15	97527503	F
Red	CTGCACT	37	19	345306	CGCAAGC	19	296306	R
	TATGAGG	37	15	83332065	CGCATTT	15	81129120	F
	GTCCTTG	37	2	10037561	CGCAGCA	2	9955012	F
	TCGGTTC	37	1	17394374	CGATTGA	1	17266961	F
	GTATATG	37	X	37765018	TGTGTTG	X	37649962	R
	AAGTGTC	37	1	28843736	CGAGAAA	1	28716323	F
	TCTCCTT	37	1	161349116	CGCTGAC	1	159615740	R
	GTGCAGC	37	3	50306456	CCTGAGG	3	50281460	R
	AGATCAT	37	6	32634245	CGGCTCT	6	32742223	F
	TTCTGCT	37	2	114151353	CGGCGCC	2	113867823	R
	GAATTTG	37	12	129337339	CGTGCGG	12	127903292	F
	GGGGCAC	37	19	17434267	AATACTG	19	17295267	R
Grn	CTCTAAA	37	3	47397852	GGCCCAC	3	47372856	R
	GCATGGC	37	11	126976228	GTCCTCA	11	126481438	R
Red	CCTGGGA	37	1	23495577	CGCGGGC	1	23368164	R
Red	GCAAGCA	37	3	197121419	CGGGAGC	3	198605816	F
Grn	CAGCTCC	37	5	177823856	TTGAAGT	5	177756462	F
Red	CAACGCC	37	8	143561205	TGAGGGC	8	143558207	R
	GAGCTGC	37	2	241644166	GGAATGT	2	241292839	F
	TGAGAGC	37	16	2848409	AACAGCC	16	2788410	R
	TCCTTCC	37	10	31939075	GGAGGCT	10	31979081	R
	CCTGGTG	37	11	8707082	CGGTGCC	11	8663658	F
	AAGGAGT	37	5	78599729	CGGAATA	5	78635485	F
	ATTTTCC	37	22	26952678	CGCTGCC	22	25282678	F
	TCTTACC	37	6	46652700	CACAATG	6	46760659	F
	GTTTTCC	37	12	132965879	CGAGGCT	12	131475952	F
	AAGGCAC	37	5	33050111	CGGGGCC	5	33085868	F
	TGGAAGA	37	19	3030324	CCCCGGG	19	2981324	F
	AGTGATC	37	3	46521313	ATCTCAC	3	46496317	F
	GAATAAA	37	3	177309023	CGGTCAT	3	178791717	R

	ACCATAT	37	15	77748245	CGGAAA	15	75535300	R
	TTGGCCC	37	2	240019300	TCCTCTG	2	239684237	R
	GACAAGT	37	6	30652202	TCTAAGA	6	30760181	R
	ACCAGGC	37	6	32522905	CGTGATA	6	32630883	F
	CAGGAGC	37	12	71148346	AAAGAAC	12	69434613	F
	ACCTAGG	37	4	89667785	CGGAGGC	4	89886808	R
	CACAGCC	37	12	103325781	AACCCCT	12	101849911	F
	TCTAAGA	37	12	107347673	CGAAGAA	12	105871803	F
	CTCCCAG	37	3	11178758	GCCTGAC	3	11153758	R
	TTTATAG	37	17	41522193	CGGCATG	17	38877719	F
Red	CACCTCC	37	17	4439481	CGGGGCT	17	4386230	R
	AAAGGTA	37	17	79258813	CGGGGCA	17	76873408	F
	TGGCCAC	37	3	139724110	CGGATGT	3	141206800	R
	TGTAAAA	37	20	17582752	CGAGGTC	20	17530752	F
Red	GCAACGC	37	X	136512132	GTATGCG	X	136339798	R
Red	GACGGTT	37	19	291986	TGAAATG	19	242986	F
	GTCTGCT	37	3	57969522	CGGTGCT	3	57944562	R
Red	GTGTGTG	37	Y	9307448	CGGGTGT	Y	9917448	F
	TGCTAAA	37	3	34884326	CGGTAAC	3	34859330	F
	ATCCCCG	37	13	111281144	AGGCTCT	13	110079145	R
	AATGGGT	37	2	286830	TACAAAC	2	276830	F
	TAGAAAA	37	6	170732120	CGCCTCA	6	170574045	R
Red	AGCCATC	37	17	48263204	CGAGATC	17	45618203	R
Red	TCGTCTC	37	3	61235869	TGGCCGC	3	61210909	F
	TCGCACC	37	6	160182554	CGCATAG	6	160102544	F
	GGGAGCC	37	17	3848506	CGACCCC	17	3795255	F
Red	CCCAGCT	37	1	202129865	CTCACCC	1	200396488	F
	GACTCAG	37	1	115722330	AGCCACC	1	115523853	R
	TGGTGTG	37	10	3823907	CGGTGCC	10	3813907	R
Red	CAACGCC	37	6	25732923	TAAGCCA	6	25840902	F
	ACTGTGC	37	2	200904751	CGACTAA	2	200612996	F
	AACAGCT	37	1	9335794	CGGGTAA	1	9258381	F
	GCACCAC	37	19	38039469	CGGGTCA	19	42731309	F
	GGTCTTG	37	1	207039833	CCTGTCC	1	205106456	F
	TCAAAAA	37	1	13184954	CATTCAT	1	13107541	R
	AGTCTGA	37	3	121307887	CGGCCAC	3	122790577	F
	ATTCCCA	37	3	30140788	CGAGCTC	3	30115792	F
	ACTCTGC	37	1	247420421	CGCCAAT	1	245487044	F
	TGCTTTC	37	5	14348251	CGACATA	5	14401251	R
	TGCGGGC	37	4	13537089	TTACTTT	4	13146187	F
	GGTCTCC	37	7	4180723	CTCACTT	7	4147249	F
	TTGTGCA	37	18	32289350	CGGGGGC	18	30543348	F
	ACCAAGC	37	4	10034580	CAGCTCG	4	9643678	F

	CATAACT	37	4	2627014	ATTCTGT	4	2596812	R
	TGTCAAG	37	10	29834263	CGGCGGC	10	29874269	F
	CACGCAC	37	4	7788342	CGGATGA	4	7839242	R
	GCTGGGA	37	12	127631198	CGCCTCC	12	126197151	F
	GTCATAT	37	17	15255513	CGACTCG	17	15196238	F
	CAGTCTG	37	13	49672483	CGGCAGT	13	48570484	R
Red	CCCGGCC	37	X	153096039	AAAAAG	X	152749233	R
Red	CAACACA	37	X	25021346	CGGAAG	X	24931267	F
Red	GCTAGCG	37	X	73756753	CGCCCTC	X	73673478	R
	TGCTGTG	37	7	143028708	GCAGTGA	7	142738830	F
	CCCAGAC	37	17	81014413	TCAGGAC	17	78607702	R
	AGAAACA	37	15	65272560	CGGCTCA	15	63059613	R
	ACCCAGC	37	1	47900630	GCCCCTC	1	47673217	R
Red	CACAGAA	37	11	50257625	CGCACAT	11	50214201	F
	GAAGGA	37	X	130423014	GAGATAT	X	130250695	R
	GTTCAAA	37	10	3666169	ATTCGAA	10	3656169	F
Red	ACCCGCG	37	13	59398086	TGGGGCT	13	58296087	F
	TCCTGTT	37	10	33342522	CGGAGGC	10	33382528	R
	GAGGCCC	37	7	157405965	CGCTGTC	7	157098726	F
	TCTTCCG	37	4	7844982	GGAAGGC	4	7895882	R
	ACCTGCT	37	Y	24452543	TGCGGTA	Y	22861931	F
Red	GTTGGCC	37	13	100150906	CGCCCCC	13	98948907	F
	TGTCCAC	37	17	39597601	CGGGGTT	17	36851127	R
Red	ATTCCAG	37	7	102107737	CGGACCC	7	101894742	R
Grn	CACGGCC	37	8	58172855	CGGTGGC	8	58335409	F
	GAAATAC	37	21	46001680	CAAATGA	21	44826108	F
Grn	CCCCGGG	37	2	177016619	GAGGCGC	2	176724865	F
	GATCGAC	37	2	232349118	CGGAAGC	2	232057362	R
	GCCTCCA	37	15	71092216	GTTTTGA	15	68879270	R
	AATCAGA	37	6	31323677	CGGTTCC	6	31431656	F
	TTTGAGT	37	3	168822459	CGTGTTT	3	170305153	R
	GTCATGT	37	10	47696803	ACTTTCC	10	47166809	R
	TCTTTAC	37	3	50855436	CGGCAGA	3	50830440	R
	AATCTCT	37	8	17207503	TGATACT	8	17251874	R
	ATTGGAG	37	7	55516751	CGCGGCC	7	55484245	R
	GATCAGC	37	7	140955751	CGCCTAG	7	140602220	R
Red	GCTTTTT	37	1	16163967	AGAAAG	1	16036554	R
Red	GGGCGCC	37	20	57465439	CGTCGCT	20	56898834	R
Grn	TGCTTGA	37	7	65971099	GTGCTCT	7	65608534	R
	CTCAGGT	37	20	60713905	CGCCCAC	20	60147300	F
Grn	ATTTATT	37	13	20531342	TTTAGTG	13	19429342	F
	AGCCAAC	37	2	42328001	GCCCAGC	2	42181505	F
	GGTTTTA	37	2	228331319	CGGTTTT	2	228039563	R

	AAGAAAT	37	2	133104748	CGCCTTT	2	132821218	F
	GAGGTCA	37	X	43741890	CGGTATT	X	43626834	F
Red	GGTGCGC	37	19	2251067	CTCGAGT	19	2202067	F
Red	GCCCCTT	37	1	178456093	TGGAGGC	1	176722716	R
Red	AGCTCTC	37	1	182921660	CGAGTTT	1	181188283	R
Red	AAGCCCC	37	3	127347876	CTCGGCG	3	128830566	R
	GAAACAA	37	6	36821364	CGTGGGC	6	36929342	R
Red	CCCGGCG	37	1	92952467	GCCTTTA	1	92725055	F
	ATCCTTG	37	11	117110208	TCTCTGA	11	116615418	R
	GGACCCC	37	1	209982407	CGTTAAC	1	208049030	R
	CGGGATA	37	X	153059444	GTGACTG	X	152712638	R
	TTGCTTC	37	11	120417671	TAATCCC	11	119922881	R
	AATGGTA	37	8	131265658	AAGAGAC	8	131334840	R
Red	AGGGCAC	37	2	89064631	CGCCGCG	2	88845746	R
	ATTACAT	37	7	123252579	TCGCACT	7	123039815	F
	CACACTA	37	11	124613956	CGGAGAC	11	124119166	R
	TCGGCCC	37	17	49021653	GCAGGAT	17	46376652	R
	GGTGGTT	37	7	80080213	CGACTGT	7	79918149	F
	AAATGTC	37	12	120930045	CGGTATA	12	119414428	R
	TACCTTT	37	8	10049871	CGCTCAC	8	10087281	R
Red	TTAGGAG	37	17	10204251	ATTTCTC	17	10144976	R
Red	TTTGGGG	37	4	132652001	TGAAGGC	4	132871451	R
	CGATGGC	37	20	43371550	GATAAAC	20	42804964	R
	TCGCGCC	37	7	100202882	GGACACA	7	100040818	F
	AGGAGTC	37	12	119591664	CGGGACT	12	118076047	R
	GAAGATC	37	4	154515617	CGGAATC	4	154735067	R
Red	CTCGGCC	37	X	37430775	CTTGGCT	X	37315694	F
Red	GAGGACC	37	3	138739916	TAGAGGC	3	140222606	R
	GCCGGAC	37	5	173191648	CTCTTGC	5	173124254	R
	CAGCTGT	37	11	46765391	CGCTGAC	11	46721967	F
	CGAGTCA	37	12	132970851	GGTGACT	12	131480924	F
	AACTGGA	37	4	119095240	CAGAGAA	4	119314688	F
	CCGTCAG	37	12	14926744	CGTTCAC	12	14818011	R
Red	TGAGGAC	37	5	179059668	CGCAGGC	5	178992274	F
	CACCACA	37	6	31747041	ACCTTTC	6	31855020	F
	AGGGCTA	37	8	126525558	GAGGAGA	8	126594740	R
Red	AAGACCT	37	1	29446085	CGGGGCC	1	29318672	R
	TCTTCCT	37	11	12309622	CGCACCA	11	12266198	F
	TCCTTCC	37	1	27881600	CGCCGTG	1	27754187	F
	GTGGCTT	37	6	6614447	AGGCAGT	6	6559446	F
	ACAAAAT	37	13	34371837	CGGTGGC	13	33269837	F
Grn	GGGCGGC	37	2	130986931	CGCCCCA	2	130703401	R
Red	AGCAGCC	37	7	158075624	CGGTGGT	7	157768385	F

	AAGCCTC	37	11	3534637	GGTGCTC	11	3491213	R
	AAATTGT	37	17	39072167	CGAGAAC	17	36325693	F
	ACTCAGG	37	4	114389632	TTCATTT	4	114609081	F
	AAATAAA	37	8	125274483	CGGAAAA	8	125343664	R
	GAGGGGT	37	2	153355619	CGGGAGC	2	153063865	F
	CAAGGCC	37	3	104078476	CGAAGTC	3	105561166	F
	CCATATG	37	4	103172826	CGCTTCT	4	103391849	F
	TATATAT	37	10	76983413	AGCCACC	10	76653419	F
	CTCGTGT	37	5	1222775	TATGTGT	5	1275775	F
	GAATTGG	37	10	766041	CGAGTAT	10	756041	F
	CACACCT	37	19	56154382	CGCCTCC	19	60846194	F
	AGGTTTA	37	18	57636670	CGGAATT	18	55787650	R
	CACGGAC	37	5	1075733	CGCCTGA	5	1128733	F
Red	GGCAGAC	37	1	2121039	ATCACAA	1	2110899	R
Red	GAAGACA	37	14	73392919	CGGCCCC	14	72462672	F
	AAGCCAA	37	7	11456440	TTACATA	7	11422965	R
	CTACAGA	37	6	27521330	CAGCATG	6	27629309	R
	AACCTTT	37	5	74303397	GTTTACA	5	74339153	F
	TTGGGAG	37	1	247511469	GCTGCAG	1	245578092	F
	CACTTGC	37	4	5960351	TGCTGAT	4	6011252	R
Red	CGCTGCC	37	19	58554479	GCTAACA	19	63246291	R
Red	TATTGCA	37	5	79378955	CGAAGCC	5	79414711	R
	CTCCCAT	37	17	74086286	CCTGGCC	17	71597881	F
	GGCCAGA	37	17	77923675	CGGCAAA	17	75538270	F
	CCCAGCC	37	6	30019655	ATACTAT	6	30127634	R
	GCCACTG	37	5	152502171	GCTTTCA	5	152482364	R
	AGTGGCT	37	3	151460366	CGGATTT	3	152943056	F
	TCCTAGT	37	6	5442953	CGACTTC	6	5387952	R
	CTGTGGC	37	X	13588301	CGCAGCC	X	13498222	R
Red	TGCTCCT	37	17	71024449	GTTAGAC	17	68536044	R
Red	ACGCTGG	37	14	24780540	TAGGGGC	14	23850380	F
	GATGCTC	37	6	101846967	CGCCAAC	6	101953688	R
	ACTGTGG	37	2	86248333	CTGAGGA	2	86101844	R
Red	GGGCGCC	37	X	53461386	CGGCCCG	X	53478111	R
Red	TGTGGAG	37	5	135416394	CGCCCGC	5	135444293	F
	CCTGCCC	37	6	112620506	CGGGGTT	6	112727199	F
	GTTTTAT	37	17	19807272	CGGTAAC	17	19747864	R
Grn	CTCAATC	37	X	18693413	CGCCCCC	X	18603334	F
	CAAGATA	37	14	23005866	CGGCTGT	14	22075706	R
	TGCTCCC	37	12	133013600	TGTGTTC	12	131523673	F
	ATAAGCT	37	1	14824776	CGACCTG	1	14697363	R
	CGTTAGA	37	1	149156606	GCTTGCT	1	147423230	R
	GGACAAC	37	11	10921186	CGGTGCC	11	10877762	R

	ACAAGTA	37	12	2445561	AAAATAC	12	2315822	F
Red	CCCCACG	37	X	30671338	AGCAAAC	X	30581259	F
Red	GGGCGGC	37	6	157041268	TCCTGGG	6	157082960	F
Red	TGGAGAA	37	6	111888446	CGCAGGC	6	111995139	R
	TCTTTTT	37	11	28642652	CGTGCCA	11	28599228	R
	GGCTCGG	37	7	155299687	AAGCTGT	7	154992448	F
	TTGTTTT	37	13	49323899	CGTTGTG	13	48221900	R
	CTAGAGC	37	14	21191859	CATACAG	14	20261699	F
Grn	AGAGCAA	37	4	7844952	CCGGCAC	4	7895852	F
	AGGTTGG	37	3	4783306	CGGAAGC	3	4758306	R
	GGGACAC	37	7	107700124	CGCTTCT	7	107487360	F
	GTCCTTG	37	4	33062845	AAGCTTG	4	32739240	R
	CGGAGAC	37	13	19919158	GCTCTGA	13	18817158	F
	GTGGATG	37	3	62665094	CGGGACT	3	62640134	R
	CTCCTCA	37	10	80076484	CGAGCTC	10	79746490	R
	CAAACAC	37	14	52482697	AAATGGT	14	51552447	R
	AGCCCCG	37	1	3561008	CGGGTCT	1	3550868	F
	GCCGGGT	37	22	46481785	CGGGGTC	22	44860449	R
	GTGTTGC	37	2	233734820	CGGGGCT	2	233443064	F
	ATTTACT	37	7	5186528	ATCCGGC	7	5153054	R
	CAAATAA	37	5	177882205	CGGGTTG	5	177814811	R
	GTCTCCC	37	1	221057573	CGGCACT	1	219124196	F
	AAAAGGC	37	8	61626625	TTCATTC	8	61789179	R
	ACAGCGC	37	4	2432313	GGTGAAA	4	2402111	R
	TCAGCGC	37	7	140263173	TACACAG	7	139909642	R
	TTGGGGC	37	7	47375903	CGCCCTG	7	47342428	F
Grn	GATTGCA	37	10	99912042	GGCCAAC	10	99902032	F
	ACAAGTC	37	6	47666248	AAGGCTT	6	47774207	F
Red	CCCTCCT	37	15	74494900	ACACACC	15	72281953	F
	TGGGTGT	37	19	50862121	CGGGTTC	19	55553933	F
	CCAGACC	37	7	95026121	GACAGGT	7	94864057	F
	AACTAAC	37	2	37962248	CGCTAGG	2	37815752	R
	TCATGCC	37	4	155662795	CGGCCAC	4	155882245	F
	TTCAGAT	37	10	91470135	CGCCACC	10	91460115	F
	CCCAAGA	37	2	175307665	CGGCCTT	2	175015911	F
	TGTCCTG	37	11	35611044	CCAGCCA	11	35567620	F
Red	GGGCTGC	37	16	1098847	CGTGCAG	16	1038848	R
	GAGGGAA	37	15	31846670	CGGGCCT	15	29633962	F
	CTTGCTG	37	2	240143798	CGCTGGC	2	239808735	R
Red	TCTCTGG	37	5	1594282	CGGGGGT	5	1647282	F
	CGGCGGC	37	5	140480941	CGACAAT	5	140461125	F
	CTGACTC	37	16	10723694	CAAAGGC	16	10631195	R
	GATTTGC	37	5	148832884	CAATGCC	5	148813077	R

	ACTCTCC	37	Y	24331358	CTTGCAA	Y	22740746	R
Red	TTTCCCC	37	19	2037662	GCCAGCT	19	1988662	F
	AACCAGC	37	17	6339466	GTGTAGG	17	6280190	F
	AATTTAA	37	6	90192032	CGGCCAT	6	90248751	R
	CTAGGGA	37	6	31382102	CGCAGCT	6	31490081	R
	AGGACCA	37	16	88990409	CGCTGTG	16	87517910	R
Grn	ACAAGCC	37	16	46603021	CGCACCT	16	45160522	F
Grn	GCTTCTG	37	13	113688268	TGGGGAC	13	112736269	R
	CCACTAT	37	4	141419962	CGGGACC	4	141639412	F
	CTGGGAC	37	6	30000200	CGGCAAC	6	30108179	F
Grn	CCCCCCC	37	10	42672589	GCCGCGC	10	41992595	F
	GCAGCAC	37	6	109871787	CGGGATC	6	109978480	F
	AGGGATC	37	4	40336255	ACTCATC	4	40031012	R
	AAAGAAC	37	6	26746687	CGCCCGA	6	26854666	F
Red	GAGTGGC	37	22	48730391	CGGCCCT	22	47109055	F
	TTTCAAC	37	5	142527658	CGCCTTT	5	142507851	F
	CAGTCCC	37	19	475587	CGGGGAC	19	426587	F
Grn	GGCGCGC	37	6	74072376	GACACCA	6	74129097	F
Red	CAGGGAA	37	5	180028767	CGGGGAC	5	179961373	F
	GGTGTCA	37	15	87197932	CGGTGAC	15	84998936	R
	ACCCCTC	37	6	116382179	CGGCTGC	6	116488872	R
	GGAAGTT	37	7	42278096	ATAAAGT	7	42244621	F
	CTCTGGT	37	6	31096127	TTCTTGG	6	31204106	R
	ACCCAAC	37	11	5384517	CGGTGAC	11	5341093	F
	TTCTCCT	37	11	131758433	CGGGATC	11	131263643	R
	GACTCTA	37	1	248756151	AGAGGAC	1	246822774	R
Grn	GACAGGA	37	6	30419576	ATGGAAC	6	30527555	F
	ACTACTG	37	10	126135176	CAAAGTA	10	126125166	R
Red	AGTAGGC	37	X	119443941	CCCGCAG	X	119327969	F
	CTAAAGT	37	16	23313240	CGCCCCC	16	23220741	R
	TCTTCCT	37	6	32548321	CGAGAGC	6	32656299	R
	CCCAAGT	37	16	2749429	CTGCCGC	16	2689430	R
Red	CGGTCAG	37	X	110653460	ACAGCGT	X	110540116	R
	GATGCCT	37	5	1298965	CCCTGCT	5	1351965	F
Grn	CTAGCAC	37	7	64403082	CCCGCCT	7	64040517	R
	GTCCGGT	37	1	9602701	CGCCAGC	1	9525288	R
Grn	CCGCTGC	37	8	1497078	AGTGCGA	8	1484485	F
	CATGATG	37	5	140213825	CTTTACC	5	140194009	R
Grn	AGGTTGA	37	12	115102726	ACTAAGC	12	113587109	R
	ACCTTCA	37	4	120726319	ATAAGAC	4	120945767	F
	CCTGGAG	37	19	18170383	CTGGGTT	19	18031383	R
Red	CTTGGCG	37	19	36485282	AGCCCTG	19	41177122	F
Grn	TGTGAGA	37	19	57276917	ACAAACA	19	61968729	F

	TGATGCC	37	10	3138505	GGGTGCA	10	3128505	R
	CCCGCAG	37	6	33048502	CGCTGTG	6	33156480	R
	TCACTCT	37	21	32927013	CGCAGGC	21	31848884	R
	AGGCCTG	37	16	88909028	ACCTGCC	16	87436529	R
Red	CAGTTTC	37	7	158533204	CGTGGCT	7	158225965	R
	CCAACAC	37	11	3225550	GTGCCTG	11	3182126	F
Grn	GGCGATC	37	19	2251588	CGAGCGC	19	2202588	R
Red	CACATGC	37	11	2919763	GTGCGGC	11	2876339	F
	TGTTTGT	37	11	65352232	AGCGTTT	11	65108808	R
	TTTGGCA	37	5	177209285	CCTCTGA	5	177141891	R
	ATATTTG	37	15	86133334	CGGGGTA	15	83934338	R
	CGGCAGA	37	11	1248959	GGCTGAC	11	1205535	R
Red	TTGTAAA	37	10	88023135	CTTGGAG	10	88013115	R
	TCATTCC	37	6	136915556	AAGGTCA	6	136957249	R
Red	CCTTGGG	37	7	140135365	CGCGCTG	7	139781834	F
	TCCCATC	37	19	33623091	GAGGGTC	19	38314931	F
	AAAACTC	37	5	5887642	CGGGTGC	5	5940642	R
	ATTCCCT	37	3	195384694	CGGGGCT	3	196869875	F
	ATGAGTC	37	18	13375474	CGCACTG	18	13365474	R
	CTTGGCC	37	13	111745598	GGTCGCT	13	110543599	R
Grn	CCAGGCT	37	6	43248039	CTATTTG	6	43356017	R
Grn	CCTCTTC	37	6	30419491	CGAGGCC	6	30527470	R
Red	TGGGTCC	37	17	40835920	GTTGGCA	17	38089446	F
Red	GGTGCGC	37	19	853334	CGCCGTG	19	804334	F
Red	GCAAAAC	37	17	80921188	CGCCCTT	17	78514477	F
	ATAGTCA	37	6	30039600	TGCCCAG	6	30147579	F
	GGCGGGA	37	X	12994598	TGCAAAA	X	12904519	F
	TTTTTTTC	37	6	33228461	CGTTGTT	6	33336439	F
Red	TCAGAAC	37	17	78997350	AGCGCCT	17	76611945	F
	CTGCGGC	37	6	29906977	CGGCTGG	6	30014956	R
Red	TGTCTCT	37	19	50249584	ACGGGGC	19	54941396	F
Grn	CACCCTG	37	20	43945364	CGGCCTT	20	43378778	F
Red	CACTTGG	37	11	888956	CGGCTGG	11	878956	F
	GTGAGCC	37	11	102191336	CGTAAAC	11	101696546	R
	TGTTTTG	37	3	46263244	GCCTTCA	3	46238248	R
	GGGCTGT	37	2	240143979	GAGGGAC	2	239808916	R
	ATAGATG	37	21	44110482	ACATTAT	21	42983551	F
	GATGGGT	37	16	819440	CGGGCCA	16	759441	R
	TCTGCAC	37	16	701656	CGGCCCC	16	641657	R
Red	ATCCTCA	37	5	150050950	TCGAGAA	5	150031143	R
	AGGGGGC	37	16	86593603	ATTGAGA	16	85151104	R
Red	CCCCCTT	37	20	25128777	TCTCACT	20	25076777	R
	CTCTGGC	37	2	102844110	TCAGAAA	2	102210542	F

Red	CGATCTG	37	X	153200109	GCGATTC	X	152853303	F
	AAGAGCC	37	11	56587595	CCATGGC	11	56344171	F
Red	CCCGCCC	37	4	7472958	TGTGTTC	4	7523858	F
	CTTTTCA	37	7	13985664	CGCAGAT	7	13952189	R
	TTTATTG	37	7	4228948	CGCCAAT	7	4195474	F
	AGTCAGA	37	16	47495768	CGCCGGC	16	46053269	R
Red	AATATCT	37	5	78281964	ACAGAGT	5	78317720	F
Red	GGACAAA	37	10	18549536	TGACGGT	10	18589542	R
	GGAACCC	37	16	2886233	CGTTCCC	16	2826234	F
Red	AGAGCCC	37	11	118781408	CGCCTCC	11	118286618	R
	CAGAGTC	37	13	111980537	GGCATCG	13	110778538	F
	AACTGCT	37	6	55956315	CATCCTT	6	56064274	R
	CTAATTA	37	6	19812885	CGCTGAA	6	19920864	F
	TTCATTA	37	5	40841493	CAAGCAA	5	40877250	F
	GTCCCAC	37	6	51953096	CGCCAGA	6	52061055	R
	GGTAAGT	37	22	27018010	ATTCAGG	22	25348010	F
	TTCCGGT	37	19	10231701	CGGTTGT	19	10092701	R
	CATGCTC	37	11	68842998	AGATGCT	11	68599574	R
	TCGGTCT	37	17	46622454	CCCTGTA	17	43977453	F
	TTCATGT	37	2	215887370	CGGATGA	2	215595615	F
	GGTGGGC	37	17	38440015	CGTCACT	17	35693541	F
	AGTTGCC	37	12	91729835	CGGTGTA	12	90253966	F
	CTACGAA	37	7	32526065	ACAGCAA	7	32492590	R
	TGTTATC	37	11	33760479	CCTTTTG	11	33717055	R
	CGGTAGT	37	3	125105935	CGCTGCT	3	126588625	R
	TGCAGGC	37	6	160023689	CGCACCA	6	159943679	F
Red	GGCTCAC	37	2	105853672	CGGCTCC	2	105220104	F
	TCTGCAT	37	15	92238013	CGGGGTT	15	90039017	F
	GAAAAAA	37	11	94782548	CACAGAC	11	94422196	F
	GTTTGGA	37	5	150677867	CGTCATT	5	150658060	R
	AGCTCTT	37	1	201852272	CCACCTA	1	200118895	R
Red	TCTGTGG	37	1	178456270	CGCGCGC	1	176722893	F
	CTGTCAT	37	10	19002068	CGTGGCT	10	19042074	F
Red	TGCCCCA	37	4	132896405	CGAGAAA	4	133115855	R
	CTTCTGC	37	Y	22682393	CGTAATA	Y	21091781	R
Red	ACGAGGC	37	5	138714136	CGGGGTT	5	138742035	R
	ACACCTC	37	16	71458897	ACGTGGA	16	70016398	R
	TCGGGGA	37	14	92410260	CGCACCC	14	91480013	F
	CTTCTCC	37	17	19314395	CAGAATC	17	19254988	F
	ACCTGTT	37	13	27825886	CGCTGCT	13	26723886	R
	TATCATC	37	12	76023400	CGGGGAC	12	74309667	R
Red	CCGGCTG	37	16	88598739	CGGTGCC	16	87126240	F
	AAATAGC	37	6	13408158	CGGAGAT	6	13516137	F

	ATTAAAA	37	12	109214864	AAAGCAT	12	107738993	F
	GGAAACT	37	15	34144832	CGCCATT	15	31932124	F
Grn	GACACCA	37	19	56612697	GCTTGGG	19	61304509	R
	TAAAAGA	37	17	7015607	GGGCTGC	17	6956331	F
	TACCGGC	37	X	21393407	AGGGGA	X	21303328	F
	AGTTTT	37	6	28447087	TCAGGGC	6	28555066	R
	ATTTGGA	37	11	111815419	CGGCCAC	11	111320629	F
	TGGGAAC	37	5	126409454	CGGACTC	5	126437353	R
Red	CTCTCCT	37	7	140267040	CGGCTGA	7	139913509	R
	CAGATCT	37	6	90714949	CGGAAGT	6	90771670	F
	CTCGTTT	37	17	76676673	CGGAGAC	17	74188268	F
	ATTGTCA	37	14	56991775	CGCCATT	14	56061528	R
Grn	CTGCCCG	37	8	48677407	CGGAGCT	8	48839960	R
	TTTTTAG	37	15	62767926	CCTTAAT	15	60555218	F
Grn	CTTCCGC	37	5	140568535	GCGGGTA	5	140548719	F
	ATAGTAC	37	2	145226929	CGAAGGC	2	144943399	R
	GGAGGTC	37	10	131560029	CGCCGAC	10	131450019	R
Red	TCGAGGC	37	8	142231004	GTGGGCT	8	142300186	F
	AGACCTC	37	19	1950427	CGCGCCT	19	1901427	F
	ATTAGAC	37	17	13972210	GGTGGAA	17	13912935	R
	ATCCCCA	37	12	119591747	CGCACCA	12	118076130	F
	CTAAAGT	37	6	31607674	CGGGATT	6	31715653	F
	AGCAGCC	37	16	8943122	CACTTTA	16	8850623	F
	AATGTGT	37	15	90796557	TGGGTAC	15	88597561	F
Red	GTCTTGA	37	6	144643175	CGGGCGT	6	144684868	F
Red	GTGAGTG	37	16	51393415	AGCTCCT	16	49950916	F
	TGGACCT	37	17	80848259	CGGGAAC	17	78441548	R
	TTTTTACT	37	15	61327619	CGGCAGC	15	59114911	F
	TGTCCTT	37	16	57836960	CGCTCCA	16	56394461	F
Red	CCTCCCC	37	7	96652115	TCAAGGA	7	96490051	R
	CAATCCT	37	14	70321227	CGGGTTC	14	69390980	F
	GATCAAT	37	11	124439146	CGGGGCA	11	123944356	R
Red	TGCGCAA	37	Y	21906893	CGAAGGA	Y	20366281	F
	AGCTTTC	37	6	24832728	CGCATGA	6	24940707	R
Red	GGTCCCT	37	13	100548780	GGGCTTC	13	99346781	F
	TCTTCAT	37	X	19361727	AGTGTAC	X	19271648	R
	CTGCAGC	37	16	67009163	CGCATCT	16	65566664	F
Grn	GAGTTCC	37	5	140531474	GGGTACA	5	140511658	F
	TAAAGAA	37	7	30810504	TTTCCCG	7	30777029	F
Red	AAAGCGC	37	7	39649443	TGCTGCA	7	39615968	F
	AAAATCC	37	4	3640481	CGTCTTT	4	3610279	R
Red	ATTAAGA	37	6	101847318	CGGCTGC	6	101954039	R
	GGGATGC	37	2	37684473	CTTTTCC	2	37537977	F

	CTTGTAG	37	19	17953473	GGGCCGC	19	17814473	F
	ATAAAAT	37	11	4389638	ACATTCT	11	4346214	R
	CCAGGTT	37	14	32350428	GAGCACT	14	31420179	R
Red	CGGGGGC	37	5	140182129	TTCACTG	5	140162313	R
Grn	GGAAATC	37	6	33386103	CGGCTCT	6	33494081	R
Red	GCGTCAT	37	3	11610239	CGCCTCC	3	11585239	F
	AAGATGA	37	7	6836436	TGGAAGC	7	6802961	R
	CCACGGC	37	19	468830	CGCAGTG	19	419830	F
	GGATCAC	37	13	114872606	CGTACCC	13	113890708	F
	TTAACCT	37	7	154720213	AAAAGTC	7	154351146	R
	CTTATTT	37	3	11178798	CGGCAGC	3	11153798	F
Red	GGCGGAC	37	5	126409153	CGCCGCC	5	126437052	F
	GTAAGGA	37	12	122129167	CGAGTGC	12	120613550	R
	TTCTGTC	37	6	32547167	CCTTATC	6	32655145	R
	AAGATGA	37	18	76629213	CGGCTGT	18	74730201	F
Red	GGGGCAC	37	16	89147812	TGGTCAG	16	87675313	R
Red	CAGAGGA	37	22	37921640	CGCCAGC	22	36251586	R
Grn	TTTGAAC	37	21	40759574	CGCAGCC	21	39681444	R
	AACTTGA	37	7	15555129	CGGGAAT	7	15521654	R
	GGCCCAT	37	12	31149418	CGCATAG	12	31040685	F
	CTCTCCT	37	8	1365049	ATTTGTT	8	1352456	R
	GGCAGCT	37	7	9767724	CGGCTGA	7	9734249	F
Red	TGAGGGT	37	16	2892782	CGCACAC	16	2832783	R
Red	GCCGCAC	37	11	842605	CGGCTCC	11	832605	F
Red	GGGCTCT	37	4	102712216	CGCCCTG	4	102931239	R
	AAAATGA	37	10	50231850	CGGAGTG	10	49901856	F
	CAGAGCT	37	3	140786844	CGAGTGC	3	142269534	R
	CAACCAT	37	11	67795659	TCAGAGC	11	67552235	F
	CTTTGGC	37	2	215362367	CGGAAAT	2	215070612	R
Grn	CTCGGGG	37	17	41477350	ACAAACA	17	38832876	F
	AGCCCGC	37	5	1594330	GGCTGGC	5	1647330	F
	GAGCCCG	37	17	74868725	CTCATGC	17	72380320	R
	GTCACGG	37	17	78472016	CGCCTGC	17	76086611	F
Grn	AGCATTA	37	16	49620536	CCCTGGC	16	48178037	F
Red	TCACTAC	37	13	20139028	GCGGCGA	13	19037028	F
	CCCAGCC	37	17	19277143	CATGGAC	17	19217736	F
Red	GCCCTGT	37	19	292210	GGCACCC	19	243210	R
	TAACTCT	37	7	158578750	CGTACTC	7	158271511	R
	TCGGCAA	37	22	49498376	CTCAACC	22	47884380	F
Red	AGCCAGC	37	X	11683995	CGCCGCT	X	11593916	R
Red	TACAACA	37	4	1203001	CGGCTGG	4	1193001	F
	AGACAAC	37	2	11515031	AATGGCC	2	11432482	R
	AGGTTCT	37	1	184121585	CGGGGCT	1	182388208	R

	CTGTCAT	37	12	54371246	ATGGTAG	12	52657513	R
Grn	ACATCAC	37	22	22987126	CGCGGGT	22	21317126	R
	AGCTGCT	37	1	1226776	GATGCTG	1	1216639	F
Red	GGCAAGA	37	15	74249189	CGGATGC	15	72036242	F
	GTCTATA	37	1	233636022	CGCCAAA	1	231702645	F
	AGTGATC	37	11	46732376	GTGCTGG	11	46688952	F
	GTTTACC	37	7	94034528	CGGGTTT	7	93872464	R
	TAAGAAA	37	17	48067475	GAGGTGC	17	45422474	F
	CAGAGAC	37	17	79816678	CGACAGC	17	77409967	F
	TGGGAAC	37	4	7763703	GTCACGG	4	7814603	R
	TCAGCCT	37	16	89258862	CACTGGT	16	87786363	R
Grn	GCGCGGC	37	10	135343280	TTGTGAT	10	135193270	F
	GGCCCCT	37	17	70680294	CGGATAA	17	68191889	R
Red	GAGCTCC	37	6	27447492	CACGTCA	6	27555471	R
Grn	GCGGGGC	37	20	43935291	GTGGTGG	20	43368705	R
	CAGTGTT	37	2	127772338	ACCTCTG	2	127488808	F
	GAAGAGC	37	6	29706048	CCACTAG	6	29814027	R
	CCCATCC	37	11	45628269	CGAGGCA	11	45584845	F
	AAGTCAC	37	4	82057467	CTGAACC	4	82276491	R
Red	AGTTCCG	37	21	47716529	AGCAGTT	21	46540957	F
Red	GGGAGGC	37	2	87018054	GCGGGGC	2	86871565	F
	TACCCAG	37	X	118892422	TGGAGCT	X	118776450	R
Red	AAAAGGT	37	4	8155589	AGACGGA	4	8206489	R
Red	GCGTCCG	37	X	15353768	CGTCCGA	X	15263689	F
	GAGGGCC	37	X	67913388	CGCCAGA	X	67830113	R
	CCCAGGC	37	19	43709360	CGTGCAC	19	48401200	R
	GCTCTTT	37	6	31275767	CGACAAC	6	31383746	R
	GCTGTGG	37	11	1891872	CGGCACC	11	1848448	R
	GGTGTAG	37	11	2171007	CTTAGAG	11	2127583	R
Grn	GCTTAGC	37	1	1992046	CGGCGTG	1	1981906	F
	GTAACTG	37	16	51475605	CGAGCAC	16	50033106	F
	GCCAGAC	37	3	38664451	TGTGCAG	3	38639455	F
	ACAAGTT	37	7	81481504	CACAGCT	7	81319440	R
	CACATCA	37	2	20793466	ATACACA	2	20656947	F
	CCGGGGT	37	19	52302551	CCCAGGT	19	56994363	F
	CGGCGGC	37	4	1044797	CAGTGCT	4	1034797	F
	GTGTCAG	37	19	22193479	CCTCCAT	19	21985319	R
	ACTATAT	37	1	47488934	CGGCAGC	1	47261521	F
	TGGGATC	37	1	39853529	TATTCTT	1	39626116	F
	TCTTCAG	37	6	30980847	GTGATCC	6	31088826	R
	GCATGAC	37	2	207042563	CGGTTAT	2	206750808	F
	ATTGGGA	37	14	53878048	GGCCAGC	14	52947798	F
Grn	GGTGGTC	37	11	49914049	AGAACTC	11	49870625	F

Grn	GGGATGC	37	21	37442289	AGAGACT	21	36364159	F
	AAAGAG	37	10	105357975	CGGGCTG	10	105347965	R
Red	GGGAAA	37	X	64196642	CGCTCCC	X	64113367	F
	ACTCGCA	37	5	140625750	GGGGATC	5	140605934	R
	GATTTTA	37	19	6746538	TTGCCCC	19	6697538	R
	GACAGGC	37	9	130516695	GCCTCTC	9	129556516	F
Red	AGATGAA	37	15	96887867	TGGCGCG	15	94688871	R
	GACTCTC	37	5	180033511	CGCTCAG	5	179966117	F
Red	GGTTTTC	37	6	30079256	CGCTATT	6	30187235	R
Red	GAAATAC	37	19	52134296	TTCCTTG	19	56826108	R
Red	GGAGGAC	37	X	100914892	ACGACGC	X	100801548	R
	CAAACTT	37	17	56273748	TGCTGTG	17	53628747	F
	GGGGAAC	37	Y	6778543	CGCCTCC	Y	6838543	R
Red	GGCCCCC	37	17	5019638	CGGGGCT	17	4960362	F
	CTGTAGT	37	6	32492198	CGTGAGT	6	32600176	R
Grn	TTCTAGT	37	6	30038929	ACGAGAC	6	30146908	R
	AAAAAA	37	5	123036376	CAAGCAC	5	123064275	F
Red	TTGGCCT	37	17	56565286	CGCCGCG	17	53920285	R
Red	GCCGAGC	37	5	2169769	CGCCCTC	5	2222769	F
	GGCTCCA	37	10	103406305	CGCCTTG	10	103396295	R
Red	CCGGTTT	37	15	101715819	CGAGCTC	15	99533342	F
	TATTCCG	37	5	1594863	GTGTTGG	5	1647863	R
Grn	TAAGCCA	37	22	22987059	TTATTAA	22	21317059	F
	AGTGACC	37	2	232055581	TTCGTTA	2	231763825	R
Red	AAACATT	37	1	1672644	CGTGTTT	1	1662504	R
	GCAGCCG	37	19	50400714	GATCCTA	19	55092526	F
Red	TTCCTCC	37	2	127839539	GTCCTCT	2	127556009	F
	AAAATCC	37	6	29575566	GTCCTTC	6	29683545	R
Red	GCCGCCA	37	6	2958808	CGCTGGG	6	2903807	R
	TTGGGAA	37	10	11387394	ATGATAT	10	11427400	F
Grn	ATGCGCT	37	6	29648564	GCTCAGA	6	29756543	R
	GAAGTGT	37	3	32748004	CTTGTGG	3	32723008	R
	TTAATAA	37	7	1715242	GATACAA	7	1681768	R
Red	CAGTCCG	37	13	23270850	GCGGTGA	13	22168850	R
Red	GAAACTG	37	7	148638192	CGGGATT	7	148269125	F
	TAGGCGA	37	1	1687481	TGGGGCC	1	1677341	F
	GGGGGAC	37	19	19650978	TGAGACA	19	19511978	R
	TTCCTGA	37	2	178197762	CGTTGGT	2	177906008	F
	GTGCTGA	37	7	128731386	AGCTTGA	7	128518622	F
	TGAATCA	37	Y	16634795	CGGCGAT	Y	15144189	F
	TGCAGGA	37	8	143645661	CGCAGCA	8	143642663	F
	TTGCAAC	37	6	101846650	CGGCCAC	6	101953371	R
	CCACTCT	37	1	85686316	CAGGCTT	1	85458904	R

Red	ATGGGGA	37	16	88361648	CGGCGAC	16	86919149	F
	GTTTCCT	37	10	32428473	CGCCTTG	10	32468479	R
	TTTGCTG	37	20	39135472	TGGGGTC	20	38568886	R
	GGCTGAC	37	8	22266134	GCTGCTC	8	22322079	R
Red	CCTGGGT	37	7	965995	GAGGTGC	7	932521	F
Red	CAAGACC	37	10	99338074	GGACCTG	10	99328064	R
	CAGGGGC	37	7	155623690	GCTTCGG	7	155316451	F
Red	GCAGAAC	37	18	77126192	CGGTCAC	18	75227180	R
Grn	CGGAGGC	37	2	26951130	ACATGGA	2	26804634	F
	TGACCTC	37	19	48374536	GCATCTC	19	53066348	F
Red	CGGTGCC	37	16	87022483	CGGCGGT	16	85579984	R
	GAAGATT	37	2	151061125	GTGAAGA	2	150769371	F
Grn	AGCCCCT	37	12	9555721	GTCCCAA	12	9446988	F
	AAAAGCA	37	6	160024002	CGCGGGC	6	159943992	R
	GCATTTT	37	7	94039079	GTCCTCT	7	93877015	F
	TCAAAGT	37	18	14427976	CGTCCAA	18	14417976	R
	TACCTAG	37	Y	21877683	CGTCCCC	Y	20337071	F
Grn	TGGGTCC	37	15	23035493	TGGGGGC	15	20586934	R
	ATGTGCG	37	3	131068941	CGGCTTC	3	132551631	R
	AAACAGA	37	16	90095949	CGTCACA	16	88623450	R
Grn	CCCGGCC	37	20	61447330	CGCCCGG	20	60917775	F
	TTTGTGT	37	3	38346525	CGGCAAC	3	38321529	R
Grn	TGATGAG	37	19	43711249	AGGGAGC	19	48403089	R
Red	GGGCTCG	37	12	57780104	GCGGGAC	12	56066371	R
	TGAAAAC	37	1	235099089	CGGGTTC	1	233165712	R
	AAGAGAT	37	X	48124969	AGAGCTC	X	48009913	R
	AAATTTC	37	1	2885085	GGACCAC	1	2874945	F
	GCTTGCG	37	1	1571801	TGTTGTA	1	1561664	R
Red	CCACTGT	37	15	75248086	CGCAACA	15	73035139	F
	GGTCTAG	37	1	247802703	CCCGAAC	1	245869326	R
	TCTGCAT	37	10	129685902	CGGCTTT	10	129575892	F
	ATAGCTC	37	15	24673917	GACACAA	15	22225010	F
	AAGAGGA	37	17	76858248	CGAGTCG	17	74369843	R
Grn	CCTCGCA	37	12	9722091	CGGCTGG	12	9613358	F
Red	GTTCCAG	37	2	97136508	CGGTCCC	2	96500235	F
	GGGTAAT	37	3	127256188	CGCCTGG	3	128738878	R
	TATTGCT	37	1	78602941	ATTAAGA	1	78375529	F
Grn	CGCGGGT	37	6	30419551	AACCCGA	6	30527530	F
	CAGGGGT	37	17	203392	CTCCACA	17	203392	F
Red	GCTGCTG	37	5	140712441	CGCCTCC	5	140692625	R
	CCGAGGA	37	1	16472728	AATCCGG	1	16345315	R
Red	TTGACGT	37	2	200320750	CGCCGCT	2	200028995	F
	ATTAGAG	37	2	15498900	AACCAAC	2	15416351	R

	ATTTCTT	37	6	161459571	CTGCAAC	6	161379561	R
	GGGTTCT	37	2	102759782	CGTAGCC	2	102126214	R
	ACGATAC	37	22	31498863	GCTGGAA	22	29828863	R
	TGACAAC	37	12	133177383	GGGGCTC	12	131687456	F
Red	TTTTCCA	37	5	140569144	TCTGGTG	5	140549328	R
	AGACCAC	37	3	189901160	CGCTGAA	3	191383854	F
	CCCCACT	37	11	60608634	GTGAGCA	11	60365210	F
	TTCAACA	37	13	113105794	CGGCTCT	13	112153795	R
Grn	CCGCTCT	37	17	73056755	GCCAGGT	17	70568350	R
	GTTGGCA	37	15	81666528	CGGGCAC	15	79453583	R
	CTAATAA	37	2	169920014	CGAGTAC	2	169628260	F
Grn	CGCTGCA	37	6	117802710	CGCGCTG	6	117909403	R
	CGGGGTC	37	22	46460338	AGAGATC	22	44839002	F
	TGTGCAG	37	19	10928172	TGTACAC	19	10789172	R
Red	AAAGGG	37	12	95840848	CGGCCCT	12	94364979	R
Grn	GGGAGCT	37	12	115173713	GGTTGAT	12	113658096	R
	CCTAGAT	37	17	1053794	GTTGCCT	17	1000544	F
	AGTGTAG	36	22	49888838	ACTGACT	22	48274842	F
Red								
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PROBE_SN	PROBE_SN	RANDOM_	METHYL2	UCSC_REF	UCSC_REF	UCSC_REF	UCSC_CP	RELATION
				AGAP1;AC	NM_01491	Body;Body	chr2:23702	N_Shore
				IL1RAPL2	NM_01741	TSS200	chrX:10381	N_Shore
rs78011553	rs74038932							
	rs5024308			SNTG2	NM_01896	Body	chr2:11630	S_Shore
	rs59476302			PIGQ;PIG	NM_14892	Body;Body	chr16:6294	N_Shore
							chr6:31650	Island
rs8192525				HTR1D	NM_00086	TSS200		
rs35314525								
rs79733927	rs60223258			CLEC16A	NM_01522	Body		
							chr12:5408	S_Shore
rs75093195	rs9925461			NAT15;NA	NM_00108	5'UTR;5'U	chr16:3507	S_Shelf
				TOP1MT	NM_05296	Body	chr8:14439	Island
				CROT;CR	NM_02115	Body;Body		
							chr6:16953	Island
				GALP;GA	NM_00114	5'UTR;5'UTR		
	rs79738529			PRKCE	NM_00540	Body		
	rs75239392						chr2:24283	S_Shelf
				PCSK9	NM_17493	TSS1500	chr1:55505	N_Shore
				LOC73227	NR_02440	Body		
							chr2:23708	N_Shore
				TRPC3;TR	NM_00330	1stExon;Bo	chr4:12285	Island
rs3760027				ALG1	NM_01910	TSS1500	chr16:5121	N_Shore
				C1orf57	NM_03232	Body	chr1:23308	S_Shelf
rs28421229								
				ATP1A4;A	NM_14469	1stExon;5'UTR		
rs2182924							chr13:1129	N_Shore
				CDH20	NM_03189	Body	chr18:5922	N_Shelf
	rs3751568			CYFIP1;C	NM_01460	Body;Body		
	rs75038007			MRPL28	NM_00642	Body	chr16:4198	Island
			TRUE	MPZ	NM_00053	TSS1500	chr1:16128	N_Shelf
				ASCC1	NM_01594	Body		
rs12518292				DPYSL3	NM_00138	Body		
				GLIPR1L2	NM_15243	TSS200	chr12:7578	Island
							chr16:1069	Island

			BCORL2	NR_00292	Body	chrY:21664	N_Shore
		TRUE					
			TNXB	NM_01910	Body		
	rs1160317		RWDD3;R	NM_00112	Body;Body	chr1:95699	S_Shelf
	rs1467834		C1orf94;C1	NM_00113	Body;5'UTI	chr1:34642	S_Shelf
			MIR886	NR_03058	TSS200	chr5:13541	Island
	rs55999058		THSD4	NM_02481	Body		
			DST;DST;I	NM_00114	Body;TSS200;Body;TSS200;TSS20		
			SPSB1	NM_02510	5'UTR		
	rs72193420					chr8:12456	Island
rs9493599	rs11753937		EYA4;EYA	NM_17210	Body;Body;Body		
	rs33913065		PFN4	NM_19934	Body	chr2:24345	N_Shore
rs2424830						chr20:2955	Island
			PKD1L2;PI	NM_05289	TSS1500;TSS1500		
			C3orf24;C3	NM_00116	TSS200;TS	chr3:10149	Island
	rs2085323					chr3:11771	S_Shelf
rs11589175	rs35026651		MEGF6	NM_00140	Body	chr1:34474	N_Shore
			ITGB5	NM_00221	Body		
			SSBP3;SSE	NM_00100	Body;Body	chr1:54821	Island
			EP300	NM_00142	Body	chr22:4148	S_Shelf
			MFAP4	NM_00240	TSS1500		
			ATP11A;A	NM_01520	Body;Body	chr13:1134	N_Shore
	rs72616127					chr4:66656	N_Shore
			EBF1	NM_02400	Body		
rs67999531	rs9269968		HLA-DRB	NM_00212	Body	chr6:32551	Island
			TTTY14	NR_00154	TSS200	chrY:21238	Island
			AIFM1;AIF	NM_14581	TSS1500;T	chrX:12929	Island
			DDX11;DD	NM_00439	Body;Body;Body		
			KIAA1949;	NM_00113	Body;1stEx	chr6:30654	N_Shelf
rs11541079	rs6746		LOC33879	NR_00280	Body	chr12:1222	N_Shore
			LOC10029	NR_02841	TSS1500		
	rs36101953		C10orf46	NM_15381	TSS1500	chr10:1205	S_Shore
			ABR;ABR;	NM_02196	Body;Body	chr17:9262	S_Shelf
			KIAA0319	NM_02487	5'UTR	chr1:36022	N_Shore
	rs73426852		CYFIP1	NM_01460	5'UTR		
						chr8:13412	N_Shore

			LOC73178	NR_02679	TSS200		
			TMSB4X;T	NM_02110	TSS200;TS	chrX:12993	Island
rs17325066	rs77812985		RPL32P3;S	NR_003111	Body;TSS1500		
rs11651991	rs66505868		TBC1D16	NM_01902	Body	chr17:7792	Island
	rs2234570		WHSC2	NM_00566	Body	chr4:19874	N_Shore
			CTSK	NM_00039	5'UTR		
	rs6507921		RPL17;SN	NM_00098	Body;TSS1	chr18:4701	N_Shelf
						chr12:1263	Island
			WDR33;W	NM_00100	TSS1500;T	chr2:12856	S_Shore
			ESRRG	NM_00113	5'UTR	chr1:21730	N_Shore
			NXN	NM_02246	Body		
rs57102073	rs10046752		CSMD1	NM_03322	Body		
			PCDHB16	NM_02095	1stExon	chr5:14056	N_Shore
						chrY:14649	S_Shore
	rs4818734		UBE2G2;U	NM_18268	5'UTR;Bod	chr21:4622	N_Shore
						chr16:2830	N_Shelf
	rs12446637					chr16:8823	S_Shore
			KRTAP2-4	NM_03318	TSS1500		
						chr2:23185	Island
	rs35405169		GATA5	NM_08047	Body	chr20:6104	N_Shore
						chr8:13145	N_Shore
			EIF2C2;EI	NM_01215	Body;Body	chr8:14155	N_Shelf
						chr11:6738	Island
		TRUE	LGALS1	NM_00230	TSS1500	chr22:3807	N_Shore
rs72806131			ANK3	NM_02098	Body		
			MYOM2	NM_00397	Body		
						chr9:90621	N_Shore
			NAPSA	NM_00485	3'UTR	chr19:5086	Island
						chr1:16158	S_Shore
rs72360220	rs76383292					chr4:19022	Island
						chr1:24780	S_Shore
			CDRT4	NM_17362	3'UTR		
			CYP2E1	NM_00077	Body	chr10:1353	Island
rs61432632							
			SELL;SEL	NM_00065	Body;Body		
			KIF13B	NM_01525	Body		

			ACTN2	NM_00110	Body		
rs3846891	rs58350918						
			DCHS2;DC	NM_01763	Body;Body	chr4:15525	Island
rs1467013						chr1:83777	Island
			BTBD9;BT	NM_00109	Body;Body;Body		
			TBX3;TBX	NM_00599	Body;Body	chr12:1151	Island
rs7408083	rs7408082		NFATC1;N	NM_00616	Body;Body	chr18:7723	Island
						chr9:13545	N_Shore
			ARHGEF1	NM_01478	Body;Body		
rs17159355			SLC43A3;S	NM_19932	TSS1500;T	chr11:5719	S_Shore
			ASPDH;AS	NM_00111	TSS200;Bo	chr19:5102	N_Shelf
			NOTCH4	NM_00455	Body		
			ZSCAN18;	NM_00114	Body;5'UT	chr19:5860	N_Shore
			HPCAL1;H	NM_00214	5'UTR;5'UTR		
			TAGLN3;T	NM_00100	Body;Body;Body		
						chr15:2472	Island
						chr16:3057	Island
						chr3:13974	Island
rs2571420	rs74218766		HLA-A	NM_00211	TSS1500	chr6:29910	N_Shore
			NUDT17	NM_00101	TSS200	chr1:14558	Island
		TRUE	AGA	NM_00002	TSS1500	chr4:17836	S_Shore
			NXPH1	NM_15274	Body	chr7:84731	S_Shore
rs33685			FAM134B;	NM_01900	TSS1500;Body		
			HLA-DPA1	NM_03355	Body		
rs61023017						chr7:14013	Island
rs77215738							
	rs41307264		ARMCX1	NM_01660	5'UTR	chrX:10080	Island
		TRUE	STC1	NM_00315	TSS200		
						chr1:28470	Island
	rs76859177		TRIM24;T	NM_00385	Body;Body		
rs2385400			RESP18	NM_00100	Body	chr2:22019	S_Shore
			HLA-DRB	NM_00212	Body	chr6:32489	S_Shelf
						chr8:59990	N_Shore
						chr10:4934	Island
						chr2:17693	Island
			ROR1;ROR	NM_00501	Body;Body		
	rs12752760						
			SBNO2;SB	NM_00110	Body;Body	chr19:1118	Island
			CYTH1;CY	NM_01745	Body;Body		
			AEBP2;AE	NM_15320	Body;Body		

rs922217			PRX;PRX	NM_02095	Body;Body	chr19:4090	Island
			NCRNA00	NR_00154	Body		
rs17505733			SH3D19;S	NM_00112	TSS200;5'UTR;5'UTR		
						chr19:4153	Island
			GTF2A1L;	NM_17219	TSS200;Bo	chr2:48844	Island
			CRCP;CRC	NM_00104	Body;Body;Body;Body;Body		
			MED12L	NM_05300	Body		
			OTOF;OTC	NM_00480	TSS1500;TSS1500;TSS1500;Body		
			MAB21L1;	NM_00558	1stExon;Bo	chr13:3604	Island
	rs6934989		TMEM63B	NM_01842	Body	chr6:44119	N_Shore
			RLTPR	NM_00101	Body	chr16:6768	Island
			PIK3CG;PI	NM_00264	5'UTR;1stE	chr7:10650	N_Shelf
			NRN1L	NM_19844	1stExon	chr16:6791	Island
		TRUE					
	rs28662301		BANP;BA	NM_01786	Body;Body		
rs74740134							
			TMEM165	NM_01847	Body		
	rs8060043		ACSF3;AC	NM_17491	Body;Body	chr16:8916	Island
			VEGFA;VE	NM_00117	TSS1500;T	chr6:43737	N_Shore
rs11145847	rs3739939		FAM69B	NM_15242	Body	chr9:13961	N_Shore
						chr5:17084	N_Shore
rs17841362							
			SPATS2	NM_02307	5'UTR	chr12:4976	S_Shelf
			LOC28569	NR_02711	Body		
						chr1:20940	Island
	rs35980577		GALNT2	NM_00448	Body		
			DNHD1	NM_14466	Body	chr11:6591	N_Shore
	rs73700237		NCALD	NM_00104	TSS1500	chr8:10313	S_Shore
			RAB1A;RA	NM_00416	Body;Body	chr2:65356	N_Shore
			SRPK2;SR	NM_18269	Body;Body	chr7:10488	N_Shelf
			PLD6	NM_17883	TSS200	chr17:1710	N_Shore
rs78475669							
			LOC10010	NR_00358	Body;Body		
						chr10:1299	Island
						chr6:15671	N_Shore
			PMM1	NM_00267	Body	chr22:4198	N_Shore

	rs9796214					chr13:1147	N_Shelf
						chr8:72917	N_Shore
rs7682744			COPS4	NM_01612	TSS1500		
			ASPSCR1	NM_02408	Body	chr17:7996	N_Shore
						chr5:74907	S_Shore
	rs7571693		FMNL2	NM_05290	Body		
	rs7204640		TEKT5	NM_14467	Body		
			AKR1B15	NM_00108	TSS200		
						chr19:5083	Island
			CCHCR1;C	NM_00110	Body;Body	chr6:31125	N_Shore
rs994379							
	rs6863024		ADAMTS2	NM_01424	Body	chr5:17855	N_Shore
			PLXNC1	NM_00576	Body		
			LOC64259	NM_00114	Body	chr18:5196	N_Shelf
			WFDC6	NM_08082	TSS1500		
rs72653146	rs72653147		COL1A1	NM_00008	Body		
			FANCI;FA	NM_00111	TSS1500;T	chr15:8978	N_Shore
			CPNE2	NM_15272	Body		
			TACSTD2	NM_00235	1stExon	chr1:59042	Island
						chr13:1006	S_Shore
	rs79274715		STK32C	NM_17357	Body		
						chrY:17567	Island
						chr17:7895	S_Shelf
						chr18:7607	N_Shore
	rs7768524						
						chr1:11328	N_Shore
			AKR1E2	NM_00104	TSS200	chr10:4868	Island
	rs894418		PRRX2	NM_01630	Body	chr9:13245	N_Shore
						chr7:17840	S_Shore
rs11124201						chr2:23988	S_Shore
			WHSC1;W	NM_13333	Body;Body;3'UTR;Body;Body;Bod		
						chr7:31003	Island
						chr8:23380	N_Shore
	rs55719509	TRUE	LASS3	NM_17884	5'UTR	chr15:1010	Island
			TUBB4Q	NM_02004	TSS200	chr4:19090	Island
	rs12483886		MPPED1	NM_00104	5'UTR	chr22:4380	S_Shelf

		ACCN1;AC	NM_00109	3'UTR;3'UTR		
	rs80312210	NUBP1	NM_00248	Body		
	rs9601330					
	rs76507469	ANO6;AN	NM_00114	Body;Body;Body;Body		
		RXRA	NM_00295	Body	chr9:13729	N_Shore
		PTPRN2;P	NM_00284	Body;Body;Body		
	rs76188937	CBFA2T3;	NM_17593	5'UTR;Bod	chr16:8899	N_Shelf
		ITGAM;IT	NM_00114	3'UTR;3'U	chr16:3134	S_Shore
		ERRFI1	NM_01894	5'UTR	chr1:80855	N_Shore
		TAS2R7	NM_02391	1stExon		
		ESX1	NM_15344	Body	chrX:10349	N_Shore
	rs3215400	CDA;CDA	NM_00178	1stExon;5'UTR		
		OR2L13;O	NM_17591	1stExon;5'U	chr1:24810	Island
	rs3094136	TRIM31	NM_00702	Body	chr6:30071	S_Shore
					chr6:15936	Island
		TRPM8	NM_02408	Body	chr2:23484	Island
		OR2T3	NM_00100	TSS1500		
		PRKCB;PR	NM_00273	Body;Body		
rs61986373	rs61986372					
	rs10131376	SLC25A21	NM_03063	Body;Body		
rs74361853		SPON1	NM_00610	Body	chr11:1398	Island
rs35176217		OR2T11	NM_00100	TSS1500		
rs35732565	rs35629555	KCNAB2;	NM_00363	TSS1500;T	chr1:60862	N_Shore
rs77207688		AGBL4	NM_03278	Body	chr1:49364	Island
		CXorf22	NM_15263	TSS200		
		THBS1	NM_00324	Body	chr15:3987	S_Shelf
	rs71390811					
	rs79295829				chr1:14655	Island
rs10100209		SOX7	NM_03143	Body	chr8:10583	Island
	rs78980985	KCNK2;K	NM_00101	1stExon;5'UTR		
		SYTL1	NM_03287	Body	chr1:27675	Island
					chr18:7672	Island
		TRPM8	NM_02408	Body	chr2:23484	Island
	rs13308736	PTPRN2;P	NM_00284	Body;Body	chr7:15824	N_Shore
rs74631495	rs12143527	CR1L	NM_17571	Body		
					chr11:6738	Island
	rs72629157	ZNF835	NM_00100	Body	chr19:5718	N_Shelf
	rs7954579					
					chr16:3348	S_Shore
		HSF5;HSF	NM_00108	5'UTR;1stE	chr17:5656	Island

	rs11665759				chr19:3803	Island
		VMAC	NM_00101	Body	chr19:5903	S_Shelf
		C14orf166	NM_01603	Body		
	rs59490038	SCN1A;SC	NM_00116	TSS1500;TSS1500;TSS1500		
					chr14:1052	Island
rs7533656		HRNR	NM_00100	TSS200		
		PPP1R2P1	NR_027771	Body	chr6:32847	Island
	rs55784104	GRB2;GR	NM_00208	Body;Body		
		TRIP12	NM_00423	Body		
					chr7:27208	N_Shore
rs73911131						
		FOXO4;FO	NM_00593	3'UTR;3'UTR		
		STK40	NM_03201	TSS1500	chr1:36851	S_Shore
					chr18:1194	Island
rs79421768		LOC14869	NR_02681	TSS1500		
		LHCGR	NM_00023	Body		
rs2669153		CUBN	NM_00108	Body		
					chr22:2045	S_Shelf
rs34779657		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		SUMO3	NM_00693	Body	chr21:4623	Island
		ADAMTS1	NM_00698	Body	chr21:2821	N_Shore
		SLC2A14	NM_15344	TSS1500	chr12:8025	Island
rs940453		ZNF775	NM_17368	Body	chr7:15009	Island
		C4orf31	NM_02457	5'UTR	chr4:12199	N_Shore
		CAPZB	NM_00493	Body	chr1:19811	N_Shore
		ARMCX5;	NM_00116	5'UTR;TSS	chrX:10185	Island
rs35682610	rs56280220	HSPA1B	NM_00534	1stExon	chr6:31795	S_Shore
		PRDM7;PR	NM_05299	3'UTR;3'UTR		
		CBFA2T3;	NM_17593	5'UTR;Bod	chr16:8899	N_Shelf
					chr1:16141	N_Shore
rs9282000	rs9272416	HLA-DQA	NM_00212	TSS200		
rs31852		PCDHB2	NM_01893	1stExon	chr5:14047	Island
					chrX:39680	Island
		SHF	NM_13835	TSS200	chr15:4549	S_Shelf
					chr1:21731	S_Shelf
	rs56142053	ATXN1;AT	NM_00112	5'UTR;5'UTR		
		VWA5B2	NM_13834	Body	chr3:18394	S_Shelf
		MATN2;M	NM_03058	Body;Body		
		UBE2H;U	NM_00334	Body;Body		

		MARK3;M	NM_00112	Body;Body;Body;Body;Body		
rs1063349		HLA-DQB	NM_00212	3'UTR		
		ARHGAP2	NM_01507	Body;Body		
	rs7543016	CMPK1;CM	NM_00113	1stExon;1st	chr1:47799	Island
					chr12:6613	S_Shelf
		ZNF254	NM_20328	Body		
					chr4:36711	N_Shore
		PRKAG2;P	NM_01620	Body;Body		
					chr3:13245	Island
		TMPRSS8	NR_02686	TSS200	chr16:2892	Island
		RPS10P7	NR_02666	TSS1500		
					chr1:40598	N_Shore
		SLC14A1;S	NM_01586	5'UTR;5'UTR;TSS1500;5'UTR		
rs12025174		PKP1;PKP	NM_00029	Body;Body		
	rs79977228				chr1:24531	N_Shelf
		DIP2C	NM_01497	Body		
	rs2491259	HLX	NM_02195	Body	chr1:22105	N_Shore
		BAIAP3	NM_00393	Body	chr16:1393	Island
rs16872792						
		SDHAP1	NR_00326	Body		
rs34884782		PCDHA6;P	NM_03184	Body;Body	chr5:14022	N_Shore
		GTF3C1	NM_00152	Body		
		PCDHA6;P	NM_03184	Body;Body	chr5:14024	Island
		CCDC57	NM_19808	5'UTR	chr17:8017	N_Shore
	rs10934303	GAP43;GA	NM_00204	Body;5'UT	chr3:11537	N_Shore
					chr6:16425	Island
					chr1:17215	Island
		GLIS1	NM_14719	5'UTR		
		WBP2NL	NM_15261	1stExon	chr22:4239	Island
		BTBD19	NM_00113	3'UTR	chr1:45278	S_Shore
rs35743243	rs35479904	FAM120B	NM_03244	Body	chr6:17068	Island
					chrY:94781	Island
		CHP2	NM_02209	TSS1500	chr16:2376	N_Shore
		RASAL3	NM_02290	Body	chr19:1556	Island
		HSD17B7;I	NM_01637	5'UTR;1stE	chr1:16276	Island
		IRX6	NM_02433	Body	chr16:5536	Island
		XYLT1	NM_02216	Body		
		EIF2AK4	NM_00101	Body	chr15:4026	Island
		PALLD;PA	NM_01608	Body;Body		

		PHF1;PHF1	NR_027692	TSS1500;T	chr6:33377	Island
		PCDHB16	NM_02095	1stExon	chr5:14056	Island
					chr2:44314	N_Shore
	rs2412045					
		ZFX;ZFX	NM_00341	5'UTR;1stE	chrX:24167	S_Shore
	rs79939347	SGCZ	NM_13916	Body	chr8:15094	N_Shore
		RFPL2;RFI	NM_00109	TSS200;5'UTR;TSS1500		
		LMX1B	NM_00231	Body	chr9:12937	Island
		CASP7;CA	NM_03333	Body;Body;Body;Body		
	rs2533872	GNA12	NM_00735	Body	chr7:28834	N_Shore
	rs57272256	MSLN;MIF	NM_00582	3'UTR;TSS1500;3'UTR		
		BICD1;BIC	NM_00171	Body;Body		
		MIR2117	NR_031751	TSS1500		
		PNLIPRP2	NM_00539	Body	chr10:1183	Island
		ODZ3	NM_00108	Body		
		ZDHHC14;	NM_15374	Body;Body		
	rs2297428	GMEB2	NM_01238	Body	chr20:6222	Island
	rs229545				chr22:3759	N_Shore
rs80278387					chr7:56855	Island
rs12895946					chr14:1011	Island
		LOC10013	NR_033182	Body	chr4:11881	N_Shore
					chr11:8564	Island
		PSORS1C1	NM_01406	5'UTR		
					chrX:12925	Island
		BRF1;BRF	NM_00151	Body;Body		
		PCDHB7	NM_01894	1stExon	chr5:14055	N_Shore
					chr2:19551	N_Shore
		RBPMS2	NM_19427	3'UTR		
					chr2:24161	Island
		PRSS21;PR	NM_14495	Body;Body	chr16:2867	Island
	rs2223709				chr20:1187	N_Shore
		PCDHB16	NM_02095	1stExon	chr5:14056	N_Shore
		SRRM4	NM_19428	Body	chr12:1195	Island
	rs75580812					
		MUC5B	NM_00245	Body	chr11:1262	Island

rs3735106	rs3735105	C7orf27	NM_15274	Body	chr7:25832	N_Shore
rs2159234		LRRC61;A	NM_02394	1stExon;5'U	chr7:15001	Island
		PCDHB9	NM_01911	1stExon	chr5:14056	N_Shore
rs10475117					chr5:18567	Island
	rs6461991	HOXA9	NM_15273	TSS1500	chr7:27203	Island
					chr7:56242	Island
		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
					chr8:14593	Island
		SUPT7L;SI	NM_01486	TSS1500;1s	chr2:27886	Island
	rs73340969	HELZ	NM_01487	3'UTR		
rs11677287						
					chr3:18424	N_Shore
rs35670997		MYOM2	NM_00397	Body	chr8:20754	Island
		LHX2	NM_00478	TSS1500	chr9:12677	N_Shore
	rs72280493	RAD52	NM_13442	Body		
					chr1:28850	Island
					chr7:25898	S_Shore
		STAG2;ST	NM_00104	1stExon;TS	chrX:12309	S_Shore
		SEPT9;SE	NM_00111	Body;Body;Body;Body;Body		
		ESR1;ESR	NM_00112	5'UTR;TSS	chr6:15212	N_Shelf
rs12610907	rs1968241	ETFB	NM_00198	Body	chr19:5186	N_Shelf
		KIAA0513	NM_01473	3'UTR		
	rs2423084	SLC23A2;S	NM_20332	5'UTR;TSS1500		
rs2835668		DSCR9	NR_02671	TSS1500		
		HLA-DRB	NM_00212	Body	chr6:32489	N_Shore
	rs300537	RADIL	NM_01805	Body		
					chr7:15726	N_Shore
		ITPR2	NM_00222	Body		
		ETS2	NM_00523	TSS1500	chr21:4017	N_Shore
		PCDHA7;P	NM_01891	Body;Body	chr5:14024	N_Shore
					chr2:33824	S_Shelf
		TNRC6B;T	NM_00102	Body;TSS1500;TSS1500		
		TRPM4	NM_01763	Body	chr19:4969	Island
rs34993694	rs2303639	ADAMTS2	NM_01424	Body	chr5:17856	N_Shore
	rs2233631	SPDEF	NM_01239	TSS1500		

							chr2:13649	N_Shelf
			TRUE	FAM83H	NM_19848	Body	chr8:14480	Island
				RORA	NM_13426	Body		
rs2065724								
				TMEM49	NM_03093	Body		
	rs77985030			COL6A3;C	NM_05716	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR		
				MYO1B;M	NM_00113	Body;Body;Body		
				PLD6	NM_17883	1stExon	chr17:1710	Island
rs2213944				KIAA1949;	NM_00113	Body;1stEx	chr6:30654	N_Shore
				PRDM16;P	NM_02211	Body;Body	chr1:30809	Island
				HOXD4	NM_01462	Body	chr2:17701	Island
				PCDHA6;P	NM_03184	Body;Body	chr5:14023	Island
				CCDC62;C	NM_20143	Body;Body;Body		
							chr2:17693	Island
				ELF1;ELF1	NM_17237	5'UTR;1stExon		
				RASSF5;R	NM_18266	Body;TSS1	chr1:20673	N_Shore
				WDR60	NM_01805	Body		
rs12948785				CAMKK1;	NM_17220	Body;Body	chr17:3771	Island
		TRUE					chr3:13350	Island
							chr16:7309	N_Shore
				CCDC36;C	NM_00113	TSS200;5'U	chr3:49236	Island
				CYP24A1;	NM_00112	Body;Body	chr20:5278	N_Shelf
							chrY:14649	N_Shore
				CPLX2;CP	NM_00100	5'UTR;5'U	chr5:17529	Island
	rs2358390			SP3;SP3	NM_00311	Body;Body	chr2:17482	N_Shore
rs6610361	rs76720014			LANCL3;L	NM_19851	TSS200;TS	chrX:37430	N_Shore
	rs75367100			FAT1	NM_00524	Body		
				ZNF714	NM_18251	TSS200	chr19:2126	N_Shore
							chr19:5427	S_Shelf
							chr8:72917	Island
	rs45452892			ABCA3	NM_00108	Body	chr16:2334	Island
	rs60004847			FOXO1	NM_00201	Body		
							chr6:29894	Island
rs404607	rs2517742						chr6:29894	S_Shelf
							chr8:14307	Island
	rs2517764						chr6:29894	Island
							chr16:8641	Island
				TSPY4	NM_00116	Body	chrY:92342	Island
				CREB5	NM_18289	5'UTR	chr7:28448	N_Shore

	rs74924576	C14orf149	NM_14458	Body	chr14:5995	N_Shelf
	rs75603638					
		FAM180A	NM_20585	TSS200		
rs79857560	rs75890562					
rs3768224		DDAH1;DI	NM_00113	Body;Body		
		FAM193B;	NM_01905	Body;Body	chr5:17695	Island
rs9992037	rs13105517	TLR2	NM_00326	5'UTR		
		EHD2	NM_01460	3'UTR	chr19:4824	N_Shore
rs74410832						
					chr19:5251	S_Shelf
		PCDHGA2	NM_01891	Body;1stEx	chr5:14072	Island
		NUP210	NM_02492	Body		
	rs78775756	CACNA2D	NM_01839	Body		
		MIR1304;S	NR_03163	TSS200;TSS1500;TSS1500;TSS150		
	rs10097189	MAK16	NM_03250	TSS1500	chr8:33342	Island
					chrX:25020	N_Shore
					chr22:3205	N_Shore
rs62039242					chr16:3373	S_Shelf
		WDR27	NM_18255	3'UTR		
	rs78552162				chr2:88251	S_Shelf
		ACTR3C	NM_00116	5'UTR	chr7:15001	N_Shore
		FAM83H	NM_19848	Body	chr8:14480	Island
	rs78181720	AFAP1;AF	NM_00113	3'UTR;3'UTR;Body		
					chr12:1151	N_Shore
		PXDN	NM_01229	Body		
		HS3ST3A1	NM_00604	Body		
		CARKD	NM_01821	Body	chr13:1112	S_Shelf
rs75506928		OXSM;OX	NR_02693	Body;Body;Body		
		FAHD1;FA	NM_00114	Body;Body	chr16:1876	S_Shelf
		THBS1	NM_00324	Body	chr15:3987	S_Shelf
		LOC10013	NR_02456	TSS200;TS	chr4:12029	N_Shore
	rs34438310	USP10	NM_00515	Body		
		THADA;TI	NM_02206	Body;Body		
		ARPC1A	NM_00640	Body		
		DPPA5	NM_00102	TSS200	chr6:74063	Island
	rs9391807	HLA-L	NR_02782	Body	chr6:30227	Island
		RNH1;RNI	NM_20338	Body;Body	chr11:4948	S_Shelf
rs2817054					chr6:35733	Island

	rs1043060		FAM102A;	NM_20330	3'UTR;3'U	chr9:13070	N_Shore
			DCHS2;DC	NM_01763	Body;Body	chr4:15525	Island
						chr7:10809	S_Shelf
						chr17:8025	N_Shelf
			TSSC1	NM_00331	Body	chr2:33176	N_Shore
	rs11074139		RGMA;RG	NM_02021	Body;5'UT	chr15:9363	N_Shore
			GMDS	NM_00150	Body		
						chr16:1501	Island
rs35955010			ANAPC10;	NM_01488	5'UTR;TSS	chr4:14601	N_Shore
			GRIK2;GR	NM_00116	Body;Body	chr6:10184	S_Shore
			PPP1R2P9	NR_002191	TSS1500	chrX:42637	S_Shore
	rs58867145					chr16:2507	N_Shelf
rs6519497			GSTT1;GS	NM_00085	5'UTR;1stE	chr22:2438	Island
	rs58481121		ANKFN1	NM_15322	Body		
rs73907520			WISP2	NM_00388	TSS1500		
						chr8:43131	Island
rs2599251	rs55793262					chr2:91634	Island
rs11785793						chr8:13651	S_Shore
	rs12439297		SLCO3A1;	NM_00114	Body;Body	chr15:9245	S_Shore
rs12906774			SNRPN;SN	NM_02280	5'UTR;5'U	chr15:2512	Island
		TRUE	CPA4;CPA	NM_00116	1stExon;1stExon;5'UTR;5'UTR		
			OTOA;OT	NM_17066	Body;Body;Body		
	rs7153897		FLJ31306;	NR_02943	Body;Body	chr14:5876	N_Shelf
			HLA-DPA1	NM_03355	Body		
rs67418040			HLA-DRB	NR_00129	Body		
rs74589225			GMDS	NM_00150	Body		
						chr4:48664	N_Shore
			FBN1	NM_00013	Body		
			C6orf127	NM_00101	Body	chr6:35754	Island
	rs10259248					chr7:10146	S_Shelf
			KRTAP5-1	NM_00101	1stExon		
	rs1944694						
	rs7740081		KHDC1	NM_03056	TSS1500	chr6:73972	S_Shore
			KIAA1529	NM_02089	Body	chr9:10006	Island

			DYSFIP1	NM_00100	TSS200	chr17:7979	S_Shore
			ZCCHC14	NM_01514	Body		
rs77153132							
rs9365910							
rs76745887			SNX29	NM_00108	Body		
	rs4809352					chr20:6243	Island
			PCDHB3	NM_01893	1stExon	chr5:14048	N_Shore
			VCX3B	NM_00100	Body		
rs209140						chr6:28863	Island
			DKFZp686	NR_002801	TSS1500		
			SGCZ	NM_13916	Body	chr8:15094	N_Shore
			PON1	NM_00044	TSS200	chr7:94953	S_Shore
			CSF1R	NM_00521	TSS200		
			GPR75;LO	NM_00679	5'UTR;1stE	chr2:54086	Island
		TRUE	CDH13	NM_00125	TSS1500	chr16:8266	N_Shore
			KLHL21	NM_01485	Body	chr1:66617	N_Shore
rs34777947						chr7:10522	Island
	rs7460592					chr8:98368	N_Shelf
	rs34756202		OTUB2	NM_02311	TSS1500	chr14:9449	N_Shore
rs76469054			H1F0	NM_00531	1stExon	chr22:3820	N_Shore
			ERRFI1	NM_01894	5'UTR	chr1:80855	N_Shore
			USP7	NM_00347	Body		
			LITAF;LIT	NM_00113	5'UTR;5'UTR;Body;5'UTR		
			C1orf86;LC	NM_00114	Body;Body	chr1:21210	Island
						chr16:8831	N_Shelf
rs4649016							
			DCAF12L1	NM_17847	TSS200	chrX:12568	S_Shore
			ABLIM3	NM_01494	Body		
			ADORA3	NM_00108	TSS1500		
	rs35650130		SLC45A4	NM_00108	TSS1500	chr8:14223	S_Shelf
rs17844388			PCDHB3	NM_01893	1stExon	chr5:14048	N_Shore
			PRR23A	NM_00113	TSS200	chr3:13872	Island
			C1orf86;LC	NM_00114	Body;Body	chr1:21210	Island
			KLHL17	NM_19831	Body	chr1:89431	Island

			PPIE;PPIE;	NM_20345	TSS1500;T	chr1:40204	N_Shore
	rs76327981		TNFAIP6	NM_00711	TSS200		
	rs77675604		RPL19P12;	NR_02666	TSS1500;5'UTR;5'UTR		
rs5743496			BPI	NM_00172	TSS200		
	rs6940682						
			AKAP13;A	NM_14476	Body;Body;Body		
		TRUE	DEFB125	NM_15332	1stExon		
			TRIM31	NM_00702	Body		
rs12668093			PCLO	NM_03302	Body		
			DLG2;DLC	NM_00114	Body;Body		
			EPS15	NM_00198	TSS1500	chr1:51984	S_Shore
			TBL1X;TB	NM_00113	5'UTR;5'U	chrX:94328	N_Shore
			EPS8	NM_00444	5'UTR		
			SIM1	NM_00506	Body	chr6:10089	N_Shore
rs12947905	rs2256987		ABR;ABR;	NM_02196	Body;Body	chr17:9755	N_Shore
			RHAG	NM_00032	TSS1500		
			HLA-DPB1	NM_00212	Body		
						chr19:4658	S_Shore
			NHSL2;RG	NM_00101	Body;TSS2	chrX:71350	Island
			TRPM4	NM_01763	Body	chr19:4968	S_Shelf
			EXPH5;EX	NM_00114	Body;Body;TSS200		
	rs11354		GNA12	NM_00735	3'UTR		
			GRIK2;GR	NM_00116	Body;Body	chr6:10184	S_Shore
			TNPO2;TN	NM_00113	5'UTR;5'U	chr19:1283	Island
			RPS4Y2	NM_00103	TSS200		
			DIAPH2;D	NM_00672	Body;Body	chrX:95939	S_Shore
						chr9:10379	N_Shore
			PITPNC1;P	NM_18167	Body;Body		
rs34242076			MDM1	NM_01744	Body		
			CCNH	NM_00123	Body	chr5:86708	N_Shore
rs72732970	rs75575681		MAPK6	NM_00274	5'UTR		
rs35509575			PRR23B	NM_00101	TSS200	chr3:13873	Island
			TMEM40	NM_01830	5'UTR		
	rs12731347		PADI4	NM_01238	Body		
			SLC7A3;SI	NM_03280	TSS200;TS	chrX:70150	S_Shore
rs9891975						chr17:2068	Island
			GCNT3;GC	NM_00475	1stExon;5'UTR		
			LOC10018	NR_024467	Body;Body	chr10:9316	S_Shelf

			SNX27	NM_03091	Body		
rs6686649							
			NNMT	NM_00616	TSS1500		
	rs7187759						
						chr4:12920	S_Shelf
rs73494349			RAB11FIP	NM_01470	TSS1500	chr16:4749	N_Shore
			NFIL3	NM_00538	5'UTR	chr9:94183	N_Shore
rs61613048			MYO1B;M	NM_00113	Body;Body;Body		
						chr21:4700	Island
	rs41279230		ACSBG1	NM_01516	Body		
	rs7131580						
			C1orf172	NM_15236	5'UTR	chr1:27286	N_Shore
	rs74875985						
	rs78629934		CMYA5	NM_15361	Body		
			MYST4	NM_01233	Body		
			FAM198B;	NM_00103	Body;Body;Body		
	rs17884389		SFTPA2	NM_00109	TSS1500		
			MICAL2	NM_01463	3'UTR		
			OPRD1	NM_00091	Body	chr1:29189	Island
rs78207116							
	rs9278239						
						chr17:7945	S_Shelf
			PHKA2	NM_00029	TSS1500	chrX:19002	Island
						chr5:58870	Island
						chr2:17297	N_Shore
						chr6:31650	Island
			MRPS18B	NM_01404	Body	chr6:30584	S_Shelf
						chr10:4384	Island
						chr17:3738	S_Shelf
			NCRNA00	NR_026751	Body		
rs71330028						chr21:1543	N_Shore
	rs2506015		RET;RET	NM_02063	Body;Body	chr10:4357	S_Shelf
		TRUE	RDH5;RD	NM_00290	1stExon;5'	chr12:5610	S_Shelf
	rs67410356		ACSM3;A	NM_00562	5'UTR;5'UTR		
rs71384648	rs12930897		TPSG1	NM_01246	TSS1500		
rs1024576							
rs76309452			C21orf81	NR_02727	TSS200	chr21:1535	S_Shore
	rs2270194		VENTX	NM_01446	Body	chr10:1350	S_Shore

			NCRNA00	NR_02679	TSS1500		
rs5987137		TRUE	BCAP31;B	NR_02445	Body;TSS1	chrX:15298	Island
			ZMYM3;Z	NM_00117	5'UTR;TSS	chrX:70473	S_Shore
			FAM171A1	NM_00101	Body		
rs56057807	rs77541628		STAG1	NM_00586	Body		
		TRUE	PTPN20B;	NM_00104	TSS200;TS	chr10:4882	Island
			CELSR3	NM_00140	Body	chr3:48693	Island
			BCL11B;B	NM_02289	Body;Body	chr14:9964	Island
			CAMK2G;	NM_17217	Body;Body;Body;Body;Body		
			TNFAIP8L	NM_20738	Body	chr15:5138	S_Shelf
			XIRP1	NM_19429	TSS1500		
			KIAA0922;	NM_01519	TSS1500;T	chr4:15438	N_Shore
						chr10:5243	Island
			PANX1	NM_01536	Body		
			LOC44160	NR_00303	Body	chr11:5025	Island
	rs1163860						
			MDGA1	NM_15348	Body	chr6:37616	Island
			NMT2	NM_00480	TSS1500	chr10:1520	S_Shore
	rs76244168					chr11:1346	S_Shelf
			RAI2;RAI2	NM_02178	5'UTR;1stE	chrX:17879	Island
		TRUE	ZNF254;Z	NM_20328	1stExon;5'UTR		
			SLC6A18	NM_18263	3'UTR	chr5:12459	Island
			MYO10	NM_01233	Body		
	rs62054659					chr16:9014	N_Shore
	rs78333027						
			SLC12A7	NM_00659	Body	chr5:10546	N_Shore
						chr1:11455	N_Shore
rs10108815	rs10108808					chr8:11372	S_Shore
			CACNB4;C	NM_00100	Body;Body;Body;Body		
rs12149359	rs56278207		CES1;CES	NM_00126	Body;Body	chr16:5586	Island
			FLJ44606;	NM_00116	TSS200;TS	chr5:12640	Island
						chr6:31650	Island
			RXFP3	NM_01656	1stExon	chr5:33936	Island
	rs2056481		MAD1L1;M	NM_00355	Body;Body;Body		
	rs72806843		PCDHGA1	NM_01891	1stExon;1st	chr5:14071	N_Shore
rs74515554	rs77770048						
			FTH1	NM_00203	Body	chr11:6173	N_Shelf
			MYO1C;M	NM_03337	5'UTR;Bod	chr17:1390	N_Shore

	rs35104720	SAMD7	NM_18261	Body		
		GPC6	NM_00570	Body		
rs77093485		PCDHA6;P	NM_03184	Body;Body	chr5:14022	N_Shore
		CLMN	NM_02473	Body		
					chr2:66802	N_Shore
		NLGN4Y;	NR_02831	Body;Body	chrY:16941	S_Shelf
					chr7:39649	N_Shelf
		NLRP11;N	NM_14500	TSS1500;5'UTR		
		BICC1	NM_00108	Body		
		RBMY2EP	NR_00157	Body		
	rs10248822	GIMAP1	NM_13075	TSS1500		
		PTPRN2;P	NM_00284	Body;Body	chr7:15805	N_Shore
		DOCK2	NM_00494	Body		
rs73376840	rs877430					
		CES1;CES	NM_00126	Body;Body	chr16:5586	Island
rs77028978	rs9349666					
		C6orf89	NM_15273	Body		
	rs475947	OR4N4	NM_00100	1stExon		
					chr6:31650	Island
		MIR2117	NR_031751	TSS1500		
		OXCT1	NM_00043	Body	chr5:41869	Island
		CHST5	NM_02453	Body	chr16:7556	Island
rs77153281		PLEKHG7	NM_00100	Body		
		ULBP2	NM_02521	Body	chr6:15026	S_Shelf
		HS3ST3A1	NM_00604	Body	chr17:1350	N_Shore
		ACAN;AC	NM_01322	5'UTR;5'UTR		
					chr10:1348	N_Shore
					chrY:93854	N_Shore
rs3836745		PCDHB6	NM_01893	1stExon	chr5:14053	N_Shore
		PRR25	NM_00101	Body	chr16:8573	Island
		RUNX1	NM_00175	Body		
		GLIPR1L2	NM_15243	TSS200	chr12:7578	Island
		SLC44A2;	NM_00114	Body;Body	chr19:1074	Island
		GRAMD3;	NM_00114	Body;Body;Body;Body;Body		
		LOC10013	NR_02733	TSS1500;TSS1500		
		BRD2;BRD	NM_00111	Body;Body	chr6:32939	S_Shore
	rs1552364					

			BTNL2	NM_01960	Body		
			FRMD5	NM_03289	Body		
			RYR1;RYR	NM_00054	Body;Body	chr19:3905	Island
			RYR1;RYR	NM_00054	Body;Body	chr19:3905	Island
			HLX	NM_02195	Body	chr1:22105	N_Shore
			PYCR2	NM_01332	Body	chr1:22611	N_Shore
			RORA	NM_13426	Body		
			ADAMTS5	NM_00703	TSS1500	chr21:2833	S_Shore
			STOML1	NM_00480	3'UTR		
	rs76631426		ZC3H12D	NM_20736	TSS200		
	rs7018270		DEFA3;DE	NM_00521	TSS1500;TSS1500;TSS1500		
			GTF2A1L;	NM_17219	TSS200;Bo	chr2:48844	Island
			SLC39A14;	NM_00112	5'UTR;5'UTR;5'UTR;5'UTR		
			NUAK1	NM_01484	Body		
						chr5:21367	N_Shore
rs79683292						chr8:13651	Island
rs3834611	rs1135519		MIR122	NR_029667	TSS1500		
rs4760673	rs76081873		TMEM106	NM_00114	TSS1500;T	chr12:4835	N_Shore
			ACMSD	NM_13832	TSS1500		
			PDE4D;PD	NM_00116	Body;Body		
			SOS1	NM_00563	Body		
			PTPRN2;P	NM_00284	Body;Body	chr7:15734	S_Shore
	rs74759139	TRUE	C20orf177;	NM_02210	1stExon;5'U	chr20:5851	Island
		TRUE	HPD	NM_00215	TSS1500		
			CLEC1A;C	NM_01651	5'UTR;1stExon		
			OR5H15	NM_00100	1stExon		
			MIR21	NR_029493	TSS200		
	rs3741704					chr12:5220	N_Shore
						chr1:24780	Island
			HAR1B;HA	NR_003245	Body;TSS1	chr20:6173	N_Shore
			TTTY10	NR_001542	Body		
rs4468809	rs4359646		C2orf54	NM_00108	1stExon		
		TRUE	BTG3;BTG	NM_00113	5'UTR;5'U	chr21:1898	Island
	rs4750963						
rs72884175	rs72799821						
rs7559444	rs7559434						
						chr6:17033	Island

			SNTB2	NM_00675	Body		
			SLC12A4;S	NM_00114	3'UTR;3'UTR;3'UTR;3'UTR;3'UTR		
						chr4:30430	Island
			RASGEF1	NM_17506	5'UTR	chr5:17958	Island
			C1orf187	NM_19854	5'UTR		
						chr2:23185	Island
						chr12:1326	N_Shore
			FLJ42289;	NR_02814	TSS1500;T	chr15:1008	S_Shore
			MUM1L1	NM_15242	5'UTR		
			GREB1	NM_01466	TSS200		
			KCNK12	NM_02205	Body		
rs12220734							
			GRM3	NM_00084	5'UTR		
			AP2A2	NM_01230	Body	chr11:9752	S_Shore
						chrX:39547	Island
rs2278269							
			NSUN5;NS	NM_01804	TSS1500;T	chr7:72722	S_Shore
			FNBP1L;F	NM_00102	TSS200;TS	chr1:93913	N_Shore
rs75096987			RAB21	NM_01499	Body	chr12:7214	S_Shore
						chr10:1245	Island
			AFAP1;AF	NM_19859	Body;Body		
						chr1:22769	N_Shore
			CD99L2;C	NM_13444	TSS200;TS	chrX:15006	Island
	rs75105531		FBXO31;F	NR_02456	Body;Body	chr16:8736	N_Shore
			KLHL24	NM_01764	Body		
			ELF1;ELF1	NM_17237	5'UTR;1stExon		
			SLCO3A1;	NM_00114	Body;Body		
			KCNIP1;K	NM_00103	Body;Body;Body		
			CDKAL1	NM_01777	Body		
			VEZT	NM_01759	Body		
rs7200011			CES4	NR_00327	Body	chr16:5579	Island
			BRD2;BRD	NM_00111	5'UTR;1stE	chr6:32939	N_Shore
			N4BP3	NM_01511	Body		
			ZCCHC14	NM_01514	Body		
		TRUE	TMTC2	NM_15258	Body		
			EVPL	NM_00198	3'UTR	chr17:7400	N_Shore

rs35123101							
		TRUE	PPAP2C;PI	NM_17752	TSS1500;T	chr19:2905	Island
	rs73208690		ALG1L2	NM_00113	TSS1500		
rs736138			RGR;RGR;	NM_00101	Body;Body;Body		
			DIP2C	NM_01497	Body	chr10:6690	S_Shelf
			PTN	NM_00282	5'UTR		
			KAL1	NM_00021	Body	chrX:86988	N_Shore
	rs35800443		MYO5C	NM_01872	Body		
			C1orf14	NM_03093	Body	chr1:18292	Island
			FDFT1	NM_00446	Body	chr8:11665	N_Shore
			EIF2AK4	NM_00101	Body	chr15:4026	N_Shore
						chr4:19095	Island
	rs28631219					chr2:24298	N_Shore
			NLRC3	NM_17884	Body	chr16:3613	Island
rs11822294		TRUE	SLC22A18	NM_00710	1stExon;Bo	chr11:2923	S_Shore
			PCDHGA4	NM_01891	Body;1stEx	chr5:14076	N_Shore
			HIRA;MRF	NM_00332	TSS1500;B	chr22:1941	Island
			KCNMA1;I	NM_00116	Body;Body;Body;Body		
	rs10750667						
rs8054657							
			HLA-DRB	NM_00212	Body	chr6:32489	Island
			NAV2;NA	NM_18296	Body;Body;Body;Body		
	rs3214699		TMEM163	NM_03092	3'UTR		
			HLX	NM_02195	Body	chr1:22105	N_Shore
			PDE11A	NM_00107	5'UTR		
	rs7573831						
rs74822384						chr1:15216	Island
						chr10:9944	S_Shelf
rs4887023	rs4886565						
			CELSR3	NM_00140	1stExon	chr3:48698	Island
			MAG;MAC	NM_00236	Body;Body	chr19:3580	N_Shore
						chr11:6862	S_Shore
			PNOC;PNC	NM_00622	5'UTR;1stExon		
			DTNA;DT	NM_00112	5'UTR;TSS1500;5'UTR;5'UTR;5'U		
	rs9272544		HLA-DQA	NM_00212	Body		
	rs77086859		UBE2E2	NM_15265	TSS1500	chr3:23244	N_Shore
			CHD7	NM_01778	5'UTR	chr8:61626	N_Shore
			TSPY4;FA	NM_00116	TSS1500;T	chrY:92154	N_Shore

	rs1556329		COL18A1;	NM_13044	Body;Body	chr21:4691	Island
			ECEL1P2	NR_028501	TSS200	chr2:23325	Island
	rs34190657						
			PDE11A;PI	NM_00107	Body;Body		
	rs78469864						
			CDK2;CDK	NM_00179	3'UTR;3'U	chr12:5636	N_Shore
rs72653142			COL1A1	NM_00008	Body		
			FLJ22536	NR_01541	Body		
	rs4303160					chr10:1347	Island
			AJAP1;AJA	NM_01883	Body;Body	chr1:47716	Island
						chrX:11913	N_Shore
rs13281473						chr8:72917	Island
			PLD1;PLD	NM_00113	5'UTR;5'UTR		
			SMYD3;SM	NM_02274	Body;Body		
			GPR64;GPI	NM_00575	5'UTR;5'U	chrX:19139	Island
			C20orf94	NM_00100	Body		
			SPACA1	NM_03096	TSS1500	chr6:88757	Island
			PLK5P	NR_02655	Body	chr19:1525	Island
						chr4:18606	N_Shelf
			VPS13B;V	NM_01789	Body;Body		
			MICA	NM_00024	3'UTR		
	rs12610801	TRUE					
			HSPB7;HS	NM_01442	1stExon;5'UTR		
			GNAS;GN	NM_08042	TSS1500;T	chr20:5742	N_Shore
			PVT1	NR_00336	Body		
	rs62023627						
			NCAN	NM_00438	5'UTR	chr19:1932	S_Shore
rs9272467	rs9272466		HLA-DQA	NM_00212	Body		
			TNFRSF21	NM_01445	Body		
rs1047993	rs1130034		HLA-DQA	NM_00212	1stExon		
			CARKD	NM_01821	Body	chr13:1112	S_Shelf
rs1181251			MAOB;MA	NM_00089	1stExon;5'U	chrX:43741	Island
			DPPA5	NM_00102	TSS1500	chr6:74063	Island
			TK2	NM_00461	3'UTR		
	rs7110676						

			ZFYVE28	NM_02097	Body	chr4:23664	Island
			NFKBIL2	NM_01343	Body	chr8:14565	S_Shelf
			TSPAN10	NM_03194	Body	chr17:7961	N_Shore
						chr4:15217	N_Shore
			RLTPR	NM_00101	Body	chr16:6768	Island
			NOS1	NM_00062	TSS200	chr12:1177	S_Shore
		TRUE	STK38	NM_00727	TSS1500	chr6:36514	S_Shore
			ANKRD44	NM_15369	Body		
			CDH11	NM_00179	5'UTR		
			GALNT8	NM_01741	TSS200		
			PRM1	NM_00276	Body		
	rs3132696		HLA-H	NR_00143	TSS200	chr6:29855	Island
			IL21R;IL21	NM_02179	TSS1500;5'UTR;5'UTR		
rs5743496			BPI	NM_00172	TSS200		
			FTO	NM_00108	Body		
rs8013454							
rs62157588							
			ACAP3	NM_03064	Body	chr1:12287	Island
	rs35309178		CDKN2D;C	NM_07942	TSS200;TS	chr19:1067	Island
			ANKRD30	NM_00114	1stExon;5'U	chr18:1474	S_Shore
						chr7:55516	Island
rs76247422	rs36112562						
rs9260857	rs2246069		HCG9	NR_02803	Body	chr6:29944	Island
			ALS2CR11	NM_00116	1stExon;1st	chr2:20248	Island
rs57595633	rs11882452		PTGER1	NM_00095	TSS1500	chr19:1458	S_Shore
			THSD4	NM_02481	Body		
	rs686389		TNNT3;TN	NM_00104	Body;Body	chr11:1947	Island
						chr2:87036	S_Shelf
			SMG6;SM	NM_01757	Body;Body		
			FGF17	NM_00386	Body	chr8:21905	Island
	rs11312232		SERPINE2;	NM_00621	5'UTR;TSS1500;Body;5'UTR		
rs77501163			GNASAS;N	NR_00278	Body;TSS1500;TSS1500		
			ZNF469	NM_00112	Body	chr16:8849	Island
	rs12131215		DNAJC8	NM_01428	TSS1500	chr1:28562	N_Shore
			F2R	NM_00199	TSS1500	chr5:76011	N_Shore
			RILP	NM_03143	TSS200	chr17:1551	S_Shore
			NCOR2;NC	NM_00631	Body;Body	chr12:1249	Island
						chr1:15736	N_Shelf
	rs55815224		ICOSLG	NM_01525	Body	chr21:4566	N_Shore

	rs72653727					
rs55694997		FAM197Y	NR_00155	TSS1500	chrY:91935	N_Shore
	rs8182339	ABR;ABR	NM_02196	Body;5'UT	chr17:1028	S_Shore
rs72651656		COL1A1	NM_00008	Body		
	rs76461368				chr1:48174	N_Shore
		ARFGAP1;	NM_17560	5'UTR;5'U	chr20:6190	S_Shore
rs74939166					chr10:6186	N_Shelf
rs75579016					chr2:10816	N_Shore
		ST7;ST7	NM_01841	Body;Body		
		BAG4;LSM	NM_00487	TSS1500;B	chr8:38033	Island
	rs1801368	MAD1L1;	NM_00355	Body;Body	chr7:19762	Island
	rs228894	TMPRSS6	NM_15360	Body	chr22:3749	Island
					chr12:5440	Island
		JAKMIP3	NM_00110	3'UTR		
		PCDHGA4	NM_01891	Body;Body	chr5:14074	N_Shore
					chr6:28554	S_Shelf
	rs79327861	CTNNA2;	NM_00438	Body;Body		
		B3GALT4	NM_00378	1stExon	chr6:33244	Island
	rs12031232					
	rs7258606				chr19:4885	S_Shore
	rs1233664	LOC22269	NR_00293	Body	chr6:28186	N_Shore
		C16orf45	NM_03320	Body		
					chr12:1252	Island
					chr13:1149	Island
		TMSB4X;T	NM_02110	TSS200;TS	chrX:12993	Island
rs7807851	rs7808948					
		TMSB4Y	NM_00420	3'UTR	chrY:15815	S_Shelf
	rs9397060	RAET1E	NM_13916	Body		
rs72659543		RASA3	NM_00736	Body		
		MAP2K6	NM_00275	Body		
rs79672239						
rs370633						
					chr5:10087	N_Shore
	rs11165878	BRDT;BRD	NM_20718	5'UTR;1stE	chr1:92414	S_Shore
rs75576061		SNAP47	NM_05305	Body		
	rs11787205	DLGAP2	NM_00474	5'UTR		
		GAN	NM_02204	Body	chr16:8134	S_Shelf

				PROCR	NM_00640	Body	chr20:3376	Island
				TNRC6A	NM_01449	Body		
				ITGBL1	NM_00479	Body	chr13:1021	Island
				APC2	NM_00588	Body	chr19:1456	Island
			TRUE					
rs61273184	rs57256805			ANK1	NM_00114	Body		
				MIR2117	NR_031751	TSS200		
				LRRC61;A	NM_00114	TSS200;5'U	chr7:15001	Island
rs11230590				OR4C6	NM_00100	TSS1500		
							chr8:43132	N_Shore
				TMEM187;	NM_00349	TSS1500;T	chrX:15323	Island
		TRUE					chr10:6960	S_Shore
rs9274425	rs9274422			HLA-DQB	NM_00212	Body	chr6:32632	Island
				ZMYM3;Z	NM_00117	5'UTR;1stE	chrX:70473	Island
							chr1:24780	S_Shore
				SEPT9;SEF	NM_00111	5'UTR;Body;TSS1500		
							chr2:12949	Island
							chr1:14655	Island
							chr6:26614	S_Shore
							chr11:1032	S_Shore
rs12719790	rs34739518							
			TRUE	ZFP112;ZF	NM_01338	1stExon;1st	chr19:4486	Island
	rs7040790			SMARCA2	NM_00307	TSS1500;T	chr9:20148	N_Shore
				UBL4B	NM_20341	TSS1500		
							chr6:25882	Island
				GNAS;GN	NM_00107	3'UTR;TSS	chr20:5746	Island
	rs78424466			DEFB135	NM_00103	TSS200		
							chr22:5000	N_Shore
	rs800126							
			TRUE	MGMT	NM_00241	Body		
				PCDH9;PC	NM_20348	Body;Body		
				BDH2	NM_02013	TSS1500		
	rs2272719			DEFA5	NM_02101	Body		
				AFG3L1;C	NR_00322	TSS1500;1s	chr16:9003	N_Shore
				CHN2;CHN	NM_00103	TSS200;Body		
	rs2668855			TNNT3;TN	NM_00104	Body;Body	chr11:1958	N_Shore
				ANKRD26	NR_02655	TSS200		

		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
	rs12277188	DEAF1	NM_02100	Body		
rs7236430					chr18:7655	N_Shelf
rs6583331						
rs61931997	rs12310440					
	rs9258593				chr6:29818	S_Shore
rs34141184		A2BP1;A2I	NM_00114	5'UTR;5'UTR;5'UTR		
		ZNF469	NM_00112	1stExon	chr16:8849	Island
					chr10:4384	Island
		STOML1	NM_00480	Body	chr15:7428	N_Shelf
		MYH15	NM_01498	Body		
		ARHGEF1	NM_01531	Body;Body	chr19:7528	N_Shelf
					chr12:5247	Island
		PCDHB17	NR_00128	Body	chr5:14053	Island
		TSKS	NM_02173	Body	chr19:5024	Island
		PCDHB4	NM_01893	1stExon	chr5:14050	N_Shore
		ARHGAP2	NM_02122	Body	chr10:4981	N_Shelf
		GPC6	NM_00570	Body		
rs34779657		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		PCDHB3	NM_01893	1stExon	chr5:14048	N_Shore
rs12787856					chr11:9779	S_Shore
		BCKDHB;I	NM_18305	Body;Body		
		MAB21L1;	NM_00558	1stExon;Bo	chr13:3604	N_Shore
					chr7:55516	N_Shore
		DMD;DMD	NM_00401	Body;Body	chrX:31284	Island
rs12089221	rs5029884	AK3L1	NM_20346	TSS1500	chr1:65613	N_Shore
		MS4A15;M	NM_15271	5'UTR;Bod	chr11:6053	Island
		PRDM16;P	NM_02211	Body;Body	chr1:31551	N_Shore
rs76490604					chr22:1686	Island
	rs6905572	C6orf26	NM_00103	Body		
	rs11691716					
	rs9395225					
		ADAMTS2	NM_02159	Body;Body	chr5:17868	Island
	rs11578682	CR1L	NM_17571	Body	chr1:20784	Island
		SMOX;SM	NM_17583	TSS1500;T	chr20:4129	N_Shore
		LOC40093	NR_02703	TSS1500	chr22:4648	N_Shore
					chr15:1010	Island
		IFFO2	NM_00113	Body		
	rs78754292					
		TRABD	NM_02520	5'UTR	chr22:5063	N_Shore

			ACSL1	NM_00199	3'UTR		
	rs57431226		CRIM1	NM_01644	Body		
			RYR3	NM_00103	Body		
			CUX1;CUX	NM_18150	Body;Body	chr7:10155	N_Shelf
	rs35698355		ITIH5;ITIH	NM_03056	Body;Body;Body		
	rs9860273		ATP2B2;M	NM_00168	Body;TSS1500;Body		
			MIR662	NR_03038	TSS1500		
						chr11:1283	S_Shore
			TAP2;TAP	NM_00054	Body;Body	chr6:32806	N_Shore
						chrY:14074	Island
						chr1:16136	Island
			TSPY4;FA	NM_00116	Body;TSS1	chrY:93636	N_Shore
			ANKFN1	NM_15322	Body		
						chr15:6251	Island
		TRUE	RPL10;RP	NM_00601	Body;Body	chrX:15362	Island
rs74488676	rs28688712		EXD3	NM_01782	Body	chr9:14024	N_Shore
						chr20:2100	S_Shelf
rs35751029							
rs11647917			ZNRF1	NM_03226	3'UTR		
			ZNF503	NM_03277	Body	chr10:7715	Island
			MPP5	NM_02247	5'UTR		
	rs76614892					chr3:54121	N_Shore
			SH3BP5;S	NM_00101	Body;Body		
			TMEM151	NM_00113	Body	chr6:44243	Island
			NCOR2;N	NM_00631	Body;Body	chr12:1249	N_Shore
rs2690601	rs1799200		DTX2;DTX	NM_00110	5'UTR;5'U	chr7:76090	S_Shelf
			KSR2	NM_17359	Body		
						chr6:25882	S_Shore
						chr4:25097	S_Shore
			POU2F2	NM_00269	3'UTR		
			PCDHB17	NR_00128	Body	chr5:14053	S_Shore
			HOXA3	NM_15363	5'UTR	chr7:27163	Island
						chr21:4425	Island
			SNRPF	NM_00309	TSS1500	chr12:9625	N_Shore
rs13005035							
	rs35329406		ESPNL	NM_19431	Body		
rs77812984	rs10947050		RNF39;RN	NM_17076	Body;Body	chr6:30038	S_Shore
			RNU5E;SS	NR_00275	Body;3'UTR;Body		

						chr17:4070	Island
	rs11666328		MYH14;M	NM_00114	Body;Body	chr19:5073	S_Shore
			FBXO42	NM_01899	TSS1500	chr1:16678	S_Shore
			STYXL1	NM_01608	5'UTR		
	rs74849098	TRUE	GAS7	NM_20143	Body		
			ANKRD11	NM_01327	Body	chr16:8933	S_Shelf
			KCNIP3	NM_01343	Body		
			RYR1;RY	NM_00054	Body;Body	chr19:3905	Island
			MIR187	NR_02961	TSS1500		
			DDX3Y;D	NM_00112	5'UTR;1stE	chrY:15016	N_Shore
	rs1885304		RASSF2;R	NM_01473	5'UTR;5'UTR		
			ZNF497	NM_19845	Body	chr19:5886	Island
rs2910329			PCDHB13	NM_01893	1stExon	chr5:14059	Island
						chr8:49427	Island
	rs67293537						
			ANKRD11	NM_01327	5'UTR	chr16:8955	N_Shore
rs72746636	rs3935295		PTPN7;PT	NM_08058	TSS1500;TSS200		
			C5orf56	NM_00101	Body		
			GNA12	NM_00735	3'UTR		
rs17721037						chr12:5438	Island
			BMPR1B	NM_00120	5'UTR		
rs7084544							
			MC2R	NM_00052	TSS1500		
			ZNF143	NM_00344	3'UTR		
			TAF3	NM_03192	TSS1500	chr10:7860	N_Shore
			NHSL2;RG	NM_00101	Body;TSS2	chrX:71350	Island
rs62103176			KCNG2	NM_01228	TSS200	chr18:7762	Island
			C2orf68	NM_00101	3'UTR	chr2:85829	S_Shelf
						chr6:28583	Island
			ZFY;ZFY;	NM_00341	TSS1500;T	chrY:28029	Island
			FAM38A	NM_00114	Body	chr16:8885	N_Shore
			HNRNPF;H	NM_00109	Body;Body;Body;Body;Body;Body		
			MAML2	NM_03242	Body		
	rs28600230					chr6:31276	N_Shore
rs56035420						chr12:5437	N_Shelf
	rs532797		CTDP1;CT	NM_04836	Body;Body	chr18:7750	S_Shore
	rs4470910		MAD1L1;M	NM_00355	Body;Body;Body		
			HLA-E	NM_00551	Body	chr6:30457	Island
			HMHA1	NM_01229	Body	chr19:1070	Island

rs75221891						chr6:15936	Island
			COL1A1	NM_00008	Body		
			CES1;CES1	NM_00102	1stExon;5'U	chr16:5586	S_Shore
			DENND1C	NM_02489	Body	chr19:6476	Island
			OR2L13;O	NM_17591	1stExon;5'U	chr1:24810	Island
			PRR25	NM_00101	Body	chr16:8573	Island
			EIF1AY	NM_00468	Body	chrY:22737	Island
			FCGBP	NM_00389	Body	chr19:4042	Island
			EPS15	NM_00198	TSS1500	chr1:51984	S_Shore
						chrY:26578	Island
			ELMO1	NM_01480	Body		
			BOLL;BOL	NM_19797	1stExon;5'U	chr2:19864	Island
rs73619461						chr20:6180	S_Shelf
	rs72953612		ME3;ME3;	NM_00668	Body;Body;Body		
rs80120024							
rs77642711						chr2:69533	S_Shelf
			MIPEP	NM_00593	Body		
			COL9A3	NM_00185	TSS1500	chr20:6144	N_Shore
rs7903137							
	rs9892163		MXRA7;M	NM_00100	Body;3'UTR;Body		
	rs73221121		PCGF3	NM_00631	5'UTR	chr4:72433	N_Shore
			ZC3H12D	NM_20736	Body	chr6:14977	Island
			CSF1R	NM_00521	TSS200		
			SNX29	NM_00108	Body		
			OR52I1	NM_00100	TSS1500		
		TRUE	CYB5R2	NM_01622	TSS1500	chr11:7694	Island
rs17006416			RAB5A	NM_00416	TSS1500	chr3:19988	N_Shore
	rs12449776		ENPP7	NM_17854	Body	chr17:7770	N_Shore
			NXPH1	NM_15274	Body	chr7:84731	S_Shelf
	rs79962772		SLC43A3;S	NM_19932	TSS1500;T	chr11:5719	S_Shore
	rs80257472		FAM65B	NM_01472	5'UTR		
			ACTC1	NM_00515	Body		
			XKRX;XK	NM_21255	5'UTR;1stE	chrX:10018	Island
rs10562732							
			HSPA12A	NM_02501	Body		
						chr6:28583	Island

rs79520425		ZNF365;Z	NM_19945	5'UTR;Body		
		MGC45800	NR_027107	Body	chr4:18306	Island
		RNF215	NM_00101	TSS1500	chr22:3078	S_Shore
	rs56268665				chr5:17738	N_Shore
					chr7:64029	S_Shelf
		HCG4P6	NR_001317	TSS200	chr6:29894	N_Shore
					chr12:1326	N_Shore
		RGMB	NM_00101	Body	chr5:98108	N_Shore
	rs79164274					
	rs75460389	OPCML	NM_00101	Body		
					chr1:20813	N_Shore
		NCRNA00	NR_026675	TSS1500;5'	chr16:2131	N_Shore
					chr7:65509	S_Shelf
	rs12166094	TTLL8	NM_00108	Body	chr22:5049	N_Shelf
		PTPRN2;P	NM_00284	Body;Body	chr7:15799	N_Shore
	rs3088174	ZNF117	NM_01585	TSS200		
		MIR196A2	NR_029617	TSS1500	chr12:5438	N_Shelf
		HEY2	NM_01225	Body	chr6:12606	S_Shelf
		FAM66D;U	NR_027425	Body;1stExon		
rs34608530						
	rs76776700	FOXR1	NM_18172	TSS200	chr11:1188	Island
		PRPS1	NM_00276	TSS200	chrX:10687	N_Shore
	rs3129877	HLA-DRA	NM_01911	Body		
		KIAA0649	NM_01481	Body	chr9:13837	Island
					chr16:1437	S_Shore
		LDLRAD2	NM_00101	Body	chr1:22140	S_Shelf
		CR1L	NM_17571	Body	chr1:20784	N_Shelf
	rs4636091					
		DEAF1	NM_02100	Body	chr11:6604	Island
		KIAA1949;	NM_00113	Body;1stEx	chr6:30654	N_Shore
		FLG2	NM_00101	TSS1500		
rs56317026		PLEC1;PL	NM_20137	Body;Body	chr8:14501	N_Shore
	rs17029184	CHD5	NM_01555	Body	chr1:61888	S_Shore
		C1orf65;C1	NM_15261	5'UTR;1stE	chr1:22356	Island
rs7805092		GNA12	NM_00735	3'UTR		

		CHML;OP	NM_00182	TSS1500;B	chr1:24180	N_Shelf
		KCTD5	NM_01899	Body	chr16:2746	S_Shelf
		ATF3	NM_00103	5'UTR		
rs62523609	rs58477175	EEF1D;EE	NM_00113	Body;Body;Body;Body;Body;Body;		
		ST5;ST5;S	NM_13915	Body;Body	chr11:8752	S_Shore
					chr4:19023	S_Shore
	rs78139923	FAM129A	NM_05296	Body		
rs1531283		B3GNTL1	NM_00100	Body	chr17:8096	S_Shore
		ZNF232	NM_01451	5'UTR	chr17:5019	S_Shore
		CES4	NR_00327	Body	chr16:5579	Island
					chr3:19738	S_Shore
		PGA5	NM_01422	TSS1500		
rs1071837	rs17885501	HLA-DRB	NM_00212	Body	chr6:32551	N_Shelf
rs6667031		OR2L13	NM_17591	TSS200	chr1:24810	Island
		KLHL13;K	NM_00116	TSS200;5'U	chrX:11725	S_Shore
rs36043556	rs9277342	HLA-DPA1	NM_03355	Body		
					chr8:11536	Island
		AMH	NM_00047	Body	chr19:2250	Island
rs9272519	rs9272518	HLA-DQA	NM_00212	Body		
		PCDHB17	NR_00128	TSS200	chr5:14053	N_Shore
	rs6011654				chr20:6182	N_Shore
		B3GNT6	NM_13870	Body	chr11:7675	Island
	rs4792929				chr17:4080	Island
	rs7404039	CBFA2T3;	NM_17593	5'UTR;Bod	chr16:8897	Island
		CPLX1	NM_00665	Body	chr4:79853	Island
	rs73726057					
		FILIP1	NM_01568	5'UTR		
	rs11753960	NCRNA00	NR_026751	Body		
		PON3	NM_00094	TSS1500	chr7:95025	Island
					chr1:48459	N_Shore

rs2493206			HSP90B3P	NR_00313	TSS1500		
			EFTUD1;E	NM_00104	Body;Body		
			TSPYL6;A	NM_00100	TSS200;Bo	chr2:54482	S_Shore
rs73044463							
rs9507472			DKFZp686	NR_002801	TSS1500		
rs10270741			RADIL	NM_01805	Body		
			MAP4K4;M	NM_00483	3'UTR;3'UTR;3'UTR		
	rs34535823		LPHN3	NM_01523	Body		
			SORBS2	NM_02106	5'UTR		
	rs3217586		MYADML	NR_00314	Body	chr2:33952	N_Shore
			LOC28573	NR_015397	Body		
			GATAD2B	NM_02069	5'UTR		
			MCC;MCC	NM_00238	Body;Body		
	rs75725719					chr1:28470	Island
			TMEM20;T	NM_15322	Body;Body	chr10:9565	S_Shelf
			LRRC2;TD	NM_02475	5'UTR;TSS	chr3:46618	Island
			SFTA2	NM_20585	3'UTR		
	rs7937152		NTM;NTM	NM_00114	Body;Body;Body;Body		
rs12031928	rs12026794		TTLL10	NM_00113	3'UTR	chr1:11328	S_Shore
			PON1	NM_00044	1stExon	chr7:94953	Island
rs60806127			KIF1A	NM_00432	Body	chr2:24171	Island
		TRUE	CACNB4;C	NM_00072	Body;Body;Body		
			SRY;SRY	NM_00314	5'UTR;1stE	chrY:26578	N_Shelf
	rs59085405		RPH3AL	NM_00698	Body		
			TTC9	NM_01535	Body		
rs71224676	rs71239275		DEFA3;DE	NM_00521	TSS1500;TSS1500;TSS1500		
			MYO1G	NM_03305	Body	chr7:45002	Island
			ZAK;ZAK	NM_01665	Body;Body		
			PFKP	NM_00262	Body		
rs79985936						chr10:6186	N_Shelf
			TBC1D4	NM_01483	Body		
			TTTY20	NR_00154	Body	chrY:91741	N_Shelf
rs3736171	rs3736173		ALDH7A1	NM_00118	TSS1500	chr5:12593	S_Shore
			SUMO3	NM_00693	3'UTR	chr21:4622	S_Shelf

			GDNF;GD	NM_19923	TSS1500;5'	chr5:37836	N_Shore
rs75815364			WWTR1;W	NM_01547	Body;Body;Body		
			ESRRG	NM_00113	5'UTR	chr1:21730	N_Shore
rs7733158	rs73730940					chr5:75587	S_Shelf
						chr21:4524	N_Shore
	rs57185755						
			FAM129A	NM_05296	Body		
			ADARB1;A	NM_01583	Body;Body;Body;Body;Body;Body;		
						chr22:3843	S_Shore
			PRAME;PF	NM_20695	TSS1500;T	chr22:2290	S_Shore
rs78540027			IL31RA	NM_13901	Body		
	rs9940875		CRAMP1L	NM_02082	Body		
	rs3129547		CNST;CNS	NM_00113	Body;Body	chr1:24678	S_Shore
			NFIC;NFIC	NM_00559	Body;Body	chr19:3456	S_Shore
	rs80337757		EMX2OS	NR_002791	Body	chr10:1192	N_Shore
						chr16:6385	N_Shelf
rs10489601							
			CARHSP1;	NM_01431	TSS1500;T	chr16:8962	S_Shore
rs78087665			ZC3H12D	NM_20736	TSS200		
			MIR21	NR_02949	TSS200		
rs62338224	rs10002013					chr4:18574	S_Shelf
						chr10:1245	Island
			POLD2;PO	NM_00623	TSS1500;T	chr7:44162	S_Shore
			C14orf43;C	NM_19427	Body;Body		
	rs78266363		PRNP;PRN	NM_00108	TSS1500;T	chr20:4666	N_Shore
						chr8:49890	S_Shore
	rs66593238		SLC26A9;S	NM_05293	TSS1500;TSS1500		
			LDB2;LDB	NM_00129	Body;Body		
rs17111739	rs55646062						
rs34326829			SIGLEC6;S	NM_00124	3'UTR;3'UTR;3'UTR		
			GPR64;GP	NM_00575	5'UTR;5'U	chrX:19140	N_Shore
			CCDC144	NM_01469	TSS200	chr17:1659	Island
			NR2F2	NM_00114	TSS200	chr15:9686	S_Shelf
	rs9567177		ENOX1;EN	NM_01799	5'UTR;5'UTR		
		TRUE	LOC40093	NR_02703	TSS1500	chr22:4648	N_Shore
			TLL1	NM_01246	Body		
						chr6:44041	N_Shore
rs4908606			CAMTA1	NM_01521	Body		

			WWOX;W	NM_01637	Body;Body		
			FAM46A	NM_01763	Body	chr6:82461	N_Shore
						chr16:1107	N_Shore
			ABCA4	NM_00035	Body		
	rs55801685	TRUE	TCF7L1	NM_03128	Body		
			KLC3	NM_17741	Body	chr19:4584	Island
						chr6:44041	N_Shore
			SGPL1	NM_00390	Body		
			MYO15A	NM_01623	Body	chr17:1802	Island
			PKD1;PKD	NM_00100	Body;Body	chr16:2165	N_Shore
			IGF2BP2;I	NM_00100	Body;Body		
			HLX	NM_02195	Body	chr1:22105	Island
rs11002311			DLG5	NM_00474	Body		
	rs11866753		GALNS	NM_00051	Body	chr16:8888	S_Shore
rs11609162	rs59836757		PARP11	NM_02036	Body	chr12:3947	Island
	rs55665837		COPB1;CO	NM_01645	Body;Body;Body		
			MICAL2	NM_01463	5'UTR		
			RPTOR;RP	NM_00116	Body;Body	chr17:7883	N_Shore
			KRT85	NM_00228	TSS1500	chr12:5276	S_Shore
			SCFD2	NM_15254	Body		
						chr10:1317	Island
			ART3	NM_00113	5'UTR		
			HEATR2	NM_01780	Body	chr7:81362	S_Shelf
			MIR886	NR_03058	Body	chr5:13541	Island
			C4orf22	NM_15277	Body		
			C1orf192	NM_00101	3'UTR		
			TBCD	NM_00599	Body	chr17:8086	N_Shelf
						chr5:15920	S_Shelf
			SOAT1	NM_00310	Body		
			SPIB	NM_00312	3'UTR	chr19:5093	Island
	rs2289917		CRYGB	NM_00521	TSS200		
rs77540987							

			AQP11	NM_17303	TSS1500	chr11:7730	N_Shore
	rs9362278						
rs1056522			CHST13	NM_15288	Body	chr3:12626	Island
						chr19:2921	Island
			SPON1	NM_00610	Body	chr11:1398	Island
			SYNC;SYN	NM_03078	TSS1500;T	chr1:33168	S_Shore
						chr7:72984	N_Shelf
						chrY:93854	S_Shelf
			MIR759	NR_031582	TSS1500		
						chr14:3806	S_Shelf
			CLYBL	NM_20680	Body		
			INPP5A	NM_00553	Body	chr10:1344	Island
			ZNF254;ZN	NM_20328	1stExon;5'UTR		
			MIR519D	NR_030202	Body		
			GNG4;GN	NM_00448	5'UTR;5'UTR;5'UTR		
			KCTD5	NM_01899	Body	chr16:2746	S_Shelf
rs17706479			SDHAF1	NM_00104	TSS1500	chr19:3648	Island
			C6orf174	NM_00101	Body	chr6:12779	Island
			CCDC36;C	NM_00113	TSS200;5'U	chr3:49236	Island
			HMHA1	NM_01229	Body	chr19:1070	Island
	rs76833705		MGAT5B;N	NM_14467	Body;Body		
			PGBD5	NM_02455	TSS1500		
rs10645			CD81	NM_00435	3'UTR	chr11:2417	S_Shore
	rs2732798		EMR2;EMI	NM_15291	3'UTR;3'UTR;3'UTR;3'UTR;3'UTR		
			TRPS1	NM_01411	5'UTR	chr8:11666	S_Shelf
		TRUE	CFHR3;CF	NM_00116	TSS1500;TSS1500		
			KIAA1324	NM_02077	Body		
rs36065777	rs61842432					chr10:1842	N_Shelf
			HLA-J;NCI	NR_02424	TSS1500;B	chr6:29974	N_Shore
			CCL2	NM_00298	TSS1500		
	rs62574262					chr9:96623	Island
rs34313934	rs76369321						
						chr6:28583	Island
						chr19:5245	Island
			NFIX	NM_00250	Body	chr19:1311	Island
rs55687522			TRIO	NM_00711	Body		
						chr11:6738	S_Shore
	rs2060458		TDH	NR_00157	Body		
			SEPT9;SEF	NM_00111	5'UTR;TSS200;Body		
	rs59759265					chr17:2302	S_Shelf

rs415552			ATP11A;A	NM_01520	Body;Body	chr13:1134	N_Shelf
			HSPE1;HS	NM_00215	1stExon;5'U	chr2:19836	Island
			LILRB4;LI	NM_00684	TSS1500;TSS1500		
rs6961385	rs62476509		WDR60	NM_01805	Body	chr7:15871	Island
			AKR1C2;A	NM_00113	TSS1500;5'UTR;5'UTR		
		TRUE	FRMD4A	NM_01802	Body	chr10:1369	N_Shore
	rs55686239					chr8:14242	N_Shore
			TIMP2	NM_00325	Body	chr17:7689	N_Shore
rs7902414			VWA2	NM_19849	Body		
			PRKY	NR_02806	Body	chrY:71415	Island
						chr5:18064	N_Shore
	rs28746820		HLA-DQB	NM_00212	Body	chr6:32632	S_Shore
			ITGAL;IT	NM_00220	Body;Body	chr16:3048	Island
			WBP2NL	NM_15261	TSS200	chr22:4239	Island
						chr4:13264	N_Shore
	rs80273550		ANKRD36	NR_02684	Body		
			LRRFIP1;L	NM_00113	Body;Body	chr2:23864	S_Shelf
	rs10425751					chr19:5427	N_Shelf
			JARID2	NM_00497	Body		
	rs72036516					chr12:1330	S_Shelf
						chr4:58061	Island
	rs12462347		ZNF578	NM_00109	3'UTR		
			HSD11B2	NM_00019	3'UTR		
			OLAH;OL	NM_00103	Body;Body		
			TMEM187;	NM_00349	TSS1500;T	chrX:15323	Island
			VAC14	NM_01805	Body		
			KANK2;K	NM_01549	3'UTR;3'U	chr19:1128	N_Shelf
rs9273554	rs9273555		HLA-DQB	NM_00212	Body	chr6:32632	N_Shelf
			LMF1	NM_02277	Body	chr16:9281	S_Shore
rs66872330							
			TBC1D16	NM_01902	Body	chr17:7792	N_Shore
	rs11436158		SMYD3	NM_00116	Body	chr1:24667	N_Shore
			WHSC2	NM_00566	Body	chr4:19946	Island
			GDPD4	NM_18283	TSS1500		

			VHL;VHL	NM_19815	TSS1500;T	chr3:10183	N_Shore
rs35108070							
rs78565274		TRUE					
	rs222722						
			FAM157B	NM_00114	TSS1500		
rs11617629	rs7328454					chr13:1131	S_Shore
			CCDC41;C	NM_00104	Body;Body		
			PCDHB16	NM_02095	1stExon	chr5:14056	N_Shore
			ZFY;ZFY;Z	NM_00341	5'UTR;5'UT	chrY:28029	S_Shore
rs7057491			DDX26B	NM_18254	TSS1500	chrX:13465	N_Shore
			C10orf68	NM_02468	Body		
			SORCS1;S	NM_05291	Body;Body	chr10:1089	N_Shelf
			CCL4L2;C	NM_20700	Body;Body		
rs2789698			PLAC9	NM_00101	Body	chr10:8189	S_Shelf
	rs78855265						
			PTGER2	NM_00095	Body	chr14:5278	S_Shore
			SHF;SHF	NM_13835	5'UTR;1stE	chr15:4549	S_Shelf
	rs12438736						
	rs62064075					chr17:1758	N_Shelf
						chr8:43132	Island
			SLC2A5;SI	NM_00303	Body;Body	chr1:90992	Island
	rs35096193						
			HMGA2;H	NM_00348	Body;Body		
	rs78242245		CYFIP1	NM_01460	5'UTR		
			HDAC9;HI	NM_17842	Body;Body;Body		
	rs56736921		IKZF1	NM_00606	5'UTR	chr7:50343	S_Shelf
rs9324066	rs9324065		TDRD9;TD	NM_15304	5'UTR;1stE	chr14:1043	Island
rs11548298			HLA-E	NM_00551	Body	chr6:30457	S_Shore
			ADCY5	NM_18335	1stExon	chr3:12316	Island
			TLN2	NM_01505	Body		
	rs76760146						
			ERRFI1	NM_01894	5'UTR	chr1:80855	N_Shelf
			RTP4	NM_02214	Body		
			RBP1;RBP	NM_00289	Body;Body;Body		
						chr2:16076	S_Shelf

						chr2:13258	Island
rs2273434						chr14:1024	S_Shore
			VPS41;VPS	NM_01439	Body;Body		
						chr17:1565	Island
			CLUAP1;C	NM_01504	Body;Body		
		TRUE	WNT7A	NM_00462	TSS1500	chr3:13919	Island
			BTNL2	NM_01960	Body		
			LOC15038	NR_02703	Body;TSS1	chr22:4644	S_Shore
			C20orf166;	NM_17846	Body;TSS1500		
						chr1:89380	S_Shore
						chr1:28573	N_Shore
rs1982911			USP29	NM_02090	TSS1500	chr19:5763	Island
	rs4754965						
			FLJ44606;F	NM_00116	TSS200;TS	chr5:12640	S_Shore
			CHTF18	NM_02209	Body	chr16:8413	Island
						chr19:1851	Island
rs67745466	rs72658141		COL1A2	NM_00008	Body		
			ELN;ELN;I	NM_00108	Body;Body;Body;Body;Body		
	rs76776700		FOXR1	NM_18172	TSS200	chr11:1188	Island
rs67506493	rs10153593		NDUFA10	NM_00454	TSS1500	chr2:24096	S_Shore
rs9914089			RFFL;RFFI	NM_00101	TSS200;5'UTR		
			GPR98;GPI	NR_00314	Body;Body		
			FCRLA	NM_03273	TSS1500		
			ZDHHC7;Z	NM_00114	5'UTR;5'UTR		
	rs34172802		C8orf34	NM_05295	Body		
rs34905461			CCDC88C	NM_00108	Body	chr14:9188	N_Shore
			DOCK5	NM_02494	Body		
			BAMBI	NM_01234	Body	chr10:2896	S_Shelf
						chr14:9973	S_Shelf
						chrY:23566	Island
rs12598001			LOC14633	NR_027242	Body	chr16:1122	S_Shore
			XYLT1	NM_02216	Body		
	rs77750217		GRM8;GRI	NM_00084	TSS1500;TSS1500;5'UTR		
			ZNF589	NM_01608	3'UTR		
			IRF2	NM_00219	Body		
						chr16:5536	Island
			VIPR2	NM_00338	Body	chr7:15885	Island
			UBD	NM_00639	TSS200		
						chrX:15267	Island

rs231772	rs16840252	CTLA4;CT	NM_00103	TSS1500;TSS1500		
	rs7898778	LRIT2	NM_00101	TSS200		
		MYT1L	NM_01502	5'UTR		
		NR2F2	NM_00114	TSS200	chr15:9686	S_Shelf
rs41311635		HOXA3;H	NM_15363	3'UTR;3'U	chr7:27146	Island
rs79596037		OR2H1	NM_03088	5'UTR		
rs4983578	rs12147310				chr14:1055	S_Shore
		BSN	NM_00345	Body		
		ETV1;ETV	NM_00116	TSS1500;T	chr7:14030	S_Shore
	rs555512					
	rs45445194	HLA-B	NM_00551	Body	chr6:31323	N_Shore
rs7725504		PLEKHG4	NM_05290	Body	chr5:16957	N_Shore
		RIN3	NM_02483	Body	chr14:9315	Island
		USH2A	NM_20693	Body		
	rs426439	SEPT9;SE	NM_00111	5'UTR;5'UTR;Body;Body;Body		
rs72545015	rs68087359					
rs55832910	rs56331243				chr10:1354	S_Shore
	rs74740078				chr18:9707	N_Shelf
		TDRD9	NM_15304	Body		
rs75545097		CD82;CD8	NM_00223	5'UTR;5'UTR		
rs12355323						
		OSGIN1;O	NM_18298	TSS200;TSS200		
					chr12:1311	N_Shore
	rs62485930					
		CYP2E1	NM_00077	Body	chr10:1353	S_Shore
rs76266017	rs17054431	CYFIP2;C	NM_00103	Body;Body;Body		
rs61870421		GALNTL4	NM_19851	Body	chr11:1164	N_Shore
		SRGAP1	NM_02076	Body		
	rs405185	KIAA1609	NM_02094	Body		
rs10139444	rs74694293					
rs78357128		ESYT2	NM_02072	Body		
		PLXDC1	NM_02040	TSS1500	chr17:3730	S_Shore
	rs3814743	GAL3ST3	NM_03303	Body	chr11:6580	Island
					chr9:44401	Island
		GPT	NM_00530	TSS1500	chr8:14573	N_Shore

rs10479519	rs62393076		ZNF879	NM_00113	TSS200	chr5:17845	Island
			ATP5C1;A	NM_00100	Body;Body		
		TRUE	SLC39A2	NM_01457	TSS200		
	rs2075720		FSCN2;FS	NM_00107	1stExon;5'U	chr17:7949	Island
			TNNT1;TN	NM_00112	3'UTR;3'UTR;3'UTR		
rs6453003							
						chr10:2668	S_Shore
			ARHGAP2	NM_02122	Body		
			ASIP	NM_00167	Body	chr20:3285	Island
	rs3757423		REPIN1;RE	NM_00109	5'UTR;Bod	chr7:15006	N_Shore
			PRDM7	NM_00109	TSS1500	chr16:9014	Island
						chr17:1656	Island
	rs11222213						
			ASPSCR1	NM_02408	Body	chr17:7996	Island
			TCP10	NM_00461	Body		
	rs35461532		WHSC1	NM_00104	5'UTR	chr4:18721	S_Shore
			C3orf64	NM_17365	Body	chr3:69062	N_Shelf
	rs10089341					chr8:10375	Island
						chr6:28554	S_Shelf
rs78271486			COL1A1	NM_00008	Body	chr17:4827	N_Shore
	rs4320987		RIMBP2	NM_01534	5'UTR		
	rs35659211						
			ZNF85	NM_00342	TSS200		
			ZNF497	NM_19845	Body	chr19:5886	Island
	rs58174822						
			ASPG	NM_00108	Body	chr14:1045	Island
			CDH5	NM_00179	Body	chr16:6643	Island
	rs4789801		FOXK2	NM_00451	Body	chr17:8053	S_Shore
			LRP2	NM_00452	Body		
			C1orf86;LC	NM_00114	Body;Body	chr1:21210	Island
			RAB36	NM_00491	Body	chr22:2348	S_Shore
			ODZ3	NM_00108	Body		
			NEK9	NM_03311	Body	chr14:7559	N_Shelf
			C19orf77	NM_00113	Body	chr19:3481	N_Shelf
			AMH	NM_00047	Body	chr19:2250	Island

	rs35964739	C13orf29	NR_027701	TSS200		
		NMT1	NM_02107	Body		
		RPH3AL	NM_00698	Body	chr17:1136	N_Shore
		LOC10013	NR_02446	Body;TSS1	chr11:6713	S_Shore
		TMEM106	NM_00114	1stExon;5'U	chr12:4835	Island
rs9288597		DOCK10	NM_01468	Body		
		ZNF232	NM_01451	5'UTR	chr17:5019	Island
		CRTC1;CR	NM_01532	3'UTR;3'U	chr19:1888	S_Shore
					chr4:16408	S_Shelf
rs34197320	rs13196639	HLA-DPA1	NM_03355	Body		
		DYNLT3	NM_00652	1stExon	chrX:37706	Island
		UPK3B;UP	NM_18268	3'UTR;3'U	chr7:76145	Island
	rs77211393	C14orf23	NR_026731	Body	chr14:2925	N_Shelf
		KLRD1	NM_00111	TSS200		
		TTTY8;TT	NR_00153	TSS1500;TSS1500		
	rs9270058	HLA-DRB	NM_00212	Body	chr6:32551	S_Shore
		D2HGDH	NM_15278	Body		
					chr10:1248	N_Shore
	rs903905	MORN1	NM_02484	Body	chr1:22660	S_Shore
					chrX:48748	Island
		ARHGEF3	NM_00112	Body		
	rs73110892	SYNPR;SY	NM_14464	TSS200;Body		
rs10831109	rs4753510				chr11:9358	S_Shelf
					chrY:61344	S_Shore
		MIR196A2	NR_029617	TSS1500	chr12:5438	N_Shelf
		SCGN	NM_00699	3'UTR		
		GALNTL2	NM_05411	Body		
		DCC	NM_00521	TSS1500	chr18:4986	N_Shelf
		NRN1	NM_01658	Body	chr6:60024	N_Shore
		HNRNPH2	NM_00103	TSS200;TS	chrX:10066	Island
rs76063193		HLA-DQA	NM_02005	Body		
		C10orf11	NM_03202	Body		
rs80228460		CCL2	NM_00298	TSS1500		
		DIP2C	NM_01497	Body		
rs56054748					chr18:7729	N_Shore
					chr8:47528	Island
		LOC16847	NR_00278	TSS200		
rs34804164		IL17C	NM_01327	Body	chr16:8870	Island

						chr17:8025	S_Shelf
						chr8:72917	Island
			ACTN3	NM_00110	Body	chr11:6632	Island
			CMTM1;C	NM_18126	1stExon;1st	chr16:6660	Island
						chr16:8670	S_Shore
			TM4SF4;T	NM_00461	1stExon;5'UTR		
			GALNT9	NM_00112	Body	chr12:1328	N_Shore
rs34433626							
			C7orf28A	NM_01562	TSS1500	chr7:59381	N_Shore
			KCNU1	NM_00103	TSS1500		
			SMOC2;S	NM_02213	Body;Body	chr6:16891	Island
	rs76801084		CTNNA2;C	NM_00438	Body;Body		
			MGAT5B;	NM_14467	Body;TSS2	chr17:7486	S_Shelf
	rs3837775		CDH5	NM_00179	5'UTR		
			CSF1R	NM_00521	TSS1500		
			IFT122;IFT	NM_05299	Body;Body;Body;Body		
rs56040263	rs2272481		MAEA;MA	NM_00588	Body;Body	chr4:13092	Island
						chr17:5611	Island
			CPNE4	NM_13080	5'UTR		
			SLC30A8	NM_17385	3'UTR		
			RILP	NM_03143	TSS200	chr17:1551	S_Shore
			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
			RXFP3	NM_01656	1stExon	chr5:33936	Island
						chr6:10643	Island
			CBFA2T3;	NM_17593	5'UTR;Body		
			PCDHGA1	NM_01891	1stExon;1st	chr5:14071	Island
			ARHGAP1	NM_00100	Body;Body		
rs80186030							
rs12946521		TRUE	PLD6	NM_17883	1stExon	chr17:1710	Island
			PCBD1	NM_00028	Body	chr10:7264	N_Shore
	rs7312853					chr12:5406	S_Shelf
			HECW1	NM_01505	Body	chr7:43288	Island
						chr6:42694	Island
	rs35508110		CYorf15A	NM_00100	TSS200	chrY:21729	N_Shore
			GALP;GA	NM_03310	3'UTR;3'UTR		
			LASS2;LA	NM_18174	TSS1500;T	chr1:15094	S_Shore

	rs2676754		ADARB2	NM_01870	Body	chr10:1516	Island
			CDH6	NM_00493	5'UTR	chr5:31193	S_Shelf
	rs73546638	TRUE	TNFRSF10	NM_00384	TSS200	chr8:22960	Island
rs71336124	rs9789900		COL18A1;	NM_13044	Body;Body	chr21:4691	S_Shelf
			CARKD	NM_01821	Body	chr13:1112	N_Shelf
	rs11271642					chr3:19526	S_Shelf
			LOC64533	NR_02424	Body	chr11:6757	N_Shelf
	rs4998914						
	rs34177912						
			FZD9	NM_00350	1stExon	chr7:72847	Island
			PFN2;PFN	NM_00262	Body;Body	chr3:14968	N_Shelf
rs1309311							
			MED20	NM_00427	Body	chr6:41888	N_Shelf
			GDF6	NM_00100	Body	chr8:97156	Island
			KIAA1522	NM_02088	Body	chr1:33235	N_Shore
			NAV1	NM_02044	Body		
			MRTO4	NM_01618	Body	chr1:19577	S_Shelf
			CMIP	NM_19839	Body		
rs79532341			SAMD12;S	NM_00110	Body;Body		
			ARHGEF3	NM_00112	Body		
rs35022151			CREB3L2	NM_19407	Body		
rs1049057	rs1049072		HLA-DQB	NM_00212	1stExon	chr6:32632	S_Shore
			PDPK1;PD	NM_03126	Body;Body	chr16:2629	S_Shore
			SPAG16	NM_02453	Body		
	rs9256982		HLA-A	NM_00211	Body	chr6:29910	Island
	rs13216344						
			KDM2A;K	NR_02747	TSS1500;T	chr11:6688	N_Shore
rs56046206	rs1042434		HLA-DPA1	NM_03355	Body		
	rs36054392		SLC9A4	NM_00101	TSS200		
			DDX56	NM_01908	TSS200	chr7:44613	S_Shore
			TRIM61	NM_00101	TSS200		
rs35836361							
rs9324268	rs9577308						
rs77176014	rs80080478						
	rs4725996		AGAP3	NM_03194	Body	chr7:15082	N_Shore

			NOX3	NM_01571	Body		
			PLXNB2	NM_01240	Body	chr22:5071	Island
			PPP1R3B	NM_02460	TSS1500	chr8:90080	Island
			KRTAP27-	NM_00107	1stExon		
rs76480899			FLOT1	NM_00580	Body	chr6:30710	N_Shelf
			C1QTNF9	NM_17854	TSS1500	chr13:2488	Island
	rs45447300		TFAM	NM_00320	Body	chr10:6014	S_Shelf
			CUGBP2;C	NM_00656	Body;Body		
rs193828							
						chr6:42694	Island
	rs1136700		HLA-A	NM_00211	Body	chr6:29910	Island
			SULT1A1;	NM_17753	5'UTR;1stE	chr16:2863	Island
rs61925230							
			PCDHB11	NM_01893	1stExon	chr5:14058	N_Shore
						chr6:31650	Island
			SLC6A12;	NM_00112	Body;Body	chr12:3125	Island
			TSPY2	NM_02257	TSS200	chrY:61140	Island
rs10525917	rs73916643		ZBTB46	NM_02522	Body	chr20:6240	Island
			SLC6A18	NM_18263	3'UTR	chr5:12459	Island
						chr2:23234	Island
			SLC38A7	NM_01823	Body		
	rs77067369		ZP3;SRCR	NM_00715	5'UTR;Bod	chr7:76029	S_Shore
			EXT1	NM_00012	Body		
			ARHGEF1	NM_01462	Body		
	rs75175183		C20orf186	NM_18251	TSS1500		
						chr4:94755	S_Shelf
		TRUE	GALR1	NM_00148	Body	chr18:7496	S_Shore
						chr19:3746	S_Shelf
			PTPRN2;P	NM_00284	Body;Body;Body		
			LDLRAD3	NM_17490	Body		
			SHISA2	NM_00100	Body	chr13:2662	N_Shore
						chr20:1856	N_Shore
			DCHS2;DC	NM_01763	Body;Body	chr4:15525	N_Shore
			DGKK	NM_00101	TSS1500	chrX:50213	Island
	rs77697480		C7orf50;C7	NM_00113	Body;Body	chr7:10759	N_Shore
			PRKAG2	NM_01620	Body		
rs78724076			SLN	NM_00306	TSS1500		
						chr20:6295	N_Shore
						chr6:17040	S_Shelf
			OTOP1	NM_17799	TSS200	chr4:42280	Island
rs41562819	rs41544215		HLA-DRB	NM_00212	Body	chr6:32489	Island

			FOXR1;FO	NM_18172	5'UTR;1stE	chr11:1188	Island
						chr10:4450	Island
			GRIK2;GR	NM_02195	TSS200;TS	chr6:10184	Island
			MIR212	NR_02962	TSS1500	chr17:1952	Island
	rs78988312		GALNT9	NM_00112	Body	chr12:1328	N_Shelf
			SPON1	NM_00610	Body		
rs7106869		TRUE	SLC5A12;S	NM_17849	5'UTR;1stExon		
			LMF1	NM_02277	TSS1500	chr16:1020	S_Shore
	rs3842457		AGPAT3;A	NM_00103	5'UTR;5'U	chr21:4536	N_Shelf
rs11802071			CAMTA1	NM_01521	Body	chr1:70220	S_Shore
						chr2:37508	S_Shore
			SETD2	NM_01415	TSS200	chr3:47204	Island
			CARD6	NM_03258	1stExon		
			CXorf39	NM_20731	TSS200	chrX:10341	Island
			PARP12	NM_02275	Body	chr7:13976	N_Shore
rs73657846			CSMD1	NM_03322	Body		
			CCL11	NM_00298	TSS200		
			LOC39995	NR_02443	Body		
rs41316148	rs62402681		TNXB;TN	NM_03247	Body;Body		
	rs12490206		EPHB3	NM_00444	Body	chr3:18427	Island
			PCDHB6	NM_01893	1stExon	chr5:14053	N_Shore
			MAP7D2;M	NM_00116	Body;Body	chrX:20134	Island
			FLT1	NM_00201	Body		
	rs1646648						
rs2280092			ADAM33;A	NM_15320	Body;Body	chr20:3653	Island
rs2747430	rs3129057						
			ARHGEF4;	NM_03299	Body;Body	chr2:13172	S_Shore
		TRUE	PDZD4	NM_03251	TSS1500	chrX:15309	S_Shore
			EGFR;EGF	NM_20128	Body;Body;Body;Body		
	rs5016957						
			AQP11	NM_17303	TSS1500	chr11:7730	N_Shore
			BCORL2	NR_00292	TSS1500	chrY:21664	S_Shore
rs76222887	rs2245786		RASSF2;R	NM_01473	5'UTR;5'UTR		
rs34435641			PRSS22	NM_02211	Body	chr16:2902	Island
rs4908900			PLEKHG5	NM_19868	Body	chr1:65575	S_Shelf
	rs2748976		KIAA1751	NM_00108	3'UTR	chr1:18863	Island
						chr7:75779	S_Shore
			OLIG1;OL	NM_13898	1stExon;3'U	chr21:3444	Island

	rs56226325			MAD1L1;	NM_00355	Body;Body;Body		
							chr8:37822	N_Shelf
				OSBPL5;O	NM_02089	5'UTR;5'UTR;5'UTR		
	rs2185151						chr1:25071	N_Shore
rs6655476				DOCK11	NM_14465	Body	chrX:11762	S_Shelf
							chr4:17442	Island
				UPF3B;UP	NM_02301	Body;Body	chrX:11898	Island
				PSORS1C1	NM_01406	1stExon;5'UTR		
	rs11246985			GALNT9;C	NM_00112	Body;Body	chr12:1326	Island
							chr2:24294	Island
				FDXR;FDX	NM_02441	Body;Body	chr17:7285	S_Shelf
							chr22:1898	Island
	rs35411568			LONRF2	NM_19846	Body		
		TRUE		HRNBP3	NM_00108	5'UTR		
				COL9A3	NM_00185	Body	chr20:6145	S_Shore
				TMEM175	NM_03232	Body	chr4:94061	S_Shore
							chr10:4384	Island
							chr16:9014	Island
				C1QTNF7;	NM_03191	TSS200;Body;5'UTR		
			TRUE	SERPINA3	NM_00108	TSS200		
	rs10173220							
				HOXC10	NM_01740	3'UTR	chr12:5437	S_Shelf
	rs56402179			PSAPL1;S	NM_00108	1stExon;Body		
				KCTD1	NM_19899	5'UTR	chr18:2412	S_Shore
							chr16:3232	N_Shelf
	rs6750127			PSD4;LOC	NM_01245	Body;Body		
							chr9:68809	Island
							chrY:21729	N_Shelf
	rs8101412			ZNF714	NM_18251	5'UTR	chr19:2126	Island
				C11orf46	NM_15231	TSS1500	chr11:3034	N_Shore
				FAM100B	NM_18256	TSS1500	chr17:7426	N_Shore
				GRIK2;GR	NM_02195	TSS200;TS	chr6:10184	Island
	rs58644696						chr1:41349	Island
rs2301753				RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
rs646709				CDC42BP	NM_01752	Body	chr11:6459	N_Shore
							chr2:23328	N_Shore

			ATP11A;A	NM_01520	3'UTR;Bod	chr13:1135	N_Shore
			FAM38B	NM_02206	Body	chr18:1114	N_Shore
			A2BP1;A2	NM_00114	Body;Body;Body		
rs6961978							
						chrX:13959	Island
			ZNF267	NM_00341	Body	chr16:3188	S_Shelf
						chr21:3477	N_Shelf
	rs56134303		KCNQ1OT	NR_00272	TSS1500;B	chr11:2720	S_Shore
rs76753455	rs2213565		HLA-DQA	NM_02005	Body		
rs60548246			PLEKHG4;	NM_00112	TSS1500;1	chr16:6731	Island
			LOC15482	NR_02439	Body		
			CD80	NM_00519	TSS1500		
			BHLHB9;B	NM_00114	TSS200;5'U	chrX:10200	Island
			ZBP1;ZBP	NM_00116	3'UTR;3'UTR;3'UTR		
	rs11133451		HOPX;HO	NM_13921	5'UTR;5'UTR;5'UTR		
			CNNM1	NM_02034	TSS200	chr10:1010	N_Shore
rs35291527	rs7759327		FARS2	NM_00656	Body		
			FAM118A;	NM_01791	TSS1500;T	chr22:4570	N_Shore
	rs1632938		HLA-G	NM_00212	Body	chr6:29795	S_Shore
			RPS4Y2	NM_00103	TSS200		
			KRT34	NM_02101	Body		
			CREG2	NM_15383	3'UTR		
			IRAK1;IRA	NM_00102	Body;Body	chrX:15328	Island
						chr16:1088	N_Shore
	rs1317505		MCF2L	NM_00111	Body	chr13:1136	N_Shelf
	rs12596752		CCDC154	NM_00114	Body	chr16:1493	Island
rs11802845							
rs13306642			SCNN1D;S	NM_00113	3'UTR;3'U	chr1:12287	N_Shore
			FHIT;FHIT	NM_00201	3'UTR;3'UTR		
						chr2:24298	Island
			GMEB2	NM_01238	Body	chr20:6222	S_Shore
			ATG4C;AT	NM_17822	TSS1500;TSS1500		
	rs10414886					chr19:2061	N_Shelf
			ZNF598	NM_17816	Body	chr16:2052	N_Shore
			CCDC86	NM_02409	TSS1500	chr11:6060	N_Shore
			ZNF80;ZN	NM_00713	5'UTR;1stExon		
			PRKCE	NM_00540	Body		
	rs2953211						
		TRUE	TSPAN6;T	NM_00327	5'UTR;1stE	chrX:99891	Island

rs35454254		SSTR5;LO	NM_00105	TSS200;Bo	chr16:1128	Island
		PXT1;KCT	NM_15299	5'UTR;TSS	chr6:36410	N_Shore
		STRADB	NM_01857	Body		
	rs57606101					
		SPOCK1	NM_00459	Body		
		CDH18;CD	NM_00116	Body;Body		
rs11707701		HRH1	NM_00109	TSS200		
		EPB41L3	NM_01230	Body		
	rs34942729	CMIP;CMI	NM_03062	Body;Body		
rs7120146	rs7108672	RBMXL2	NM_01446	TSS200	chr11:7110	Island
	rs2427567	DNAJC5	NM_02521	5'UTR	chr20:6256	N_Shore
					chr19:7937	Island
					chr13:1129	Island
					chr10:5243	Island
		ADAMTS8	NM_00703	Body		
		HDAC4	NM_00603	Body		
					chr19:5310	S_Shelf
rs1811359	rs9277441	HLA-DPB1	NM_00212	Body	chr6:33048	S_Shelf
	rs1387561	RADIL	NM_01805	Body	chr7:48559	N_Shore
		FAM178B	NM_00112	Body		
		NFATC1;N	NM_00616	Body;Body	chr18:7728	N_Shore
		DND1	NM_19424	TSS200	chr5:14005	Island
rs75900625	rs62390862				chr6:29855	S_Shelf
		COX6A2	NM_00520	Body	chr16:3143	Island
		FAM58A;F	NM_00113	TSS200;TS	chrX:15286	Island
rs11402061						
		SYNRG;SY	NM_00116	TSS200;TS	chr17:3596	Island
		CBFA2T3;	NM_17593	5'UTR;Bod	chr16:8899	N_Shelf
		ESRRG;ES	NM_20659	5'UTR;5'UTR;5'UTR		
		C20orf96	NM_15326	Body	chr20:2597	Island
		CPT2	NM_00009	TSS1500	chr1:53662	N_Shore
		PRR25	NM_00101	Body	chr16:8573	Island
	rs77322225	FHAD1	NM_05292	Body		
	rs77247387	C11orf75	NM_02017	TSS1500	chr11:9327	S_Shore
rs921921					chr12:1252	S_Shore
		LRRC8B	NM_00113	5'UTR	chr1:89989	Island

	rs1792264		DHCR7;D	NM_00116	Body;Body	chr11:7114	S_Shelf
			IGFBP6	NM_00217	TSS1500	chr12:5349	N_Shore
			ARHGEF1	NM_01462	5'UTR		
						chr18:4782	S_Shore
			SPINT4	NM_17845	Body		
			SORCS2	NM_02077	Body		
rs4969385			BAIAP2;B	NM_01745	Body;Body;Body;Body		
			IRF2BP1	NM_01564	1stExon	chr19:4638	Island
						chr5:26431	Island
	rs73934484		ZNF71	NM_02121	5'UTR	chr19:5710	S_Shelf
			TSPY4	NM_00116	3'UTR	chrY:93645	S_Shelf
rs35864573			LDHAL6A	NM_14497	TSS200;TS	chr11:1847	Island
			OPCML	NM_00101	Body		
			MRVI1;M	NM_00110	TSS1500;TSS1500;TSS1500		
rs34050526							
rs77140801	rs78978157					chr8:14415	S_Shelf
rs7941689						chr11:3235	N_Shore
						chr12:5437	N_Shelf
rs77833200			CTNNA2;C	NM_00438	Body;Body		
rs71445125			CD4	NM_00061	TSS200		
rs13303829	rs13303801		TTTY14	NR_00154	TSS1500	chrY:21238	Island
			REPS2;RE	NM_00472	TSS200;TS	chrX:16964	Island
	rs4076044					chr12:1329	Island
rs6503269	rs6503268		RCVRN	NM_00290	Body	chr17:9808	N_Shore
			FEZ2;FEZ2	NM_00510	Body;Body		
			RERE;RER	NM_00104	5'UTR;Body;Body		
			GALP;GA	NM_00114	5'UTR;5'UTR		
			SLC2A14	NM_15344	5'UTR	chr12:8025	Island
			PRR5-ARH	NM_18133	Body	chr22:4513	S_Shelf
			IQSEC2	NM_00111	1stExon	chrX:53349	Island
			MAPKAPK	NM_03296	Body;Body		
		TRUE	NOTCH3	NM_00043	TSS1500	chr19:1531	S_Shore
			HCN2	NM_00119	Body	chr19:6129	Island
			SLC7A5	NM_00348	Body		
rs1372570			RCAN2	NM_00582	TSS200		
			RHOT1;R	NM_00103	Body;Body;Body		
rs56073209						chr18:7729	Island

	rs62388030				chr5:17417	N_Shelf
rs66771331	rs7259679	CLPTM1	NM_00129	TSS1500	chr19:4545	N_Shore
		METAP1	NM_01514	Body		
	rs56002604	KALRN;K	NM_00102	Body;Body		
		S100A10	NM_00296	TSS1500	chr1:15196	S_Shore
	rs6940600					
	rs78820219				chr11:7030	Island
					chr3:39447	N_Shelf
		C19orf22	NM_13877	Body	chr19:9116	Island
		C2orf48	NM_18262	Body		
		MT2A	NM_00595	3'UTR	chr16:5664	S_Shore
		LOC10013	NR_02447	Body;Body		
rs61737979	rs12949998					
					chr2:13311	Island
		SDHAP3	NR_00326	TSS200	chr5:15942	Island
		CECR1;CE	NM_17740	Body;Body		
		ABT1	NM_01337	Body	chr6:26598	Island
	rs6669420				chr1:23748	N_Shore
		ENPP6	NM_15334	Body	chr4:18501	S_Shelf
		MLLT4;MI	NM_00104	3'UTR;Body		
rs72803483						
		NAPSA	NM_00485	Body	chr19:5086	Island
	rs13089	LPCAT1	NM_02483	3'UTR	chr5:14633	N_Shore
		AFAP1;AF	NM_19859	Body;Body		
		MYT1L	NM_01502	Body		
	rs1681851				chr1:43389	N_Shore
		RNF150	NM_02072	Body		
		FLJ16779;	NR_02438	TSS200;Bo	chr20:6188	Island
rs56699267	rs61474285	PTPRN2;P	NM_00284	Body;Body;Body		
		GXYLT2	NM_00108	Body		
	rs6911125	HLA-J;NC	NR_02424	TSS1500;B	chr6:29974	N_Shore
		ZNF167	NM_02516	Body	chr3:44622	Island
	rs3095323	CDSN;PSO	NM_00126	Body;5'UTR		
		LTB4R2;L	NM_00116	Body;1stEx	chr14:2477	Island
		MEIS1	NM_00239	Body	chr2:66661	S_Shelf

			LELP1	NM_00101	TSS1500		
			EHHADH;	NM_00116	Body;Body		
			C1orf69	NM_00101	Body	chr1:22836	N_Shelf
rs13241610							
			BRSK2	NM_00395	Body		
						chr2:11391	N_Shelf
			LDB2;LDB	NM_00129	Body;Body		
			ABO	NM_02046	TSS1500	chr9:13615	S_Shore
	rs34923004		KRT40	NM_18249	TSS200		
			LTB4R;LT	NM_00114	5'UTR;Bod	chr14:2477	Island
						chr14:1024	Island
			CASKIN1	NM_02076	Body	chr16:2228	Island
rs2242660	rs2736163		BAT2	NM_08068	Body	chr6:31599	N_Shore
			KIAA1751	NM_00108	Body		
	rs3781353		SH3PXD2A	NM_01463	Body		
			SLC12A4;S	NM_00114	3'UTR;3'UTR;3'UTR;3'UTR;3'UTR		
	rs4782153						
			ABLIM1;A	NM_00100	Body;Body;Body		
			FRMD4A	NM_01802	Body		
			BRD1;LOC	NM_01457	Body;TSS2	chr22:5017	N_Shelf
rs78014167			FAM38A	NM_00114	Body	chr16:8882	S_Shore
			TTLL3	NM_00102	TSS1500	chr3:98514	N_Shore
			VPS53;VPS	NM_01828	Body;Body		
			CXorf22	NM_15263	TSS200		
			TDRD9	NM_15304	TSS200	chr14:1043	Island
rs1004903			DYNC1H1	NM_00137	Body		
rs35864573			LDHAL6A	NM_14497	TSS200;TS	chr11:1847	Island
rs79939347			SGCZ	NM_13916	Body	chr8:15094	N_Shore
			PCDHB19	NR_00128	Body	chr5:14062	N_Shore
			TRAPPC9;	NM_00116	Body;Body		
rs1279736			GNB2L1;S	NM_00609	TSS1500;T	chr5:18067	N_Shore
			ST3GAL5;	NM_00104	Body;Body		
						chr14:1024	Island
	rs2119876		ZFAT;ZFA	NM_00116	Body;Body;TSS1500		
rs2839091							
		TRUE					
			GLIS3;GLI	NM_15262	Body;Body	chr9:41178	N_Shore

	rs10067182		PCDHA6;P	NM_03184	Body;Body	chr5:14021	Island
			FOXN3;FO	NM_00519	Body;Body		
	rs3187207		VAV3;VA	NM_00611	3'UTR;3'UTR		
rs79326925			PCDHB15	NM_01893	1stExon	chr5:14062	Island
rs6580012			PCDHA6;P	NM_03184	Body;Body	chr5:14022	Island
	rs11164142		ATP4B	NM_00070	Body		
rs78322754			TGFB3	NM_00323	Body	chr14:7644	N_Shelf
	rs16841702						
rs59352401	rs35512631						
	rs79725671		MIR329-2	NR_02996	TSS200		
	rs4939450		MS4A15;M	NM_15271	5'UTR;Bod	chr11:6053	Island
			LRRC61;A	NM_00114	TSS1500;5'	chr7:15001	Island
rs1969877						chr1:44568	Island
		TRUE	NFAT5;NF	NM_13871	5'UTR;Body;Body;5'UTR;Body		
rs615557	rs413095						
	rs10840167					chr11:2017	S_Shelf
	rs76423190		FAM176A;	NM_03218	5'UTR;5'U	chr2:75787	N_Shore
			LPCAT1	NM_02483	Body		
	rs541		PFKP	NM_00262	3'UTR	chr10:3180	N_Shore
			MMP16;M	NM_00594	Body;Body		
						chr2:47499	N_Shelf
rs35629555	rs35471643		KCNAB2;K	NM_00363	TSS1500;T	chr1:60862	N_Shore
			ZFP2	NM_03061	TSS200	chr5:17832	Island
rs28623392	rs74365204					chr7:15896	S_Shore
			BCL11B;B	NM_02289	Body;Body		
			PXDN	NM_01229	Body		
rs7319234						chr13:2426	Island
			TBC1D2B;	NM_01507	3'UTR;TSS1500;3'UTR		
			PCDHA1;P	NM_03141	Body;Body	chr5:14017	Island
	rs76499425		C5orf54	NM_02209	TSS1500	chr5:15982	S_Shore
			CACNG3	NM_00653	TSS1500	chr16:2426	N_Shore
			C1orf86	NM_00114	TSS200	chr1:21368	S_Shore
			GK;GK;GK	NM_00112	TSS200;TS	chrX:30670	Island
			PTPRE	NM_00650	5'UTR		
	rs74971938						
						chr6:25882	Island
			LOC64174	NR_03324	Body		
						chr18:2930	Island

							chr8:14496	Island
rs1129638				PGAM2	NM_00029	1stExon	chr7:44104	Island
	rs66581054							
				SH3BP5;SH	NM_00101	Body;Body		
				EGR3	NM_00443	3'UTR	chr8:22547	Island
				KIAA1683;	NM_02524	TSS1500;TSS1500;TSS1500		
				CCDC83	NM_17355	Body		
	rs73881125						chr3:17409	N_Shelf
rs62079552				SEPT9;SEP	NM_00111	5'UTR;TSS200;Body		
				B3GNTL1	NM_00100	Body	chr17:8096	Island
							chr1:35586	Island
				LY9;LY9	NM_00103	Body;Body	chr1:16077	N_Shelf
							chr12:5225	S_Shore
							chr16:3345	Island
							chr15:9688	Island
				TNFRSF18	NM_14890	TSS1500;T	chr1:11416	S_Shore
	rs10074268							
		TRUE		C16orf74	NM_20696	Body	chr16:8574	S_Shelf
				TSNAX-DI	NR_028394	Body;Body;Body;Body;Body;Body;		
			TRUE	HFE2;HFE	NM_20200	TSS1500;T	chr1:14541	N_Shelf
rs11206167	rs72906949							
				COLEC12	NM_13038	TSS1500	chr18:4993	S_Shore
				B3GNTL1	NM_00100	Body	chr17:8096	N_Shore
				WDR45	NM_00707	5'UTR	chrX:48957	N_Shore
				SFTPB;SFT	NM_00054	Body;Body		
				IGSF22	NM_17358	Body	chr11:1872	S_Shore
rs35559353				RNF39;RN	NM_17076	Body;Body	chr6:30038	S_Shore
				MIR21	NR_029493	Body		
	rs36063234			NPAS3;NP	NM_00116	Body;Body;Body;Body		
	rs432263							
							chr1:14885	Island
	rs78460632			PLXNC1	NM_00576	3'UTR		
rs77662651								
rs2276014				ESRRA	NM_00445	Body	chr11:6408	N_Shelf
				RAMP1	NM_00585	Body		
				PTPRN2;P	NM_00284	Body;Body	chr7:15834	N_Shore
rs9924504				ZNF469	NM_00112	1stExon	chr16:8849	Island

			PCDHA6;P	NM_03184	Body;Body	chr5:14021	Island
rs59597720			ACTA2;AC	NM_00161	TSS200;5'UTR		
rs6576615	rs6576614						
			PEX10;RE	NM_00261	3'UTR;3'U	chr1:23398	N_Shelf
	rs61972401						
						chr7:63652	Island
rs7826035			CHD7	NM_01778	5'UTR	chr8:61626	S_Shore
	rs78915409						
			BAMBI	NM_01234	3'UTR		
			CAMK1D;	NM_02039	Body;Body		
			TNS3	NM_02274	5'UTR		
	rs11147024		ANKLE2	NM_01511	Body	chr12:1333	S_Shore
	rs79029484		SLC1A3;S	NM_00417	Body;Body		
						chr6:17073	Island
	rs7601196		TSSC1	NM_00331	Body	chr2:33210	S_Shore
	rs8089792					chr18:4225	N_Shelf
		TRUE				chr6:16110	Island
	rs7284165					chr22:3803	N_Shelf
			CACNA1C	NM_00112	Body;Body;Body;Body;Body;Body;		
			TMEM132	NM_01787	Body;Body	chr11:6070	Island
			CES4	NR_00327	TSS1500	chr16:5579	N_Shore
rs73796318			CSF1R	NM_00521	TSS200		
			TGFBR2;T	NM_00102	Body;Body		
rs4688362	rs9836779						
	rs78635760		HLA-DOA	NM_00211	Body	chr6:32975	S_Shore
			SH3KBP1	NM_03189	Body	chrX:19905	N_Shore
			GLIPR1L2	NM_15243	1stExon	chr12:7578	Island
	rs61757948		GRB2;GR	NM_00208	Body;Body		
			CD19	NM_00177	Body	chr16:2894	Island
			PSRC1;PS	NM_00103	TSS1500;T	chr1:10982	Island
			BARX2	NM_00365	Body	chr11:1292	S_Shore
						chr19:1851	Island
rs34467568						chr7:12151	Island
						chr6:17047	S_Shelf
	rs75461049						

rs4781022			CIITA	NM_00024	Body		
			LCK;LCK	NM_00535	Body;Body	chr1:32740	Island
			FBN1	NM_00013	Body		
			ATP6AP2	NM_00576	TSS200	chrX:40439	Island
			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
rs2302398			CDSN;CDS	NM_00126	5'UTR;1stExon;5'UTR		
		TRUE	PON1	NM_00044	Body	chr7:94953	N_Shore
			TRIM40	NM_13870	Body		
			CYB5B	NM_03057	Body		
						chr4:13962	Island
	rs77768851		EFHA2	NM_18172	Body		
			DNAJA3;D	NM_00113	3'UTR;3'UTR		
			SLC6A6;SI	NM_00113	5'UTR;5'U	chr3:14443	S_Shelf
						chr18:1194	Island
			TNIK;TNIK	NM_00116	Body;Body;Body;Body;Body;Body;		
						chr6:31650	Island
	rs8003746		VSX2	NM_18289	TSS1500	chr14:7470	N_Shore
	rs3925325					chr6:66804	Island
			TAF9B	NM_01597	1stExon	chrX:77394	Island
			NCOR2;NC	NM_00631	Body;Body	chr12:1248	N_Shore
						chr17:7946	S_Shore
						chr13:2167	S_Shelf
			RNMTL1	NM_01814	Body		
			TNS3	NM_02274	5'UTR		
			ANKRD23	NM_14499	Body	chr2:97505	Island
rs6149381			LOC72967	NR_02718	Body	chr5:18025	N_Shore
						chr17:3481	N_Shelf
	rs59628701		FHOD3	NM_02513	Body	chr18:3432	Island
						chr10:1346	S_Shore
			STARD13	NM_17800	Body		
			KIF26B	NM_01801	Body		
			EBF3	NM_00100	Body	chr10:1316	N_Shore
			LTB4R2;L	NM_00116	1stExon;1st	chr14:2477	Island
	rs77290902					chr10:1323	N_Shore

			LMF1	NM_02277	Body	chr16:9233	N_Shore
			CDKL5	NM_00315	TSS200	chrX:18443	Island
			TMEM140	NM_01829	5'UTR		
rs80173385	rs75928006		MIR519A1	NR_03021	TSS1500;TSS200		
	rs28649010					chr7:13285	S_Shelf
						chr21:4705	S_Shore
			FIGLA	NM_00100	TSS1500	chr2:71017	S_Shore
			MATN4;M	NM_00383	5'UTR;5'U	chr20:4393	Island
			CRTAM	NM_01960	Body		
			VAC14	NM_01805	Body	chr16:7079	N_Shore
	rs6926983						
						chr11:1345	S_Shelf
			ESR1;ESR	NM_00112	5'UTR;TSS	chr6:15212	N_Shelf
	rs2843147		MORN1	NM_02484	Body	chr1:22660	N_Shore
			HLX	NM_02195	Body	chr1:22105	Island
			NPPB	NM_00252	3'UTR	chr1:11919	N_Shore
	rs72972615		KALRN;K	NR_02813	Body;Body;Body		
						chr16:5536	Island
	rs28508407		ALDH4A1;	NM_17072	Body;Body	chr1:19209	S_Shore
		TRUE	CD19	NM_00177	TSS1500		
	rs41289829		NMBR	NM_00251	1stExon	chr6:14240	Island
rs73038957			AHRR	NM_02073	Body		
	rs78357128		ESYT2	NM_02072	Body		
			PRKY	NR_02806	Body	chrY:71415	Island
			TRIO	NM_00711	Body		
	rs13407128					chr2:13966	Island
			ESR1;ESR	NM_00112	5'UTR;TSS	chr6:15212	N_Shelf
	rs3791865		GAD1;GA	NM_00081	Body;Body	chr2:17167	S_Shore
	rs6872104						
rs75650125			CBFA2T3	NM_00518	Body	chr16:8903	S_Shore
			JAKMIP3	NM_00110	Body		
	rs12973147					chr19:2186	Island
	rs74111910	TRUE	AKR1C1	NM_00135	TSS1500		
	rs56127449		CYP2D7P1	NR_00257	Body	chr22:4253	N_Shore
rs2998115	rs3008367					chr10:1350	Island
			GPN3;GPN	NM_00116	Body;TSS2	chr12:1109	Island
rs78281277							
rs34367740	rs34237790		NANOG	NM_02486	3'UTR		
			TMEM132	NM_20731	Body	chr17:3290	S_Shore
			MPV17L;M	NM_17380	1stExon;1st	chr16:1548	Island
			SLC6A3	NM_00104	Body	chr5:14167	S_Shelf
			ACRV1;A	NM_02011	TSS1500;TSS1500;TSS1500;TSS15		

			ZNF232	NM_01451	5'UTR	chr17:5019	Island
rs41317006			PNPLA7;P	NM_15228	Body;Body	chr9:14035	Island
			NRK	NM_19846	TSS200	chrX:10506	Island
						chr16:8096	S_Shore
			SCML1;SC	NM_00674	1stExon;1st	chrX:17755	Island
		TRUE					
			OTUD4;O	NM_01749	5'UTR;5'U	chr4:14610	N_Shelf
			PCGF3	NM_00631	5'UTR	chr4:71628	S_Shelf
			LOC10012	NM_00116	Body		
			ADAMTS1	NM_03095	Body		
	rs1559979						
rs35357264	rs34406003		NKAIN4	NM_15286	Body	chr20:6187	Island
	rs9390		TBCD	NM_00599	Body	chr17:8089	Island
			SYCP1	NM_00317	TSS200	chr1:11539	N_Shore
rs55839918			NFATC1;N	NM_00616	Body;Body	chr18:7724	Island
			ZNF469	NM_00112	1stExon	chr16:8849	Island
			RPS4Y2	NM_00103	TSS1500		
rs72551055			RASGEF1	NM_17506	5'UTR	chr5:17958	S_Shore
rs34355311	rs35383103		PPP1R9A;	NM_00116	TSS1500;5'	chr7:94536	S_Shore
			TTTY1;LO	NR_00153	Body;Body		
			STC1	NM_00315	TSS200		
						chr8:14469	S_Shelf
			FOXR1	NM_18172	TSS200	chr11:1188	Island
			CBLB	NM_17066	Body		
	rs5875223		HCG9	NR_02803	TSS200	chr6:29944	N_Shore
			FLT4	NM_18292	3'UTR		
			STK24	NM_00103	Body		
			TRIM40	NM_13870	Body		
			PIK3CD	NM_00502	Body	chr1:97757	S_Shelf
	rs4791758					chr17:8702	N_Shelf
	rs745023						
			PCDHB17	NR_00128	Body	chr5:14053	N_Shore
	rs75489507		FAM188B	NM_03222	Body		

			SYCP1	NM_00317	TSS200	chr1:11539	N_Shore
						chr10:1217	Island
						chr4:18781	Island
			THSD7A	NM_01520	Body		
	rs11086026		FAM32A	NM_01407	3'UTR		
	rs67048105		CNTN4;CN	NM_17561	Body;Body		
	rs45579944		SEMA6B	NM_03210	Body	chr19:4552	Island
rs4868229			ERGIC1	NM_00103	Body		
			SIRPA;SIR	NM_08079	Body;Body	chr20:1918	N_Shelf
			SEPT9;SEF	NM_00111	5'UTR;Body;TSS1500		
			SLC6A12;S	NM_00112	Body;Body	chr12:3125	Island
						chr17:2068	N_Shore
rs28825688						chr12:2834	S_Shelf
			TMCO3	NM_01790	Body	chr13:1141	N_Shelf
	rs10248661		ZNF783	NR_01535	Body	chr7:14897	N_Shore
			SMAD3;SM	NM_00590	Body;TSS1500		
			SCN8A	NM_01419	Body		
rs34923246	rs3205684		HLA-DRB	NM_00212	3'UTR		
			PRKCZ;PR	NM_00103	Body;Body;Body		
	rs35359742						
			KCNQ4;KC	NM_00470	Body;Body	chr1:41303	Island
			ZACN	NM_18099	TSS1500	chr17:7407	S_Shore
			HOXC4;HC	NM_01462	5'UTR;Bod	chr12:5441	S_Shore
			RXFP3	NM_01656	1stExon	chr5:33936	Island
			LOC10013	NR_02733	TSS200;TSS1500		
			PSMB9;PS	NM_00280	Body;Body	chr6:32820	S_Shore
			TPO;TPO;T	NM_17571	Body;Body	chr2:14807	Island
rs71394100			ZFPM1	NM_15381	Body	chr16:8853	N_Shelf
rs3821186			DLX1;DLX	NM_00103	3'UTR;3'U	chr2:17295	Island
			TIAM2;TIA	NM_01245	Body;Body		
		TRUE	UTY;UTY;	NM_18266	Body;Body;Body		
			UGT2B15;	NM_00107	TSS1500;TSS1500		
			SAMD12	NM_00110	3'UTR		
			FAM83H	NM_19848	Body	chr8:14480	Island
			COL18A1	NM_13044	Body	chr21:4684	S_Shore

rs9392815			LOC28578	NR_02697	Body;Body		
	rs76488732						
	rs6858064		UGT2B15;	NM_00107	TSS1500;TSS1500		
						chr20:3520	N_Shelf
	rs28780111						
rs9281864	rs35287346		HLA-DRB	NM_00212	Body		
rs3757651			DOCK4	NM_01470	Body		
						chr11:3157	Island
			SH3BP5;S	NM_00101	Body;Body		
rs73954213		TRUE	TCEB3C;K	NM_14565	TSS1500;5'	chr18:4455	S_Shore
	rs67035222		HLA-DPA1	NM_03355	Body		
			NAPRT1	NM_14520	Body	chr8:14465	Island
			SCARNA1	NR_00301	TSS1500;T	chr17:7508	N_Shore
						chr16:2827	Island
	rs77795436		SNCA;SNC	NM_00730	Body;Body;Body;Body		
			CPA5;CPA	NM_00112	Body;Body;Body		
			FOXP1;FO	NM_03268	5'UTR;5'UTR		
rs17878838			HLA-A	NM_00211	Body	chr6:29910	Island
	rs2747432						
						chr3:13350	Island
			MIR196A2	NR_029617	TSS200	chr12:5438	N_Shelf
	rs77811883		TECPR2	NM_01484	Body		
						chr15:9819	Island
			C19orf44;C	NM_03220	TSS1500;B	chr19:1660	N_Shore
						chr16:5431	Island
			MBNL2;M	NM_14477	5'UTR;5'UTR		
			TESSP1	NM_00113	1stExon	chr16:2848	Island
			ASPSCR1	NM_02408	Body	chr17:7996	Island
			KRTAP11-	NM_17585	TSS1500		
			DLX5	NM_00522	Body	chr7:96651	Island
			SLC47A2;S	NM_00109	TSS1500;T	chr17:1961	S_Shelf
rs76200428	rs603787					chr15:4073	N_Shore
			SMYD3;SM	NM_02274	Body;Body		
rs72849316			CCDC40	NM_01795	Body	chr17:7803	N_Shelf
	rs6943605						
rs3766807			SLC1A7	NM_00667	Body		
						chr1:24885	Island

	rs80247741		FLJ42875;F	NR_024371	Body;Body	chr1:29792	S_Shore
		TRUE	FBXL13;LI	NM_14503	Body;Body;3'UTR;Body		
			HECTD1	NM_01538	Body		
	rs76343291					chr16:8946	N_Shore
			MIA3	NM_19855	TSS1500	chr1:22279	N_Shore
			MMP2;MM	NM_00112	Body;Body		
			HECA	NM_01621	Body		
rs10737337						chr1:17181	N_Shelf
	rs3197223		NME6	NM_00579	3'UTR		
						chr16:3242	Island
	rs7303493		BRI3BP	NM_08062	Body	chr12:1255	N_Shore
						chrY:81478	S_Shelf
						chr1:40598	Island
			SNX29	NM_00108	3'UTR		
			ZNF319	NM_02080	3'UTR	chr16:5803	N_Shore
	rs73657729		MYOM2	NM_00397	Body	chr8:20780	Island
			IPO5	NM_00227	TSS200		
			COMP	NM_00009	TSS1500	chr19:1889	S_Shore
			BTN2A1;B	NM_07847	TSS1500;T	chr6:26458	N_Shore
			NAPSA	NM_00485	Body	chr19:5086	Island
			FHIT;FHIT	NM_00116	5'UTR;5'U	chr3:61236	N_Shore
rs75034630			C1orf86;LC	NM_00114	Body;Body	chr1:21210	Island
rs73323532			OR4D2	NM_00100	1stExon		
			SYT17	NM_01652	Body		
			PCDHB6	NM_01893	1stExon	chr5:14053	N_Shore
	rs34035778		C1QTNF7;	NM_00113	3'UTR;3'UTR;3'UTR		
			GSTT1	NM_00085	TSS1500	chr22:2438	S_Shore
			LRBA;MA	NM_00672	Body;1stEx	chr4:15150	N_Shore
			TRIM31	NM_00702	Body		
			TMEM175	NM_03232	5'UTR	chr4:94061	Island
			CLCNKA;	NM_00104	5'UTR;5'UTR		
	rs7207886		METRNL	NM_00100	Body	chr17:8104	Island
						chr8:98368	N_Shore
	rs11743226		AHRR;LO	NM_02073	Body;TSS200		
			MCC;MCC	NM_00238	Body;Body		
			SAE1;SAE	NM_00550	Body;Body	chr19:4763	S_Shelf
						chr2:86393	Island
			IMPDH1;I	NM_00114	3'UTR;3'UTR;3'UTR;3'UTR;3'UTR		
			PPP1R13L;	NM_00114	5'UTR;5'U	chr19:4590	N_Shelf

		C14orf119	NM_01792	3'UTR	chr14:2356	S_Shelf
		TSPY4;TS	NM_00116	Body;Body	chrY:92358	S_Shore
rs60911997					chr1:32859	S_Shelf
rs74359683		PRKAG2;P	NM_01620	Body;Body;Body		
rs12361485		GDPD4	NM_18283	TSS1500		
		ELANE	NM_00197	Body	chr19:8528	Island
	rs2080822					
	rs76048097	EXTL3	NM_00144	Body	chr8:28573	S_Shelf
		SHF;SHF	NM_13835	5'UTR;1stE	chr15:4549	S_Shore
		IL21R;IL21	NM_02179	TSS1500;5'UTR;5'UTR		
		AKAP13;A	NM_00720	Body;Body		
	rs35039554				chr2:24158	N_Shore
rs74986280	rs1663456	MGAT5B;	NM_14467	Body;Body	chr17:7487	Island
					chr11:6524	Island
					chr13:1129	Island
	rs79553680	MT1IP	NR_00366	Body	chr16:5670	S_Shore
	rs75258887					
	rs73193383	RGS12;RG	NM_19822	Body;Body;Body		
		PECI;PECI	NM_20683	Body;Body	chr6:41351	N_Shelf
					chr6:15035	N_Shore
		CRABP1	NM_00437	TSS1500	chr15:7863	N_Shore
		HRNBP3	NM_00108	3'UTR		
		CLCN4	NM_00183	5'UTR	chrX:10126	Island
	rs72819323	C16orf81	NR_02434	TSS200	chr16:8922	N_Shore
		SKIL;SKIL	NM_00114	TSS1500;5'	chr3:17007	S_Shore
		LOC15482	NR_02439	Body		
					chr11:6738	Island
		HSF5;HSF	NM_00108	5'UTR;1stE	chr17:5656	Island
		SYT7	NM_00420	Body	chr11:6132	Island
		RGMB	NM_00101	Body	chr5:98108	S_Shore
		PRPH2	NM_00032	Body		
	rs76340337	VGLL3	NM_01620	Body	chr3:87039	N_Shelf
rs7757853	rs55708070	HSPA1L	NM_00552	5'UTR	chr6:31782	N_Shelf
		TM4SF4	NM_00461	TSS1500		
		MIER2	NM_01755	Body	chr19:3102	Island

		TRUE	CDKN2BA	NR_00352	Body;3'UT	chr9:22005	N_Shore
			PUS7	NM_01904	Body		
			CTCF	NM_00656	5'UTR		
	rs28743077		PCGF3	NM_00631	5'UTR		
			PRR25	NM_00101	Body	chr16:8573	S_Shore
rs66573219			NCRNA00	NR_026751	Body		
			ABTB2	NM_14580	Body		
			PTPRN2;P	NM_00284	Body;Body;Body		
			MYO16	NM_01501	Body	chr13:1097	Island
rs80342458			BAZ1B	NM_03240	Body		
						chr12:1021	S_Shelf
rs74863748							
						chr15:9397	S_Shelf
			SDHAP3	NR_00326	TSS200	chr5:15942	Island
			HDAC9;HI	NM_17842	Body;Body;Body;Body		
	rs10407949		GNG7	NM_05284	5'UTR	chr19:2578	S_Shelf
			MYH11;M	NM_02284	Body;Body;Body;Body		
		TRUE	WBP2NL	NM_15261	TSS200	chr22:4239	Island
			GMDS	NM_00150	Body		
						chr3:13350	N_Shore
			DNAH5	NM_00136	Body		
rs7607108							
			PDE10A;PI	NM_00113	Body;Body		
			GNA15	NM_00206	TSS1500		
						chr3:88089	S_Shelf
rs16896166	rs1611714					chr6:29831	N_Shelf
	rs68094000		PON3	NM_00094	TSS1500	chr7:95025	S_Shore
			BCAN	NM_02194	Body	chr1:15662	Island
			GK;GK;GK	NM_00112	TSS200;TS	chrX:30670	Island
			SEMA5B	NM_00103	5'UTR		
						chr11:7812	S_Shelf
			CBFA2T3;	NM_17593	5'UTR;Bod	chr16:8897	S_Shore
	rs9261293		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
			SLIT3	NM_00306	Body		
			LOC61920	NR_00293	Body	chr10:1352	Island
						chr8:70790	Island
	rs76237713					chr6:15552	Island
	rs35839865		ZNF497	NM_19845	Body	chr19:5886	Island
						chr10:8229	Island
	rs582244					chr5:39622	N_Shelf

	rs73289713		NXN	NM_02246	Body	chr17:7388	Island
	rs2838613		KRTAP12-	NM_19869	TSS1500;Body		
			PTPRN2;P	NM_00284	Body;Body;Body		
			TNXB	NM_01910	Body	chr6:32063	Island
			HAS1	NM_00152	Body	chr19:5221	S_Shore
			TAGLN3;T	NM_00100	Body;Body;Body		
			DDX3Y;DI	NM_00112	TSS200;TS	chrY:15016	N_Shore
			SPEF2	NM_02486	Body		
						chr18:7588	Island
			RUNX3;RU	NM_00103	Body;Body		
rs12669395						chr7:11785	Island
	rs10832746					chr11:1724	Island
			ZNRF2	NM_14712	Body		
			ARFRP1;A	NM_00322	3'UTR;3'U	chr20:6232	S_Shelf
						chr16:3345	Island
	rs73582059		YAP1;YAP	NM_00113	Body;Body		
rs76560607	rs76536279		LMF1	NM_02277	Body	chr16:9672	Island
			NCRNA00	NR_02706	Body	chr2:11096	Island
		TRUE	TH;TH;TH	NM_19929	TSS200;TSS200;TSS200		
	rs59440261		MICA	NM_00024	TSS1500	chr6:31370	Island
						chrX:87512	Island
						chr5:18059	N_Shelf
	rs10892498						
		TRUE	OXCT1	NM_00043	Body	chr5:41869	Island
						chrY:15863	S_Shore
	rs11641227					chr16:2009	N_Shore
			PRHOXNB	NM_00110	TSS200		
			C8orf74	NM_00104	Body		
			TUBGCP3	NM_00632	TSS1500	chr13:1132	S_Shore
			EIF3E	NM_00156	Body		
			IZUMO1	NM_18257	5'UTR		
			LOC10030	NM_00116	TSS200;TS	chr2:54086	Island
rs9891975						chr17:2068	Island
			NFIX	NM_00250	Body	chr19:1311	Island
			MIER2	NM_01755	TSS1500	chr19:3452	Island
rs79796940			WDR33;W	NM_00100	TSS1500;T	chr2:12856	S_Shore
			PNKD	NM_01548	Body		
rs74149217			CHRM3	NM_00074	5'UTR		

rs8046452	rs4889672	AHSP	NM_01663	TSS1500		
					chrX:53123	Island
					chr12:9618	S_Shelf
					chr7:65970	Island
		USP29	NM_02090	TSS1500	chr19:5763	Island
	rs71700743					
		TSPY4;FA	NM_00116	TSS1500;T	chrY:92154	N_Shore
		CELSR3	NM_00140	Body	chr3:48693	Island
		PLCH2	NM_01463	Body		
		DEFB128	NM_00103	TSS1500		
	rs58924691	IRF2	NM_00219	5'UTR	chr4:18537	S_Shelf
rs60716049	rs62336823	SCFD2	NM_15254	Body		
		RPS4Y1	NM_00100	TSS1500		
rs34662611		RFX2;RFX	NM_00063	3'UTR;3'U	chr19:5994	N_Shore
					chr19:3828	N_Shore
rs72653160	rs72653162	COL1A1	NM_00008	Body		
		PGLYRP1	NM_00509	TSS200	chr19:4652	S_Shore
		TBPL1	NM_00486	5'UTR		
	rs62441317				chr7:66547	N_Shore
		PGLYRP1	NM_00509	TSS200	chr19:4652	Island
					chr13:1126	N_Shore
					chr17:8101	N_Shore
		PXK	NM_01777	Body	chr3:58318	S_Shore
		CBFA2T3;	NM_17593	5'UTR;Body		
					chr17:4489	S_Shore
		SPRED3	NM_00104	3'UTR	chr19:3888	S_Shore
	rs564448	OPCML	NM_00101	Body		
					chr4:13289	Island
		C20orf43;C	NM_01640	1stExon;5'U	chr20:5504	Island
		NBPF22P	NR_00371	TSS1500		
		CACNA2D	NM_17236	Body	chr12:1973	Island
		MAST4;M	NM_01518	Body;Body	chr5:66459	S_Shelf
rs9327740	rs71589303	MIR886	NR_03058	TSS1500	chr5:13541	S_Shore
	rs59108884				chr11:1283	Island

rs4471400	rs74681539						
	rs11271675		SLC22A23;	NM_02194	Body;Body		
			LSP1;LSP1	NM_00101	5'UTR;5'U	chr11:1892	Island
						chr6:31276	N_Shore
rs4957000						chr5:50805	Island
						chr4:41880	Island
			SDHAP3	NR_00326	Body	chr5:15942	Island
						chr6:42694	Island
			IFT172	NM_01566	TSS1500	chr2:27712	S_Shore
rs10277412							
		TRUE	NSDHL;NS	NM_01592	5'UTR;5'U	chrX:15199	S_Shore
	rs35117389		TMEM190	NM_13917	TSS200	chr19:5588	N_Shore
			BANP;BAN	NM_01786	Body;Body	chr16:8805	Island
			POLR1A	NM_01542	Body		
	rs59192026					chr17:2074	Island
			DNAH5	NM_00136	Body	chr5:13810	Island
rs464516						chr22:1853	Island
			EIF1AY	NM_00468	Body	chrY:22737	Island
	rs2074374		PAPSS1	NM_00544	TSS200	chr4:10864	Island
			HRH1	NM_00109	TSS200		
rs28732995			DLX5	NM_00522	Body	chr7:96653	N_Shore
	rs57257499						
			GMIP	NM_01657	Body	chr19:1974	Island
						chr3:13906	N_Shelf
			C21orf7	NM_02015	Body		
			C10orf10;R	NM_00702	TSS200;Body		
			C3orf26;FI	NM_03235	Body;5'UTR;5'UTR		
			OTUD7B	NM_02020	5'UTR	chr1:14998	N_Shelf
			AHRR	NM_02073	Body	chr5:34344	S_Shore
			FAM20A	NM_01756	Body		
	rs4304906					chr13:1120	Island
						chr1:33772	Island
			ACACB	NM_00109	Body	chr12:1095	S_Shelf
			HRNBP3	NM_00108	Body		

					chr13:2167	S_Shore
	rs10889705				chr1:41349	Island
		MRPS5	NM_03190	TSS1500	chr2:95787	S_Shore
		CTU1	NM_14523	Body	chr19:5160	Island
					chr1:16157	N_Shelf
		C3orf24;C3	NM_00116	TSS200;TS	chr3:10149	Island
		PCDH21	NM_03310	Body	chr10:8595	Island
rs176398					chr15:8995	N_Shore
		LOC10012	NR_024447	Body		
		AHRR	NM_02073	Body		
	rs12221520	KCNQ1;KC	NM_00021	Body;Body		
		CAMTA1	NM_01521	Body		
		MRPL28	NM_00642	5'UTR	chr16:4198	Island
	rs28738959					
		TTLL10	NM_00113	5'UTR	chr1:11093	S_Shore
rs41315938		HOXA10;H	NM_01895	3'UTR;3'U	chr7:27212	N_Shore
rs27355		EFNA5	NM_00196	Body		
		OR2L13;O	NM_17591	1stExon;5'U	chr1:24810	Island
		OPCML	NM_00101	Body		
		LRRTM4	NM_00113	Body		
	rs3830059	HLA-DQB	NM_00212	Body	chr6:32632	S_Shore
	rs11529778					
	rs6458151					
rs75562000		TCERG1L	NM_17493	Body		
		C3orf50	NR_02148	Body		
		PDE1A;PD	NM_00501	Body;Body		
		PCDHB12	NM_01893	1stExon	chr5:14058	Island
		MGC45800	NR_02710	Body	chr4:18306	N_Shore
		GRM8;GR	NM_00112	Body;Body;Body		
rs35590611		GNG7	NM_05284	5'UTR	chr19:2525	Island
rs2496219		UPF3B;UP	NM_02301	TSS200;TS	chrX:11898	Island

			OGT;BCY	NM_18167	TSS1500;B	chrX:70752	Island
	rs2077037						
		TRUE	SLC12A5;S	NM_02070	TSS1500;B	chr20:4465	N_Shore
			PTPRN2;P	NM_00284	Body;Body	chr7:15811	N_Shore
			UBE2MP1	NR_00283	Body	chr16:3440	N_Shore
			ZNF217;Z	NM_00652	5'UTR;1stE	chr20:5219	S_Shore
rs80222444							
						chr16:8520	N_Shore
	rs4347019					chr8:13651	Island
rs34951704							
rs9272870	rs9272865		HLA-DQA	NM_00212	3'UTR		
			KIF15;KIA	NM_02024	TSS1500;B	chr3:44802	N_Shore
rs78379193			TBX3;TBX	NM_00599	Body;Body	chr12:1151	N_Shelf
			CRAMP1L	NM_02082	Body	chr16:1705	S_Shelf
			CORO7	NM_02453	Body	chr16:4465	N_Shelf
rs55819742							
	rs11644978		ZSCAN10	NM_03280	TSS200	chr16:3139	S_Shelf
			WNT3A	NM_03313	Body	chr1:22824	Island
			SLC6A18	NM_18263	Body	chr5:12459	Island
			NUBP1	NM_00248	TSS1500	chr16:1083	N_Shore
rs62052310			CDRT15P	NR_003261	TSS200		
			CCDC6	NM_00543	Body		
			CDK2AP1	NM_00464	TSS1500	chr12:1237	S_Shore
rs78566649			AHRR	NM_02073	Body	chr5:34344	S_Shore
						chr15:9688	S_Shore
			LMF1	NM_02277	Body		
rs34773621						chr8:48676	N_Shore
						chr8:48676	N_Shore
	rs4866831		C5orf34	NM_19856	Body	chr5:43483	S_Shelf
	rs5854137						
			YEATS4	NM_00653	Body		
			TGM6	NM_19899	TSS200		
			COX6A2	NM_00520	Body	chr16:3143	Island
						chrX:11913	N_Shore
						chr8:10375	Island
			PCDHB15	NM_01893	1stExon	chr5:14062	N_Shore
			MAML2	NM_03242	Body		
						chr1:22106	S_Shore

	rs2367654						chrX:13852	N_Shelf
rs1977269	rs28519456						chr1:17006	N_Shore
				H2AFJ;H2A	NM_17792	TSS1500;T	chr12:1492	N_Shore
rs74126346				C13orf16	NM_15232	Body		
				COL9A3	NM_00185	Body	chr20:6145	N_Shore
	rs72747049			LPGAT1	NM_01487	Body		
	rs73177799						chr20:5566	N_Shore
							chr6:10643	Island
				HLA-H	NR_00143	Body	chr6:29855	Island
	rs2400685			CCDC85C	NM_00114	Body		
rs2601207				IQGAP1	NM_00387	Body		
				RHCE;RHC	NM_13861	Body;Body;Body;Body		
				ABCA4	NM_00035	Body		
							chr19:3842	Island
rs5010982								
				RNMTL1	NM_01814	3'UTR		
				PTPRK;PT	NM_00284	Body;Body		
				TRIP12	NM_00423	Body		
		TRUE		GNG2	NM_05306	5'UTR		
	rs60253582			SCARF1;S	NM_14535	Body;Body	chr17:1546	N_Shore
							chr1:14780	N_Shore
				RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
rs34986666	rs10846601							
				SHANK1	NM_01614	Body	chr19:5118	S_Shore
							chrX:14855	S_Shelf
							chr3:18452	N_Shore
				HLA-F;HL	NM_00109	Body;Body	chr6:29691	Island
							chr7:57324	Island
	rs2268967			ACTN1;AC	NM_00113	Body;Body;Body		
			TRUE	PSMD11	NM_00281	TSS1500	chr17:3077	Island
	rs71542459			HLA-DQB	NM_00212	Body	chr6:32632	N_Shore
							chr6:10643	Island
rs11325819	rs3214864			DTX1	NM_00441	3'UTR	chr12:1135	S_Shelf
							chr2:17693	Island

			TRUE	GEMIN8;G	NM_00104	TSS1500;T	chrX:14047	Island
	rs72828989			CTBP2;CT	NM_00132	Body;Body	chr10:1266	Island
				HEATR4;C	NM_20330	Body;1stEx	chr14:7395	Island
				CTTN;CTT	NM_13856	Body;Body		
				ZNF714	NM_18251	5'UTR	chr19:2126	Island
							chr16:8524	Island
				PRKCH	NM_00625	Body		
				DLX5	NM_00522	Body	chr7:96650	N_Shore
rs11803374				ABCA4	NM_00035	TSS1500		
							chr2:23171	S_Shelf
							chr1:24222	Island
	rs73089432			HSD11B1;I	NM_18175	5'UTR;TSS1500		
				DHX32	NM_01818	Body		
	rs79625042							
	rs6920813			GPX6	NM_18270	Body		
				PCTP;PCT	NM_02121	Body;Body		
rs62494191								
				ASCC3;AS	NM_02209	3'UTR;Body		
				EVI2A;EV	NM_00100	Body;Body;Body;Body		
		TRUE						
							chrY:20499	S_Shore
	rs28383376			HLA-DQA	NM_00212	Body		
	rs12919931							
				CLEC16A	NM_01522	Body	chr16:1126	N_Shore
							chr1:16494	N_Shelf
				DAG1;DA	NM_00116	5'UTR;5'UTR		
				C21orf57	NM_05818	Body	chr21:4771	N_Shore
rs72298225			TRUE	PSMD5;LC	NM_00504	TSS1500;B	chr9:12360	S_Shore
				PDE8A;PD	NM_17345	Body;Body		
				ACSF3;AC	NR_02331	Body;5'UT	chr16:8916	N_Shore
	rs10808557			POU5F1B	NM_00115	TSS1500		
	rs73042941			SLC9A3	NM_00417	Body	chr5:50038	N_Shore
				WWOX	NM_01637	Body		
	rs7672848			FAT1	NM_00524	Body		
	rs2706513							
				ARRDC4	NM_18337	3'UTR		
	rs61752492			FAM46A	NM_01763	Body	chr6:82461	N_Shore
				NCLN	NM_02017	Body	chr19:3190	Island

				FEZ2;FEZ2	NM_00104	TSS1500;T	chr2:36824	S_Shore
				RPTOR;RP	NM_00116	Body;Body	chr17:7893	Island
				JPH3	NM_02065	Body	chr16:8771	N_Shelf
				C5orf62	NM_03294	Body		
				RYR1;RYR	NM_0054	Body;Body	chr19:3905	Island
				HLA-DPB2	NR_00143	Body		
				RPTOR;RP	NM_00116	Body;Body		
				UST	NM_00571	Body		
				PGCP	NM_01613	5'UTR		
	rs77180248			MRPL15	NM_01417	3'UTR		
rs160516								
	rs2274245			PYROXD2	NM_03270	TSS200		
							chr2:24177	S_Shelf
				CACNA1C	NM_00112	Body;Body	chr12:2339	Island
	rs997868			DYRK4	NM_00384	TSS200		
	rs7129689			LDHA;LDH	NM_00556	TSS1500;T	chr11:1841	N_Shore
			TRUE	HPR	NM_02099	TSS200		
							chr17:3702	N_Shore
rs71759945				DAXX;DA	NM_00114	Body;Body	chr6:33288	N_Shore
							chrX:14952	Island
rs73126196				MIR548A2	NR_03031	Body		
				FOXP1;FO	NM_03268	5'UTR;5'UTR		
rs80066344	rs72061684			ADAMTS9	NM_18292	Body	chr3:64671	N_Shore
rs5747958							chr22:1898	Island
rs62323829	rs62323827			TLR2;TLR	NM_00326	5'UTR;1stE	chr4:15460	Island
				HYALP1	NR_002731	Body		
				FAM20C	NM_02022	Body	chr7:23127	N_Shore
			TRUE	NNMT	NM_00616	TSS1500		
				ATP9B	NM_19853	Body	chr18:7713	Island
				ZPBP2;ZPI	NM_19932	TSS200;TS	chr17:3802	Island
rs78400686							chr7:15878	Island
							chr16:8524	Island
				ABCC12	NM_03322	Body		
				GMEB2	NM_01238	Body	chr20:6222	S_Shelf
rs73454814	rs35088836							
		TRUE		NEGR1	NM_17380	Body		
			TRUE	SHROOM2	NM_00164	Body	chrX:97535	S_Shore

			UBQLN2;U	NM_01344	1stExon;5'U	chrX:56589	Island
			ZNF879	NM_00113	Body	chr5:17845	S_Shelf
rs79270468			S100A3	NM_00296	TSS200		
			PTPRN2;P	NM_00284	Body;Body	chr7:15763	N_Shelf
			CPLX2	NM_00665	5'UTR		
		TRUE				chr16:8519	N_Shore
						chr13:1126	N_Shore
	rs62377743		STK32A;S	NM_00111	Body;Body		
			KIF13A;KI	NM_02211	Body;Body;Body;Body		
rs73508538			SNX29	NM_00108	Body		
			CARD11	NM_03241	Body		
			GRHL2	NM_02491	Body		
rs61736219	rs7951297		SCGB1C1;	NM_14565	1stExon;1stExon		
rs73906668			AGPAT3	NM_02013	5'UTR		
						chr12:1252	Island
						chr4:10496	N_Shelf
			GPC3;GPC	NM_00116	Body;Body	chrX:13311	Island
			SLN	NM_00306	TSS1500		
						chr20:3285	Island
			AGPAT3	NM_02013	5'UTR		
			ZNF254	NM_20328	TSS200		
rs2739765							
	rs11633657		ANXA2;A	NM_00113	Body;Body;Body;Body		
			KREMEN2	NM_02450	Body;Body	chr16:3016	N_Shore
			MGC45800	NR_02710	Body	chr4:18306	N_Shore
	rs76058981		SCD	NM_00506	Body	chr10:1021	S_Shelf
			MGC45800	NR_02710	Body	chr4:18306	Island
						chr6:16881	S_Shore
	rs60968917						
			RD3;RD3	NM_18305	Body;Body	chr1:21165	Island
			SCHIP1	NM_01457	Body		
	rs78336103	TRUE	DYSF;DYS	NM_00113	Body;Body;Body;Body;Body;Body;		
		TRUE	ZFY;ZFY;	NM_00114	Body;Body;5'UTR		
			P4HA2;P4	NM_00101	5'UTR;5'U	chr5:13156	N_Shelf
			NCOR2;NC	NM_00631	Body;Body		
						chr1:35586	Island

		TRUE	PLXNB1;P	NM_00113	5'UTR;5'U	chr3:48470	N_Shelf
rs940367							
rs35980577			GALNT2	NM_00448	Body		
rs227651	rs11087488		CST7	NM_00365	TSS200		
						chr10:1319	N_Shelf
			DDX3Y;DI	NM_00466	TSS200;5'U	chrY:15016	Island
	rs11917613		SLC12A8	NM_02462	Body	chr3:12486	S_Shore
	rs73294763						
						chr4:66656	N_Shore
	rs35462285		PTPRN2;P	NM_00284	Body;Body;Body		
	rs6538643		USP44;USI	NM_00104	TSS1500;5'	chr12:9594	S_Shore
			ZFYVE28	NM_02097	Body	chr4:23664	Island
			GNAS;GN	NM_00107	3'UTR;TSS	chr20:5746	Island
			LOC12195	NR_02696	TSS200		
			SRRM1	NM_00583	TSS1500	chr1:24969	N_Shore
						chr6:28583	Island
			FAM173B	NM_19913	3'UTR		
			SEPT9;SEF	NM_00111	5'UTR;Body;TSS1500		
rs60335230	rs56393137		LHFPL2	NM_00577	5'UTR	chr5:77805	S_Shelf
			PCSK6;PC	NM_00257	Body;Body	chr15:1020	N_Shelf
			CUX2	NM_01526	Body		
rs79244768	rs4843570					chr16:8725	N_Shore
rs7581359			MYT1L	NM_01502	Body		
	rs79415057						
	rs12874739					chr13:1120	Island
			GPT	NM_00530	TSS1500	chr8:14573	N_Shore
	rs59956200		ADCY9	NM_00111	Body	chr16:4016	S_Shore
			PNPLA4;P	NM_00114	Body;Body	chrX:78950	N_Shelf
						chr2:11861	N_Shelf
rs60575307						chr10:8229	Island
			FBLN7;FB	NM_15321	Body;Body	chr2:11289	S_Shore
	rs4990367					chr15:2434	Island
			ST3GAL3;S	NM_17496	Body;Body;Body;Body;Body;Body;		
			TTLL5	NM_01507	Body		
			MGMT	NM_00241	Body		
			C11orf17;C	NM_18290	TSS1500;T	chr11:8932	N_Shore
			AKAP6	NM_00427	Body		
			MAP3K7IP	NM_15278	1stExon;5'U	chrX:30906	Island
						chr2:65086	N_Shore
			CR1;CR1	NM_00065	Body;Body	chr1:20766	Island

rs6944877	rs59729366		MAD1L1;	NM_00355	Body;Body	chr7:19502	S_Shelf
			C21orf81	NR_02727	TSS1500	chr21:1535	S_Shore
	rs9931360						
	rs75453246		FLJ39653;	NR_02769	Body;Body	chr4:16257	N_Shelf
			EEPD1	NM_03063	Body	chr7:36192	S_Shore
			FLJ37201	NR_02683	Body		
			AMHR2;A	NM_00116	Body;Body;Body		
			DIP2C	NM_01497	Body		
	rs2293269		GTF2A1L;	NM_17219	1stExon;Bo	chr2:48844	Island
			TTTY11	NR_00154	Body		
			PAX8;PAX	NM_01395	TSS1500;T	chr2:11403	S_Shore
rs11768077	rs78867640						
			SH3D19;SH	NM_00100	TSS1500;TSS1500		
	rs3739231		DENND3	NM_01495	5'UTR	chr8:14213	Island
			CYorf15A	NM_00100	TSS200	chrY:21729	Island
			LONRF2	NM_19846	Body		
			C12orf23	NM_15226	TSS1500	chr12:1073	N_Shore
						chr7:25990	S_Shore
			CCDC84	NM_19848	Body	chr11:1188	S_Shore
						chr8:12458	Island
						chr1:28470	N_Shelf
			CPT1A;CP	NM_00187	Body;Body	chr11:6855	Island
	rs10841068		PLCZ1	NM_03312	Body		
rs11062654							
	rs78553485		HLA-DRB	NR_00129	Body		
			FRAS1;FR	NM_02507	Body;Body		
			CYTSB;CY	NM_00103	Body;Body		
			SYN2;TIM	NM_13362	Body;Body	chr3:12200	N_Shelf
rs36061309			ST7L;ST7L	NM_01774	3'UTR;3'UTR;3'UTR		
rs34561980	rs34161953		CSNK2B	NM_00132	Body	chr6:31632	S_Shore
	rs599134		DENND2D	NM_02490	Body		
	rs9771330		PRKAR1B;	NM_00116	Body;Body;Body;Body;Body;Body		
rs8018356							
	rs56119510		ARHGEF7;	NM_00111	Body;Body	chr13:1119	Island
			USP29	NM_02090	TSS1500	chr19:5763	Island
		TRUE	SLC5A8	NM_14591	1stExon	chr12:1016	Island
			CEACAM1	NM_02021	3'UTR;3'UTR		

	rs74068805					chr1:43472	S_Shore
			ST18	NM_01468	5'UTR		
			TTLL8	NM_00108	Body	chr22:5048	N_Shore
	rs78643977		TC2N;TC2	NM_15233	TSS1500;5'	chr14:9230	S_Shore
			PRNT;PRN	NR_02426	TSS1500;TSS1500;TSS1500		
	rs621635		COL23A1	NM_17346	Body		
			OGFRL1	NM_02457	Body		
						chr1:22874	Island
	rs57995724		CGNL1	NM_03286	Body		
rs7182446	rs9919986		PLA2G4E	NM_00108	TSS1500		
			TNIK;TNI	NM_00116	Body;Body;Body;Body;Body;Body;		
			SVOPL;SV	NM_00113	Body;TSS2	chr7:13834	Island
			LTB4R2;L	NM_00116	Body;1stEx	chr14:2477	Island
	rs11784329		MYOM2	NM_00397	Body	chr8:20377	N_Shelf
			FLJ44606;F	NM_00116	5'UTR;5'U	chr5:12640	Island
rs61649802			BANP;BAN	NM_01786	Body;Body	chr16:8805	Island
rs78643977			TC2N;TC2	NM_15233	TSS1500;5'	chr14:9230	S_Shore
	rs55966917					chr5:25190	Island
			PCDHA6;P	NM_03184	Body;Body	chr5:14021	Island
			ZFY;ZFY;Z	NM_00341	TSS1500;T	chrY:28029	Island
rs4722586							
rs1050269	rs1050268		UPP1;UPP	NM_18159	5'UTR;5'U	chr7:48128	Island
rs28383373	rs28383372		HLA-DQA	NM_00212	Body		
			FGGY;FG	NM_01829	Body;Body		
		TRUE	FAM113B	NM_13837	5'UTR		
	rs72623166		B3GALT1	NM_02098	TSS1500		
	rs370061		CPNE7;CP	NM_01442	Body;Body	chr16:8964	Island
						chr12:6586	N_Shore
			ZNF469	NM_00112	Body	chr16:8849	Island
		TRUE					
			ITGBL1;IT	NM_00479	1stExon;5'U	chr13:1021	N_Shore
rs66550714	rs56218113		C4orf11;C4	NR_024087	Body;Body		
						chrY:20508	Island
			IDO1	NM_00216	TSS1500		
	rs2083624						
rs7058338			LOC72960	NR_02444	TSS1500	chrX:20008	Island
rs77763351			CNTNAP5	NM_13077	Body		
			CHL1	NM_00661	5'UTR		
			NR0B1	NM_00047	TSS200	chrX:30326	Island

				ADARB2	NM_01870	Body		
				JAG2;JAG	NM_00222	Body;Body	chr14:1056	N_Shore
							chr4:18788	Island
				ZMYM3;Z	NM_20159	TSS1500;1	chrX:70473	S_Shore
				MMP27	NM_02212	1stExon		
				BPGM;BP	NM_00172	Body;Body		
rs28721783	rs28993612						chr6:29818	N_Shelf
							chr1:32538	N_Shelf
	rs73082997							
				MGLL;MG	NM_00728	Body;Body		
	rs75963540			C2orf76	NM_00101	Body		
	rs7265027			SS18L1	NM_19893	Body	chr20:6074	S_Shore
			TRUE	PON3	NM_00094	TSS1500	chr7:95025	S_Shore
	rs7835987			ATP6V1H;	NM_21361	3'UTR;3'UTR;3'UTR		
							chr11:1283	Island
rs72982581	rs73232946			ACPL2;AC	NM_15228	Body;Body		
				SRY	NM_00314	TSS200	chrY:26578	N_Shore
							chr16:2875	N_Shore
				ATP6AP2	NM_00576	TSS200	chrX:40439	Island
				RXFP3	NM_01656	1stExon	chr5:33936	Island
				MTSS1	NM_01475	Body		
				LOC40093	NR_02703	TSS1500	chr22:4648	N_Shore
							chr19:1237	Island
	rs78542675			CEACAM2	NM_00110	TSS200;TSS200;TSS200;TSS200		
rs75526663							chr9:45733	N_Shore
rs9270371	rs9270366			HLA-DRB	NM_00212	TSS1500		
				EZH2;EZH	NM_15299	Body;Body		
			TRUE	HLA-C	NM_00211	Body	chr6:31238	Island
				CYFIP1	NM_01460	5'UTR		
		TRUE						
	rs4367979							
				CPA6;CPA	NM_02036	Body;Body		
				C6orf201;C	NM_00108	TSS200;5'U	chr6:40790	Island
				ATP2A1;A	NM_17320	TSS1500;T	chr16:2889	N_Shore
				SYCP1	NM_00317	5'UTR	chr1:11539	Island
				STX2;STX	NM_00198	Body;Body	chr12:1313	N_Shelf

			JAM2	NM_02121	TSS1500	chr21:2701	N_Shore
			MTCP1NB	NM_00101	5'UTR;Body		
			CDK6;CDK	NM_00125	Body;Body	chr7:92462	N_Shelf
	rs78056730		CCR6	NM_00436	TSS1500		
						chr13:1122	S_Shelf
			CHCHD3	NM_01781	Body		
			NDUFS2;A	NM_00455	TSS200;TS	chr1:16117	N_Shelf
			BEST1;BES	NM_00418	Body;Body		
			MTMR1	NM_00382	TSS200		
			FLG	NM_00201	TSS1500		
			TNFAIP2	NM_00629	Body	chr14:1035	Island
rs61821292							
	rs80267389						
rs79556808	rs1054411		SCD;SCD	NM_00506	5'UTR;1stE	chr10:1021	Island
						chr7:65970	Island
	rs34989027						
rs9392474			SLC22A23;	NM_02194	Body;Body		
			UBE2J2;UI	NM_19445	3'UTR;3'U	chr1:11905	Island
	rs2292474		SYT8	NM_13856	Body		
rs45604837	rs45574533		TNFRSF25	NM_00379	TSS200;3'U	chr1:65259	S_Shore
rs79244006			PPP1R13B	NM_01531	TSS1500	chr14:1043	S_Shore
rs11626310	rs12586680					chr14:1015	S_Shelf
			PCDHB19P	NR_001282	TSS200	chr5:14062	N_Shore
	rs4666457		GDF7	NM_18282	3'UTR	chr2:20870	Island
	rs7961916						
			CAMTA1	NM_01521	Body	chr1:70220	S_Shore
rs61653552			PRDM16;P	NM_02211	Body;Body		
	rs78210990		GLI2	NM_00527	Body		
			CLASP1;CI	NM_00114	Body;Body;Body		
	rs79641401						
			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		TRUE	NRN1L	NM_19844	TSS200	chr16:6791	Island
			PCNXL2	NM_01480	Body		
						chr12:7781	Island
			SLC6A6;SI	NM_00304	Body;Body		
			MAB21L1;	NM_00558	1stExon;Bo	chr13:3604	N_Shore
						chrX:10674	Island
			PCDHGA1	NM_01891	TSS1500;T	chr5:14071	N_Shore
			SLCO4A1	NM_01635	Body	chr20:6128	Island

rs7255531						chr19:5621	Island
			PAG1	NM_01844	5'UTR		
						chr11:1283	Island
rs60648910			PTPRN2;P	NM_00284	Body;Body	chr7:15828	N_Shore
			ZFYVE28	NM_02097	Body	chr4:23664	Island
			ABCA13	NM_15270	Body		
			EBPL	NM_03256	Body		
			UGT2B15;	NM_00107	TSS1500;TSS1500		
rs28405322	rs76432766		KIAA1199	NM_01868	5'UTR		
rs41287319	rs36177427		HLA-DRB	NM_00212	Body	chr6:32551	S_Shore
			CACNA1C	NM_00112	Body;Body	chr12:2339	Island
			LOC10013	NR_02445	TSS1500		
						chrX:45710	Island
			MCTP2;M	NM_01834	Body;Body;Body		
			MIR196A2	NR_02961	TSS1500	chr12:5438	N_Shelf
			C13orf30	NM_18250	Body		
			PLA1A	NM_01590	3'UTR		
			GPRASP1;	NM_01471	5'UTR;5'U	chrX:10190	Island
rs2746400			SKIV2L	NM_00692	Body	chr6:31939	N_Shelf
						chr19:4807	S_Shore
						chr3:13451	N_Shore
			MYBPC2	NM_00453	Body	chr19:5096	Island
			GDF7	NM_18282	Body	chr2:20870	Island
						chr17:3529	Island
			DDAH2	NM_01397	TSS200	chr6:31695	Island
rs6981256							
			PSD3;PSD	NM_20690	Body;Body		
			FOXO1	NM_00201	Body		
			CYTH1;CY	NM_01745	Body;Body		
			BMP8A	NM_18180	Body	chr1:39980	Island
	rs11976257						
						chr13:1126	Island
	rs12475572		COLEC11;	NM_02402	Body;Body		
		TRUE	FAM180A	NM_20585	TSS200		
	rs78391197		YPEL1	NM_01331	3'UTR	chr22:2205	N_Shelf

	rs4725997			AGAP3	NM_03194	Body	chr7:15082	S_Shore
				C3orf24;C3	NM_00116	TSS200;TS	chr3:10149	Island
							chr13:1129	Island
			TRUE	TMEM109	NM_02409	TSS1500	chr11:6068	N_Shore
	rs78517604			PTPRN2;P	NM_00284	Body;Body;Body		
rs3759383	rs3759384			ARPC3	NM_00571	TSS1500	chr12:1108	S_Shore
							chr14:7392	S_Shelf
	rs12436604						chr14:7681	Island
rs62131624	rs76168174						chr19:5503	Island
				KCNS3	NM_00225	5'UTR	chr2:18059	S_Shelf
	rs35184018			ITGB3	NM_00021	Body	chr17:4533	S_Shelf
				PTPRN2;P	NM_00284	Body;Body	chr7:15811	N_Shore
	rs35785418			HSP90B3P	NR_00313	Body		
	rs2249670			PRKCZ;PR	NM_00274	Body;5'UT	chr1:20252	N_Shore
							chr15:9690	Island
	rs3742722			C14orf145;	NM_15244	1stExon;5'U	chr14:8140	N_Shore
rs6456718								
				TGFB3	NM_00323	Body	chr14:7644	N_Shelf
							chr12:5437	N_Shelf
	rs10885596			ABLIM1;A	NM_00100	1stExon;1stExon;5'UTR;5'UTR		
				ORAI2;AL	NM_03283	3'UTR;3'U	chr7:10209	N_Shore
				RASA3	NM_00736	Body		
				HOXD4	NM_01462	Body	chr2:17701	N_Shore
				PCDHB14	NM_01893	1stExon	chr5:14060	N_Shore
rs78779376	rs78743240			TUBB4Q	NM_02004	TSS200	chr4:19090	Island
				ASAP2;AS	NM_00113	Body;Body		
				FLJ44606;F	NM_00116	TSS200;TS	chr5:12640	Island
	rs76932150			SPRR2D	NM_00694	TSS1500		
				PPAP2C;P	NM_17754	Body;Body	chr19:2905	N_Shore
							chr2:19817	N_Shore
				B3GNTL1	NM_00100	Body	chr17:8096	S_Shore
				EIF2AK4	NM_00101	Body	chr15:4026	S_Shore
	rs73525929	TRUE		CLEC5A	NM_01325	Body		
				RPH3AL	NM_00698	Body	chr17:1373	S_Shore
				STX2;STX	NM_00198	Body;Body	chr12:1313	Island
				LCK;LCK	NM_00535	Body;Body	chr1:32740	Island
			TRUE	TBL1X;TB	NM_00113	5'UTR;5'U	chrX:94328	Island

	rs80028898		GPR115	NM_15383	TSS1500		
	rs73581032					chr20:8252	S_Shelf
						chr2:11959	Island
rs78651079	rs7800149		SDK1;SDK	NR_02781	Body;Body		
rs943975	rs28371741		CYP2E1	NM_00077	Body	chr10:1353	Island
	rs55645419	TRUE	PGLYRP1	NM_00509	TSS200	chr19:4652	S_Shore
rs6542986	rs6731211						
rs78345829	rs10947970						
rs2075702			STK19;SKI	NR_02671	TSS1500;B	chr6:31939	N_Shelf
			LNPEP;LN	NM_17592	Body;Body		
		TRUE	C2orf39	NM_14503	TSS200	chr2:26624	Island
			DTYMK;D	NM_00116	Body;Body	chr2:24261	S_Shelf
rs4881436	rs4881435		TUBAL3	NM_02480	TSS200		
rs2453648			SPAG1;SP	NM_17221	5'UTR;5'U	chr8:10117	S_Shelf
						chr12:5437	N_Shore
						chr7:56242	Island
			SH3D19;S	NM_00112	1stExon;5'UTR;1stExon;5'UTR		
			KLHL35	NM_00103	Body	chr11:7513	Island
			SCARB1;S	NM_00108	Body;Body		
			TMEM185	NM_03250	TSS200	chrX:14871	Island
	rs12259153		KNDC1	NM_15264	Body	chr10:1349	S_Shore
			PPP2R2B;P	NM_18167	Body;Body	chr5:14625	N_Shelf
			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
			HRNBP3	NM_00108	TSS200		
			FAM153C	NM_00107	TSS1500	chr5:17743	S_Shore
			C5orf33	NM_15301	TSS1500	chr5:36241	S_Shore
			C10orf53;C	NM_18255	Body;Body	chr10:5088	S_Shelf
			PPAPDC1A	NM_00103	Body		
			APAF1;AP	NM_18186	Body;Body;Body;Body;Body		
						chr12:1151	N_Shore
	rs2104231		FLJ22536	NR_01541	Body		
	rs12725787		MIB2;MIB	NM_00117	Body;Body	chr1:15585	N_Shelf
			IMMT;IMM	NM_00110	TSS1500;T	chr2:86422	S_Shore
rs55885018	rs34211819		TNS3	NM_02274	5'UTR		
			VPS13A;V	NM_00101	TSS1500;T	chr9:79792	Island
rs2523988			TRIM31	NM_00702	Body		
						chr22:2148	N_Shelf
			TNFRSF25	NM_14897	3'UTR;3'U	chr1:65205	Island
			LYSMD2;L	NM_15337	Body;5'UTR		
						chr3:75704	Island

		UBTD1	NM_02495	Body		
rs41542812	rs41544112	HLA-DQB	NM_00212	Body	chr6:32632	N_Shelf
		DOCK1	NM_00138	Body		
		NLGN4Y;	NR_02831	Body;5'UT	chrY:16635	S_Shore
		C6orf182;C	NM_17383	TSS200;5'UTR		
	rs11576030	LCK;LCK	NM_00535	Body;Body	chr1:32740	Island
		GRIPAP1;	NM_20767	Body;Body		
rs36215042	rs34041546	HLA-DRB	NR_00129	Body		
		ZBTB20;Z	NM_00116	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR		
	rs58223673				chr7:55411	Island
	rs12637576	CCDC36;C	NM_00113	5'UTR;5'U	chr3:49236	Island
rs17854367		PCDHB12	NM_01893	1stExon	chr5:14058	Island
		LDOC1	NM_01231	TSS200	chrX:14027	Island
		LOC28326	NR_015451	TSS1500		
	rs13309471					
		STX2;STX	NM_00198	Body;Body	chr12:1313	Island
rs13043488		RTEL1;RT	NM_01643	Body;Body	chr20:6231	N_Shelf
		ST3GAL5	NM_00389	Body		
		FAM19A5	NM_00108	Body	chr22:4889	Island
		SLC7A3;SL	NM_03280	5'UTR;5'U	chrX:70150	Island
	rs36060608	GABRB3	NM_02191	TSS1500	chr15:2701	S_Shore
rs67316991		BAHCC1	NM_00108	Body	chr17:7937	S_Shore
		ANO10	NM_01807	Body		
	rs1610642	HCG4	NR_00213	Body	chr6:29759	N_Shore
					chr10:5053	S_Shelf
rs73832379	rs80066344	ADAMTS9	NM_18292	Body	chr3:64671	N_Shore
rs74685485		CACNA1C	NM_00112	Body;Body;Body;Body;Body;Body;		
	rs9324560					
					chr17:8045	N_Shelf
rs439797		RNF182;R	NM_00116	TSS1500;T	chr6:13925	N_Shore
		BANP;BA	NM_01786	Body;Body	chr16:8805	Island
					chr2:12845	Island
		HOXB3	NM_00214	TSS1500	chr17:4665	N_Shore
	rs1248643	DLG5	NM_00474	Body		
	rs79648471	OR11H6	NM_00100	TSS200		
	rs34557407				chr2:24158	S_Shore

		GAB2	NM_08049	TSS1500	chr11:7812	S_Shore
		RPS6KA2;	NM_02113	Body;Body		
rs58639797						
rs78092115		TAF3	NM_03192	TSS1500	chr10:7860	N_Shore
		LOC10010	NR_02724	TSS200	chr13:1991	Island
		MGC45800	NR_02710	Body	chr4:18306	Island
		ZAK;ZAK	NM_01665	Body;Body		
rs10826790	rs2245761					
		LSM1	NM_01446	Body	chr8:38033	N_Shore
		RNU5E;RN	NR_00275	Body;Body	chr5:80597	N_Shelf
		PTPRN2;P	NM_00284	Body;Body	chr7:15828	N_Shore
		SCARA5	NM_17383	Body	chr8:27779	Island
	rs73163142					
		PTRF	NM_01223	Body	chr17:4055	S_Shelf
		CDH9	NM_01627	TSS200		
		LPCAT1	NM_02483	Body	chr5:14897	S_Shore
rs79898337					chr1:24768	Island
					chr5:18567	Island
		LOC10013	NR_02446	Body;TSS1	chr11:6713	S_Shore
		FMNL2	NM_05290	Body		
		SCD5;SCD	NM_00103	Body;Body	chr4:83719	N_Shore
rs9393102		LOC28576	NR_02711	Body;Body		
		ADAM5P	NR_00144	TSS200		
		ZNF192	NM_00629	Body		
		HLA-F;HL	NM_00109	TSS1500;T	chr6:29691	N_Shore
		MAGI2	NM_01230	Body		
		MPZ	NM_00053	TSS1500	chr1:16128	N_Shelf
rs77462072		PGBD5	NM_02455	Body	chr1:23049	S_Shore
		FMNL1	NM_00589	Body	chr17:4331	Island
		EIF1AY;EI	NM_00468	5'UTR;1stE	chrY:22737	N_Shore
		ARHGEF3	NM_00112	Body		
rs10172321	rs77758395					
		NPHP1;NP	NM_00112	Body;Body;Body;Body		
		PCDHGA2	NM_01891	Body;1stEx	chr5:14072	N_Shore

			TMEM47	NM_03144	Body	chrX:34674	Island
			FAM138D	NR_02682	TSS200		
			TRIM66	NM_01481	5'UTR		
	rs72648853						
			MOV10;M	NM_02096	Body;Body		
	rs10522738		B3GNTL1	NM_00100	Body	chr17:8096	Island
rs73169210	rs78139649		LOC15482	NR_02439	Body	chr7:15881	N_Shore
rs77969743	rs71594797						
			MAGT1	NM_03212	TSS1500	chrX:77150	S_Shore
			GPC6	NM_00570	Body		
			BMP8B;O	NM_00172	Body;1stEx	chr1:40235	Island
	rs2304283		DENND3	NM_01495	Body		
			HNRNPUL	NM_00704	Body;Body		
			MSC	NM_00509	TSS1500	chr8:72755	S_Shore
			PGM5P2	NR_00283	Body	chr9:69147	Island
			LRCH2	NM_02087	1stExon	chrX:11446	Island
		TRUE	LY6G6C;L	NM_02526	5'UTR;1stE	chr6:3169	N_Shore
						chrX:12911	Island
						chr17:3516	N_Shelf
			CDK16;CD	NM_03301	1stExon;TS	chrX:47077	Island
						chr17:1568	Island
		TRUE	JAM2	NM_02121	TSS1500	chr21:2701	N_Shore
rs55783427						chr6:16850	Island
			CFHR3;CF	NM_02102	Body;Body		
rs34765785							
	rs77449817					chr2:22036	Island
			DLX5	NM_00522	Body	chr7:96651	Island
		TRUE	AKR7L;AK	NM_00114	TSS200;TS	chr1:19600	Island
			IGLON5	NM_00110	Body	chr19:5181	S_Shelf
						chr5:43040	N_Shore
						chr8:43132	S_Shelf
rs1340493	rs74603131						
		TRUE	HSPB3	NM_00630	1stExon		
rs11650811			CDRT15	NM_00100	Body		
	rs11072475						
						chr6:17045	S_Shore

				COL6A1	NM_00184	Body	chr21:4740	Island
				EFTUD1;E	NM_00104	Body;Body		
	rs72354906			CYFIP1	NM_01460	5'UTR		
				GALE;GAI	NM_00112	Body;Body	chr1:24126	N_Shelf
							chr15:6732	N_Shelf
	rs75473167			SLC12A7	NM_00659	Body	chr5:11113	N_Shore
	rs72648059			GALNT2	NM_00448	Body		
							chr5:26431	Island
							chr19:1851	Island
				PON3	NM_00094	TSS1500	chr7:95025	Island
rs2308928	rs2308929			HLA-DPA1	NM_03355	Body		
	rs9515189			COL4A2	NM_00184	Body	chr13:1109	S_Shelf
				CYP2E1	NM_00077	Body	chr10:1353	S_Shore
				SMC1A;RI	NM_00630	TSS200;TS	chrX:53448	Island
				PHPT1;PHI	NM_01417	TSS1500;T	chr9:13973	Island
				WASF3	NM_00664	5'UTR		
		TRUE		SLC23A1;S	NM_15268	Body;Body	chr5:13871	Island
							chr15:3260	Island
				SFRP2	NM_00301	Body	chr4:15470	N_Shelf
				DIP2C	NM_01497	Body	chr10:6690	S_Shore
			TRUE	KRT6A	NM_00555	TSS1500		
	rs4809555			KCNQ2;KC	NM_17210	Body;Body	chr20:6205	Island
							chr9:72026	Island
				CAMTA1	NM_01521	Body	chr1:70220	S_Shore
	rs55678474			MAD1L1;M	NM_00355	Body;Body	chr7:19772	S_Shelf
				CLIC6	NM_05327	TSS200	chr21:3604	Island
	rs73795197							
rs56268625				FLT4	NM_18292	3'UTR		
							chr22:4692	S_Shore
				LOR	NM_00042	Body		
				SND1	NM_01439	TSS1500	chr7:12729	N_Shore
	rs75104428			IDE;IDE	NM_00496	Body;5'UTR		
rs10040651	rs75514521			RASGRF2;	NM_00690	Body;TSS200;TSS200		
rs75678647	rs72869469			NCRNA00	NR_02702	Body;TSS2	chr2:13301	Island
				INPP4A;IN	NM_00156	5'UTR;5'UTR;5'UTR;5'UTR		
	rs57636116			PCDHB11	NM_01893	1stExon	chr5:14058	Island
				TOP1MT	NM_05296	Body	chr8:14440	S_Shelf
							chr2:24164	S_Shelf
				TBC1D15;	NR_02744	TSS1500;T	chr12:7223	N_Shore
							chr22:3095	N_Shelf
				CLIP1;CLI	NM_00295	Body;Body		

rs397654		PPP1R3G;F	NM_00114	3'UTR;1stE	chr6:50845	Island
		DHDPSL;D	NM_13841	Body;Body		
		ADAM5P	NR_00144	TSS200		
		SHISA4;SH	NM_19814	TSS1500;TSS1500		
	rs12499983				chr4:14665	S_Shore
		ITPR1;ITP	NM_00222	Body;Body;Body;TSS1500		
rs45497893					chr5:17743	Island
					chr5:13541	N_Shore
					chr6:11466	N_Shelf
		KIAA0408;	NM_01470	5'UTR;3'UTR;1stExon		
	rs77448028	COL1A1	NM_00008	Body		
		NSDHL;NS	NM_01592	5'UTR;5'U	chrX:15199	S_Shore
		BAIAP2;B	NM_01745	Body;Body	chr17:7900	S_Shore
					chr13:2531	Island
	rs10247312	HIPK2;HIP	NM_00111	Body;Body		
		NPAS4	NM_17886	3'UTR		
		FNIP2	NM_02084	Body		
		ITIH4;ITIH	NM_00116	5'UTR;1stExon;1stExon;5'UTR		
		DDO;DDO	NM_00403	Body;Body		
	rs10103800				chr8:13273	Island
		ETV6	NM_00198	Body		
		CCDC88B	NM_03225	Body	chr11:6411	S_Shelf
		COL20A1	NM_02088	TSS200	chr20:6192	N_Shelf
rs41279106		MBNL2;M	NM_14477	5'UTR;5'UTR		
		HNRNPH2	NM_00103	1stExon;TS	chrX:10066	Island
	rs2052769				chr4:11975	S_Shelf
	rs9624216	IGLL1;IGL	NM_02007	TSS200;TSS200		
	rs943037	CNNM2;C	NM_19907	Body;Body		
rs80134795						
		KCNN2	NM_02161	Body	chr5:11369	S_Shore
		GPR119	NM_17847	TSS1500		
		MAP7D2;M	NM_00116	Body;Body	chrX:20134	Island
					chr13:1128	N_Shelf
		HIBADH	NM_15274	TSS1500	chr7:27702	S_Shore
	rs55990625	PCGF3	NM_00631	Body	chr4:73842	N_Shore
		CPVL;CPV	NM_03131	Body;Body		

							chr1:28850	Island
				INPP5A	NM_00553	Body		
				TMEM220	NM_00100	TSS1500	chr17:1063	S_Shore
rs34823482	rs34195497			HLA-DRB	NR_00129	Body		
			TRUE	EFNB1	NM_00442	Body	chrX:68048	Island
	rs4725236			KIAA1908;	NR_02732	Body;Body;Body		
				DLG5	NM_00474	Body		
				PCDHA2;P	NM_01890	Body;Body	chr5:14020	Island
rs1142447	rs1130156			HLA-DQA	NM_00212	3'UTR		
		TRUE		RANBP3L;	NM_14500	Body;Body		
	rs6425762			LOC28455	NR_02708	Body		
				NCRNA00	NR_02706	Body		
rs6699055							chr1:22865	Island
				ELAC2;EL	NM_01812	TSS1500;T	chr17:1292	S_Shore
				VTRNA1-2	NR_02670	TSS200		
rs1059467	rs61760912			HLA-A	NM_00211	Body	chr6:29910	Island
	rs11146085						chr10:1348	N_Shelf
				B3GNTL1	NM_00100	Body	chr17:8096	S_Shore
				TFE3	NM_00652	TSS200	chrX:48900	Island
							chr8:43131	Island
	rs3128781			ZFYVE28	NM_02097	Body	chr4:24015	S_Shore
	rs4368927			PTPRN2;P	NM_00284	Body;Body	chr7:15828	N_Shore
				DOCK1	NM_00138	Body		
				MST1R	NM_00244	1stExon	chr3:49940	Island
							chr12:1151	N_Shore
				TOP2B	NM_00106	Body		
							chr14:1004	S_Shelf
				GREM2	NM_02246	TSS1500		
				PPYR1	NM_00597	TSS200	chr10:4708	Island
							chr5:17604	N_Shore
				ANKFN1	NM_15322	1stExon		
			TRUE	ZCCHC12	NM_17379	TSS200	chrX:11795	Island
							chr14:1019	Island
				IMMP2L	NM_03254	Body		
				OPRM1;O	NM_00114	Body;Body;Body;1stExon;Body;Bo		

	rs2925323	LOC15222	NR_02693	TSS1500		
	rs73361268	TG;SLA;SL	NM_00323	Body;Body;5'UTR		
	rs28736751				chr6:16763	N_Shelf
		ESYT3	NM_03191	TSS1500	chr3:13815	N_Shore
		DLX5	NM_00522	Body	chr7:96651	Island
	rs34291637					
		CST9L	NM_08061	TSS1500		
		SRY	NM_00314	TSS200	chrY:26578	N_Shore
	rs34025887	MIR196A2	NR_02961	TSS1500	chr12:5438	N_Shelf
		VRK3;VRK	NM_01644	3'UTR;3'UTR		
	rs6822582	WDR17;W	NM_18126	1stExon;5'U	chr4:17698	Island
		DCHS2;DC	NM_01763	Body;Body	chr4:15525	Island
					chr3:13350	Island
	rs2108488	PSG1	NM_00690	TSS200		
					chr2:23321	Island
		ZRANB3	NM_03214	Body		
		HTR1D	NM_00086	TSS200		
					chr4:39528	S_Shelf
		CACNA2D	NM_17236	Body	chr12:2017	N_Shore
		PIKFYVE;	NM_01504	Body;Body		
		ISPD;ISPD	NM_00110	Body;Body	chr7:16460	N_Shelf
		EID2	NM_15323	TSS1500	chr19:4003	S_Shore
		EXOSC9;E	NM_00503	TSS1500;T	chr4:12272	N_Shore
					chr1:98519	N_Shore
	rs1049060	HLA-DQB	NM_00212	1stExon	chr6:32632	S_Shore
		B4GALT6	NM_00477	3'UTR		
rs71684644	rs2294487	SLC35E2	NM_18283	3'UTR		
rs17879746	rs9270296	HLA-DRB	NM_00212	Body		
		C10orf119	NM_02483	Body		
	rs67550272					
					chr13:1126	N_Shore
	rs6856550	KIAA1530	NM_02089	Body	chr4:13664	Island
		DIP2C	NM_01497	Body		

rs11755610					chr6:90597	Island
	rs10693671					
		NIN	NM_02092	3'UTR		
		HAUS7	NM_01751	1stExon	chrX:15273	Island
rs73724324		MESTIT1;	NR_00438	Body;5'UT	chr7:13013	N_Shore
rs12617802		CYBRD1;	NM_00112	TSS1500;T	chr2:17237	N_Shore
		TCERG1L	NM_17493	Body		
rs3873388					chr6:31276	N_Shore
rs9295884					chr6:30418	Island
	rs6310	HTR2A;HT	NM_00062	5'UTR;Body		
					chr6:16409	N_Shore
		ZBTB4;ZB	NM_00112	5'UTR;5'U	chr17:7382	N_Shore
		ATP5G2;A	NM_00100	Body;Body	chr12:5406	N_Shore
		CACNA1A	NM_00112	Body;Body	chr19:1331	S_Shore
					chrX:12571	Island
					chr8:14485	N_Shelf
rs2072122	rs11670098				chr19:6156	Island
		ANKDD1A	NM_18270	Body		
					chr13:2511	Island
		HOXB2	NM_00214	Body	chr17:4662	S_Shore
		NCR1;NC	NR_02704	TSS200;TSS200;TSS200;TSS200;T		
	rs8177656	IL15RA;IL	NM_00218	Body;5'UT	chr10:6018	N_Shelf
					chrX:15278	Island
rs56165058		HCN2	NM_00119	Body	chr19:6129	Island
	rs9639699	SDK1	NM_15274	Body		
		USP35	NM_02079	Body	chr11:7790	Island
rs2041083		PASK	NM_01514	Body		
rs2308931		HLA-DPA1	NM_03355	Body		
					chr6:17033	Island
		SMOC2;S	NM_02213	Body;Body	chr6:16891	N_Shore
		HRH1	NM_00109	TSS200		
		ACTN3	NM_00110	Body	chr11:6631	S_Shelf
	rs76422091				chr17:5334	N_Shelf
		SLC35E2	NM_18283	Body	chr1:16707	N_Shelf
		FBXO18;F	NM_03280	1stExon;Body;5'UTR		

rs2729762			PAK1;PAK	NM_00257	3'UTR;3'UTR		
			C15orf27	NM_15233	Body	chr15:7648	Island
			FMNL2	NM_05290	3'UTR		
rs79487751		TRUE	LONRF2	NM_19846	Body		
rs7410432			LOC15038	NR_02703	Body;TSS1	chr22:4644	S_Shore
			TRPM1	NM_00242	Body		
			USP29	NM_02090	TSS1500	chr19:5763	Island
			GABRG3	NM_03322	Body		
			AKR1E2	NM_00104	TSS200	chr10:4868	Island
rs2287922			RASIP1	NM_01780	Body	chr19:4923	Island
rs17769193	rs4940456		CPLX4	NM_18165	3'UTR		
rs2269834			LEF1;LEF1	NM_01626	3'UTR;3'UTR;Body;3'UTR		
	rs34755906		MORF4	NM_00679	TSS1500		
			HLA-DQB	NR_00393	Body	chr6:32729	N_Shore
rs79506788			ZDHHC14;	NM_15374	Body;Body		
			ARHGAP1	NM_03351	TSS1500		
			NUAK2	NM_03095	Body		
			DYNC2H1	NM_00137	Body;Body		
						chr6:25882	Island
			MTMR8	NM_01767	TSS200	chrX:63614	Island
rs7454567	rs34622008		HLA-C	NM_00211	TSS1500	chr6:31238	S_Shore
			RASAL3	NM_02290	Body	chr19:1556	Island
			ZPBP;ZPB	NM_00115	Body;Body		
			MAML2	NM_03242	Body		
rs73556753							
	rs6658590						
	rs78141882		SEMA4B;S	NM_02021	Body;Body		
			HLA-DPA1	NM_03355	Body		
			PCDHB17	NR_00128	Body	chr5:14053	Island
rs75639866						chr5:11960	Island
	rs6786975					chr3:18054	Island
rs59879723			SPOCK1	NM_00459	Body		
			ABLIM1;A	NM_00100	Body;Body	chr10:1163	S_Shelf
						chr1:14654	N_Shore
			PCSK6;PC	NM_13832	Body;Body;Body;Body;Body;Body;		
			RHCE;RH	NM_13861	Body;Body;Body;Body		
			KIAA0495	NM_20730	3'UTR	chr1:36629	N_Shelf

			PQBP1;PQ	NM_00103	5'UTR;5'U	chrX:48754	S_Shore
			VTRNA1-1	NR_02670	TSS1500		
	rs12783621		C10orf110;	NR_02462	Body;Body;Body;Body		
			PACS2;PA	NM_01519	Body;Body	chr14:1058	Island
			SFT2D2	NM_19934	Body	chr1:16819	S_Shelf
			C21orf91;C	NM_01744	5'UTR;5'U	chr21:1919	Island
			KRT23	NM_01551	TSS1500		
rs10279869			PTPRN2;P	NM_00284	Body;Body	chr7:15834	N_Shore
	rs12945000					chr17:1962	N_Shore
						chr1:17006	N_Shore
			TMEM68;T	NM_15241	5'UTR;TSS	chr8:56685	Island
rs57970013			RGMB	NM_00101	Body	chr5:98108	S_Shelf
			LCLAT1;L	NM_18255	TSS1500;T	chr2:30669	N_Shore
rs3021478						chr1:15814	Island
			CCDC36;C	NM_00113	TSS200;5'U	chr3:49236	Island
rs56026845						chrX:15315	Island
rs2520165		TRUE	C17orf48;S	NM_02023	5'UTR;TSS	chr17:1060	S_Shore
	rs60269219		EXOC3L2	NM_13856	Body	chr19:4572	S_Shelf
	rs77440597		LUZP1;LU	NM_03363	5'UTR;5'UTR		
						chr15:3478	N_Shelf
			CLTC	NM_00485	Body		
rs72381545	rs10870326						
	rs2493899		INPP5A	NM_00553	Body	chr10:1344	Island
rs6736791			NDUFA10	NM_00454	3'UTR		
			ADK	NM_00672	Body	chr10:7591	S_Shelf
rs76143368			RBKS	NM_02212	Body		
			FAM134B	NM_00103	Body	chr5:16616	N_Shelf
			PDZD4	NM_03251	Body	chrX:15308	Island
			TOM1L2;L	NM_00103	Body;TSS1	chr17:1787	Island
rs35842320							
			RAP1GAP	NM_01508	Body;Body		
			HOXD4;H	NM_01462	5'UTR;1stE	chr2:17701	N_Shore
	rs11533868						
			OR6C74	NM_00100	TSS1500		
			APOA5;AP	NM_05296	TSS1500;T	chr11:1166	S_Shelf
			SLC6A19	NM_00100	Body	chr5:12184	S_Shore
			COL1A2	NM_00008	Body		
						chr2:24164	S_Shelf
	rs35709241					chr18:1114	S_Shore

				EXOC6B	NM_01518	Body		
							chr13:1129	Island
	rs71708436			C7orf50;C7	NM_00113	Body;Body	chr7:10808	Island
							chr13:1149	Island
				AQP11	NM_17303	TSS1500	chr11:7730	N_Shore
rs34359792								
rs61521042	rs75467749			RPTOR;RP	NM_00116	Body;Body		
							chr17:8025	S_Shelf
				MCF2L;M	NM_00111	Body;Body	chr13:1136	N_Shelf
				RASA1;RA	NM_02265	3'UTR;3'UTR		
				AKAP7	NM_01637	Body		
				TRIM40	NM_13870	TSS1500		
				MFHAS1	NM_00422	Body		
rs72364780				CXorf64	NM_00112	Body		
rs2719375	rs58553660							
	rs12037089							
				ANKRD36	NM_00116	TSS1500	chr2:97778	Island
				RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
							chr12:1213	S_Shelf
				SH3PXD2	NM_01463	Body		
							chr4:14945	S_Shelf
				CIDEA;CI	NM_00127	Body;Body	chr18:1225	S_Shore
				IQGAP2;F2	NM_00663	Body;Body		
rs34631567							chr17:3530	N_Shore
	rs11145836			FAM69B	NM_15242	Body	chr9:13960	Island
				CARKD	NM_01821	Body	chr13:1112	S_Shelf
				COL18A1	NM_13044	Body	chr21:4685	S_Shore
							chr6:42384	N_Shore
				CACNA2D	NM_17236	Body	chr12:2017	Island
			TRUE	RPH3A;RP	NM_01495	5'UTR;5'UTR		
							chr17:1988	Island
rs79598406				PPBPL2	NR_02676	TSS1500		
							chr4:15789	S_Shelf
	rs443767							
				CCL2	NM_00298	TSS1500		
		TRUE		MEGF6	NM_00140	Body	chr1:34999	S_Shelf
							chr8:13113	S_Shore
				GALNT9;L	NM_00112	Body;Body	chr12:1328	N_Shore
	rs77587514			MGLL;MG	NM_00728	Body;Body		
				PLSCR4;PL	NM_00112	TSS1500;T	chr3:14596	S_Shore
				RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
				TRIM24;T	NM_00385	Body;Body		

		SYTL1	NM_03287	Body	chr1:27675	Island
					chr6:33588	N_Shelf
					chr22:1853	N_Shore
		AKR7L;AK	NM_00114	TSS200;TS	chr1:19600	Island
rs6889353						
		SYCP1	NM_00317	Body	chr1:11539	S_Shore
rs6744070					chr2:10816	N_Shelf
	rs35462366	VPS13B;V	NM_01789	Body;Body		
	rs11775641	CHD7	NM_01778	5'UTR	chr8:61626	Island
		TCEA1;TC	NM_20143	TSS1500;T	chr8:54934	S_Shore
		ABHD2;A	NM_15292	5'UTR;5'UTR		
		MMP16;M	NM_00594	Body;Body		
		NCRNA00	NR_026751	Body		
	rs34470543	DGKZ;DG	NM_00110	Body;Body	chr11:4638	Island
	rs36030612	HLA-DPA1	NM_03355	3'UTR		
	rs94598	SEPT9;SE	NM_00111	5'UTR;5'UTR;Body;Body;Body		
rs9296074	rs9296073	HLA-DPB1	NM_00212	TSS1500;TSS1500		
rs36070756	rs34450868	HLA-DRB	NM_00212	Body	chr6:32551	N_Shelf
	rs11059611	TMEM132	NM_00113	Body	chr12:1287	Island
					chr10:4418	Island
					chr5:83428	N_Shelf
	rs73597928					
		VTRNA1-2	NR_02670	TSS1500		
rs6926096	rs41439948					
		RFPL2;RF	NM_00109	TSS200;5'UTR;TSS1500		
rs11242928						
					chr6:10961	Island
					chr6:28554	S_Shelf
					chr1:92001	S_Shore
					chr7:15882	N_Shelf
		MAP1B	NM_00590	Body		
		TMEM196	NM_15277	3'UTR		
		RASGEF1	NM_17506	5'UTR	chr5:17958	Island
		PTPRN2;P	NM_00284	Body;Body;Body		
					chr3:13175	S_Shelf

						chr7:69062	N_Shelf
rs12361485		TRUE	GDPD4	NM_18283	TSS1500		
			CCDC67	NM_18164	TSS1500	chr11:9306	Island
	rs2297890		PYGL;PYG	NM_00116	TSS1500;T	chr14:5141	S_Shore
rs1129740	rs1129737		HLA-DQA	NM_00212	Body		
			KBTBD5	NM_15239	TSS1500	chr3:42727	N_Shore
	rs6849		ZMAT2	NM_14472	3'UTR		
	rs79653773						
	rs1050462		HLA-B	NM_00551	1stExon	chr6:31323	Island
			SH3PXD2	NM_00101	Body		
	rs12630564					chr3:16016	S_Shelf
			LAMB1	NM_00229	Body		
			SSH1;SSH	NM_00116	Body;Body	chr12:1092	N_Shelf
			LOC10013	NR_02446	Body;TSS1	chr11:6713	S_Shore
			ZSCAN16	NM_02523	TSS1500		
			SLC43A3;	NM_19932	TSS1500;T	chr11:5719	S_Shore
rs41263830	rs41263829		HLA-DQB	NM_00212	Body	chr6:32632	S_Shore
			C3orf24;C3	NM_00116	1stExon;1st	chr3:10149	Island
rs6693843						chr1:20668	N_Shelf
rs7104093							
			WDR63	NM_14517	Body		
	rs74147564		SLC35F3	NM_17350	Body	chr1:23434	S_Shore
			MRGPRX2	NM_05403	5'UTR		
	rs62011567		CYFIP1	NM_01460	Body	chr15:2294	S_Shelf
rs71535461			HLA-DRB	NR_00129	Body		
						chr12:1151	N_Shore
			TGFBR3	NM_00324	Body		
			GRIK2;GR	NM_02195	TSS200;TS	chr6:10184	Island
	rs870038		HSPB7	NM_01442	TSS200		
rs77211383			COX16	NM_01646	TSS1500	chr14:7082	S_Shore
rs9374425							
			C1orf14	NM_03093	Body	chr1:18292	N_Shore
	rs10846657		NCOR2;NC	NM_00631	Body;Body	chr12:1248	N_Shore
			THRAP3	NM_00511	TSS1500	chr1:36689	N_Shore
rs41304915			GNA12	NM_00735	3'UTR		
			ECEL1P2	NR_028501	TSS200	chr2:23325	Island
						chr6:42694	Island

rs528340	rs528212		LOC39995	NR_02443	Body		
			SGCG;SGC	NM_00023	1stExon;5'UTR		
			SGK269	NM_02477	5'UTR		
			TMEM88B	NM_00114	Body	chr1:13629	N_Shore
			RNF39;RN	NM_02523	TSS1500;T	chr6:30042	S_Shore
			RGS17	NM_01241	5'UTR		
	rs7222331		KRTAP3-3	NM_03318	TSS1500		
			LRRFIP1;L	NM_00113	Body;Body	chr2:23864	S_Shelf
rs2301753			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
			MTUS2;M	NM_01523	Body;Body		
						chr1:27060	N_Shore
			MSX1	NM_00244	TSS1500	chr4:48596	Island
rs2788469	rs1201424		ESYT2	NM_02072	Body		
	rs9893356		ITGA3;ITG	NM_00550	Body;Body	chr17:4813	S_Shelf
	rs3828198		HDAC4	NM_00603	Body		
			SYNE1;SY	NM_18296	Body;TSS1500;Body		
			KIAA0753	NM_01480	Body		
			RIN3	NM_02483	Body	chr14:9310	Island
						chr1:27527	N_Shelf
			KIAA1109	NM_01531	TSS1500		
			MAB21L1;	NM_00558	1stExon;Bo	chr13:3604	Island
rs4501554							
						chr14:1019	N_Shore
			AKAP13;A	NM_00720	Body;Body		
	rs3791367		HDAC4	NM_00603	Body		
			CACNG2	NM_00607	Body	chr22:3696	Island
			MAML2;M	NM_03242	5'UTR;1stExon		
			UBE2K;UE	NM_00111	Body;Body	chr4:39772	Island
rs79522772						chr2:12141	Island
rs73734198	rs36054513		RBM33	NM_05304	Body		
			ENAH;EN	NM_00100	Body;Body	chr1:22584	N_Shelf
						chr5:71713	Island
	rs6147224		NMUR1	NM_00605	TSS200	chr2:23239	Island
		TRUE	CYP2E1	NM_00077	Body	chr10:1353	Island
rs36093353			ANAPC10;	NM_01488	5'UTR;TSS	chr4:14601	N_Shore
			OR4A47	NM_00100	TSS1500		

					chr1:21731	S_Shelf
rs58854534		ARHGEF1	NM_01462	Body		
		COL21A1	NM_03082	Body		
	rs56069317				chr12:1252	N_Shore
		MAGI2	NM_01230	TSS1500	chr7:79082	S_Shore
	rs62642841	ITIH5;ITIH	NM_03056	Body;Body		
	rs34927789	RPH3AL	NM_00698	Body		
		DDR1;DD	NM_01399	TSS200;5'U	chr6:30852	S_Shelf
rs1130366	rs12722106	HLA-DQB	NM_00212	1stExon	chr6:32632	S_Shore
		LOC10030	NM_00116	TSS200;TS	chr2:54086	Island
		BOLL;BOL	NM_19797	TSS200;TS	chr2:19864	Island
rs2144295		GALNT2	NM_00448	Body		
rs2236781		GABRB1	NM_00081	Body	chr4:47034	S_Shore
		TTTY4B;T	NR_00217	Body;Body;Body		
rs73262629		C12orf59	NM_15302	Body		
		IQSEC2	NM_00111	TSS1500	chrX:53349	S_Shore
		AHDC1	NM_00102	5'UTR	chr1:27901	N_Shelf
		FCGBP	NM_00389	Body	chr19:4037	N_Shore
rs11755446	rs35215894				chr6:30418	Island
		PHLPP1	NM_19444	Body		
					chr13:2521	Island
		RERE;RER	NM_00104	5'UTR;Bod	chr1:84833	N_Shelf
		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		BSPRY	NM_01768	3'UTR		
		MFSD6	NM_01769	3'UTR		
	rs60360399					
		CARKD	NM_01821	Body	chr13:1112	N_Shelf
		ZNF473;ZN	NM_00100	3'UTR;3'U	chr19:5055	N_Shelf
		ATG7;AT	NM_00113	Body;Body;Body		
		TGFBR1;T	NM_00461	Body;Body	chr9:10186	S_Shore
	rs12946584	P2RX1	NM_00255	Body		
					chr1:99027	S_Shore
		EXOSC3;E	NM_00100	3'UTR;3'UTR		
					chr6:88760	Island
rs74701654					chr10:4384	Island
	rs7033479					
		KLF6;KLF	NR_02765	Body;Body	chr10:3823	N_Shore
		ZNF782	NM_00100	5'UTR	chr9:99616	N_Shore
		PTCHD3	NM_00103	1stExon	chr10:2770	N_Shore

				INADL	NM_17687	Body		
				TRIM37;TI	NM_00100	Body;Body		
							chr4:10496	N_Shelf
				TRUB2	NM_01567	Body	chr9:13108	N_Shelf
				BNC2	NM_01763	Body		
	rs12023538							
				MAP2K3	NM_14510	Body	chr17:2118	S_Shelf
				ESRRG;ES	NM_20659	5'UTR;5'UTR;5'UTR		
	rs74822384						chr1:15216	Island
							chr2:17699	S_Shore
				MTUS2	NM_00103	Body	chr13:2991	Island
			TRUE	SLC5A4	NM_01422	Body		
				NCR1;NCR	NR_02704	TSS200;TSS200;TSS200;TSS200;T		
				LOC61920	NR_00293	Body	chr10:1352	Island
				OSBPL5;O	NM_02089	Body;Body	chr11:3114	S_Shelf
				ENTPD8;E	NM_19858	Body;Body	chr9:14033	Island
				PTPRN2;P	NM_00284	Body;Body;Body		
				LOC61920	NR_00293	Body	chr10:1352	N_Shore
				MCC	NM_00108	TSS1500	chr5:11282	S_Shore
rs9557654				ITGBL1	NM_00479	Body	chr13:1021	S_Shore
rs75981550		TRUE		ACO1	NM_00219	Body		
							chr6:11268	Island
							chr1:21000	N_Shelf
				PRKCH	NM_00625	Body		
rs756776	rs635739			VAV2;VA	NM_00113	Body;Body		
	rs6600405							
				DUOX1;DU	NM_17594	Body;Body		
	rs1545347			PIAS4	NM_01589	Body	chr19:4032	S_Shore
				TNFRSF10	NM_14718	Body;Body	chr8:22925	N_Shore
	rs56155140							
rs34577747							chr5:13541	N_Shore
	rs11955589			ERGIC1	NM_00103	Body		
	rs13395215							
				SPTBN5	NM_01664	TSS1500		
				OPCML;OI	NM_00254	Body;Body		
	rs72774438			COL5A1	NM_00009	Body	chr9:13766	S_Shelf
				NR6A1;NR	NM_00148	TSS1500;T	chr9:12753	S_Shore

				CCDC46	NM_14503	Body		
	rs62125277			GPATCH1;	NM_01802	1stExon;5'U	chr19:3357	Island
				KCNJ16;K	NM_17074	TSS1500;TSS1500		
				LRIG3;LRI	NM_00113	Body;Body		
				LOC38879	NR_027241	Body;TSS1500;Body		
	rs56016226			HOXC10	NM_01740	Body	chr12:5437	S_Shore
				PPP1R2P1	NR_027771	TSS1500		
				MSC	NM_00509	Body	chr8:72755	N_Shore
				PDZD11;PI	NM_01648	1stExon;5'U	chrX:69509	Island
				SPON1	NM_00610	Body	chr11:1398	S_Shore
	rs62533774			KDM4C;KI	NM_01506	Body;Body;Body;Body		
				GABBR2	NM_00545	Body		
	rs72763937	TRUE		ASTN2;AS	NM_19818	Body;Body;Body		
				LTBP1;LTI	NM_20694	Body;TSS1500;TSS1500;TSS1500;		
rs76245433	rs2296633			DOCK1	NM_00138	Body	chr10:1291	S_Shore
rs73400034				HLA-DPA1	NM_03355	3'UTR		
rs17886590				INS-IGF2;I	NR_00351	Body;Body	chr11:2176	Island
rs1015674	rs72987107			PTPRS;PTI	NM_13085	5'UTR;5'U	chr19:5335	Island
							chr12:5438	N_Shore
	rs56236217			NTNG2	NM_03253	Body	chr9:1351	N_Shelf
rs8176631	rs8176632						chr9:13615	S_Shore
				ADARB2	NM_01870	Body		
				CTNND2	NM_00133	Body		
				PPP1R9B	NM_03259	3'UTR	chr17:4820	S_Shelf
				ACP6	NM_01636	TSS1500	chr1:14714	S_Shore
				BAT2	NM_08068	TSS1500	chr6:31587	N_Shore
				FIBIN	NM_20337	1stExon		
rs59458614				C13orf29	NR_027701	Body		
				GK;GK;GK	NM_00112	TSS200;TS	chrX:30670	Island
				LOC90784	NR_02698	TSS1500		
rs3001386								
				UNC119B	NM_00108	TSS200	chr12:1211	N_Shore
				KIAA1529	NM_02089	TSS1500	chr9:10000	N_Shore
	rs10963785			ADAMTSL	NM_00104	Body		
				FGF1;FGF	NM_00080	5'UTR;TSS200;5'UTR;5'UTR;5'UT		
			TRUE	MBD3L1	NM_14520	1stExon		
							chr6:13891	N_Shore
							chr19:5295	Island
				FAM83H	NM_19848	Body	chr8:14480	Island

				PAX5	NM_01673	Body	chr9:36985	S_Shelf
	rs2511404			HEPHL1	NM_00109	TSS200		
rs6962576	rs12531150			NUDT1;NU	NM_19894	Body;Body	chr7:22932	N_Shelf
							chr15:2450	Island
							chr14:7572	N_Shelf
				SOHLH1;S	NM_00110	TSS1500;T	chr9:13859	N_Shore
	rs78494548						chr9:38478	N_Shore
				LCN10	NM_00100	Body	chr9:13963	S_Shore
				ITSN2;ITS	NM_14715	5'UTR;5'U	chr2:24582	Island
				SOHLH1;S	NM_00101	Body;Body		
				INCA1;INC	NM_21372	TSS200;TS	chr17:4900	Island
	rs12974000	TRUE						
	rs72705782						chr14:1055	N_Shelf
				CRHBP	NM_00188	Body	chr5:76249	Island
	rs1048122			HLA-DQA	NM_00212	Body		
				THADA;TH	NM_02206	Body;Body		
							chr7:75831	N_Shore
				MKX	NM_17357	Body	chr10:2803	N_Shore
				RBMY1F;	NM_15258	TSS1500;T	chrY:24454	N_Shore
				RECK	NM_02111	Body		
							chr9:34957	N_Shelf
							chrX:87512	Island
				TBX3;TBX	NM_00599	Body;Body	chr12:1151	N_Shore
	rs77368007			SIN3B	NM_01526	3'UTR	chr19:1698	Island
				MAMDC2	NM_15326	Body		
							chr9:38487	Island
rs74420579							chr15:2467	S_Shelf
rs9261309							chr6:30042	S_Shelf
				PNPLA7;P	NM_15228	Body;Body	chr9:14035	Island
				ENTPD7	NM_02035	Body	chr10:1014	S_Shore
				VOPP1	NM_03079	Body	chr7:55639	N_Shore
	rs12526206							
				PLCE1;PL	NM_00116	TSS200;Body		
							chr9:11583	Island
	rs28502318			ENPP7	NM_17854	TSS1500		
rs11669378			TRUE	ZNF132	NM_00343	TSS200	chr19:5895	Island

rs73468084	rs77547622			TLE1	NM_00507	Body		
rs72634815				MIB2;MIB	NM_00117	TSS1500;T	chr1:15504	N_Shore
		TRUE		RORB	NM_00691	Body		
				PIWIL1	NM_00476	5'UTR	chr12:1308	Island
							chr5:14148	N_Shelf
rs9269827	rs9269825			HLA-DRB	NM_00212	Body	chr6:32551	N_Shelf
	rs6868964			PLEKHG4	NM_05290	Body	chr5:16957	S_Shelf
			TRUE	DUSP9	NM_00139	5'UTR	chrX:15290	Island
							chr11:3563	S_Shelf
	rs61754472			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
	rs2381176						chr9:34809	Island
				C1orf43;U	NM_00109	TSS1500;5'	chr1:15419	S_Shore
				SDF4;SDF	NM_01654	TSS1500;T	chr1:11670	Island
				FAM163A	NM_17350	5'UTR		
	rs34134095			C9orf72	NM_14500	TSS1500	chr9:27572	S_Shore
				TMEM187;	NM_00349	TSS1500;T	chrX:15323	Island
				PLEKHO2	NM_02520	Body		
				AFF1;AFF	NM_00116	Body;Body		
				ROR2	NM_00456	Body		
			TRUE	ZFR	NM_01610	TSS1500	chr5:32443	S_Shore
				DNM2;MI	NM_00494	Body;TSS1500;Body;Body;Body		
				SND1	NM_01439	Body		
rs72774438				COL5A1	NM_00009	Body	chr9:13766	S_Shelf
rs6861101							chr5:74348	N_Shelf
	rs2491811			HIATL2	NR_00289	TSS1500	chr9:99775	S_Shore
				RENBP;RE	NM_00291	1stExon;5'UTR		
				GCC1	NM_02452	Body	chr7:12722	N_Shelf
				MYH13	NM_00380	Body		
				SKA2;SKA	NM_18262	3'UTR;3'U	chr17:5718	S_Shelf
							chr9:13469	S_Shore
				LOC10013	NR_02447	TSS1500;TSS1500		
				AKNA	NM_03076	Body		
				IQSEC2	NM_00111	1stExon	chrX:53349	Island
				PGLYRP1;	NM_00509	1stExon;5'U	chr19:4652	Island
				AUH	NM_00169	Body		

							chr2:13104	Island
				C10orf26;C	NM_01778	TSS1500;Body		
rs41541015	rs1059542			HLA-A	NM_00211	Body	chr6:29910	Island
rs4742450								
				ENTPD2;E	NM_20346	Body;Body	chr9:13994	Island
				MARCH8;	NM_00100	Body;Body;Body		
rs17273728	rs6824020							
	rs62333915			PALLD;PA	NM_01608	Body;Body;Body		
				NDRG1;NI	NM_00609	Body;Body		
	rs7383143			C6orf10	NM_00678	Body		
				HCG26	NR_002812	Body		
				ELANE	NM_00197	Body	chr19:8528	Island
							chr2:24185	S_Shelf
				LOC16983	NM_00110	5'UTR	chr9:11577	N_Shelf
				C9orf78;U	NM_01652	TSS1500;5'	chr9:13259	S_Shore
	rs1052564			CCDC124;	NM_00113	3'UTR;3'UTR		
				NOTCH1	NM_01761	Body	chr9:13940	S_Shore
				PCDHB11	NM_01893	TSS200	chr5:14058	N_Shore
				MYO16	NM_01501	Body		
rs1819730	rs4430148						chr9:11022	S_Shelf
rs28724134	rs9269983			HLA-DRB	NM_00212	Body	chr6:32551	S_Shore
				FAM20C	NM_02022	Body	chr7:23127	Island
				C6orf174	NM_00101	Body	chr6:12779	Island
							chr21:4478	Island
rs41276208				STXBP1;S	NM_00103	3'UTR;3'U	chr9:13045	Island
				TMEM8B;	NM_00104	Body;Body	chr9:35846	S_Shore
				CCDC88C	NM_00108	Body		
	rs36046152			HCCA2	NM_05300	Body		
							chr13:2341	Island
rs11671499	rs78558181			KHSRP	NM_00368	TSS1500	chr19:6425	Island
				CLCF1;LO	NM_00116	1stExon;Bo	chr11:6713	S_Shore
	rs79505548	TRUE		APTX;APT	NM_17507	Body;Body;Body;Body;Body		
	rs11619305						chr13:2189	N_Shelf
				GPR115;GI	NM_15383	5'UTR;1stExon		
			TRUE	TBL1X;TB	NM_00113	5'UTR;5'U	chrX:94328	Island
				MYH14;M	NM_00114	Body;Body	chr19:5073	Island
				MYO1F	NM_01233	Body	chr19:8620	N_Shore
				COX7B	NM_00186	TSS200	chrX:77150	S_Shelf
				GIPC1;GIP	NM_00571	TSS200;TS	chr19:1460	Island

			L3MBTL4	NM_17346	Body	chr18:6284	N_Shore
						chr9:10050	N_Shore
						chrY:14649	S_Shelf
						chrY:19679	N_Shore
			LINGO2	NM_15257	5'UTR		
			PGM3	NM_01559	Body		
			FREQ	NM_01428	Body	chr9:13293	S_Shelf
			NRP2;NRP	NM_20127	Body;Body;Body;Body;Body;Body		
			CAMSAP1	NM_01544	Body		
			ASPG	NM_00108	Body		
rs11236715	rs11236714		SHANK2;S	NM_01230	Body;Body		
	rs11977692						
			UBASH3A	NM_01896	Body;Body		
			HIP1	NM_00533	Body	chr7:75268	S_Shore
			TLE4	NM_00700	Body		
			SORCS2	NM_02077	Body		
rs4258447							
			FAM178B	NM_00112	5'UTR	chr2:97651	N_Shore
rs35108070							
			CAPRIN2;	NM_00100	Body;Body;Body		
			SGK269	NM_02477	Body		
			EHBP1L1	NM_00109	TSS1500	chr11:6534	Island
			NANOS2	NM_00102	1stExon	chr19:4641	Island
rs73366955	rs12938918		TBCD	NM_00599	Body		
rs7684622							
	rs7160944		TMEM229	NM_18252	TSS1500	chr14:6798	S_Shore
			MGC45800	NR_02710	Body	chr4:18306	Island
	rs3800550		C6orf122;C	NR_026781	Body;Body	chr6:17019	Island
		TRUE	NNMT;NN	NM_00616	5'UTR;1stExon		
						chr8:38508	Island
rs61999782						chr14:2443	Island
	rs41311635		HOXA3;H	NM_15363	3'UTR;3'U	chr7:27146	Island
			PRR25	NM_00101	Body	chr16:8573	Island
rs13422242			RGPD8;RG	NM_00116	Body;Body	chr2:11319	Island
	rs10255150		PTN	NM_00282	5'UTR		
rs60569739	rs72875573	TRUE	CELA3A	NM_00574	TSS200		

						chr7:48128	N_Shelf
						chr19:1525	N_Shelf
	rs35050898						
			LTBP1	NM_20694	Body		
			KLF1	NM_00656	3'UTR	chr19:1299	N_Shore
rs34641102			ARHGEF7;	NM_00111	Body;Body	chr13:1119	Island
			MLPH;ML	NM_00104	Body;Body		
			DPPA5	NM_00102	TSS1500	chr6:74063	Island
			DDX58	NM_01431	3'UTR		
			TNNI3	NM_00036	TSS200	chr19:5566	S_Shore
			IRS1	NM_00554	1stExon	chr2:22766	N_Shore
rs34302635	rs28362335		HCG27	NR_026791	TSS1500	chr6:31165	N_Shore
			PBX3;PBX	NM_00113	Body;Body	chr9:12850	S_Shore
			RAD51L1;	NM_13350	Body;Body;Body		
						chr10:1899	N_Shelf
	rs4877074						
			ABO	NM_02046	Body	chr9:13613	S_Shelf
	rs1042926		HLA-DPA1	NM_03355	3'UTR		
			KLK15;KL	NM_01750	Body;Body	chr19:5133	Island
			SUSD1	NM_02248	Body		
rs74995957	rs9270991						
			KIF25;KIF	NM_00535	Body;Body	chr6:16843	S_Shore
						chr9:11585	Island
						chr8:21635	Island
						chr19:2280	Island
rs9273500	rs9273499		HLA-DQB	NM_00212	Body	chr6:32632	N_Shelf
						chr7:63498	Island
		TRUE	EPB41L1	NM_17799	5'UTR		
			PRR23C	NM_00113	TSS200	chr3:13876	Island
						chr22:2102	Island
						chr7:75779	Island
rs78788865							
			MYOCD;M	NM_00114	Body;Body;Body		
rs34845477			TBC1D16	NM_01902	Body	chr17:7792	Island
			FOXO4;FO	NM_00593	Body;Body	chrX:70316	S_Shore
						chr19:5866	N_Shore
			FLJ44606;	NM_00116	5'UTR;5'U	chr5:12640	N_Shore
rs1810684	rs13283491					chr9:84137	N_Shore
			COL18A1;	NM_13044	Body;Body	chr21:4689	Island

rs36029197							chr13:1114	Island
rs3130059				BAT1;SNO	NM_00464	5'UTR;TSS	chr6:31509	N_Shore
rs56663793							chr1:28415	S_Shelf
				MYOZ3;M	NM_13337	Body;Body	chr5:15005	Island
							chr13:2341	Island
				DDC;DDC	NM_00079	Body;Body		
							chr18:7783	S_Shore
							chr2:13100	Island
				DOCK10	NM_01468	Body		
	rs7768561			FTSJD2	NM_01505	Body		
	rs6742343						chr2:19866	N_Shelf
				LHX2	NM_00478	Body		
rs7867501	rs7864589	TRUE		ASTN2;AS	NM_19818	Body;Body;Body		
				LRRC10;L	NM_20155	1stExon;3'UTR		
							chr7:15726	N_Shore
							chr12:1151	N_Shore
				KIAA0020	NM_01487	Body		
				RAP1GDS1	NM_00110	Body;Body;Body;Body;Body;Body		
	rs72308270			CDK5RAP	NM_00101	Body;Body	chr9:12325	Island
				GRIK4	NM_01461	Body		
				TMSB4Y	NM_00420	3'UTR	chrY:15815	S_Shore
				TTTY13	NR_001537	TSS1500		
				RAPGEF1;	NM_19867	Body;Body		
							chr4:13289	Island
	rs59564702			PIGG;PIG	NM_01773	Body;Body	chr4:52916	N_Shore
rs2932988				FNDC1	NM_03253	Body	chr6:15965	Island
	rs13388294			DIRC3	NR_026597	Body		
							chr2:63612	Island
rs2249189				SEMA3E	NM_01243	Body		
							chr7:15726	S_Shore
				PCDHB11;	NM_01893	1stExon;3'U	chr5:14058	S_Shore
				TTC7B	NM_00101	Body		
				ANKRD9	NM_15232	Body	chr14:1029	Island
				CGREF1;C	NM_00116	5'UTR;TSS	chr2:27341	Island
				KCNE1;KC	NM_00112	TSS200;5'U	chr21:3583	Island
				ROCK2	NM_00485	Body		
			TRUE	NCR1;NCR	NR_02704	TSS200;TSS200;TSS200;TSS200;T		

				SMYD1	NM_19827	TSS200		
				FAM75A3	NM_00108	TSS1500		
				DENND1A	NM_02482	Body;Body		
				C12orf23	NM_15226	TSS1500	chr12:1073	N_Shore
							chr9:13278	S_Shore
				TMEM111	NM_01844	Body		
							chr15:3174	S_Shelf
rs72451347	rs4975612							
							chr9:96623	Island
				ADAMTSL	NM_20751	Body		
				PHF6;PHF	NM_03233	5'UTR;5'U	chrX:13350	Island
	rs58879463			ADAMTS2	NM_01424	Body		
							chr9:93879	S_Shore
rs76869359	rs1864006			NXNL1	NM_13845	TSS200		
				MXI1;MXI	NM_13043	Body;Body	chr10:1119	S_Shelf
							chr1:35586	S_Shore
				KCNK7;K	NM_03334	1stExon;5'U	chr11:6536	N_Shelf
				KIAA1529	NM_02089	TSS1500	chr9:10000	N_Shore
rs3810665	rs3810666			ZNF157	NM_00344	TSS200		
	rs7797542			PRRT4	NM_00111	TSS1500	chr7:12800	S_Shore
				ABO	NM_02046	Body	chr9:13613	S_Shore
			TRUE	PAMR1;PA	NM_00100	TSS1500;T	chr11:3554	S_Shore
		TRUE		MOBKL2B	NM_02476	Body		
	rs28724107			HLA-DRB	NM_00212	Body	chr6:32551	Island
	rs11819368			LHPP;LHP	NM_02212	Body;Body		
	rs1059752			DNAJB6	NM_05824	3'UTR	chr7:15720	S_Shore
				CYTH1;CY	NM_01745	Body;Body		
				GARNL3	NM_03229	Body		
				C2orf76	NM_00101	Body		
rs1048998				ALPP	NM_00163	Body	chr2:23324	Island
				GLIS1	NM_14719	5'UTR		
	rs894462						chr11:6421	Island
							chr19:3573	N_Shelf
				STK19;DO	NR_026717	TSS1500;B	chr6:31939	N_Shore
	rs6861166			MCC;MCC	NM_00238	Body;Body		
				HCN3	NM_02089	Body	chr1:15524	Island
	rs74178195						chr19:1023	S_Shelf
				MIR196A2	NR_029617	Body	chr12:5438	N_Shelf
				ACSL3;AC	NM_20337	Body;Body		
	rs73398146							
rs73082997								

					chr7:16867	S_Shore
rs72869469	rs72869468	NCRNA00	NR_02702	Body;TSS2	chr2:13301	Island
		KCNN1	NM_00224	Body	chr19:1809	N_Shore
		USP11	NM_00465	Body	chrX:47092	Island
		ZNF365;ZN	NM_19945	Body;Body		
		SNORA49;	NR_00297	TSS1500;B	chr12:1325	S_Shore
		NUMA1	NM_00618	Body		
	rs2241608	SLC12A7	NM_00659	Body	chr5:10605	Island
	rs2819493				chr1:22769	N_Shelf
		ACAD9	NM_01404	TSS1500	chr3:12859	N_Shore
		HRNBP3	NM_00108	5'UTR	chr17:7712	Island
	rs1058932	CYP2C8	NM_00077	3'UTR		
		PTPRE	NM_00650	5'UTR		
					chr6:24720	S_Shelf
					chr12:1151	Island
		PARD3	NM_01961	Body		
		ASCC2	NM_03220	Body		
					chrY:17567	S_Shore
	rs12807866	HSD17B12	NM_01614	Body		
rs2851915					chr18:1203	S_Shelf
		RBPJL	NM_01427	Body	chr20:4394	Island
		DCHS2;DC	NM_01763	Body;Body	chr4:15525	Island
		GDF7	NM_18282	Body	chr2:20870	Island
	rs9405002	COL11A2;	NM_08067	Body;Body	chr6:33129	S_Shelf
		TPO;TPO;T	NM_17571	Body;Body	chr2:14807	Island
	rs2609858	PLSCR1	NM_02110	5'UTR	chr3:14626	N_Shore
	rs55874919					
	rs34158381				chr5:72598	S_Shelf
	rs28383404	HLA-DQA	NM_00212	Body		
		IMMT;IM	NM_00683	Body;Body	chr2:86422	N_Shelf
		KCTD2	NM_01535	Body		
					chr10:1033	S_Shelf
	rs34747756	FRG1B	NR_00357	Body	chr20:2961	Island
		C3orf63	NM_00111	TSS1500	chr3:56716	Island
rs78418641		JMY	NM_15240	TSS1500	chr5:78531	Island
	rs12354378	C1orf130	NM_00101	5'UTR		
	rs2599396	TAS2R30;	NM_00109	TSS1500;5'UTR;5'UTR		
		GK;GK;GK	NM_00112	TSS200;TS	chrX:30670	Island

				COL1A1	NM_00008	Body	chr17:4827	N_Shore
			TRUE	GPR75;LO	NM_00679	5'UTR;1stE	chr2:54086	Island
	rs11404509							
				OTUD3	NM_01520	3'UTR		
				DYNC1H1	NM_00137	Body		
				ARSI	NM_00101	TSS1500	chr5:14968	S_Shore
rs74056623	rs11274442						chr1:19110	S_Shore
				PLEKHG6;	NM_00114	Body;Body	chr12:6438	N_Shore
rs75103809	rs2307621			UBAP2L	NM_01484	Body		
		TRUE		ZNF827	NM_17883	Body		
				ATP6V1C1	NM_00169	TSS1500	chr8:10403	N_Shore
		TRUE						
							chr2:36991	Island
				KLHL14	NM_02080	TSS200	chr18:3034	S_Shore
				HSP90AA1	NM_00534	TSS1500;B	chr14:1025	S_Shore
			TRUE	CATSPER1	NM_05305	TSS1500		
	rs78299948			KIF13B	NM_01525	Body	chr8:28928	S_Shore
	rs2285774			SORCS2	NM_02077	Body		
							chr2:13104	Island
				TEAD3	NM_00321	Body	chr6:35453	Island
				MATN4;M	NM_00383	5'UTR;5'U	chr20:4393	Island
				MDGA1	NM_15348	Body	chr6:37616	Island
	rs2340980			FAM38A	NM_00114	Body	chr16:8879	Island
rs76628753							chr2:24156	Island
rs9264653				HLA-C	NM_00211	Body	chr6:31238	N_Shore
rs7077451				DIP2C	NM_01497	Body	chr10:3674	S_Shore
				TBXA2R;T	NM_20163	Body;Body	chr19:3595	Island
				DOCK1;FA	NM_00138	Body;Body		
				DDB2	NM_00010	Body		
rs75689774				TCF23	NM_17576	Body	chr2:27373	Island
			TRUE	HMOX2;H	NM_00112	TSS1500;T	chr16:4526	N_Shore
				AGK	NM_01823	Body		
rs3840959				COL6A2;C	NM_00184	5'UTR;5'U	chr21:4753	N_Shore
							chr19:3779	Island
rs73080778				TMEM44;T	NM_00101	Body;Body;Body;Body		
rs79910532				ADD2;ADI	NM_01748	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR		
rs1050269				UPP1;UPP	NM_18159	5'UTR;5'U	chr7:48128	Island

rs7259294						chr19:2921	Island
			RARRES1;	NM_20696	Body;Body		
						chr12:1151	Island
			VCAN;VC	NM_00438	5'UTR;5'U	chr5:82770	S_Shore
			CRISP2;CR	NM_00114	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR		
rs77547816						chr9:11582	Island
			PDGFRL	NM_00620	Body		
			SPIB	NM_00312	Body	chr19:5093	Island
			AGBL4	NM_03278	Body		
rs3208105	rs1142326		HLA-DQA	NM_00212	Body		
						chr13:9182	Island
	rs488223		CALCOCO	NM_00583	TSS200	chr17:4690	Island
						chr1:15216	N_Shore
			STS	NM_00035	TSS200		
rs262669	rs262670		PRKCZ;PR	NM_00103	Body;Body	chr1:20823	Island
			CAPN2	NM_00114	TSS200		
rs76078031	rs79354455		ACACA;A	NM_19883	Body;Body;Body;Body;Body		
			FAM53B	NM_01466	TSS1500	chr10:1264	S_Shore
			PCDHB4	NM_01893	1stExon	chr5:14050	N_Shore
rs67775324	rs76462367		POTEH	NM_00113	TSS1500	chr22:1628	S_Shore
			SYNE1;SY	NM_18296	Body;Body;Body;Body		
		TRUE	BARX2	NM_00365	Body	chr11:1293	S_Shelf
			EIF1AY	NM_00468	TSS200	chrY:22737	N_Shore
rs80132126							
						chr3:13974	Island
	rs73724324		MESTIT1;	NR_00438	Body;5'UT	chr7:13013	N_Shore
						chr13:1125	Island
			LSP1;LSP1	NM_00101	5'UTR;5'U	chr11:1892	Island
	rs3828326		LY75	NM_00234	Body	chr2:16076	N_Shelf
			CHCHD4;	NM_00109	Body;Body		
rs75020383			PFKP	NM_00262	Body		
rs76561716			MSX1	NM_00244	TSS1500	chr4:48596	Island
						chr19:3036	S_Shore
			TMEM175	NM_03232	5'UTR	chr4:94061	Island
			PCDHA1;P	NM_03141	1stExon;1st	chr5:14016	N_Shore
			KLK15;KL	NM_01750	Body;Body	chr19:5133	Island
			C3orf24;C3	NM_00116	TSS200;TS	chr3:10149	S_Shore

			PCDHA7;P	NM_01891	Body;Body	chr5:14025	Island
	rs80319185		DNAH17	NM_17362	Body		
			PLEKHM2	NM_01516	3'UTR	chr1:16058	S_Shelf
			LTBP1;LT	NM_20694	Body;TSS1500;TSS1500;TSS1500;		
rs61072203						chr2:66802	S_Shore
rs9277419	rs9277418		HLA-DPB1	NM_00212	Body	chr6:33048	S_Shelf
			CELSR3	NM_00140	Body	chr3:48693	Island
			POLS	NM_00699	3'UTR	chr5:67551	Island
rs35706896		TRUE	NUPR1;NU	NM_01238	TSS200;TSS200		
rs79251455							
rs73388549			EIF2AK4	NM_00101	Body	chr15:4026	S_Shelf
			ZNF714	NM_18251	5'UTR	chr19:2126	Island
			TSKS	NM_02173	Body	chr19:5024	Island
			CRTC1;CR	NM_01532	3'UTR;3'U	chr19:1888	Island
						chr17:1988	Island
			GMDS	NM_00150	Body		
	rs11589812		FAAH	NM_00144	TSS1500	chr1:46859	N_Shore
			TNFRSF25	NM_14896	Body;Body	chr1:65259	Island
rs78923851			SH3D19;SH	NM_00112	5'UTR;1stExon;5'UTR;5'UTR		
			PDE4C	NM_00092	5'UTR	chr19:1834	S_Shore
			TULP1	NM_00332	Body	chr6:35479	Island
	rs62341548		ADCY2	NM_02054	Body		
			SLC16A2	NM_00651	Body	chrX:73642	Island
			MATN4;M	NM_00383	5'UTR;5'U	chr20:4393	Island
			STK32C	NM_17357	Body		
			GCET2;GC	NM_15278	TSS1500;TSS1500		
rs7313068							
			RAB40B	NM_00682	Body		
			SLC2A14	NM_15344	TSS200	chr12:8025	Island
			GSTT1	NM_00085	TSS200	chr22:2438	Island
			ETV1;ETV	NM_00116	TSS1500;T	chr7:14030	S_Shore
						chr10:2921	Island
rs76017150						chr6:17103	S_Shelf
			SCARB1;S	NM_00108	Body;Body	chr12:1253	N_Shore
	rs35913897		PTPRN2;P	NM_00284	Body;Body;Body		
			ZMYND11	NM_00662	Body;Body;Body		
rs75475524	rs4789864		TIMP2	NM_00325	Body	chr17:7689	Island
rs74717563	rs67964892		FOXK2	NM_00451	Body	chr17:8055	Island

	rs78327118		SNTG2	NM_01896	Body	chr2:11630	S_Shelf
		TRUE	ACAT2	NM_00589	TSS1500	chr6:16018	Island
			GLP1R	NM_00206	Body		
						chr8:13113	N_Shore
			ZNF385B;Z	NM_15252	Body;Body;TSS200		
	rs7171087						
			PTPRN2;P	NM_00284	Body;Body;Body		
			CISH;CISH	NM_14507	Body;5'UT	chr3:50648	N_Shore
			TTTY14	NR_00154	TSS200	chrY:21238	Island
			MMRN2	NM_02475	Body	chr10:8870	Island
			THRB;THR	NM_00046	Body;Body;Body		
			SLC9A9	NM_17365	TSS200		
			PCDHB17	NR_00128	Body	chr5:14053	N_Shore
		TRUE	LTB4R2;L	NM_00116	Body;1stEx	chr14:2477	Island
	rs4897076		UST	NM_00571	Body		
			COG5;CO	NM_00116	TSS1500;T	chr7:10720	S_Shore
rs61736674			KLHL34	NM_15327	1stExon	chrX:21674	Island
			PCDHB2	NM_01893	1stExon	chr5:14047	N_Shore
	rs77671502		XRRA1	NM_18296	5'UTR		
	rs4939290		OR5A1	NM_00100	TSS1500		
			MGAT4C	NM_01324	TSS200		
						chr1:95006	S_Shelf
			PSG9	NM_00278	Body		
rs67984685		TRUE	SRD5A2	NM_00034	TSS1500	chr2:31805	Island
			DPP9	NM_13915	TSS1500	chr19:4723	S_Shore
			FLJ44606;F	NM_00116	TSS200;TS	chr5:12640	Island
			TUBGCP2	NM_00665	Body	chr10:1351	S_Shore
			HOXC9	NM_00689	TSS1500	chr12:5439	N_Shore
			DPPA5	NM_00102	TSS200	chr6:74063	Island
			IL18	NM_00156	5'UTR		
			ACTN1;AC	NM_00113	Body;Body	chr14:6934	S_Shore
	rs34577522		ZNF117;Z	NM_01585	1stExon;5'UTR		
			C3orf21	NM_15253	Body		
			COL1A1	NM_00008	Body		
	rs12878371					chr14:1036	S_Shore
						chr7:12250	N_Shelf
			GLCCI1	NM_13842	Body		
			HLX	NM_02195	Body	chr1:22105	Island
			HCFC1	NM_00533	Body	chrX:15321	Island

			LEPR;LEP	NM_00100	5'UTR;5'U	chr1:65885	S_Shelf
						chr21:4457	Island
			ANKFY1;	NM_01637	Body;Body	chr17:4125	N_Shore
						chr22:1883	N_Shore
rs71475867						chr10:2543	Island
			COL9A3	NM_00185	TSS1500	chr20:6144	N_Shore
			LOC10010	NR_02724	TSS200	chr13:1991	Island
	rs13385681		NMS	NM_00101	TSS200		
		TRUE	NAPRT1	NM_14520	TSS1500	chr8:14465	S_Shore
rs11887733							
						chr1:11919	S_Shelf
			LIPT1;LIP	NM_14519	5'UTR;5'U	chr2:99771	Island
			PCDHB12	NM_01893	TSS200	chr5:14058	N_Shore
			MIR519E	NR_03018	TSS200		
			VWDE	NM_00113	Body		
	rs35986921					chr7:55661	S_Shore
rs17879599	rs16822805		HLA-DRB	NM_00212	Body	chr6:32551	Island
	rs79937362						
			FHIT;FHIT	NM_00116	5'UTR;5'U	chr3:61236	N_Shore
			MAD1L1;	NM_00355	Body;Body	chr7:20197	Island
	rs4247257		HLA-DPA1	NM_03355	Body		
rs506859							
	rs41549414		HLA-F;HL	NM_00109	Body;Body	chr6:29691	S_Shore
rs74982786			DENND2D	NM_02490	Body		
rs11273051							
rs80179123			SYNPO;SY	NM_00116	Body;Body	chr5:15000	S_Shore
			MFAP2;M	NM_00113	TSS1500;T	chr1:17306	S_Shelf
	rs7558752		SNTG2	NM_01896	Body	chr2:11630	S_Shelf
			KIAA1704;	NM_01855	TSS1500;1	chr13:4556	Island
			HOXA11A	NR_00279	TSS1500;1	chr7:27224	Island
			TXK	NM_00332	TSS1500		
						chr8:13102	N_Shelf
	rs4881107					chr10:3180	N_Shore
rs41561720	rs41555814		HLA-C	NM_00211	Body	chr6:31238	Island
rs34155920						chr10:8229	Island
			HOXC4;H	NM_15363	Body;Body	chr12:5444	S_Shore
			LCLAT1;L	NM_18255	TSS1500;T	chr2:30669	N_Shore

					chr2:43327	N_Shelf
		C13orf28;C	NM_14524	1stExon;5'UTR		
					chr6:29894	Island
	rs67652741	TSPAN18	NM_13078	5'UTR		
rs1126542	rs35171346	HLA-DPA1	NM_03355	Body		
		LOC10010	NR_00359	TSS1500;T	chrY:97455	S_Shore
		ITM2A;ITM	NM_00486	1stExon;1stExon		
		SCNN1D;S	NM_00113	Body;Body	chr1:12287	N_Shore
		ABCC8	NM_00035	TSS1500	chr11:1749	S_Shore
		SPIB	NM_00312	Body	chr19:5093	Island
		GRIK2;GR	NM_00116	Body;Body;Body		
		LOC72872	NR_02439	Body		
					chr1:10662	Island
		13-Sep	NR_024271	Body	chr7:45808	Island
		SLC9A2	NM_00304	Body	chr2:10323	S_Shelf
		GABRQ	NM_01855	TSS200	chrX:15180	Island
	rs34767965				chr22:4944	Island
		LOC73075	NM_00116	TSS1500		
rs9790401	rs58957020	AFAP1;AF	NM_19859	Body;Body;Body		
		PLEKHA2	NM_02162	Body		
		TGFBR2;T	NM_00102	Body;Body		
rs76720862		ALS2CL;A	NM_18277	TSS200;Body		
		SHANK3	NM_00108	Body	chr22:5113	Island
		CDH19	NM_02115	TSS1500		
rs4546787					chrX:14952	Island
rs80126421					chr12:1311	Island
		TBC1D23	NM_01830	Body		
rs71542466	rs9274525	HLA-DQB	NM_00212	TSS200	chr6:32632	S_Shore
					chr5:48663	Island
					chr7:15260	Island
	rs11772971	ELMO1	NM_01480	5'UTR	chr7:37487	N_Shelf
					chr18:7729	Island
		TTTY16	NR_001552	TSS1500		
		MAD1L1;M	NM_00355	Body;Body	chr7:20996	Island
					chr12:1330	N_Shore
					chr19:1583	Island
		RNH1;RNH	NM_20338	Body;Body	chr11:4948	Island
	rs60024156	TNFAIP8L	NM_15236	TSS1500	chr19:4639	N_Shore
		DTX2;DTX	NM_00110	Body;Body	chr7:76129	N_Shore

rs77936015							chr19:3834	Island
				LNX1;LNX	NM_03262	Body;Body		
rs35365032				MEG8	NR_02414	Body		
				LOC64640	NR_02673	Body	chr13:2550	Island
			TRUE	COX4NB;C	NM_00114	Body;TSS1	chr16:8583	N_Shore
	rs2467830			DUOX2	NM_01408	Body	chr15:4540	Island
				LOC28541	NR_02710	TSS1500		
rs28377211							chr1:24780	Island
	rs3111753			ITM2C;ITM	NM_00101	Body;Body	chr2:23172	S_Shelf
				COL18A1	NM_13044	Body	chr21:4685	Island
				MYO10	NM_01233	Body		
				C2;C2;CFB	NM_00006	3'UTR;3'UTR;TSS1500		
				PLCB2	NM_00457	Body	chr15:4058	Island
rs74433172	rs56353161							
				SRPK2	NM_18269	Body	chr7:10494	S_Shelf
				DAGLA	NM_00613	5'UTR	chr11:6144	S_Shelf
				MAOB;MA	NM_00089	1stExon;5'U	chrX:43741	Island
rs11753382	rs61754472			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
				SETD1B	NM_01504	Body	chr12:1222	N_Shore
							chr7:12698	N_Shelf
		TRUE						
				PLXDC2	NM_03281	Body		
	rs79473318			PTPN14	NM_00540	5'UTR		
rs59463838	rs6533344			MRPL1	NM_02023	Body		
rs67760762				GFPT1	NM_00205	Body		
				MIR592;GI	NR_03032	TSS1500;Body;Body;Body		
	rs11748337							
				OR5B12	NM_00100	TSS1500		
				PCDHB8	NM_01912	TSS1500	chr5:14055	N_Shelf
rs71606395							chr4:24317	Island
							chr14:1036	S_Shore
				CSMD3;CS	NM_19812	Body;Body;Body;TSS1500		
	rs72502525						chr6:30418	S_Shore
	rs4969465			FASN	NM_00410	Body	chr17:8004	N_Shore
				AKR7L;AK	NM_20125	1stExon;1st	chr1:19600	Island

				TRIM31	NM_00702	Body		
				PDGFC	NM_01620	3'UTR		
	rs10210434							
rs9982576	rs73238114						chr21:4676	N_Shelf
	rs76815872							
	rs28440154						chr21:4681	N_Shore
	rs28487568			AMTN	NM_21255	TSS1500		
				EXT1	NM_00012	Body		
				TRIM10;T	NM_00677	Body;Body		
				SHANK2;S	NM_01230	Body;Body	chr11:7033	S_Shelf
				LOC10013	NR_02456	Body;Body	chr4:11881	S_Shelf
rs12412456	rs12415178			PNLIPRP2	NM_00539	TSS200		
				UBD	NM_00639	Body		
	rs3791364			HDAC4	NM_00603	Body		
							chr1:24305	N_Shelf
	rs10422978			TNNI3	NM_00036	TSS1500	chr19:5566	S_Shore
rs79019553				GCET2;GC	NM_15278	TSS1500;TSS1500		
			TRUE	GRIK2;GR	NM_02195	TSS200;TS	chr6:10184	N_Shore
				SIGLEC14	NM_00109	3'UTR		
				RIT2	NM_00293	TSS1500		
				MTHFD1	NM_00595	Body		
				TMEM132	NM_13344	Body		
rs945941				MAN1C1	NM_02037	Body		
	rs79710380							
	rs77277521							
rs61861412							chr10:9435	N_Shore
				PTGFRN	NM_02044	Body	chr1:11748	Island
rs5747457							chr22:1853	N_Shore
	rs34038017						chr2:24056	S_Shore
rs74806334								
	rs74470823		TRUE	CDKL1	NM_00419	1stExon	chr14:5086	N_Shore
	rs908117			AHRR;PD	NM_02073	Body;Body	chr5:30970	N_Shore
				LOC10012	NR_02727	TSS1500		
	rs6908059			TCP11;TC	NM_00109	TSS1500;T	chr6:35108	S_Shore

			BEST1;BES	NM_00113	TSS1500;TSS1500		
						chr10:1299	Island
			ZNF354C	NM_01459	5'UTR	chr5:17848	S_Shore
rs451921	rs60584481		C12orf70	NM_00114	Body		
rs486845			CHRM5	NM_01212	5'UTR		
			KIRREL3;I	NM_00116	Body;Body		
rs3753964	rs1010502		TMEM9	NM_01645	TSS200	chr1:20112	Island
			MTOR	NM_00495	Body		
			EIF2AK4	NM_00101	Body	chr15:4026	Island
			NCOA4;NC	NM_00114	3'UTR;3'UTR;3'UTR;3'UTR;3'UTR		
rs72620404			RFPL3	NM_00660	TSS200		
			PCDHA1;P	NM_03141	Body;Body	chr5:14017	Island
						chr21:4519	S_Shore
	rs12487365						
	rs61783468						
	rs6894246		PLEKHG4I	NM_05290	Body	chr5:18172	N_Shore
						chr8:10375	N_Shore
		TRUE	FRK;FRK	NM_00203	1stExon;5'UTR		
						chr18:1003	Island
rs3743591		TRUE	TNFRSF17	NM_00119	1stExon;5'UTR		
						chr7:23245	Island
	rs61591073		TSPAN10	NM_03194	TSS200		
	rs9391924					chr6:15552	Island
						chr18:7667	Island
			TRAPPC9;	NM_00116	Body;Body		
		TRUE	PTPN20B;I	NM_00104	TSS200;TS	chr10:4882	Island
rs78176004							
	rs10150792		KIF26A	NM_01565	Body	chr14:1046	Island
						chr7:12151	Island
			SYCE1;SY	NM_00114	TSS200;TS	chr10:1353	Island
			YTHDC2	NM_02282	Body		
			C6orf132	NM_00116	Body		
			PCDHA2;P	NM_01890	Body;Body	chr5:14018	Island
			IQGAP2	NM_00663	TSS1500	chr5:75698	N_Shore
			MGMT	NM_00241	Body		
			NTM;NTM	NM_00114	Body;Body;Body;Body		
	rs76542536					chr18:5763	N_Shelf
			PCDHGA1	NM_01891	1stExon;1st	chr5:14071	N_Shore
			C3orf25	NM_20730	Body		

			SALL3	NM_17199	Body	chr18:7675	N_Shore
			HPD	NM_00215	TSS1500		
	rs1046073		ABHD12;A	NM_01560	Body;3'UTR		
rs4252757			CCNI	NM_00683	TSS200	chr4:77996	Island
			TMEM216	NM_01649	TSS1500	chr11:6115	N_Shore
rs35097027	rs35363281						
						chr14:1024	Island
			LTBP1	NM_20694	Body		
			PINX1	NM_01788	Body		
	rs34586932		SCHIP1	NM_01457	Body		
rs41263829	rs9274435		HLA-DQB	NM_00212	Body	chr6:32632	S_Shore
						chr16:1034	Island
rs35471025			PRR23B	NM_00101	TSS200	chr3:13873	Island
			PCNXL2	NM_01480	Body		
			CES4	NR_00327	Body	chr16:5579	N_Shore
	rs75581552		IL6ST;IL6S	NM_00218	5'UTR;5'U	chr5:55290	N_Shore
			MUCL1	NM_05817	TSS200		
						chr11:1492	Island
			PFKP	NM_00262	Body	chr10:3160	S_Shelf
			ADAMTS1	NM_13905	Body		
			FGGY;FG	NM_01829	Body;Body		
						chr1:91300	N_Shore
			TBX3;TBX	NM_00599	Body;Body	chr12:1151	N_Shore
	rs41317300		KIAA0284;	NM_01500	Body;Body		
						chr3:13350	Island
			DCBLD2	NM_08092	Body		
		TRUE	LOC28595	NR_02711	Body;Body	chr7:41745	N_Shelf
			DLX2;DLX	NM_00440	5'UTR;1stE	chr2:17296	Island
rs55657144							
						chr10:1299	Island
rs16855898			C2orf48	NM_18262	Body		
	rs2856411						
						chr17:4019	Island
			FER1L4	NR_02437	Body	chr20:3418	Island
						chr16:3313	S_Shelf
	rs7904554		BEND7;BE	NM_00110	1stExon;1stExon;5'UTR;5'UTR		
						chr10:4796	N_Shelf

		PIWIL4	NM_15243	Body		
		ASIP	NM_00167	Body	chr20:3285	Island
		EIF5A2	NM_02039	TSS1500	chr3:17062	Island
		MAP1B	NM_00590	Body		
		UPK3B;UP	NM_18268	3'UTR;3'U	chr7:76145	Island
		ARID1B;A	NM_01751	Body;Body;Body		
					chr15:9586	Island
		NXN	NM_02246	Body		
		NUAK1	NM_01484	Body	chr12:1064	Island
		GCK	NM_00016	TSS1500		
		PPT2;PRR	NM_00515	TSS1500;T	chr6:32121	N_Shore
	rs462432	REV3L	NM_00291	Body		
	rs17523127	SNORA14	NR_00295	TSS1500;T	chr1:23529	Island
rs4758254						
	rs13198630	HCG2P7	NR_00131	Body		
		ANKRD55	NM_02466	Body		
	rs74716954	COL11A2;	NM_08067	Body;Body	chr6:33159	N_Shore
rs17882663	rs9269958	HLA-DRB	NM_00212	Body	chr6:32551	Island
	rs72656349	COL1A1	NM_00008	Body		
	rs74006116	FAM195B;	NM_20736	5'UTR;5'U	chr17:7979	N_Shelf
		C3orf25	NM_20730	TSS1500	chr3:12914	S_Shore
		HOXC10	NM_01740	3'UTR	chr12:5437	S_Shelf
	rs2233632	SPDEF	NM_01239	TSS1500		
		MRPS35	NM_02182	Body		
rs9260590					chr6:29924	N_Shore
rs79295549						
		ARL16;HG	NM_00104	TSS1500;B	chr17:7965	S_Shore
	rs674102	KIF17;KIF	NM_00112	Body;Body	chr1:21022	Island
		MCF2L;M	NM_00111	Body;Body	chr13:1136	N_Shelf
	rs10037095				chr5:26431	N_Shore
					chr6:28984	N_Shore
		IGF2BP2;I	NM_00100	Body;Body		
					chr9:11585	N_Shore
rs80041074	rs76481776	MIR182	NR_02961	Body		
	rs10109265				chr8:61193	S_Shelf
		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		PCDHB7	NM_01894	1stExon	chr5:14055	N_Shore

					chr12:5438	Island
		C3orf24;C3	NM_00116	TSS200;TS	chr3:10149	Island
		DCP1A	NM_01840	Body	chr3:53381	N_Shore
		MIR886	NR_03058	TSS1500	chr5:13541	S_Shore
rs41386944		MGP	NM_00090	TSS1500		
		MAFK	NM_00236	5'UTR	chr7:15757	S_Shore
		PCDHB6	NM_01893	TSS200	chr5:14053	N_Shore
	rs35853657					
		INPP5A	NM_00553	Body		
	rs76293558	PTPRN2;P	NM_00284	Body;Body;Body		
		GPR64;GP	NM_00575	TSS1500;T	chrX:19139	S_Shore
		DRAP1;C1	NM_00644	TSS1500;B	chr11:6568	Island
	rs75095852					
		CAMTA1	NM_01521	Body		
	rs28506195	KDM2B;K	NM_03259	Body;Body	chr12:1220	N_Shelf
		LOC28583	NR_02697	Body;Body		
		SCML4	NM_19808	TSS1500		
		ODZ2	NM_00112	TSS200		
	rs6930591					
		GUCY2G	NR_02813	TSS200		
rs12959342		MIR187	NR_02961	TSS1500		
		C11orf95	NM_00114	3'UTR	chr11:6352	N_Shore
		UBAC2;UE	NM_00114	Body;Body;Body		
					chr10:1352	Island
		CMIP	NM_19839	Body		
rs8009724	rs8004552					
rs12668237					chr7:55516	Island
		C12orf23	NM_15226	5'UTR	chr12:1073	S_Shore
	rs72842429					
	rs906303	NCOR2;NC	NM_00631	Body;Body		
		SHF	NM_13835	TSS200	chr15:4549	S_Shelf
rs77573804		CBR1;CBR	NM_00175	1stExon;5'U	chr21:3744	Island

				HLA-L	NR_02782	Body	chr6:30227	S_Shore
							chr12:1251	S_Shelf
				LDHD;LDI	NM_19443	Body;Body	chr16:7514	S_Shore
rs79403508								
				SLITRK1	NM_05291	1stExon	chr13:8445	Island
				MRGPRF;	NM_00109	Body;Body	chr11:6877	N_Shelf
				FAM66D	NR_02742	Body		
rs75263406	rs72841739			HLA-A	NM_00211	Body	chr6:29910	Island
				B3GNT3	NM_01425	TSS1500	chr19:1790	Island
				CLECL1	NM_17200	TSS200		
	rs28788792						chr16:3154	S_Shelf
				ZNF263	NM_00574	Body	chr16:3332	S_Shore
	rs80069232			ARHGEF1	NM_01462	Body		
				PPP1R7	NM_00271	Body		
				PGCP	NM_01613	Body		
				TBCD	NM_00599	Body	chr17:8086	S_Shelf
		TRUE		KCTD5	NM_01899	Body	chr16:2746	S_Shelf
				RPH3AL	NM_00698	Body	chr17:1136	N_Shore
							chr7:17840	S_Shore
	rs63300360			TMPRSS6	NM_15360	Body	chr22:3749	Island
							chr3:15117	Island
rs72645365	rs72645366			COL1A1	NM_00008	Body	chr17:4827	N_Shelf
				PDE9A;PD	NM_00100	Body;Body	chr21:4410	Island
				SLC35B4	NM_03282	3'UTR		
			TRUE	ANKRD9	NM_15232	5'UTR	chr14:1029	Island
				LOC10013	NR_02446	Body;TSS1	chr11:6713	S_Shore
				C3orf59	NM_17849	Body		
				SKAP1;SK	NM_00107	TSS200;TS	chr17:4650	Island
	rs1183967						chr16:7309	S_Shore
				BCOR;BC	NM_00112	5'UTR;1stE	chrX:40036	Island
				GABRA5;	NM_00116	TSS1500;T	chr15:2711	N_Shore
	rs3116068			BRMS1;BR	NM_01539	3'UTR;3'U	chr11:6610	S_Shelf
	rs5893130							
				PIM2	NM_00687	TSS200	chrX:48775	Island
				PRR5L	NM_00116	5'UTR		
rs11541225	rs8068081			NPLOC4	NM_01792	3'UTR		
rs35415553	rs12949718			TOM1L1	NM_00548	Body	chr17:5297	S_Shelf
	rs12600633			RPTOR;RP	NM_00116	Body;Body		
	rs62106648			CLPP	NM_00601	Body	chr19:6361	S_Shore
				ARHGEF1	NM_01462	Body		
				NCRNA00	NR_02433	Body	chr19:5220	Island

			FYN;FYN;	NM_1530	Body;Body;Body		
rs272008			DPP10;DP	NM_02086	3'UTR;3'UTR		
		TRUE	CCK	NM_00072	5'UTR	chr3:42306	Island
			FUT2;FUT	NM_00051	5'UTR;5'U	chr19:4919	Island
			GDPD5	NM_03079	5'UTR		
			MAB21L1;	NM_0055	1stExon;Bo	chr13:3604	Island
rs75266286			HOXC10	NM_01740	TSS1500	chr12:5437	N_Shore
	rs6426133						
			GREB1;GR	NM_14890	3'UTR;Body;Body		
			JPH2	NM_02043	Body	chr20:4278	Island
	rs17551206		YES1	NM_00543	3'UTR		
rs75196460			ZNF132	NM_00343	TSS1500	chr19:5895	Island
			HRH1	NM_00109	TSS200		
			EBF4	NM_00111	Body	chr20:2731	Island
			LRIG1	NM_01554	Body		
rs62288071						chr3:19398	S_Shore
			DIP2C	NM_01497	Body		
			TGFB2;TG	NM_00323	Body;Body		
			ZNF717	NM_00112	TSS200	chr3:75834	Island
			SORCS2	NM_02077	Body		
	rs2739801		SNORD11	NR_00335	TSS1500		
			AP2A2	NM_01230	Body		
			PCDHB12;	NM_01893	5'UTR;1stE	chr5:14058	N_Shore
			TRIO	NM_00711	Body		
rs11111420			ASCL1	NM_00431	1stExon	chr12:1033	Island
rs75831139						chr6:28554	S_Shelf
	rs16862402						
			LRRFIP1;L	NM_00113	Body;Body	chr2:23864	S_Shelf
	rs614542		FLI1;FLI1	NM_00201	Body;5'UT	chr11:1285	S_Shelf
	rs2105505		DTX4	NM_01517	Body	chr11:5893	S_Shelf
			C8orf34	NM_05295	TSS1500		
	rs3749777		PCDHGB1	NM_01892	1stExon;Bo	chr5:14073	Island
			GLIPR1L2	NM_15243	Body	chr12:7578	S_Shore
rs73729763			PTPRN2;P	NM_00284	Body;Body;Body		
						chr5:25190	Island
			CSF1R	NM_00521	TSS1500		

		MCF2L	NM_00111	Body	chr13:1136	S_Shore
	rs35635923				chr12:1151	Island
		GALNTL4	NM_19851	Body	chr11:1164	Island
		LSAMP	NM_00233	3'UTR		
	rs197210	CCDC109E	NM_01791	Body		
		HLA-C	NM_00211	Body	chr6:31238	N_Shore
		PIP5K1C	NM_01239	Body	chr19:3659	N_Shelf
					chr2:24156	N_Shore
					chr7:11203	S_Shore
		MAP3K7IP	NM_15278	1stExon;5'U	chrX:30906	Island
		AKT3;AKT	NM_00546	Body;Body		
		PSMD14	NM_00580	Body		
		PRDM1;PR	NM_00119	Body;1stExon;5'UTR		
	rs6760031	AAK1	NM_01491	Body		
	rs72758352	BNC1	NM_00171	Body	chr15:8395	N_Shelf
		HDAC6	NM_00604	TSS200	chrX:48659	Island
	rs598641	ZFYVE28	NM_02097	Body	chr4:23055	Island
rs7581359		MYT1L	NM_01502	Body		
rs78685753	rs76989997	DLC1;DLC	NM_18264	Body;Body		
		GINS4	NM_03233	Body		
		PKP3	NM_00718	Body	chr11:4000	Island
		SELP	NM_00300	TSS1500		
		ABCG4;AB	NM_00114	Body;Body	chr11:1190	S_Shelf
rs13402068		NFE2L2;N	NM_00616	Body;5'UTR;5'UTR		
		PM20D1	NM_15249	Body	chr1:20581	Island
	rs79829138				chr1:31280	S_Shelf
	rs62153905	NCAPH	NM_01534	Body	chr2:97001	S_Shelf
	rs56255127	NTM;NTM	NM_00114	Body;Body;Body;Body		
		RLIM;RLI	NM_18335	TSS1500;T	chrX:73833	S_Shore
		XRCC2	NM_00543	3'UTR		
					chr22:4984	N_Shelf
rs76677712	rs80242037					

			ELF4;ELF4	NM_00142	TSS1500;T	chrX:12924	Island
		TRUE					
			PRSS37	NM_00100	Body		
			HIVEP3;HI	NM_02450	5'UTR;5'UTR		
			NPSR1	NM_20717	Body		
rs200500			HIST1H4J	NM_02196	TSS200	chr6:27791	Island
	rs35910200					chr17:2219	S_Shore
rs1886544			NEK5	NM_19928	Body	chr13:5270	N_Shore
			ACTC1	NM_00515	Body		
	rs74531854		EPCAM;M	NM_00235	Body;TSS1500		
			FEZ2;FEZ2	NM_00510	Body;Body		
						chr6:31276	N_Shore
rs67799164						chr5:13908	Island
			PET112L	NM_00456	Body		
rs28450960	rs9969009						
rs12354378			C1orf130	NM_00101	5'UTR		
			TMEM132	NM_20731	Body	chr17:3296	Island
			C2orf84	NM_00104	TSS200	chr2:24397	Island
	rs73082997						
	rs9277367		HLA-DPB1	NM_00212	Body	chr6:33048	S_Shore
			RASGRF2	NM_00690	Body	chr5:80255	S_Shore
			PON1	NM_00044	TSS200	chr7:94953	Island
			CTNNA2;C	NM_00438	Body;Body		
			CECR1;CE	NM_17740	TSS200;Body		
			KCNQ1;K	NM_00021	Body;Body		
rs11973023	rs73176136		PTPRN2;P	NM_00284	Body;Body;Body		
			DOCK1	NM_00138	Body		
			CCNH	NM_00123	TSS1500	chr5:86708	S_Shore
			MED24;M	NM_01481	Body;Body;TSS200		
rs73567426			TRMT2B;T	NM_02491	1stExon;5'U	chrX:10030	Island
			DND1	NM_19424	Body	chr5:14005	Island
	rs34766380		HEATR2	NM_01780	Body		
			NOTCH4	NM_00455	Body		

	rs28626100		PRKCZ	NM_00274	Body		
	rs58568506		HLA-DQB	NR_003937	Body		
rs28729528	rs74462848					chr10:4267	S_Shore
			HLA-DRB	NM_00212	3'UTR		
			RPL13AP3	NR_00484	Body	chr14:5623	Island
	rs72722579		GOLGA8A	NR_02740	Body	chr15:3472	N_Shelf
		TRUE	ANKRD44	NM_15369	Body		
rs2500548			UST	NM_00571	Body		
	rs73613550		SS18L1	NM_19893	Body	chr20:6074	Island
			TGFBI	NM_00035	Body		
			ACTR3	NM_00572	3'UTR		
	rs619398						
		TRUE	LOC39995	NR_02443	Body		
			TSLP	NM_03303	TSS1500	chr5:11040	N_Shelf
	rs1636643	TRUE	LOC10013	NR_029411	Body		
rs4867381	rs78219065						
			CYB561;C	NM_00101	Body;Body	chr17:6151	N_Shore
rs9272676	rs28383432		HLA-DQA	NM_00212	Body		
rs2748063	rs4849235					chr2:11426	N_Shore
			KIRREL3;	NM_00116	Body;Body		
			ACTR3C;A	NM_00116	Body;Body		
			CREM;CR	NM_18285	5'UTR;Body;Body;Body;Body;Bod		
rs7106869			SLC5A12;S	NM_17849	5'UTR;1stExon		
						chr1:91300	N_Shore
rs9886096							
			HEYL	NM_01457	TSS1500	chr1:40105	Island
	rs2337987		PCDHA2;P	NM_01890	Body;Body	chr5:14018	Island
			ZBTB20;Z	NM_01564	5'UTR;5'UTR		
			TGFBR3	NM_00324	Body		
rs2772103			ROR1;ROR	NM_00501	Body;Body		
						chr3:16093	N_Shelf
rs34789086	rs36098404		MYOM2	NM_00397	Body	chr8:20780	S_Shelf
rs62262385			ADCY5	NM_18335	Body		
			BAMBI	NM_01234	Body	chr10:2896	S_Shelf
			ZNF541	NM_00110	Body	chr19:4804	Island

	rs77272297					chr15:5309	S_Shore
						chr6:17045	Island
	rs74860689					chr13:2490	Island
			PCDHB4	NM_01893	1stExon	chr5:14050	Island
			TAF3	NM_03192	Body		
			HECW1	NM_01505	Body	chr7:43288	Island
			KIF15;KIA	NM_02024	TSS1500;B	chr3:44802	N_Shore
rs80099637						chr6:27482	Island
	rs75271579		EXOC4	NM_02180	Body		
			SF3B5	NM_03128	TSS1500	chr6:14441	S_Shore
			RGS12;RG	NM_19822	Body;TSS2	chr4:33747	N_Shelf
			MAP2K6	NM_00275	Body		
	rs55840817		TNS1	NM_02264	Body		
			KIF1A	NM_00432	Body		
			SDHAP3	NR_00326	TSS200	chr5:15942	Island
			MAP1B	NM_00590	Body		
			FGF12	NM_00411	Body		
			PRKAG2;P	NM_01620	Body;Body		
			HRNBP3	NM_00108	5'UTR		
rs78086551			ZNF662;ZN	NM_00113	TSS200;5'U	chr3:42947	Island
	rs9640385						
			CTTN;CTT	NM_13856	Body;Body		
	rs72972417		SEMA5B	NM_00103	5'UTR		
			SLC9A7	NM_03259	TSS200	chrX:46618	Island
			CARKD	NM_01821	Body	chr13:1112	S_Shelf
			ITGB5	NM_00221	Body	chr3:12460	N_Shelf
						chr13:1129	Island
			RBMS3;R	NM_00100	Body;Body;Body		
			SMC1B	NM_14867	Body	chr22:4580	N_Shelf
			ESR1;ESR	NM_00112	5'UTR;TSS	chr6:15212	N_Shelf
			MMP7	NM_00242	TSS200		
			LHFP	NM_00578	Body		
		TRUE	HIST1H2A	NM_00351	1stExon;TS	chr6:26124	Island
	rs3786698		COL5A3	NM_01571	Body	chr19:1007	S_Shore

	rs6954688		PRKAG2;P	NM_01620	Body;Body	chr7:15142	S_Shore
			FOXO4;FO	NM_00117	TSS1500;T	chrX:70315	Island
						chr10:1189	N_Shelf
rs12244105	rs60360796						
			PCDHB7	NM_01894	1stExon	chr5:14055	N_Shore
	rs74002072		AATK	NM_00108	Body		
	rs79947479		HIVEP2	NM_00673	5'UTR		
			GPC5	NM_00446	Body		
			RPS4Y2	NM_00103	TSS200		
	rs9435732		MFAP2;M	NM_00240	TSS1500;T	chr1:17306	S_Shore
		TRUE	LCLAT1;L	NM_18255	TSS1500;T	chr2:30669	N_Shore
			CPLX1	NM_00665	Body	chr4:79853	Island
rs3214680			MRPS27	NM_01508	Body		
			CRTC1;CR	NM_01532	Body;Body	chr19:1888	Island
			DPYSL2	NM_00138	Body		
			HDAC9;H	NM_17842	Body;Body;Body;Body;Body		
			HLA-DPB2	NR_00143	Body	chr6:33084	N_Shore
rs77431781							
	rs74482437						
			ZNF673;Z	NM_01777	TSS200;TS	chrX:46306	Island
						chr19:2270	Island
			SEC31A;S	NM_01493	Body;Body;Body;Body;Body		
rs13189269			PCDHB7	NM_01894	1stExon	chr5:14055	Island
			RPS6KA3	NM_00458	TSS1500	chrX:20284	Island
			FNDC3B;F	NM_02276	5'UTR;5'U	chr3:17175	S_Shore
	rs78030723		PTPRN2;P	NM_00284	Body;Body	chr7:15810	N_Shelf
			NCR1;NC	NR_02704	TSS200;TSS200;TSS200;TSS200;T		
		TRUE	UMOD;U	NM_00100	TSS1500;T	chr16:2035	S_Shelf
						chrY:15863	Island
			PTPRN2;P	NM_00284	Body;Body	chr7:15837	N_Shore
			CSMD1	NM_03322	Body		
			COL11A1;	NM_00185	3'UTR;3'UTR;3'UTR;3'UTR		
			CR1L	NM_17571	Body	chr1:20784	Island
			CLYBL	NM_20680	Body		
rs9271163	rs9271162						
			CCDC62;C	NM_20143	Body;Body;Body		
			TSPY4	NM_00116	Body	chrY:93433	N_Shelf
	rs7545953					chr1:12123	N_Shelf
			C21orf29;K	NM_14499	Body;TSS1500		
			PSMB9;P	NM_00280	Body;Body	chr6:32820	S_Shore

			TCERG1L	NM_17493	Body		
			TBC1D16	NM_01902	Body	chr17:7792	Island
			ARSB;ARS	NM_19870	TSS200;1st	chr5:78280	S_Shore
			FLJ44606;F	NM_00116	5'UTR;5'U	chr5:12640	N_Shore
			HLX	NM_02195	Body	chr1:22105	N_Shore
			TET2;TET2	NM_00112	5'UTR;5'UTR		
						chr1:22105	S_Shore
	rs3996378		AMZ1	NM_13346	5'UTR	chr7:27276	Island
						chr2:23321	Island
						chr16:8587	Island
						chr15:9011	N_Shelf
			ZNF57;ZN	NM_17348	5'UTR;1stE	chr19:2900	Island
			TCF12;TC	NM_00320	Body;Body;Body;Body		
			LIMA1;LI	NM_00111	Body;Body		
			PAPPA2;P	NM_02193	5'UTR;5'UTR		
rs77063167	rs76889504		C1orf175;C	NR_02678	Body;5'UTR		
			ITGA8	NM_00363	Body		
		TRUE	GSTM1;GS	NM_00056	1stExon;5'U	chr1:11023	Island
	rs76591184					chr10:8839	S_Shelf
	rs74001164		RPTOR;RP	NM_00116	Body;Body	chr17:7893	Island
rs2458239			SHF	NM_13835	TSS200	chr15:4549	S_Shelf
						chr17:2528	Island
			VWA3B	NM_14499	3'UTR		
			AUTS2;AU	NM_01557	Body;Body		
	rs9261291		RNF39;RN	NM_17076	3'UTR;3'U	chr6:30038	N_Shore
						chr4:58061	N_Shore
			XRCC5	NM_02114	Body		
			HSD3B2;H	NM_00116	Body;Body		
	rs11591336		ZMIZ1	NM_02033	5'UTR		
						chr6:90597	Island
						chr19:3803	Island
			SNORD12	NR_00368	TSS1500;T	chr5:95446	S_Shore
	rs28691845		DMBT1;DM	NM_00732	TSS1500;TSS1500;TSS1500		
			RAD50;RA	NM_13348	TSS1500;T	chr5:13189	N_Shore
			GRK5	NM_00530	Body		
	rs55793228						
			PHKA2	NM_00029	TSS200	chrX:19002	Island
	rs836718		B3GALT1	NM_02098	TSS1500		

	rs33961294			ITPA;ITPA	NM_18149	Body;Body		
							chr1:22874	Island
				TMEM195;	NM_00100	1stExon;5'UTR		
				PCDHA6;P	NM_03184	Body;Body	chr5:14022	Island
				KLHL14	NM_02080	Body	chr18:3034	N_Shore
				ZFY;ZFY;Z	NM_00341	5'UTR;5'U	chrY:28029	S_Shelf
				C4orf49;C4	NM_03262	5'UTR;1stE	chr4:14020	Island
				NCRNA00	NR_026751	Body		
							chr22:4645	S_Shore
							chr3:10206	N_Shelf
							chr19:5857	N_Shelf
							chr7:96653	S_Shore
				LOC10013	NR_02456	TSS200;TS	chr4:12029	N_Shore
			TRUE	SYCP1;SY	NM_00317	1stExon;5'U	chr1:11539	Island
rs12463342				RFPL4A	NM_00114	TSS1500		
	rs12808337						chr11:6128	N_Shelf
							chr14:1011	Island
				WWC2	NM_02494	Body		
				CADM1;C	NM_00109	Body;Body		
				FLRT2	NM_01323	Body		
rs12519737								
				LOC10013	NR_02446	Body;TSS1	chr11:6713	S_Shore
	rs73329999			SMTNL2;S	NM_19850	TSS200;TS	chr17:4487	N_Shore
	rs34072327							
				HEPHL1;H	NM_00109	5'UTR;1stExon		
	rs76515922			HLA-DRB	NM_00212	TSS1500		
				NLGN4Y;N	NR_02831	Body;5'UT	chrY:16636	Island
		TRUE		RCAN2	NM_00582	Body		
				LOC10013	NR_02447	Body		
				SCUBE2;S	NM_00117	TSS200;TS	chr11:9112	Island
rs8818				LOXL1	NM_00557	3'UTR		
rs2280406				MST1R	NM_00244	TSS200	chr3:49940	Island
							chr7:65338	N_Shelf
				MAOA	NM_00024	TSS200	chrX:43515	N_Shore
				SEMA6D;S	NM_15361	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR		
	rs28970277			NOP56;MI	NM_00639	Body;TSS2	chr20:2632	Island

		TRUE	PRKY	NR_02806	Body		
			ASAP1	NM_01848	Body		
			RBMS1;RE	NM_00289	Body;Body		
						chr10:3180	N_Shore
			GFI1;GFI1	NM_00112	TSS1500;T	chr1:92945	Island
			KIAA1217;	NM_01959	Body;Body;Body		
						chr10:4890	S_Shelf
						chr5:17562	Island
			IDE	NM_00496	TSS1500	chr10:9433	S_Shore
	rs76604458						
			CCDC57	NM_19808	Body		
						chr6:17073	Island
						chr10:1348	S_Shore
rs6488428							
rs497988	rs72804303						
			TMEM26	NM_17850	3'UTR		
	rs6575572						
			NXT2	NM_01869	Body	chrX:10878	Island
rs79283987							
			KRTAP2-1	NM_00112	TSS1500		
rs1059974			ARL4D	NM_00166	Body	chr17:4147	Island
rs4750015	rs79985936					chr10:6186	N_Shelf
	rs74761001					chr1:11779	S_Shelf
			GUCY2E	NR_024042	Body		
						chr6:90597	Island
rs73796371							
			CAPN2;CA	NM_00174	Body;Body	chr1:22389	S_Shelf
			USP29	NM_02090	5'UTR	chr19:5763	S_Shelf
			NUP210	NM_02492	Body		
			HAS2AS;H	NR_00283	TSS1500;5'	chr8:12265	N_Shore
		TRUE	FLJ37543	NM_17366	Body		
			WDR27	NM_18255	Body	chr6:17005	N_Shelf
rs4752658			TACC2;TA	NM_20686	Body;Body		
			TRIM31	NM_00702	Body		
			TNFRSF19	NM_14895	3'UTR		
	rs7255365		MIR518C;	NR_03019	TSS1500;TSS200		
	rs4654327		OPRD1	NM_00091	3'UTR	chr1:29189	S_Shore
	rs55652837	TRUE				chr19:8575	N_Shore

			RAMP1	NM_00585	Body		
			IGLON5	NM_00110	Body	chr19:5183	N_Shore
			PTGDR	NM_00095	TSS1500	chr14:5273	N_Shore
			SNX18;SN	NM_05287	TSS1500;T	chr5:53813	N_Shore
			HAUS7;HA	NM_01751	5'UTR;1stE	chrX:15273	S_Shore
		TRUE	PTPN7;PT	NM_08058	TSS1500;5'UTR		
			CAPN8	NM_00114	Body	chr1:22374	S_Shelf
rs77049826			SDK1	NM_15274	Body		
			SYCP1	NM_00317	5'UTR	chr1:11539	S_Shore
			PACS2;PA	NM_01519	Body;Body	chr14:1058	Island
			KIAA1217;	NM_01959	Body;Body;Body		
			MACROD1	NM_01406	Body		
rs10017302							
			PCDHB11	NM_01893	TSS200	chr5:14058	N_Shore
			GRID1	NM_01755	Body	chr10:8802	Island
	rs80177780		HLA-DRB	NM_00212	Body	chr6:32489	S_Shore
			KIAA1239	NM_00114	TSS1500	chr4:37245	Island
	rs73799819		C1QTNF7;	NM_00113	Body;1stExon;5'UTR		
			DHRS7C	NM_00110	Body	chr17:9674	S_Shelf
			DLGAP2	NM_00474	Body	chr8:14967	Island
						chr10:2563	Island
	rs11046051		PYROXD1	NM_02485	Body	chr12:2159	S_Shelf
	rs627448					chr18:1203	N_Shelf
			EEF1DP3	NR_027062	Body		
			ELF1	NM_17237	TSS200		
			CEACAM5	NM_00436	TSS1500		
			LOC10013	NR_02446	Body;TSS1	chr11:6713	S_Shore
			OR4K14	NM_00100	1stExon		
						chr5:75377	N_Shore
			RNASE4;A	NM_19443	TSS1500;T	chr14:2115	S_Shelf
			GCK	NM_00016	Body		
						chr14:7507	S_Shelf
rs72959331						chr4:85413	N_Shelf
	rs3823967		ZNF767;Z	NR_02778	TSS1500;T	chr7:14932	S_Shore
			DIP2C	NM_01497	Body	chr10:6522	N_Shore
			DIP2C	NM_01497	Body		
			DMPK;DM	NM_00440	TSS1500;T	chr19:4628	N_Shelf
rs76049498						chr8:62051	S_Shore
rs62286822						chr4:14945	S_Shelf
	rs75722464		ZNF283	NM_18184	TSS1500		
rs79735053			OXCT1	NM_00043	Body		

		TRUE	SULT1A1;	NM_17753	5'UTR;1stE	chr16:2863	Island
			HOXC8	NM_02265	3'UTR	chr12:5440	N_Shelf
			CLASP1;C	NM_00114	Body;Body;Body		
			ATL3	NM_01545	Body	chr11:6343	N_Shelf
			UST	NM_00571	Body		
			BRUNOL4	NM_00102	Body;Body	chr18:3506	N_Shore
rs41307436			PNPLA7;P	NM_15228	Body;Body	chr9:14035	Island
	rs77476480					chr1:14885	Island
			TRIM2;TR	NM_01527	Body;5'UTR		
			THOP1	NM_00324	Body	chr19:2790	S_Shore
	rs11626877					chr14:7601	S_Shelf
	rs74060478					chr14:7031	S_Shore
			KIAA1949;	NM_00113	Body;1stEx	chr6:30654	N_Shore
			C2orf84	NM_00104	TSS200	chr2:24397	Island
			OR4A16	NM_00100	1stExon		
			FREM2	NM_20736	3'UTR		
	rs72888697						
rs71633779	rs3978140					chr4:13264	N_Shore
			LOC72937	NR_02425	Body	chr3:12982	N_Shelf
rs41553315	rs41560216		HLA-A	NM_00211	Body	chr6:29910	Island
rs76741942	rs77481328		HCG9	NR_02803	Body	chr6:29944	S_Shore
			MYT1L	NM_01502	5'UTR		
			ANK1;AN	NM_02047	Body;Body	chr8:41583	Island
rs72667033			COL1A1	NM_00008	Body	chr17:4827	N_Shore
	rs1934697		DYDC1	NM_13881	5'UTR	chr10:8211	N_Shelf
			C3orf24;C3	NM_00116	TSS200;TS	chr3:10149	Island
			LOC92249	NR_01535	Body		
	rs59684608					chr19:4420	N_Shelf
			C6orf201;C	NM_00108	1stExon;TS	chr6:40790	S_Shore
	rs76068276	TRUE	LIN28	NM_02467	TSS200	chr1:26737	Island
						chr5:58870	Island
			C2orf55	NM_20736	Body	chr2:99438	Island
			PCDHB8	NM_01912	TSS1500	chr5:14055	N_Shore
			RELL1;RE	NM_00108	Body;Body		
rs35917228						chr2:23321	Island
			MIR886	NR_03058	TSS200	chr5:13541	Island
			ATP6AP2	NM_00576	TSS1500	chrX:40439	Island
			KIAA0391	NM_01467	Body		
			RYR1;RYR	NM_00054	Body;Body	chr19:3905	S_Shelf

				C6orf10	NM_00678	Body		
				PNLIPRP2	NM_00539	Body	chr10:1183	Island
rs12485273				RBP1;RBP	NM_00289	Body;Body	chr3:13925	N_Shelf
							chr18:7283	Island
				C14orf182	NM_00101	TSS1500		
				FLJ44606;F	NM_00116	5'UTR;5'U	chr5:12640	Island
				RFFL;RFFI	NM_00101	TSS200;5'UTR		
rs57400052				TRIP4	NM_01621	Body		
				HLA-DPA1	NM_03355	3'UTR		
	rs67392985			FLT4;FLT4	NM_00202	Body;Body	chr5:18004	Island
	rs57441095			USP29	NM_02090	TSS1500	chr19:5763	S_Shore
				RAI14;RAI	NM_00114	Body;Body;Body;Body;Body;Body		
				PXT1;KCT	NM_15299	5'UTR;TSS	chr6:36410	N_Shore
				DUSP5	NM_00441	Body	chr10:1122	S_Shelf
				TMCO4	NM_18171	Body		
				ARX	NM_13905	Body	chrX:25025	Island
	rs78423629						chr2:20857	N_Shelf
							chr22:1826	S_Shore
				SV2B;SV2	NM_00116	Body;Body		
							chr8:48676	N_Shore
	rs78318036			HBB	NM_00051	TSS200		
				FRK	NM_00203	TSS200		
	rs10054597			TPPP	NM_00703	Body	chr5:66794	S_Shore
			TRUE	USP51	NM_20128	TSS1500	chrX:55515	S_Shore
				C3	NM_00006	Body	chr19:6710	Island
				MIR196A2	NR_029617	TSS200	chr12:5438	N_Shelf
				IL1B	NM_00057	TSS1500		
				RASGRF2	NM_00690	Body	chr5:80255	S_Shelf
	rs12426212			LRIG3;LRI	NM_00113	Body;Body	chr12:5931	N_Shelf
				SIM1	NM_00506	Body	chr6:10089	Island
rs2375289							chr11:6983	N_Shore
	rs77759253	TRUE		WWC1;W	NM_00116	Body;Body;Body		
				UPK3B;UP	NM_18268	3'UTR;3'U	chr7:76145	Island
				MIR886	NR_03058	TSS1500	chr5:13541	S_Shore
rs6697054	rs6697061			SNAP47	NM_05305	Body		
				SNX26	NM_05294	TSS1500	chr19:3626	N_Shore
rs2489842				MAP3K8	NM_00520	TSS1500	chr10:3072	N_Shore
			TRUE	SATB1;SA	NM_00297	5'UTR;5'U	chr3:18466	N_Shore
				PLEKHG4	NM_05290	Body	chr5:16471	N_Shore

		HLA-DRB	NM_00212	Body	chr6:32489	N_Shore
	rs34897299					
		BRIP1	NM_03204	Body	chr17:5994	N_Shelf
		ARSB;ARS	NM_19870	TSS200;1st	chr5:78280	S_Shore
		JARID2	NM_00497	Body		
rs4806621		NCR1;NCR	NR_02704	TSS200;TSS200;TSS200;TSS200;T		
rs4242910					chr12:1331	N_Shore
		OR2A5	NM_01236	TSS1500		
					chr6:31276	Island
	rs78286218	ASAM	NM_02476	Body		
	rs66586255	C10orf58;C	NR_02457	Body;Body		
					chr6:16881	S_Shore
		WDR88;W	NM_17347	1stExon;5'U	chr19:3362	Island
rs71375217						
	rs7210944				chr17:2172	N_Shelf
		GOLGA3	NM_00589	Body	chr12:1333	Island
					chr11:4693	S_Shelf
rs2514184		OR9Q1	NM_00100	5'UTR		
		UCHL1	NM_00418	TSS1500	chr4:41258	N_Shore
					chr2:24298	Island
		TNKS2	NM_02523	3'UTR		
					chr4:17069	Island
		PACS2;PA	NM_01519	Body;Body	chr14:1058	S_Shore
		HPCAL1;H	NM_00214	5'UTR;5'UTR		
rs2123114	rs71742037				chr2:17559	Island
rs34779657		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		MCOLN2	NM_15325	Body		
		SLITRK1	NM_05291	1stExon	chr13:8445	S_Shore
		GSTM1;GS	NM_00056	1stExon;5'U	chr1:11023	Island
		DPP6;DPP	NM_00103	Body;TSS2	chr7:15374	Island
		ADARB2	NM_01870	Body	chr10:1516	Island
	rs2180266					
					chr11:7812	S_Shelf
		OAT	NM_00027	3'UTR		
		CYP2E1	NM_00077	Body	chr10:1353	S_Shore
	rs17281216	HDAC6	NM_00604	TSS200	chrX:48659	Island

		SFRS8	NM_00459	Body	chr12:1322	Island
		BDH1;BDH	NM_20331	Body;Body;Body		
		PARD3	NM_01961	Body		
		USP36	NM_02509	Body	chr17:7679	N_Shelf
	rs8079308	CCDC103	NM_21360	3'UTR	chr17:4297	S_Shelf
		MCF2L;MC	NM_00111	Body;Body	chr13:1136	Island
		GVIN1	NR_00394	TSS1500		
	rs4976688	RGS14	NM_00648	TSS1500		
rs74429981						
rs41556114	rs1136700	HLA-A	NM_00211	Body	chr6:29910	Island
		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
					chr17:4662	N_Shore
		TUBA1C	NM_03270	Body	chr12:4965	S_Shelf
	rs75437491	C7orf50;C7	NM_00113	Body;Body	chr7:10974	S_Shore
		PRDM1	NM_00119	Body	chr6:10653	S_Shore
		ACVR1;AC	NM_00110	5'UTR;5'UTR		
rs55704653		UBE2J2;U	NM_19445	3'UTR;3'U	chr1:11893	Island
					chr15:3836	N_Shelf
rs61731875		PFKFB3;P	NM_00456	Body;Body		
	rs9383513	WDR27	NM_18255	Body		
		SLC25A27	NM_00427	Body	chr6:46620	S_Shelf
rs56113739		LOC64174	NR_03324	Body		
					chr17:6192	Island
	rs58094600	IDO2	NM_19429	Body		
		LASS6	NM_20346	Body		
		MGC16121	NR_02460	Body	chrX:13367	Island
		RPL24	NM_00098	TSS1500	chr3:10140	S_Shore
rs9501327	rs36036203				chr6:30418	S_Shore
		EIF1AD;EI	NM_03232	1stExon;5'U	chr11:6576	Island
					chr6:15552	Island
		TBC1D16	NM_01902	Body	chr17:7792	Island
rs75490742					chr17:4885	Island
		RAPGEF4;	NM_00702	Body;Body		
		C20orf85	NM_17845	TSS200	chr20:5672	Island
	rs9556451				chr13:9565	N_Shelf
	rs59417780	GOLGA3	NM_00589	Body		

		ADAP1	NM_00686	Body	chr7:94270	S_Shore
		DDR1	NM_00195	TSS1500	chr6:30852	N_Shore
		MUC21	NM_00101	Body		
					chr20:5954	Island
rs61487242	rs56031155				chr15:3026	S_Shelf
		LRRC61;A	NM_00114	TSS200;5'U	chr7:15001	Island
					chr2:23321	Island
	rs6761527	C2orf48	NM_18262	Body		
		RBM19;RB	NM_00114	Body;Body;Body		
					chr12:1252	Island
		DDO;DDO	NM_00403	Body;Body	chr6:11072	Island
		NOV	NM_00251	Body	chr8:12042	S_Shore
					chr10:1352	Island
rs73357389		CLIC6	NM_05327	TSS200	chr21:3604	Island
		CLYBL	NM_20680	Body		
rs80002403		CYP27C1	NM_00100	Body		
rs6903652		ZNF323;ZK	NM_00113	5'UTR;5'UTR;TSS200		
rs76119325		ZNF826	NM_00103	3'UTR		
	rs7327685	COL4A2	NM_00184	Body	chr13:1111	S_Shore
rs78443201					chr12:7125	S_Shelf
					chr19:1327	S_Shelf
		ELN;ELN;I	NM_00108	Body;Body;Body;Body;Body		
rs59244063					chr10:1349	N_Shore
	rs77822212	AGPAT1;A	NM_00641	5'UTR;5'UTR		
		PMS2L11	NR_02338	Body		
rs76621072		RASSF2;R	NM_01473	5'UTR;5'UTR		
		FCGR2C	NM_20156	3'UTR		
		NLGN4Y;N	NR_02831	Body;5'UT	chrY:16636	Island
					chr10:1106	Island
	rs5784138	SVIL;SVIL	NM_02173	Body;Body		
	rs55752997	CHD3	NM_00100	Body	chr17:7788	S_Shore
		TBL1X;TB	NM_00113	5'UTR;5'U	chrX:94328	Island
					chr7:14013	Island
rs55823554		KCNQ4;KC	NM_00470	Body;Body	chr1:41303	Island
		RBMS1;RE	NM_00289	Body;Body		
rs74042535						
rs2283333		VWF	NM_00055	Body	chr12:6165	N_Shelf
		TINAG	NM_01446	Body		
rs73042944		SLC9A3	NM_00417	Body	chr5:50183	Island
		GRIP1	NM_02115	Body		

rs17304758				ZNF420	NM_14468	TSS200	chr19:3756	Island
				LOC28402	NR_02434	TSS1500	chr17:7818	S_Shore
				EPAS1	NM_00143	Body		
				NAV2	NM_00111	Body		
				EFHC1	NM_01810	Body	chr6:52284	S_Shelf
							chr12:1313	N_Shelf
rs76356885	rs12817870			DTX1	NM_00441	Body	chr12:1135	S_Shore
	rs11200296			NSMCE4A	NM_00116	Body;Body	chr10:1237	N_Shelf
rs11267707							chr8:66640	S_Shore
				OR2T11	NM_00100	TSS1500		
	rs80243330							
							chr15:7972	N_Shelf
							chr18:7729	Island
				LRRC20;L	NM_20711	5'UTR;5'U	chr10:7214	N_Shelf
				KIR3DP1	NM_00101	3'UTR		
				CD99L2;C	NM_13444	1stExon;5'U	chrX:15006	Island
rs17706479				SDHAF1	NM_00104	TSS1500	chr19:3648	Island
				AKR1E2	NM_00104	TSS200	chr10:4868	Island
				CXorf57	NM_01801	TSS200	chrX:10585	Island
							chr4:10411	S_Shelf
				RAI14;RAI	NM_00114	TSS200;Body;5'UTR;Body;Body;B		
				DGKQ;DG	NM_00134	5'UTR;1stE	chr4:96673	Island
							chr1:13881	N_Shelf
rs75147946	rs2286740			NRAP;NR	NM_00617	Body;Body		
rs7246865				MYO9B;M	NM_00113	Body;Body		
				FRAS1;FR	NM_02507	Body;Body		
				ELL2	NM_01208	Body	chr5:95296	N_Shore
				ARFGAP1;	NM_01820	3'UTR;3'U	chr20:6191	Island
rs61745639				MYH16	NR_00214	Body		
				ZXDC;ZXI	NM_00104	TSS200;TS	chr3:12619	Island
				RAI1	NM_03066	5'UTR	chr17:1762	S_Shore
	rs79507701		TRUE	TEAD1	NM_02196	5'UTR		
							chr15:9689	N_Shelf
		TRUE						
rs41299408				CYP2E1	NM_00077	Body	chr10:1353	Island
		TRUE						
	rs71715635						chr1:41826	Island

			KCNK17;K	NM_03146	Body;Body	chr6:39271	Island
			NFATC1;N	NM_00616	Body;5'UT	chr18:7717	Island
rs3217986		TRUE	CDKN2BA	NR_00352	Body;3'UT	chr9:22005	N_Shore
	rs12498258						
rs174137			NCRNA00	NR_02837	TSS200	chrX:73512	S_Shore
			IL8RBP	NR_00271	Body		
			ODF3L1	NM_17588	TSS1500		
rs12616807			CYTIP	NM_00428	TSS1500		
	rs80046497		HOXD4	NM_01462	1stExon	chr2:17701	Island
			HDX	NM_14465	TSS200		
			HLA-DRB	NM_00212	Body	chr6:32489	S_Shelf
						chr22:4971	N_Shore
			NCRNA00	NR_02435	TSS200	chrX:13455	Island
			TOP1P2;P	NR_00128	TSS1500;5'	chr22:2515	Island
			ANK1;AN	NM_02047	Body;Body	chr8:41583	Island
	rs9264		SNX6;SNX	NM_02124	3'UTR;3'UTR		
			FAM108C1	NM_02121	Body		
	rs34655830		6-Mar	NM_00588	Body		
			SLC2A14	NM_15344	TSS200	chr12:8025	Island
		TRUE	PGBD5	NM_02455	1stExon		
						chr4:57458	Island
						chr6:10723	N_Shelf
			HLA-A	NM_00211	3'UTR	chr6:29910	S_Shore
			SERPINB6	NM_00456	TSS1500	chr6:29710	S_Shore
			KIAA1024	NM_01520	5'UTR	chr15:7972	S_Shelf
			VPS13B;V	NM_01789	Body;Body		
						chr2:23171	S_Shelf
			LOC61920	NR_00293	Body	chr10:1352	Island
			CXXC5	NM_01646	5'UTR	chr5:13904	Island
						chr4:18798	N_Shore
			C6orf204;P	NM_20692	Body;5'UTR;Body		
rs3131847	rs3131848						
			LRRC25	NM_14525	Body	chr19:1849	S_Shelf
rs17844607			PCDHB13	NM_01893	1stExon	chr5:14059	N_Shore
rs6488428							
			MIR654;M	NR_03039	TSS1500;TSS1500;TSS1500;TSS15		

				PON1;PON	NM_00044	1stExon;5'U	chr7:94953	Island
							chr5:74907	S_Shore
				FARS2	NM_00656	Body		
rs34844508	rs697822			NLRP2	NM_01785	TSS200		
	rs28506183			SPTBN5	NM_01664	TSS1500		
				RREB1;RR	NM_00100	TSS1500;T	chr6:71070	N_Shore
	rs74317122							
				KIAA1671	NM_00114	Body	chr22:2557	N_Shelf
				EDIL3	NM_00571	TSS1500	chr5:83679	S_Shore
				IFRD1	NM_00100	TSS200		
	rs4245888			CMTM8	NM_17886	Body		
	rs71479760	TRUE					chr10:6186	N_Shelf
			TRUE	KCNQ1;KC	NM_00021	Body;Body	chr11:2812	Island
							chr2:74357	Island
				RDH5	NM_00290	Body		
rs2227817				F2R	NM_00199	TSS1500	chr5:76011	N_Shore
	rs73916303							
				HCCA2	NM_05300	Body	chr11:1715	N_Shelf
				GRIA1;GR	NM_00082	Body;Body		
	rs2928896			CHRDL1;C	NM_00114	5'UTR;TSS	chrX:11003	Island
	rs3744742			GEMIN4	NM_01572	Body		
		TRUE		CHAT;CH	NM_02098	Body;Body;Body;Body;Body;Body;		
rs17233820				MGC45800	NR_02710	Body	chr4:18306	Island
				MKS1;MK	NM_00116	3'UTR;3'UTR		
				EIF3G	NM_00375	TSS1500	chr19:1023	S_Shore
rs72492331	rs36183131			HLA-DRB	NR_00129	Body		
							chr3:19478	S_Shore
rs72310778							chr12:2982	N_Shore
				BCAT1	NM_00550	Body		
				RECQL4	NM_00426	Body	chr8:14573	N_Shore
							chr17:7790	S_Shelf
				BMP6	NM_00171	Body		
	rs55934941			OAS3	NM_00618	3'UTR		
				NAV1	NM_02044	1stExon	chr1:20161	Island
rs12962517				IMPACT	NM_01843	TSS1500	chr18:2200	N_Shore
				BAIAP2;B	NM_01745	Body;Body	chr17:7904	S_Shore
			TRUE	RUNX1	NM_00175	TSS1500		
							chr8:48676	N_Shore
				CDC20B;C	NM_00114	Body;Body;Body		

	rs74648832		APBA2;AP	NM_00113	TSS200;TSS200		
rs79620169							
			TC2N;TC2	NM_00112	5'UTR;5'U	chr14:9230	N_Shore
rs79379778			ITPR1;ITPI	NM_00222	Body;Body;Body		
			NAALADL	NM_00546	Body	chr11:6481	Island
			C7orf49;C7	NM_02403	TSS1500;T	chr7:13485	S_Shore
			ATXN7L1;	NM_15274	Body;Body		
						chrX:15274	Island
			HOXC10	NM_01740	3'UTR	chr12:5437	S_Shelf
			CD99L2;CI	NM_13444	1stExon;5'U	chrX:15006	Island
			MKRN3	NM_00566	1stExon		
						chr11:1021	S_Shore
	rs55686318						
						chrX:14952	Island
			COX6A2	NM_00520	Body	chr16:3143	Island
						chr9:11584	Island
rs2232691		TRUE	SERPINA1	NM_01618	TSS1500;TSS200		
						chr13:2531	Island
			C7orf50;C7	NM_00113	Body;Body;Body		
	rs76473451		EXPH5;EX	NM_00114	Body;Body;TSS200		
	rs3828250		ALPPL2	NM_03131	TSS1500	chr2:23327	N_Shore
			PCDHB17	NR_00128	Body	chr5:14053	N_Shore
			KCNMA1;I	NM_00116	Body;Body;Body;Body		
			TMPRSS2;	NM_00565	Body;Body		
			KCNQ1;KC	NM_00021	Body;Body		
	rs9675196		CCDC57	NM_19808	Body		
			PCDHA6;P	NM_03184	Body;Body	chr5:14024	N_Shelf
			SH3PXD2E	NM_00101	Body		
	rs6068087		VSTM2L	NM_08060	TSS1500	chr20:3653	N_Shore
			KIAA0922;	NM_01519	Body;Body		
			SLITRK2;S	NM_03253	5'UTR;5'U	chrX:14489	Island
			DLX5	NM_00522	3'UTR	chr7:96650	N_Shore
			RAMP1	NM_00585	Body		
	rs4642496						
rs1950503			LTB4R2;L	NM_00116	Body;1stEx	chr14:2477	Island

		SH3KBP1;	NM_03189	1stExon;5'	chrX:19905	Island
					chr7:51838	N_Shelf
rs2308765	rs78466762	HLA-DRB	NM_00212	Body	chr6:32551	N_Shelf
		MKLN1	NM_00114	Body		
		TRIM2;TR	NM_01527	Body;5'UT	chr4:15417	S_Shelf
rs35055994	rs76145852	AHSA1	NM_01211	Body	chr14:7792	S_Shelf
		CHST3	NM_00427	3'UTR	chr10:7376	S_Shelf
	rs820456	MYLK;MY	NM_05303	1stExon;5'UTR;Body;Body;Body;5'		
rs804815		MDGA1	NM_15348	Body	chr6:37617	Island
		SLC39A2	NM_01457	TSS200		
		TMSL3;T	NM_18304	5'UTR;5'U	chrX:12993	Island
		FBXL13;L	NM_14503	Body;Body;Body;Body		
		PXDNL	NM_14465	Body	chr8:52321	Island
	rs79192675	GALNTL1;	NM_00116	Body;Body		
		LOC40093	NR_02703	TSS200	chr22:4648	Island
		C22orf9;C2	NM_00100	Body;TSS1500		
rs56024124		CYP2C18;	NM_00112	TSS1500;TSS1500		
		SYCE1;SY	NM_00114	TSS200;TS	chr10:1353	Island
					chr8:13212	Island
		TSPAN9;T	NM_00667	Body;Body		
rs3781931	rs3781932	PDE2A;PD	NM_00114	Body;Body;Body;TSS1500;Body		
		SRCIN1	NM_02524	Body	chr17:3671	Island
		BRUNOL4	NM_00102	Body;Body	chr18:3491	S_Shore
	rs3823463	WDR27	NM_18255	Body	chr6:17005	N_Shore
rs3132580	rs79792575	DPCR1	NM_08087	Body	chr6:30923	N_Shelf
		NHS;NHS	NM_00113	Body;Body	chrX:17673	Island
		PON1	NM_00044	TSS1500	chr7:94953	S_Shore
		FIBIN;FIB	NM_20337	1stExon;3'UTR		
rs6589796	rs12419706					
					chr1:29291	N_Shore
rs34549987		NCR1;NC	NM_00482	TSS1500;TSS1500;TSS1500;TSS15		
		HAR1B;H	NR_00324	Body;TSS1	chr20:6173	N_Shore
					chr7:63642	Island
		ZNF365;Z	NM_19945	5'UTR;Body		
	rs76002673					
		SLC6A12;	NM_00112	Body;Body	chr12:3125	Island
		PRH2;PRH	NM_00504	TSS1500;TSS1500;Body;5'UTR		
					chr7:96645	S_Shore
		DAAM2	NM_01534	5'UTR		
		ADARB2	NM_01870	Body	chr10:1252	N_Shore

	rs34366005					
		TMEM216	NM_01649	TSS200	chr11:6115	N_Shore
					chr4:14755	N_Shore
		HRNBP3	NM_00108	TSS200		
		PQLC1;PQ	NM_00114	Body;Body	chr18:7767	Island
		ANKS1B;A	NM_02014	Body;Body		
		PTPRN2;P	NM_00284	Body;Body	chr7:15806	N_Shore
		FUT2;FUT	NM_00051	5'UTR;5'U	chr19:4920	N_Shelf
					chr19:4131	Island
		ADAMTS7	NM_01427	TSS1500	chr15:7910	Island
	rs11753382	RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
rs58263745		C17orf44	NR_026951	Body	chr17:8124	Island
		EIF2AK4	NM_00101	Body	chr15:4026	Island
		COX16	NM_01646	TSS1500	chr14:7082	S_Shore
	rs34198238	CR1L	NM_17571	Body	chr1:20784	Island
		CTNNA3;L	NM_00112	Body;Body;Body		
		C1orf198;C	NM_03280	Body;Body;TSS1500		
rs41554		ZNF467	NM_20733	5'UTR	chr7:14946	Island
		GPR124	NM_03277	Body		
	rs73955784	LYPD1;LY	NM_14458	TSS1500;T	chr2:13342	S_Shore
		KCNQ4;K	NM_00470	Body;Body	chr1:41303	Island
		CDKL5;CD	NM_00315	1stExon;5'U	chrX:18443	Island
		AKR1E2	NM_00104	TSS200	chr10:4868	Island
					chr18:3355	N_Shelf
		GPR161	NM_15383	5'UTR		
					chr19:5872	Island
	rs6696467	SMYD3;SM	NM_02274	Body;Body	chr1:24641	S_Shore
rs60980377	rs71608913					
rs11264511	rs12118077	BCAN	NM_02194	Body	chr1:15662	N_Shelf
		C1orf86;LC	NM_00114	Body;Body	chr1:21210	N_Shore
					chr2:64836	S_Shelf
		LOC28479	NR_02709	TSS200;Bo	chr20:2512	Island
		C1orf101;C	NM_00113	Body;Body		
		PXDN	NM_01229	Body	chr2:17468	N_Shore
		FER1L5	NM_00111	Body		
					chr8:62051	Island
	rs78650063					
		PFKP	NM_00262	Body		
		LSP1;LSP1	NM_00101	5'UTR;TSS	chr11:1892	Island
		ZYX;ZYX	NM_00346	Body;Body	chr7:14307	S_Shelf
rs75484905		PYCR2	NM_01332	3'UTR	chr1:22611	N_Shelf

rs62131616						chr19:5503	Island
	rs79459735		FAM101A	NM_18170	5'UTR	chr12:1247	S_Shore
	rs12269418		C10orf26	NM_00108	Body		
						chr12:5439	N_Shore
			COL18A1	NM_13044	Body	chr21:4682	S_Shelf
			NHSL2;RG	NM_00101	Body;TSS1	chrX:71350	Island
rs74445306	rs9868706		LSAMP	NM_00233	Body		
			SLC44A4	NM_02525	Body		
	rs10894647		OPCML	NM_00101	Body		
			MAP3K7IP	NM_15278	5'UTR	chrX:30906	Island
			DLX5	NM_00522	Body	chr7:96650	Island
			LOC10013	NR_02938	TSS1500	chr19:3679	S_Shelf
rs13309408			PTPRN2;P	NM_00284	Body;Body;Body		
rs77564531							
			STAT5A	NM_00315	TSS200	chr17:4044	N_Shore
			C6orf174	NM_00101	Body	chr6:12779	Island
			BCAT1	NM_00550	Body	chr12:2505	Island
		TRUE	PRKY	NR_02806	TSS1500	chrY:71415	Island
			HOXC10	NM_01740	Body	chr12:5437	S_Shore
rs59681854			HOXC10	NM_01740	TSS1500	chr12:5437	N_Shore
	rs34617298		CAMTA1	NM_01521	Body	chr1:71225	Island
	rs77697282						
			SND1;MIR	NM_01439	Body;TSS1500		
			OR2L13	NM_17591	5'UTR	chr1:24810	S_Shore
			UOX	NR_003927	Body		
			TUBB4Q	NM_02004	Body	chr4:19090	Island
						chr6:28583	Island
			ACVR1;AC	NM_00110	5'UTR;5'UTR		
			GPR115	NM_15383	5'UTR		
			WDR16;W	NM_00108	3'UTR;3'U	chr17:9548	N_Shore
			WRNIP1;W	NM_13039	Body;Body		
			POLD3	NM_00659	Body		
			ARHGAP6	NM_01342	Body;Body	chrX:11682	N_Shore
	rs2748404		FLJ43860	NM_20741	Body		
rs1190983							
	rs76697342		MC2R	NM_00052	TSS1500		
			MICB	NM_00593	Body		
			DUSP9	NM_00139	5'UTR	chrX:15291	Island
						chr6:17054	S_Shore
		TRUE	OR2L13;O	NM_17591	1stExon;5'U	chr1:24810	Island

					chr8:13145	S_Shore
		PTPRN2;P	NM_00284	Body;Body;Body		
		CRELD1;C	NM_00103	Body;Body	chr3:99743	S_Shore
		ESYT2	NM_02072	Body		
rs76001430	rs9518056	PCCA;PCC	NM_00112	Body;Body		
		GIMAP4	NM_01832	TSS1500		
		PTPRN2;P	NM_00284	Body;Body	chr7:15736	S_Shore
		MAPK14;M	NM_00131	3'UTR;3'UTR;3'UTR		
	rs61757950	GRB2;GRE	NM_00208	3'UTR;3'UTR		
	rs9261298	RNF39;RN	NM_17076	Body;Body	chr6:30038	S_Shore
rs3747422		APOOL	NM_19845	TSS200		
		KCNK2	NM_00101	TSS1500		
		KIFAP3	NM_01497	TSS1500	chr1:17004	S_Shore
		ANO4	NM_17882	Body		
		C6orf89	NM_15273	3'UTR		
					chr14:2119	Island
		HMHA1	NM_01229	Body	chr19:1070	Island
		FLJ40330	NR_01542	TSS200	chr2:89064	Island
		CEP68	NM_01514	5'UTR		
		AP3B2	NM_00464	Body		
		TP53INP2	NM_02120	TSS200	chr20:3329	Island
rs6914348		HLA-DPA1	NM_03355	Body		
		HIST1H4K	NM_00354	TSS200	chr6:27798	Island
		RBM20	NM_00113	Body	chr10:1124	S_Shore
rs35114504		TRPM1	NM_00242	Body		
					chr7:48128	N_Shelf
rs17238800		SNORA2B;	NR_002951	TSS200;Body		
		ATP8B4	NM_02483	Body		
		WNK4	NM_03238	Body	chr17:4093	N_Shore
		BRE;BRE;I	NM_19919	Body;Body;Body;Body;Body		
		PDZD4	NM_03251	Body	chrX:15309	Island
		TEKT1	NM_05328	5'UTR		
		B3GNTL1	NM_00100	Body	chr17:8096	N_Shore
rs11672316		UNC13A	NM_00108	Body	chr19:1775	S_Shelf

		HTR1D	NM_00086	TSS200		
	rs9700646	TAS1R2	NM_15223	TSS200		
		CAMK1D;	NM_02039	Body;Body		
					chrX:15039	Island
	rs1046548	OTUD3	NM_01520	3'UTR		
		DUSP14	NM_00702	5'UTR	chr17:3584	S_Shelf
rs78324415		RNF216;R	NM_20711	Body;Body		
	rs76494538				chr2:24284	N_Shore
		PTPRN2;P	NM_00284	Body;Body;Body		
		STK10	NM_00599	Body		
					chr2:36991	Island
rs6780145		ULK4	NM_01788	Body		
					chr6:42694	S_Shore
	rs4846963				chr1:23056	S_Shelf
		CCDC127;	NM_14526	5'UTR;TSS	chr5:21803	Island
		WNT5A	NM_00339	Body	chr3:55517	N_Shore
		KIRREL3;	NM_00116	Body;Body		
		HEXDC	NM_17362	Body	chr17:8039	S_Shore
		PTPRN2;P	NM_00284	Body;Body;Body		
	rs75060408				chr17:7307	S_Shore
rs7058338		LOC72960	NR_02444	TSS1500	chrX:20008	Island
		SH3D19;S	NM_00112	Body;Body;Body		
					chr1:11067	N_Shelf
		LOC34009	NR_02699	Body		
					chr5:18567	Island
	rs60928390					
					chr6:30418	Island
rs72898266	rs11657629	TK1	NM_00325	Body	chr17:7618	N_Shelf
	rs9268673					
					chr17:4661	N_Shore
		FRG1B	NR_00357	Body	chr20:2961	Island
		TMEM175	NM_03232	5'UTR	chr4:94061	Island
rs9276400		HLA-DQA	NM_02005	TSS200		
rs13221417		C7orf50;C7	NM_00113	Body;Body	chr7:10595	N_Shelf
		PCGF3	NM_00631	Body	chr4:73028	Island
					chr17:3702	N_Shore
		PIK3C2B	NM_00264	5'UTR		
rs28390109					chr11:7152	N_Shore

						chr6:28583	Island
			SEPT6;SEF	NM_01512	TSS200;TS	chrX:11882	Island
		TRUE	ZNF323;ZI	NM_00113	5'UTR;5'UTR;TSS200		
	rs10866927					chr8:13979	S_Shore
			ARHGEF1	NM_01478	Body	chr11:7305	Island
						chr6:93990	Island
						chr7:27208	N_Shore
			ATP6AP2	NM_00576	TSS200	chrX:40439	Island
rs80274390			TBC1D8	NM_00110	Body		
rs77731384							
			DEGS2	NM_20691	Body	chr14:1006	S_Shelf
	rs4247257		HLA-DPA1	NM_03355	Body		
rs6852883			RNF150	NM_02072	Body		
			KATNAL2	NM_03130	3'UTR		
	rs74500663		CPA5;CPA	NM_00112	Body;Body;Body		
			HDAC4	NM_00603	Body		
			DPPA3	NM_19928	TSS1500		
	rs78557296		HSD11B1;I	NM_18175	5'UTR;TSS200		
			C2orf65	NM_13880	TSS200	chr2:74875	Island
			FRAS1;FR	NM_02507	Body;Body		
			LAS1L;LA	NM_03120	TSS200;TS	chrX:64754	Island
rs60671061	rs71869600		BGN	NM_00171	3'UTR		
	rs7542928					chr1:18199	S_Shelf
			BMP6	NM_00171	Body		
			SCNN1D;S	NM_00113	3'UTR;3'U	chr1:12287	N_Shore
			TNFRSF8;	NM_00124	Body;TSS1500		
rs6022601			ZNF217	NM_00652	TSS200	chr20:5219	S_Shore
rs9277359	rs9277358		HLA-DPB1	NM_00212	Body	chr6:33048	S_Shore
						chr19:5295	Island
			ZHX1;ZHX	NM_00722	5'UTR;5'U	chr8:12428	N_Shore
rs77685907	rs71632111					chr1:18128	S_Shelf
rs55869163	rs56359841		MAP3K6	NM_00467	Body	chr1:27687	Island
	rs72699799						
			TMEM51;T	NM_00113	5'UTR;5'U	chr1:15541	N_Shelf
						chr14:1053	S_Shore
			TM2D2;TM	NM_03194	3'UTR;3'UTR;3'UTR;3'UTR		

rs4627431			RPH3AL	NM_00698	5'UTR	chr17:1850	N_Shelf
						chrX:13901	Island
			NAV2;NA	NM_18296	Body;Body;Body;Body		
						chr2:23321	Island
			IQCD	NM_13845	5'UTR		
						chr6:88760	Island
rs6966449	rs75180717					chr7:99340	S_Shelf
rs80281298			LOC10013	NR_02456	TSS1500;T	chr4:12029	Island
rs75400970							
rs61027870			C3orf63	NM_00111	TSS1500	chr3:56716	Island
rs4905039			ITPK1;ITP	NM_00114	Body;Body;Body		
			KDM5B	NM_00661	TSS1500	chr1:20277	N_Shore
			CR1L	NM_17571	Body	chr1:20784	Island
	rs10935008						
			ITGBL1;IT	NM_00479	1stExon;5'U	chr13:1021	N_Shore
			FCER2;FC	NM_00200	1stExon;5'UTR		
			OCLN	NM_00253	TSS1500	chr5:68788	N_Shore
			TNFAIP8	NM_00107	TSS1500	chr5:11860	N_Shore
			CD80	NM_00519	3'UTR		
			PRDM16;P	NM_02211	Body;Body		
						chr5:43313	S_Shelf
			APC2	NM_00588	Body	chr19:1456	Island
			HSD17B10	NM_00449	1stExon;1st	chrX:53461	Island
						chr20:5954	Island
						chr8:75376	Island
			PRDM16;P	NM_02211	Body;Body		
						chr9:13610	N_Shelf
rs4246747			SDHAP3	NR_00326	TSS200	chr5:15942	Island
	rs28488438		EXD3	NM_01782	Body	chr9:14026	Island
rs62281832			COL8A1;M	NM_00185	5'UTR;Body;5'UTR		
			NAPRT1	NM_14520	Body	chr8:14465	N_Shore
			KIF3C	NM_00225	TSS1500	chr2:26204	S_Shore
		TRUE	MBTPS2	NM_01588	Body	chrX:21857	S_Shore

					chr3:19358	Island
		FLJ13197	NR_02680	Body		
	rs6665208				chr1:22659	S_Shelf
		SEMA4D;S	NM_00637	Body;Body	chr9:91995	S_Shore
		SOX3	NM_00563	1stExon	chrX:13958	Island
	rs71119762				chr14:1036	S_Shore
		TRIM14;T	NM_03322	TSS1500;T	chr9:10088	S_Shore
					chr8:72917	S_Shore
					chr1:11075	Island
rs4523		TBXA2R;T	NM_20163	Body;Body	chr19:3595	Island
					chr12:1151	Island
		TRIM31	NM_00702	Body		
		AIG1	NM_01610	Body		
	rs78792335	DAB2IP	NM_03255	Body	chr9:12436	S_Shore
	rs62571853				chr9:12050	S_Shelf
		SEC16A	NM_01486	Body	chr9:13936	S_Shelf
	rs76007970					
		EXD3	NM_01782	5'UTR	chr9:14031	Island
					chr9:11582	Island
		NSDHL;N	NM_01592	5'UTR;5'U	chrX:15199	S_Shore
		NOBOX	NM_00108	TSS200		
		GLIPR1L2	NM_15243	Body	chr12:7578	Island
					chr1:15216	S_Shore
	rs9341608					
	rs75797701				chr6:15990	Island
	rs13427406	ASB18	NM_21255	Body	chr2:23712	Island
	rs12427963	GJA3	NM_02195	3'UTR	chr13:2071	N_Shore
rs35505375		C1orf100	NM_00101	5'UTR		
		PTPRN2;P	NM_00284	Body;Body	chr7:15734	S_Shore
		BEX1	NM_01847	5'UTR	chrX:10231	Island
		NPEPPS	NM_00631	Body		
	rs2065410					
		C10orf125;	NM_19847	TSS200;TS	chr10:1351	Island
		CELA3B;C	NM_00735	5'UTR;1stExon		
		LOC15056	NR_01539	Body		
		MAB21L1;	NM_00558	1stExon;Bo	chr13:3604	N_Shore
		KCTD2	NM_01535	Body		
					chr13:5273	S_Shelf

				SPON1	NM_00610	Body	chr11:1398	Island
							chr17:8025	S_Shelf
				SLCO5A1;	NM_03095	Body;Body;Body		
		TRUE		VGLL4	NM_01466	Body	chr3:11684	S_Shelf
				IFFO1;IFF	NM_08073	Body;TSS2	chr12:6657	S_Shore
							chr22:1873	S_Shore
rs2424608				GGTLC1	NM_17831	5'UTR	chr20:2396	Island
	rs75175492							
	rs56406441							
rs17043031	rs45560933		TRUE	PSD4;LOC	NM_01245	TSS1500;Body		
				C19orf20	NM_03351	3'UTR	chr19:5188	Island
rs34968596	rs78783036			PIWIL2;PI	NM_01806	5'UTR;1stE	chr8:22132	Island
rs73186185								
rs77832261								
							chr13:8122	Island
	rs55812238			ELMO1	NM_01480	5'UTR	chr7:37487	N_Shore
				UPP1;UPP	NM_18159	5'UTR;5'U	chr7:48128	S_Shore
				MIR551B;	NR_03029	TSS1500;Body		
rs9274340	rs41263817			HLA-DQB	NM_00212	Body	chr6:32632	Island
				DLGAP2	NM_00474	3'UTR	chr8:16494	S_Shore
				TLR6	NM_00606	3'UTR		
				SDCCAG8	NM_00664	Body		
				VGLL4;V	NM_01466	Body;Body	chr3:11610	Island
				ADAMTS9	NM_18292	Body		
rs75840477				SLC6A12;S	NM_00112	Body;Body	chr12:3125	N_Shelf
				LSP1;LSP1	NM_00101	5'UTR;TSS	chr11:1892	Island
				PCDHB3	NM_01893	1stExon	chr5:14048	N_Shore
				CRYBB1	NM_00188	Body		
				NUPL1;NU	NM_00100	TSS1500;T	chr13:2587	Island
				MTPN;LU	NM_14580	TSS1500;T	chr7:13566	S_Shore
				OBSCN;O	NM_05284	Body;Body	chr1:22847	S_Shore
				PCDHGA4	NM_01891	Body;Body	chr5:14079	Island
				CHRNA1;C	NM_00103	TSS200;TSS200		
				PCDHB4	NM_01893	1stExon	chr5:14050	S_Shore
				TMCO3	NM_01790	Body	chr13:1141	N_Shelf
				PCSK6;PC	NM_00257	Body;Body	chr15:1019	N_Shelf
				BMPR1B	NM_00120	Body		
rs2857945	rs2857943						chr4:24317	Island
				DLG2;DL	NM_00114	Body;Body		
	rs7405713			RPH3AL	NM_00698	Body	chr17:9971	S_Shore

				HOXC4;H	NM_01462	5'UTR;Bod	chr12:5442	N_Shelf
				ELANE	NM_00197	Body	chr19:8555	N_Shore
							chr10:8396	Island
		TRUE		UBR3	NM_17207	Body		
	rs72630209							
				IL17C	NM_01327	Body	chr16:8870	Island
				KLHL8	NM_02080	TSS1500	chr4:88140	S_Shore
		TRUE		VCAN;VC	NM_00438	5'UTR;5'U	chr5:82770	S_Shore
							chr2:24087	N_Shelf
rs58136434				APPL2	NM_01817	TSS1500	chr12:1056	S_Shore
				NPAS2	NM_00251	5'UTR		
				UBE2E1;U	NM_00334	Body;Body		
	rs72744212			TRIO	NM_00711	Body		
rs71669872				MBNL2;M	NM_14477	5'UTR;5'UTR		
				SYNPO2;S	NM_00112	Body;Body;Body		
rs79428826				HTATIP2;	NM_00109	Body;Body	chr11:2038	S_Shelf
				IQSEC3	NM_00117	Body	chr12:1756	S_Shore
	rs34192302			SGMS2	NM_00113	TSS1500	chr4:10874	N_Shore
				EDA;EDA;	NM_00100	TSS200;TS	chrX:68835	Island
				GRIK2;GR	NM_17576	1stExon;1st	chr6:10184	Island
	rs73728427			PRKAG2	NM_01620	Body		
rs55750403							chr8:14464	N_Shelf
	rs75548537			FDFT1	NM_00446	Body	chr8:11665	N_Shelf
							chr4:66756	N_Shelf
				PXDN	NM_01229	Body		
				CASQ2;CA	NM_00123	5'UTR;1stExon		
	rs6953080			C7orf50;C7	NM_00113	Body;Body	chr7:10974	Island
				C6orf174	NM_00101	3'UTR		
				ITGBL1	NM_00479	Body		
				FMN2	NM_02006	Body		
				CNTNAP1	NM_00363	Body	chr17:4083	Island
				WDR27	NM_18255	Body	chr6:16997	S_Shore
	rs6724808			AGAP1;AC	NM_01491	Body;Body		
			TRUE	PSMD5;LC	NM_00504	Body;TSS1	chr9:12360	N_Shore
				PCDHGA1	NM_01891	1stExon;1st	chr5:14071	Island
							chr7:63560	Island
				PGCP	NM_01613	Body		
rs34738237				CDKN1C;C	NM_00007	TSS1500;T	chr11:2905	S_Shore
	rs73212176						chr3:19604	S_Shelf

				CPNE5	NM_02093	Body		
rs11895800								
			TRUE	ZNF323;Z	NM_00113	5'UTR;5'UTR;5'UTR		
	rs77442133		TRUE	BNIP3	NM_00405	TSS1500	chr10:1337	Island
				BEYLA;BE	NR_02701	TSS1500;TSS1500		
rs73014517	rs56102901			IQSEC1	NM_00113	Body		
				PCDHB17	NR_00128	Body	chr5:14053	N_Shore
				MAP3K5	NM_00592	Body		
	rs75220670			BMPER	NM_13346	Body		
rs79328354				TIMM17A	NM_00633	TSS1500	chr1:20192	N_Shore
							chr7:99140	N_Shelf
				SEL1L3	NM_01518	Body		
rs78495114				C7orf58;C7	NM_00110	Body;Body		
				GGT6;GG	NM_00112	TSS1500;TSS1500		
				TRIM31	NM_00702	Body		
rs28732319	rs35043862			HLA-DRB	NM_00212	Body	chr6:32551	N_Shelf
				TBC1D16	NM_01902	Body	chr17:7792	N_Shore
	rs5840			SLC2A5;SL	NM_00303	3'UTR;Bod	chr1:90992	N_Shelf
							chr14:5317	N_Shelf
		TRUE		LOC28576	NR_02711	Body;Body		
	rs34795289			LRRK1	NM_02465	Body	chr15:1015	Island
	rs10244273			GIMAP2	NM_01566	TSS1500		
				FAM55D;F	NM_01767	5'UTR;5'UTR		
rs36076676	rs76982061							
				ADAP1	NM_00686	Body	chr7:96598	S_Shelf
rs72651656				COL1A1	NM_00008	Body		
				PDE4DIP;P	NM_02235	Body;Body;Body;Body		
							chr2:24280	Island
rs62244885				FOXP1;FO	NM_03268	5'UTR;5'UTR		
rs6121899	rs6121898						chr20:6069	N_Shelf
				C14orf132	NR_02393	Body		
				RFFL;RFF	NM_00101	1stExon;5'UTR;5'UTR		
rs56769123				C11orf17;C	NM_18290	TSS1500;T	chr11:8932	N_Shore
	rs11765692			C7orf29;LR	NM_13843	TSS1500;5'UTR;5'UTR		
	rs76846478			LHFPL2	NM_00577	5'UTR		
							chr17:1988	Island
rs78346570				NARS	NM_00453	TSS1500	chr18:5528	S_Shore
	rs60213124			BSPH1	NM_00112	1stExon		

				PCDHA2;P	NM_01890	Body;Body	chr5:14018	Island
	rs11976805			C7orf50;C7	NM_00113	Body;Body	chr7:11412	N_Shelf
				C8orf74	NM_00104	Body		
				ZFAT;ZFA	NM_00116	Body;Body	chr8:13549	S_Shelf
				SDHAP3	NR_00326	TSS200	chr5:15942	Island
				VIT	NM_05327	TSS1500		
				SHF;SHF	NM_13835	5'UTR;1stE	chr15:4549	S_Shore
							chr1:14916	Island
	rs819637						chr1:20027	Island
				NCRNA00	NR_02433	Body	chr19:5220	Island
	rs72693510							
	rs79179815							
							chr4:15952	N_Shore
	rs734894			ABR;ABR;	NM_02196	Body;Body	chr17:9517	N_Shelf
				HRNBP3	NM_00108	5'UTR		
				UMOD;UM	NM_00336	Body;Body	chr16:2035	Island
rs8069228	rs8070393			PITPNM3;I	NM_03122	Body;Body		
				DCHS2;DC	NM_00114	Body;1stExon		
				TNFAIP3	NM_00629	Body	chr6:13818	S_Shelf
				NAPSA	NM_00485	3'UTR	chr19:5086	Island
				PDZRN4;P	NM_01337	TSS1500;Body		
				AGAP1;AC	NM_01491	Body;Body	chr2:23667	S_Shore
				ARHGEF1	NM_01462	5'UTR		
				MEF2A;MI	NM_00113	5'UTR;5'UTR;5'UTR		
	rs66799959			HLA-DPA1	NM_03355	Body		
rs76999291							chr2:24161	Island
			TRUE	MRGPRX2	NM_05403	5'UTR		
		TRUE		MEGF11	NM_03244	5'UTR		
				TRIM59	NM_17308	TSS1500	chr3:16016	S_Shore
rs443767								
				NDUFB11;	NR_02423	Body;TSS1	chrX:47003	Island
				SYNPR	NM_00113	Body		
				PRDM16;P	NM_02211	Body;Body	chr1:33319	S_Shelf
	rs77813121							
				WDR91	NM_01414	Body		
				PCOLCE	NM_00259	Body	chr7:10020	Island
				ALKBH4	NM_01762	Body	chr7:10210	N_Shelf
				TRPV1;TR	NM_01872	5'UTR;5'UTR;1stExon;5'UTR		

	rs73789455	FBXL21	NM_01215	5'UTR		
		LRP5L;LR	NM_18249	TSS200;5'U	chr22:2575	S_Shelf
		ST14	NM_0197	Body		
		PTPRJ;PTP	NM_00284	Body;Body		
	rs58752696				chr2:91757	S_Shore
	rs4076232				chr13:1142	N_Shelf
		ADAMTS9	NM_18292	Body		
					chr6:28583	Island
		TRAF3IP2;	NR_02833	Body;Body;Body		
		GABARAP	NR_02828	Body	chr15:9089	N_Shelf
		KCNJ16;K	NM_17074	TSS1500;TSS1500		
		SPACA1	NM_03096	TSS200	chr6:88757	Island
		CDC42BP	NM_01752	Body	chr11:6459	Island
		INO80C;IN	NM_19428	TSS1500;T	chr18:3307	S_Shore
	rs17853691	PCDHA6;P	NM_03184	1stExon;Bo	chr5:14020	Island
	rs74334869					
		UGT2B15	NM_00107	1stExon		
		ADARB2	NM_01870	Body	chr10:1404	Island
		SEH1L;SE	NM_00101	TSS1500;T	chr18:1294	N_Shore
		WBP2NL	NM_15261	Body	chr22:4239	Island
		PCDHB7;P	NM_01894	1stExon;5'U	chr5:14055	N_Shore
		ALPI	NM_00163	Body	chr2:23332	Island
					chr13:1021	N_Shelf
rs73323496					chr12:6515	S_Shelf
					chr6:33129	N_Shore
		RASAL3	NM_02290	Body	chr19:1556	Island
		DNAH17	NM_17362	Body	chr17:7642	Island
	rs7992042	FARP1	NM_00576	Body		
rs79645032						
rs8192366		PKM2;PK	NM_18247	5'UTR;5'U	chr15:7252	N_Shelf
	rs9561316	GPC6	NM_00570	Body		
					chr1:27960	S_Shelf
	rs2276808	TRANK1	NM_01483	TSS1500	chr3:36985	Island
		SALL3	NM_17199	Body	chr18:7675	Island
rs55872757					chr17:7578	Island
		NCKAP5;N	NM_20748	TSS200;TSS200		
		ANO6;AN	NM_00114	Body;Body;Body;Body		

rs61674626						chr21:4682	N_Shelf
			TMEM108;	NM_00113	Body;Body		
rs75654158			ATXN1;AT	NM_00112	5'UTR;5'UTR		
			NEBL	NM_21356	Body	chr10:2146	Island
rs618752						chr13:3068	N_Shelf
	rs71160293		PGS1	NM_02441	3'UTR	chr17:7642	N_Shelf
			GNB2L1;S	NM_00609	Body;TSS2	chr5:18067	Island
						chr20:6064	S_Shelf
			MTCH2	NM_01434	3'UTR		
		TRUE	RAB37	NM_17573	TSS200	chr17:7266	N_Shore
			IFI16	NM_00553	Body		
	rs4801877		LGALS7	NM_00230	TSS1500	chr19:3926	S_Shelf
			MAST2	NM_01511	Body		
						chr19:2289	Island
		TRUE	ZNF541	NM_00110	Body	chr19:4804	Island
rs35871417						chr22:4628	S_Shore
rs78776377						chr7:12151	Island
			CARD11	NM_03241	Body		
			SLC9A1	NM_00304	TSS200	chr1:27481	Island
			DISC1;DIS	NM_00101	Body;Body;Body;Body;Body;Body;		
	rs76639268	TRUE	KRTAP21-	NM_18161	TSS1500		
			MTMR7	NM_00468	Body		
	rs491247		MCF2L;M	NM_00111	Body;Body	chr13:1137	S_Shelf
	rs12864509		NALCN	NM_05286	Body		
			PTPRN2;P	NM_00284	Body;Body	chr7:15799	S_Shore
			MCC;MCC	NM_00238	Body;Body		
			CAPN2;CA	NM_00174	Body;Body		
rs12191440			ZFAND3	NM_02194	Body		
	rs79437938		RNF213;R	NM_02095	Body;Body		
	rs62390377					chr6:29894	Island
						chr1:14915	N_Shore
	rs7259450		CPAMD8	NM_01569	Body		
			RAP1B;RA	NM_01564	5'UTR;5'UTR		

						chr2:91777	Island
rs77703965			PTPRN2;P	NM_00284	Body;Body	chr7:15811	N_Shore
						chr7:51838	Island
			GRIK2;GR	NM_02195	TSS200;TS	chr6:10184	Island
	rs34979811					chr3:18288	S_Shelf
			FBN1	NM_00013	Body		
						chr12:9066	N_Shore
rs62113344						chr19:5209	N_Shelf
			KANK2;K	NM_01549	3'UTR;3'UTR		
			BTNL8;BT	NM_00115	Body;Body;Body;TSS1500;Body;B		
		TRUE	CHRNA5	NM_00074	TSS1500	chr15:7885	N_Shore
rs16022			CACNA1A	NM_00112	Body;Body	chr19:1340	Island
			MIR147	NR_02960	TSS200		
	rs2073795		CYP51A1;	NM_00114	5'UTR;Bod	chr7:91763	Island
			SGCE;SGC	NM_00109	Body;Body;Body		
	rs60897780		MCC	NM_00108	Body		
			ISM1	NM_08082	TSS1500	chr20:1320	Island
			FOXP1;FO	NM_03268	5'UTR;5'UTR		
			C3P1	NR_02730	Body	chr19:1017	Island
			ANK3;AN	NM_02098	Body;TSS200		
						chr19:5308	S_Shelf
			PLA2G2A;	NM_00116	TSS1500;TSS1500;TSS1500		
			ESRRG;ES	NM_20659	5'UTR;5'UTR;5'UTR		
			CXorf36	NM_17681	Body	chrX:45016	Island
rs72844166	rs66712869		HLA-DRB	NR_00129	Body		
			TBC1D9	NM_01513	Body		
rs11252004							
rs1915959			SUNC1;SU	NM_15278	Body;Body		
			TBX3;TBX	NM_00599	Body;Body	chr12:1151	Island
		TRUE	WISP1;WI	NM_00388	Body;Body		
						chr19:2299	Island
rs12366028			NAV2;NA	NM_18296	Body;Body;Body		
			ALPPL2	NM_03131	Body	chr2:23327	Island
			PCDHB8	NM_01912	TSS200	chr5:14055	N_Shore
	rs10220034						
			HOXB1	NM_00214	TSS200	chr17:4660	Island
			ADAMTS1	NM_13363	TSS1500	chr5:12879	Island
			FRMPD4;F	NM_01472	5'UTR;1stE	chrX:12156	Island

				OR2T10	NM_00100	TSS1500		
rs35834087				KIF16B	NM_02470	Body	chr20:1655	N_Shore
							chr6:15552	N_Shore
				PNOC	NM_00622	5'UTR		
				PDE11A;PI	NM_00107	Body;Body;Body;Body		
	rs2359867							
				ATG4C;AT	NM_17822	TSS1500;TSS1500		
	rs3006087			CNST;CNS	NM_00113	Body;Body		
				ITGB2;ITG	NM_00112	5'UTR;1stE	chr21:4635	N_Shelf
							chr1:22874	Island
		TRUE	TRUE	NR0B1	NM_00047	TSS1500	chrX:30326	S_Shore
				MORN1	NM_02484	Body	chr1:22537	Island
				ONECUT1	NM_00449	Body	chr15:5307	N_Shore
				MPP7	NM_17349	Body		
							chr1:15055	S_Shelf
							chr12:2954	Island
	rs2274148			CDADC1	NM_03091	Body		
				ELF1	NM_17237	TSS200		
							chr1:16141	Island
				C11orf67;R	NM_02468	5'UTR;TSS	chr11:7753	S_Shore
				SPIB	NM_00312	3'UTR	chr19:5093	Island
							chr6:15027	S_Shore
							chr4:86324	S_Shore
				LRRC61;A	NM_00114	TSS200;5'U	chr7:15001	Island
rs11888476	rs78870007			MGAT5	NM_00241	Body		
rs77067975							chr12:5832	Island
							chr13:2490	Island
							chr20:2444	N_Shelf
	rs13169133			GMCL1L	NR_003281	Body	chr5:17761	N_Shore
				FAM187B	NM_15248	TSS1500		
	rs76410669							
				ABR;ABR;	NM_02196	Body;Body	chr17:9815	Island
							chr14:6506	Island

rs61938448	rs78598564	TMEM132	NM_00113	Body		
		C1QL1	NM_00668	3'UTR	chr17:4303	N_Shore
	rs17844417	PCDHB4	NM_01893	1stExon	chr5:14050	Island
rs61744319		ARHGEF7;	NM_00111	Body;Body	chr13:1119	Island
	rs4075035	FLJ43860	NM_20741	Body	chr8:14245	Island
		SNRNP40	NM_00481	3'UTR		
	rs2800793	PBX1	NM_00258	Body		
	rs13247141	SLC4A2	NM_00304	Body		
rs4398729	rs1129956	HLA-DQA	NM_02005	Body		
	rs61997184	OR2H2	NM_00716	1stExon		
		CDK16;CD	NM_03301	1stExon;TS	chrX:47077	Island
		KLF8;KLF	NM_00115	TSS200;TS	chrX:56258	N_Shore
	rs80093400	SLC22A18	NM_18323	Body;Body	chr11:2923	S_Shore
		RSRC1	NM_01662	Body		
		GRM5;GR	NM_00084	Body;Body		
		SNORD11	NR_00334	TSS1500;TSS1500;TSS1500;TSS15		
		GRIK2;GR	NM_00116	Body;Body	chr6:10184	S_Shore
		CYP26B1	NM_01988	Body	chr2:72371	Island
	rs2621343					
					chr5:28927	Island
	rs7806927	ZNF815	NR_023382	Body	chr7:58628	Island
		RAPGEF4	NM_00702	Body		
rs61737694		DAXX;DA	NM_00114	Body;Body	chr6:33288	N_Shore
		FLJ44606;F	NM_00116	TSS200;TS	chr5:12640	Island
		DLG2	NM_00114	Body		
	rs71239273	DEFA1B;D	NM_00104	5'UTR;5'UTR;5'UTR		
	rs9567295	CCDC122;	NM_14497	5'UTR;TSS	chr13:4445	Island
rs140517	rs3752396	C22orf41	NM_00112	TSS200	chr22:5100	Island
		HHLA2	NM_00707	TSS200		
	rs2546424	OR2V2	NM_20688	TSS200		
					chr4:12442	S_Shelf
	rs9272466	HLA-DQA	NM_00212	Body		
		PDE7B	NM_01894	Body		
		FAS;FAS;F	NM_15287	Body;Body	chr10:9075	S_Shore
		OR5D16	NM_00100	TSS200		
		SMTN;SM	NM_00693	Body;Body	chr22:3150	N_Shelf
		SLC24A3;I	NM_02068	Body;TSS1500		
		PCDHB10	NM_01893	1stExon	chr5:14057	N_Shore
rs9423005					chr10:1285	N_Shelf
rs560239					chr12:3176	S_Shelf
	rs34900851	HSF5	NM_00108	TSS1500	chr17:5656	S_Shore

rs77465066						
		PTPRN2;P	NM_00284	Body;Body	chr7:15740	Island
	rs11684511	LYPD6B	NM_17796	Body		
		CYP26B1	NM_01988	Body	chr2:72371	Island
		LOC64174	NR_03324	Body		
rs3796158	rs3796159	C3orf21	NM_15253	3'UTR	chr3:19478	S_Shelf
		C20orf85	NM_17845	TSS200	chr20:5672	Island
					chr19:2289	Island
					chr19:4785	N_Shore
		AMIGO3;R	NM_19872	1stExon;Bo	chr3:49755	Island
					chr19:3371	S_Shore
		ESPNL	NM_19431	Body	chr2:23900	S_Shelf
	rs36141123					
		KCNQ1DN	NR_02462	TSS200	chr11:2890	Island
		PCSK6;PC	NM_00257	Body;Body;Body;Body		
		IGSF21	NM_03288	Body	chr1:18703	N_Shelf
					chr14:1020	N_Shore
		PTGDR	NM_00095	TSS1500	chr14:5273	N_Shore
		C1orf100	NM_00101	Body		
	rs7977832					
					chr1:14915	N_Shore
		IFIT1L	NM_00101	TSS1500		
rs4241882	rs4266333					
rs11706886		CBLB	NM_17066	Body		
		PTPRN2;P	NM_00284	Body;Body;Body		
		TRIM62	NM_01820	Body		
		TEKT4	NM_14470	Body	chr2:95540	Island
rs7792381		PTPRN2;P	NM_00284	Body;Body;Body		
		LOC28578	NR_02697	Body	chr6:65463	N_Shelf
		PCDHGA2	NM_03200	1stExon;Bo	chr5:14071	N_Shore
		SNRPN;SN	NM_02280	5'UTR;5'UTR;5'UTR;5'UTR		
		PRAMEF5	NM_00101	Body		
		SVOPL;SV	NM_00113	Body;TSS1	chr7:13834	Island
		GSDMD	NM_00116	TSS200	chr8:14463	Island
		SLC25A12	NM_00370	Body		
		GPR123	NM_00108	Body	chr10:1349	S_Shore
					chr1:14916	Island
		KCNQ4;K	NM_00470	Body;Body	chr1:41303	Island

			TNFRSF25	NM_00379	TSS200;3'U	chr1:65259	S_Shore
						chrX:27881	Island
			SPNS2	NM_00112	Body	chr17:4439	S_Shore
			TCERG1L	NM_17493	Body		
			KCNK3	NM_00224	Body	chr2:26950	Island
						chr3:14615	Island
			PAX8;PAX	NM_00346	Body;Body	chr2:11403	N_Shore
			GALNT9	NM_00112	Body	chr12:1328	N_Shore
	rs7311355		CACNA1C	NM_00112	Body;Body;Body;Body;Body;Body;		
	rs75277606		PTPRN2;P	NM_00284	Body;Body	chr7:15734	N_Shore
rs10214030	rs76243532		ODZ2	NM_00112	Body		
	rs9525308		RASA3	NM_00736	Body	chr13:1147	Island
						chr1:86081	Island
						chr10:3500	S_Shelf
			COL23A1	NM_17346	Body	chr5:17782	Island
			SETMAR;S	NR_024022	TSS1500;T	chr3:43450	N_Shore
			C7orf50;C7	NM_00113	Body;Body	chr7:10974	S_Shore
						chr11:6738	Island
rs10214910	rs1126533		HLA-DPA1	NM_03355	Body		
			PHC2;PHC	NM_00442	Body;Body		
			SKA3;SKA	NM_14506	3'UTR;3'UTR		
			DISC1;DIS	NM_01866	Body;Body;Body;Body;Body;Body;		
			BMPR1B	NM_00120	5'UTR	chr4:95678	S_Shore
						chr2:17693	N_Shelf
			ADAM19	NM_03327	TSS1500	chr5:15700	S_Shore
			OGT;OGT;	NM_18167	TSS200;TS	chrX:70752	Island
						chr1:28850	Island
		TRUE					
			AMH	NM_00047	Body	chr19:2250	Island
			DACT1;DA	NM_00107	Body;Body	chr14:5911	N_Shelf
rs57553892			ASAP2;AS	NM_00113	Body;Body	chr2:95147	S_Shelf
			ANKRD36	NM_02519	TSS1500	chr2:98206	Island
	rs2708879		PKD1L1	NM_13829	Body		
			MACC1	NM_18276	Body		
	rs28432866		GABRB1	NM_00081	Body	chr4:47427	N_Shore
rs75617860	rs55672148						
			ARX	NM_13905	Body	chrX:25025	Island
			NSUN2;SR	NM_01775	TSS1500;5'	chr5:66327	Island
						chr6:10643	Island

		PCDHB6	NM_01893	1stExon	chr5:14053	N_Shore
		GFPT2	NM_00511	Body	chr5:17974	Island
		TPRG1	NM_19848	TSS1500		
		AKAP11	NM_01624	5'UTR	chr13:4284	S_Shore
		SPOCD1	NM_14456	Body		
		KLHDC7A	NM_15237	1stExon	chr1:18808	Island
		HSP90AA1	NM_00534	TSS1500;B	chr14:1025	S_Shore
		TBC1D1	NM_01517	Body		
		ST3GAL3;	NM_17496	Body;Body;Body;Body;Body;Body;		
	rs78016579	FBXO38;F	NM_20583	Body;Body		
rs12698235		PTPRN2;P	NM_00284	Body;Body;Body		
		PTPRN2;P	NM_00284	Body;Body	chr7:15740	Island
	rs4443669				chr8:22560	S_Shore
		ACCN1	NM_00109	Body		
					chr7:15470	S_Shore
rs9277341	rs35521473	HLA-DPA1	NM_03355	Body		
		HLA-DPB1	NM_00212	Body	chr6:33048	S_Shore
	rs3189152	HLA-DQB	NM_00212	1stExon	chr6:32632	S_Shore
		PDZRN3	NM_01500	Body		
		SH3RF3	NM_00109	Body		
		WDR37	NM_01402	Body		
					chr2:15017	S_Shelf
rs11849385	rs12589304					
					chrX:12571	Island
rs17636747						
	rs71941608	BTG2	NM_00676	Body	chr1:20327	S_Shore
	rs5935457	TMSB4X;T	NM_02110	TSS200;TS	chrX:12993	N_Shore
		CACNA1C	NM_00112	Body;Body	chr12:2339	Island
rs58157532		CTNNA2;	NM_00438	Body;Body		
rs8192769		CYP2E1	NM_00077	Body	chr10:1353	Island
		TRAPPC9;	NM_00116	Body;Body		
		LOC10013	NR_02696	Body		
	rs76190553	OR10G9	NM_00100	TSS1500		
		DPPA5	NM_00102	TSS200	chr6:74063	Island
	rs2234095	TM9SF1;T	NM_00640	TSS200;TS	chr14:2466	Island
	rs62117975					
	rs4758	PDIA6	NM_00574	Body		

						chr14:1020	Island
	rs7159093						
	rs28496961						
rs72646280			CYP4V2	NM_20735	Body		
						chr5:53730	N_Shore
	rs77751758						
	rs67303455		HLA-DQB	NM_00212	Body	chr6:32632	S_Shore
						chr5:17654	Island
	rs67637320					chr2:13098	S_Shelf
			LOC72938	NM_00110	TSS1500		
			SDHA;CC	NM_00416	1stExon;TS	chr5:21803	Island
	rs75102927		C7orf50;C7	NM_00113	Body;Body	chr7:11426	Island
rs17844631	rs3096082		PCDHB15	NM_01893	1stExon	chr5:14062	Island
	rs74945670						
	rs62068242		NTN1	NM_00482	Body		
rs76286084							
rs2290840			FAM84B	NM_17491	TSS200	chr8:12756	Island
	rs489196		LOC25516	NR_02442	TSS1500	chr5:65828	N_Shore
			KCNQ2;K	NM_17210	Body;Body	chr20:6205	Island
	rs73398423		TCERG1L	NM_17493	Body		
			SLC7A8;S	NM_01224	Body;TSS200		
						chr7:51838	Island
rs2240276			TXNDC17;	NM_03273	3'UTR;3'U	chr17:6543	S_Shelf
	rs2278796		NFASC;NF	NM_00100	Body;Body	chr1:20495	Island
rs4957035	rs6868204					chr5:83428	Island
	rs9526703		RNASEH2	NM_02457	TSS1500;T	chr13:5148	N_Shore
			TUBE1;C6	NM_01626	TSS1500;5'	chr6:11240	S_Shore
			GLIPR1L2	NM_15243	TSS200	chr12:7578	Island
rs6976552	rs6975427						
	rs72220014					chr12:1148	N_Shore
			BEST3	NM_03273	5'UTR		
			LRP4	NM_00233	3'UTR		
		TRUE	PCDHB6	NM_01893	1stExon	chr5:14053	N_Shore
	rs75825590		ARID1B;A	NM_01751	Body;Body;Body		
	rs67305932						
			FAM122B;	NM_00116	TSS1500;T	chrX:13393	S_Shore

			HSD17B1	NM_00041	Body	chr17:4070	Island
			COL4A2	NM_00184	Body	chr13:1110	N_Shore
			LRRK1	NM_02465	Body		
			DGKQ	NM_00134	TSS1500	chr4:96673	Island
						chr8:43101	N_Shore
rs71321006			TOP1P2;PI	NR_00128	TSS1500;5'	chr22:2515	Island
rs11728092							
			C2orf69	NM_15368	TSS1500	chr2:20077	N_Shore
			SPACA1	NM_03096	TSS200	chr6:88757	Island
			MGC12982	NR_02687	TSS1500;T	chr1:47902	N_Shore
			SLC25A36	NM_01815	TSS1500;T	chr3:14066	Island
			FOXR1	NM_18172	1stExon	chr11:1188	Island
			FLJ23867;	NR_02690	TSS1500;Body;3'UTR		
			MED1	NM_00477	3'UTR	chr17:3755	S_Shore
			CFLAR;CF	NM_00112	Body;Body;Body		
						chr6:29894	S_Shore
			MRGPRE	NM_00103	TSS1500	chr11:3253	Island
	rs10455835						
			TNS3	NM_02274	Body		
			TIAL1;TIA	NM_00103	Body;Body		
			FRY	NM_02303	Body		
	rs9261293		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
	rs34834085		GPR123	NM_00108	Body	chr10:1349	N_Shore
			COL1A1	NM_00008	Body		
rs79347036			HLA-DRA	NM_01911	Body		
						chr1:83969	Island
			PI16	NM_15337	Body	chr6:36929	Island
						chr15:9688	S_Shore
						chr17:4143	N_Shore
		TRUE					
			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
	rs11204985		FLG2	NM_00101	TSS1500		
			COL6A3;C	NM_00436	Body;Body;Body		
			BMPR1B	NM_00120	5'UTR		
rs67722890	rs11650261		KRTAP4-7	NM_03306	1stExon		
	rs76366552					chr12:1331	N_Shore

				GATSL3	NM_00103	TSS200	chr22:3068	Island
		TRUE		SLC39A11;	NM_00115	Body;Body		
				MGAT5B;	NM_14467	Body;TSS2	chr17:7486	S_Shore
							chr6:10723	N_Shelf
rs3826008			TRUE	MTHFS	NM_00644	TSS1500	chr15:8018	S_Shore
				AGAP1;AC	NM_01491	Body;Body		
			TRUE	CCL28	NM_14867	Body		
				BDKRB1	NM_00071	TSS200		
rs73788131				RPS6KA2	NM_00100	Body		
				PPAP2C;PI	NM_17752	TSS1500;T	chr19:2905	S_Shore
				NCOR2;NC	NM_00631	Body;Body	chr12:1248	N_Shore
				FAM110B	NM_14718	5'UTR	chr8:59058	Island
	rs10864558							
							chr1:22768	S_Shore
rs71660512	rs1064715			HLA-DRB1	NM_00212	3'UTR		
rs9279728	rs35095850			HLA-DRB1	NM_00212	Body	chr6:32551	N_Shore
				PIN4;PIN4;	NM_00622	TSS200;TSS200;TSS200		
rs61608953							chr1:16136	N_Shore
rs36113538				PCDHB3	NM_01893	TSS1500	chr5:14048	N_Shelf
rs72943296							chr2:88583	Island
							chr1:22889	Island
				PNMAL2;P	NM_02070	1stExon;3'U	chr19:4699	Island
				EXD3	NM_01782	5'UTR	chr9:14031	Island
				BCAT1	NM_00550	Body	chr12:2505	Island
				CAMTA1	NM_01521	Body	chr1:77645	N_Shelf
				TMEM175	NM_03232	5'UTR	chr4:94061	Island
							chr7:56436	S_Shore
				TANC1;TA	NM_03339	Body;Body		
rs6422194	rs6422193						chr15:2014	Island
rs8076072	rs76512695						chr17:7948	N_Shore
	rs7066839			WWC3	NM_01569	TSS1500	chrX:99825	Island
							chr8:10375	Island
				RFNG	NM_00291	Body	chr17:8000	N_Shore
				PCDHB15	NM_01893	1stExon	chr5:14062	N_Shore
				PJA1;PJA1	NM_02236	5'UTR;5'U	chrX:68384	Island

	rs4919814	HCN2	NM_00119	Body	chr19:5956	N_Shore
		GPR64;GP	NM_00575	TSS1500;T	chrX:19140	Island
	rs6435323					
rs77978034	rs2894582				chr19:5241	S_Shore
		DENND3	NM_01495	Body		
		TSPY4	NM_00116	TSS1500	chrY:91935	Island
	rs3807043	KCNK16;K	NM_00113	TSS1500;TSS1500;TSS1500;TSS15		
		PSORS1C1	NM_01406	Body;Body		
rs28690610					chr19:3779	S_Shelf
		ITGAL;IT	NM_00220	Body;Body	chr16:3048	Island
		BEGAIN;B	NM_00115	Body;Body	chr14:1010	Island
rs57250050		GALNTL4	NM_19851	Body		
		PDZD4	NM_03251	Body	chrX:15309	Island
		FABP1	NM_00144	TSS200		
	rs880303	MYCBP;G	NM_01233	TSS1500;B	chr1:39338	S_Shore
	rs9909356					
					chr6:30418	Island
rs6491711		BIVM;BIV	NM_00115	Body;Body		
		KLHDC7A	NM_15237	1stExon	chr1:18808	N_Shore
		LNX1;LNX	NM_03262	Body;Body		
		FCGBP	NM_00389	Body	chr19:4037	N_Shelf
rs241439	rs4148874	TAP2;TAP	NM_00054	Body;Body		
		ATG4C;AT	NM_17822	TSS1500;TSS1500		
rs11257762	rs11257761					
	rs869621					
	rs9368372	FLJ22536	NR_01541	Body		
rs73262713	rs13226317				chr7:13150	N_Shelf
rs75814207						
rs9261297		RNF39;RN	NM_17076	Body;Body	chr6:30038	S_Shore
					chr6:28583	Island
		WWC1;W	NM_00116	3'UTR;3'UTR;3'UTR		
rs80115060						
	rs77437493					
	rs3763384	RADIL	NM_01805	Body	chr7:48760	Island
					chr4:58217	N_Shore
		PCDHB11	NM_01893	1stExon	chr5:14058	N_Shore
		TULP3;TU	NM_00116	Body;Body		
		CNOT6	NM_01545	Body		
		KIF14	NM_01487	Body		
		TSC22D3	NM_19805	TSS1500	chrX:10701	Island

rs34173461		PTPRN2;P	NM_00284	Body;Body;Body		
	rs78244274	COL11A2;	NM_08067	Body;Body;Body		
					chr8:48676	N_Shore
		ARSB;ARS	NM_00004	TSS1500;T	chr5:78280	S_Shore
		SH3BP5;S	NM_00484	Body;5'UTR		
	rs61493992	TACC2;TA	NM_20686	Body;Body		
rs34452676		ZACN	NM_18099	TSS1500	chr17:7407	S_Shore
					chrY:93854	N_Shore
					chr7:55433	N_Shelf
		IQCE;IQC	NM_00110	Body;Body	chr7:26455	N_Shelf
rs3813153		PPAP2C;P	NM_17752	TSS1500;T	chr19:2905	Island
		ANO8	NM_02095	Body	chr19:1743	Island
		MIPEP	NM_00593	Body		
rs8107979		SIGLEC5	NM_00383	TSS200		
					chr7:22122	Island
		PGLYRP1	NM_00509	TSS1500	chr19:4652	S_Shore
		KLHL26	NM_01831	Body	chr19:1876	S_Shore
rs12266787		CPEB3	NM_01491	Body	chr10:9399	N_Shore
		ZNF33B	NM_00695	3'UTR		
	rs35240166					
		C10orf11	NM_03202	Body	chr10:7787	N_Shore
		TRAK1	NM_00104	Body		
rs55956706	rs72777425	CCDC3	NM_03145	Body		
		HLA-DPA1	NM_03355	1stExon		
		T	NM_00318	Body	chr6:16657	N_Shelf
		ATP1B1;A	NM_00100	Body;Body	chr1:16907	S_Shelf
	rs75676135	A2ML1	NM_14467	Body		
					chr1:15975	N_Shelf
		STAT3;ST	NM_21366	Body;Body;Body		
	rs185669	PRTFDC1	NM_02020	Body	chr10:2524	N_Shelf
		LGR4	NM_01849	Body		
		CCDC155;	NM_14468	1stExon;5'U	chr19:4989	Island
		FAM129A	NM_05296	TSS1500	chr1:18494	S_Shore
		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		TRPM2	NM_00330	Body	chr21:4584	N_Shelf
		SETD2	NM_01415	Body		
		HOXA3	NM_15363	5'UTR	chr7:27163	Island

			SNORD11	NR_003301	TSS200;TSS200;TSS200;TSS200		
			PSMD14	NM_00580	Body		
			ZNF662;ZN	NM_20740	5'UTR;1stE	chr3:42947	Island
	rs1990322		CACNA1C	NM_00112	Body;Body;Body;Body;Body;Body;		
						chr7:55516	Island
			B3GNTL1	NM_00100	Body	chr17:8091	N_Shelf
	rs12943352					chr17:4081	N_Shelf
						chr19:5507	S_Shelf
						chr18:1194	Island
	rs74035965		GJB2	NM_00400	5'UTR	chr13:2076	N_Shore
						chr10:8229	Island
	rs2269139		PDE9A;PD	NM_00100	Body;Body	chr21:4410	N_Shore
	rs12405005					chr1:32180	N_Shelf
			PPAP2C;P	NM_17752	TSS1500;T	chr19:2905	Island
			THBS3	NM_00711	Body	chr1:15516	S_Shelf
			FAM163A	NM_17350	5'UTR	chr1:17971	Island
						chr12:1151	N_Shore
			KCNK2	NM_00101	Body		
rs28383432	rs4455710		HLA-DQA	NM_00212	Body		
						chr12:9885	Island
rs344534			C3	NM_00006	Body	chr19:6710	Island
	rs11351590		SMYD3	NM_00116	Body		
rs5844228						chr21:4667	N_Shelf
			GSTM1;GS	NM_14642	TSS200;TS	chr1:11023	Island
			LOC14869	NR_02681	Body		
						chr10:1245	Island
	rs872727						
rs7767613							
			PCDHB11	NM_01893	TSS1500	chr5:14058	N_Shore
			LY6K;LY6	NM_00116	TSS200;TS	chr8:14378	N_Shore
						chr8:21635	Island
			MCC	NM_00108	TSS1500	chr5:11282	S_Shore
		TRUE	MRVI1;MR	NM_00110	TSS1500;1stExon;5'UTR;1stExon;5		
			C20orf123	NM_08072	Body	chr20:4517	S_Shore

			LOC10013	NR_02447	TSS1500;TSS1500		
			B3GNTL1	NM_00100	Body	chr17:8092	N_Shore
			GALNT2	NM_00448	Body		
	rs62392796					chr5:17905	Island
	rs4348729						
			SH3RF3	NM_00109	Body		
	rs9554038		LOC10010	NR_02724	Body	chr13:1991	Island
						chr12:1148	S_Shore
	rs28986217		HLA-DQB	NM_00212	Body	chr6:32632	S_Shore
	rs78105036						
			WDR44;W	NM_01904	1stExon;5'U	chrX:11747	Island
			SELI	NM_03350	Body		
rs4588232	rs28716328					chr2:91936	Island
	rs78763018						
			MRPS10	NM_01814	TSS1500		
	rs35082251		SPNS2	NM_00112	Body	chr17:4439	N_Shore
			ZNF704	NM_00103	TSS200	chr8:81785	S_Shore
			RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
			GNA12	NM_00735	Body	chr7:28024	S_Shore
		TRUE	TCEAL3;T	NM_03292	5'UTR;5'U	chrX:10286	Island
			B3GNTL1	NM_00100	Body	chr17:8096	S_Shore
			TMEM151	NM_00113	Body	chr6:44243	Island
rs6963250							
	rs9804137		C1orf107	NM_01438	Body		
			PI16	NM_15337	Body	chr6:36929	Island
			BGLAP	NM_19917	TSS200	chr1:15621	N_Shelf
rs75441000	rs77485428		OR4C45	NM_00100	TSS1500		
			PCDHA2;P	NM_01890	Body;Body	chr5:14018	S_Shore
	rs7331553		TRPC4;TR	NM_00113	Body;Body;Body;Body;Body;Body		
	rs633811		TBCD	NM_00599	Body	chr17:8073	N_Shelf
	rs78843017		KLHL29	NM_05292	5'UTR	chr2:23749	N_Shelf
			RAB27A;R	NM_18323	Body;Body;Body;Body		
			PNLIPRP2	NM_00539	Body	chr10:1183	Island
						chr11:6738	Island
rs17346574							
						chr22:4316	S_Shelf
			TRIM27	NM_00651	Body		

	rs79163776					chr10:9741	S_Shelf
rs10151296						chr14:1011	Island
			SH2B2	NM_02097	Body	chr7:10196	Island
			HTT	NM_00211	Body		
			GNAL;GN	NM_00114	Body;Body	chr18:1182	N_Shelf
			HSD17B14	NM_01624	Body	chr19:4934	N_Shore
rs1557091							
	rs12562729		SKI	NM_00303	Body	chr1:22323	N_Shelf
			TCP10L2	NM_00114	Body	chr6:16758	S_Shore
	rs74698515		THSD4	NM_02481	Body		
			GRIK2;GR	NM_02195	TSS200;TS	chr6:10184	Island
	rs62167593						
						chr14:1019	Island
rs35484182	rs9270341		HLA-DRB	NM_00212	TSS1500		
	rs78227304		ARID3A	NM_00522	Body	chr19:9395	N_Shelf
			GAB2;GAE	NM_08049	Body;1stExon;5'UTR		
			FMN1	NM_00110	Body		
			ZNF516	NM_01464	Body	chr18:7411	S_Shelf
	rs72622090		CYFIP1;CY	NM_01460	Body;Body	chr15:2298	Island
			FSTL5;FST	NM_00112	TSS200;TSS200;TSS200		
rs75350172			MDGA1	NM_15348	Body	chr6:37617	Island
	rs4493531		SORCS2	NM_02077	Body		
			FAM100B	NM_18256	TSS1500	chr17:7426	N_Shore
			ANGPT1	NM_00114	Body		
			GJD4	NM_15336	TSS1500	chr10:3589	N_Shelf
						chr13:1129	N_Shore
	rs74793004		PTPRN2;P	NM_00284	Body;Body;Body		
			FYN	NM_00203	5'UTR		
	rs9876107		C3orf58	NM_17355	TSS1500	chr3:14368	Island
			NCOR2;NC	NM_00631	Body;Body	chr12:1249	Island
			PIWIL1	NM_00476	TSS200	chr12:1308	Island
						chr6:29894	S_Shore
	rs12027339		IGSF21	NM_03288	Body		
rs75328542						chr3:12598	N_Shelf
		TRUE	SIAH2;SIA	NM_00506	5'UTR;1stE	chr3:15047	Island
			CACNA2D	NM_17236	Body	chr12:2017	Island
rs2312183			SGCD;SGC	NM_00112	Body;Body;Body		
	rs2277868		BANF2;BA	NM_17847	TSS200;TSS200;Body		
			MGAT5	NM_00241	Body		

			SLC6A18	NM_18263	Body	chr5:12269	S_Shore
			CEP350	NM_01481	Body		
		TRUE	CCL11	NM_00298	TSS200		
			HPS5;HPS	NM_18150	3'UTR;3'UTR;3'UTR		
	rs11023212						
			FGF14	NM_17592	Body		
	rs78546739		EIF4EBP2	NM_00409	TSS1500	chr10:7216	N_Shore
rs62080640						chr18:1445	N_Shore
			PPP1R14D;	NM_01772	Body;Body		
			HSPA1A;H	NM_00534	1stExon;3'U	chr6:31782	S_Shore
			PART1	NR_024617	Body		
			RGNEF	NM_00108	Body		
rs79908836						chr1:16907	N_Shelf
						chr11:1031	S_Shelf
						chr2:58478	S_Shelf
			TP53AIP1	NM_02211	TSS200		
			CCT6P1	NR_00311	Body	chr7:65229	N_Shore
		TRUE	NCRNA00	NR_027063	Body		
		TRUE	RBMXL2	NM_01446	1stExon	chr11:7110	Island
			SERP2	NM_00101	3'UTR		
	rs11689911						
	rs1039913		MFHAS1	NM_00422	Body		
			PRX;PRX	NM_02095	Body;Body	chr19:4090	Island
	rs2843153					chr1:22457	N_Shore
	rs73168563		MIR548F3;	NR_03164	Body;Body		
			FABP1	NM_00144	TSS200		
			HAR1B;HA	NR_00324	Body;TSS1	chr20:6173	N_Shore
	rs589697						
rs7684015	rs13104693						
	rs74336972					chr17:7552	N_Shelf
			MCPH1	NM_02459	Body		
			C6orf10	NM_00678	Body		
rs1820741	rs13161456		AHRR	NM_02073	Body		
			TRPM1	NM_00242	Body		
			PCDHB5	NM_01566	1stExon	chr5:14051	N_Shore
			SDHAP3	NR_003263	TSS200	chr5:15942	Island
			SMAD3	NM_00590	Body	chr15:6735	S_Shelf

					chr10:8532	N_Shelf
rs9272540		HLA-DQA	NM_00212	Body		
		UNC93B1	NM_03093	Body	chr11:6776	N_Shore
		NR1D1;TH	NM_02172	3'UTR;Bod	chr17:3824	Island
					chr7:14238	N_Shelf
		C20orf96	NM_15326	Body	chr20:2597	Island
rs1556823					chr1:24780	Island
	rs1051508	ARHGAP2	NM_02122	3'UTR	chr10:4965	N_Shelf
	rs75355423					
					chr1:24780	Island
rs41264269		CKS1B;SH	NR_02416	TSS200;TS	chr1:15494	Island
		PCDHB7;P	NM_01894	1stExon;3'U	chr5:14055	S_Shore
	rs79807096	PTPRN2;P	NM_00284	Body;Body	chr7:15749	S_Shore
		LRCH1	NM_00116	3'UTR		
					chr1:35586	Island
		HLA-G	NM_00212	TSS200	chr6:29795	N_Shore
rs11913556	rs78180672				chr22:2028	N_Shelf
					chrY:74281	S_Shelf
		LOC10018	NR_02446	Body		
		RPRD2	NM_01520	TSS1500	chr1:15033	N_Shore
		DCHS2;DC	NM_01763	Body;Body	chr4:15525	N_Shore
					chr6:15695	S_Shelf
rs11836372		ERC1;ERC	NM_17803	Body;Body;Body;Body;Body		
		SH3D19;SH	NM_00100	TSS200;TSS200		
		FAM113B;	NM_13837	5'UTR;TSS1500		
	rs4618620	DTX2;DTX	NM_00110	5'UTR;5'UTR;5'UTR;TSS1500		
		KBTBD5	NM_15239	1stExon	chr3:42727	Island
	rs72509898					
	rs62335956				chr5:16539	N_Shelf
	rs35373206	HLA-DRB	NR_00129	Body		
		SYN1;SYN	NM_00695	Body;Body	chrX:47433	Island
					chr22:1853	S_Shore
		TRAPPC9;	NM_00116	Body;Body		
		AKR1B10;	NM_02029	1stExon;5'UTR		
	rs630755	MUS81	NM_02512	Body	chr11:6562	S_Shelf
		DOCK5	NM_02494	Body		
rs714006	rs34965630				chr22:4984	S_Shelf
		PRTFDC1	NM_02020	Body		
		LOC28317	NR_02434	Body		

			KCNN2	NM_02161	Body	chr5:11369	S_Shore
			ESPNP	NR_026567	Body	chr1:17018	Island
			CDK19	NM_01507	Body	chr6:11096	N_Shelf
			FLJ32810	NM_15243	Body		
			PCDHB5;P	NM_01566	3'UTR;1stE	chr5:14051	S_Shore
	rs78254170		GNG4;GN	NM_00448	5'UTR;5'UTR;5'UTR		
rs28891411	rs9274855						
	rs1182222					chr1:24780	Island
			PCDHA6;P	NM_03184	Body;Body	chr5:14022	Island
		TRUE	ZMYM3;Z	NM_00117	5'UTR;TSS	chrX:70473	Island
			WNT8B	NM_00339	Body	chr10:1022	N_Shelf
			RTBDN;R	NM_03142	Body;5'UT	chr19:1293	S_Shore
			SDS	NM_00684	TSS1500		
	rs11062351						
						chr2:24271	S_Shelf
	rs80159287		PFKP	NM_00262	Body	chr10:3160	S_Shelf
			RBM20	NM_00113	Body		
						chr22:1853	Island
			TMTC4;T	NM_00107	Body;Body		
rs11692777						chr2:12845	S_Shore
			SND1	NM_01439	Body		
rs72500559	rs67640541		HLA-DPA1	NM_03355	3'UTR		
			GPAM	NM_02091	TSS1500	chr10:1139	S_Shore
	rs12594038		RFX7	NM_02284	Body	chr15:5653	N_Shelf
			ARPC1B	NM_00572	5'UTR	chr7:98971	S_Shelf
						chr2:23321	Island
			IRS2	NM_00374	1stExon	chr13:1104	Island
			ODF3L2	NM_18257	Body	chr19:4687	Island
rs5022251	rs56062738					chr8:14406	N_Shore
						chr7:15876	S_Shelf
			SLC25A19	NM_00112	TSS1500;T	chr17:7328	S_Shore
			MIR886	NR_030583	TSS200	chr5:13541	Island
rs79017589		TRUE	PWP1	NM_00706	TSS1500	chr12:1080	N_Shore
rs1469828			ADAMTS1	NM_13905	Body		
						chr10:7715	Island
			TSPAN1	NM_00572	Body		

			MBOAT2	NM_13879	Body		
						chr1:98510	N_Shore
			HCCA2	NM_05300	Body		
	rs79612977						
			UBE2E2	NM_15265	Body		
	rs11658272		CCDC57	NM_19808	Body	chr17:8008	N_Shore
			MST4;MST	NM_00104	5'UTR;TSS	chrX:13115	Island
rs3188121			MAST4;MA	NM_01518	Body;Body	chr5:66459	S_Shelf
	rs9419585						
	rs3762293		MATN1	NM_00237	TSS1500	chr1:31194	S_Shelf
rs74730364	rs4757025		NAV2;NA	NM_18296	Body;Body;Body;Body		
						chr6:31650	Island
			WDR41	NM_01826	Body	chr5:76787	N_Shelf
rs76653421			CDH20	NM_03189	Body	chr18:5922	Island
						chr11:6568	N_Shore
	rs61972029					chr13:1149	S_Shore
rs3091376			POM121L1	NR_024591	TSS200	chr22:2298	Island
			MRC2	NM_00603	Body	chr17:6074	N_Shore
			LIMD1	NM_01424	Body		
	rs2062335						
	rs79441096						
	rs66985080		ATP5G1;A	NM_00517	1stExon;5'U	chr17:4696	S_Shore
			CYP2D6;C	NM_00102	Body;Body	chr22:4252	Island
			CEACAM6	NM_00248	3'UTR		
rs1712517						chr10:1050	N_Shelf
			FAM83H	NM_19848	Body	chr8:14480	Island
			TBC1D5;T	NM_01474	5'UTR;5'UTR;5'UTR		
rs79333241			TMEM51;T	NM_00113	5'UTR;5'U	chr1:15541	Island
						chr1:31280	Island
			FOXP1	NM_03268	Body	chr3:71113	N_Shelf
			ULK4	NM_01788	Body		
rs77995541			PASK	NM_01514	Body		
rs77917781			THSD7B	NM_00108	Body		
			CCK	NM_00072	TSS1500	chr3:42306	Island
	rs72610839		GRIK2;GR	NM_00116	Body;Body;Body		
						chr13:1996	N_Shelf
		TRUE					

				MCC;MCC	NM_00238	Body;Body		
rs4076353				PPP2R2C	NM_02041	TSS1500	chr4:64721	S_Shore
rs1323160				ENOX1;EN	NM_01799	5'UTR;5'UTR		
				NBN	NM_00248	Body		
	rs35648800							
		TRUE						
				GNG7	NM_05284	5'UTR	chr19:2525	Island
				HPRT1;HP	NM_00019	5'UTR;1stE	chrX:13359	Island
rs78055904								
	rs67650322		TRUE	TRIML2	NM_17355	TSS1500	chr4:18902	N_Shore
				GTF2A1L;	NM_17219	TSS200;Bo	chr2:48844	Island
				LTB4R2;L	NM_00116	Body;1stEx	chr14:2477	Island
	rs8038732			TTC23;TT	NM_00104	Body;Body;Body;Body;Body;Body;		
				MIER2	NM_01755	TSS1500	chr19:3452	Island
rs2303988				AP3B2	NM_00464	Body		
				TAF1B	NM_00568	Body		
	rs12133334			PADI2	NM_00736	3'UTR		
							chrX:37765	Island
rs12239131				SNHG3-R	NR_03072	Body;TSS1	chr1:28844	N_Shore
				SEMA3B;S	NM_00100	5'UTR;5'U	chr3:50310	N_Shelf
rs28746846				HLA-DQB	NM_00212	Body	chr6:32632	S_Shore
				LOC44083	NR_02939	Body		
rs61456535	rs535676			GLT1D1	NM_14466	TSS1500	chr12:1293	N_Shore
				ANO8	NM_02095	3'UTR	chr19:1743	N_Shelf
							chr3:47397	Island
	rs74783011							
				LUZP1;LU	NM_03363	TSS1500;TSS1500		
				COL23A1	NM_17346	Body	chr5:17782	Island
				BAI1	NM_00170	Body	chr8:14355	S_Shelf
	rs1864869						chr2:24164	S_Shelf
				TESSP1	NM_00113	TSS200	chr16:2848	N_Shore
	rs2073686			RPL27A;S	NM_00099	Body;Body	chr11:8710	N_Shelf
				JMY	NM_15240	Body		
				TPST2;MI	NM_00359	5'UTR;TSS1500;5'UTR		
							chr6:46655	N_Shelf
	rs74874268						chr12:1329	Island
rs9304902				TLE2;TLE	NM_00114	TSS1500;B	chr19:3028	S_Shore
rs75957843	rs34306326							

		HMG20A	NM_01820	5'UTR		
	rs3791385	HDAC4	NM_00603	Body		
		KIAA1949;	NM_00113	Body;1stEx	chr6:30654	N_Shelf
rs35662673		HLA-DRB	NR_00129	Body		
		PTPRR;PT	NM_13084	1stExon;Body;5'UTR		
	rs74931846	FAM13A;F	NM_01488	Body;Body		
rs34068305	rs7969789					
					chr12:1073	N_Shore
		HRH1	NM_00109	TSS200		
rs7207008		MIR2117	NR_031751	Body		
		SPNS2	NM_00112	Body	chr17:4439	Island
	rs77548084	SLC38A10;	NM_00103	Body;Body	chr17:7925	N_Shore
		CLSTN2	NM_02213	Body		
		DSTN;DST	NM_00687	Body;Body		
					chrX:13651	S_Shore
		PPAP2C;P	NM_17752	TSS1500;T	chr19:2905	Island
		TSPY4	NM_00116	Body	chrY:93036	S_Shelf
		CARKD	NM_01821	Body	chr13:1112	S_Shelf
rs34884738		FAM150B	NM_00100	Body	chr2:28735	N_Shore
	rs77876371				chr6:17073	Island
		COL1A1	NM_00008	Body		
		FHIT;FHIT	NM_00116	5'UTR;5'U	chr3:61236	N_Shore
		ACAT2	NM_00589	TSS1500	chr6:16018	Island
		ATP2A3;A	NM_17495	Body;Body	chr17:3847	Island
rs3935295		PTPN7;PT	NM_08058	TSS1500;TSS200		
		KLF6;KLF	NR_02765	Body;Body	chr10:3823	Island
					chr6:25732	Island
					chr19:3803	N_Shore
		IL20	NM_01872	Body		
		LOC44056	NM_00113	TSS1500		
		ARGFX	NM_00101	3'UTR		
rs12486900						
	rs41308154	VN1R5	NM_17385	1stExon		
		TRIO	NM_00711	Body		
rs80346635					chr4:13537	N_Shore
		SDK1;SDK	NR_02781	Body;Body		
		DTNA;DT	NM_00112	5'UTR;TSS1500;5'UTR;5'UTR;5'U		
		SLC2A9	NM_00100	5'UTR		

			FAM193A	NM_00370	TSS200		
rs4578281	rs4440932		MIR604;SV	NR_03033	TSS1500;Body;Body		
			AFAP1;AF	NM_19859	Body;Body		
rs34401369						chr12:1276	Island
			FNDC3A	NM_00107	Body		
			PDZD4	NM_03251	TSS200	chrX:15309	Island
						chrX:25020	Island
						chrX:73755	Island
			CLCN1	NM_00008	Body		
rs57596330	rs67368103					chr17:8101	N_Shore
			SPG21;SPC	NM_00112	Body;Body;Body		
	rs72515118		MGC12982	NR_02687	TSS1500;T	chr1:47899	S_Shore
rs58491120			LOC44160	NR_00303	Body	chr11:5025	Island
			IGSF1;IGS	NM_20583	5'UTR;1stExon;5'UTR;5'UTR;5'UT		
	rs9527901						
			PTPRN2;P	NM_00284	Body;Body	chr7:15740	Island
			AFAP1;AF	NM_19859	Body;Body		
						chrY:24454	N_Shelf
rs36069442	rs34548643					chr13:1001	Island
			KRT38	NM_00677	TSS200		
			LRWD1	NM_15289	Body	chr7:10210	S_Shore
rs66936919						chr8:58172	Island
			C21orf29;K	NM_14499	Body;TSS1500		
			HOXD4	NM_01462	1stExon	chr2:17701	Island
						chr2:23234	S_Shore
rs41545339	rs4081559		HLA-B	NM_00551	Body	chr6:31323	N_Shore
			MECOM;M	NM_00116	Body;Body;Body;Body;Body;Body		
			ANTXRL	NR_003601	Body		
			DOCK3	NM_00494	Body		
			MTMR7	NM_00468	Body		
						chr7:55516	N_Shore
			FLJ37453	NR_02427	Body	chr1:16163	Island
		TRUE	GNAS;GN	NM_00107	3'UTR;TSS	chr20:5746	Island
						chr7:65970	Island
rs78773816	rs3827118		PSMA7	NM_00279	Body	chr20:6071	N_Shelf
rs77634732			ZMYM2;Z	NM_00345	TSS1500;T	chr13:2053	N_Shore
						chr2:42328	N_Shore

rs2459669							
rs28577261			MAOB	NM_00089	TSS200	chrX:43741	S_Shore
			AMH	NM_00047	Body	chr19:2250	Island
						chr1:17845	Island
			C1orf14	NM_03093	Body	chr1:18292	N_Shore
			PODXL2	NM_01572	TSS200	chr3:12734	Island
			GFI1;GFI1	NM_00112	TSS1500;T	chr1:92945	Island
			RNF214;RN	NM_00107	Body;Body		
						chr1:20997	S_Shelf
		TRUE	IDH3G;IDH	NM_00413	Body;Body	chrX:15305	Island
			ASAP1	NM_01848	Body		
rs34513596			FLJ40330	NR_01542	TSS1500	chr2:89064	Island
rs78708893	rs75577269		ASB15	NM_08092	5'UTR		
			NRGN;NR	NM_00617	Body;Body	chr11:1246	N_Shore
						chr17:4902	N_Shore
			DYNLL1	NM_00103	5'UTR	chr12:1209	N_Shelf
			MSRA;MS	NM_00113	Body;Body;Body		
			MYH13	NM_00380	3'UTR		
						chr4:13265	Island
						chr20:4337	N_Shelf
			PCOLCE	NM_00259	Body	chr7:10020	Island
	rs77312752		SRRM4	NM_19428	Body	chr12:1195	N_Shore
			KIAA0922;	NM_01519	Body;Body		
			LANCL3;L	NM_19851	TSS200;TS	chrX:37430	Island
			PRR23B	NM_00101	TSS200	chr3:13873	Island
			CKAP5;CK	NM_00100	3'UTR;3'UTR		
rs36123777	rs35718555					chr12:1329	N_Shore
rs34452190			NDST3	NM_00478	Body		
			H2AFJ;H2A	NM_17792	TSS1500;T	chr12:1492	N_Shore
						chr5:17905	Island
rs71750265			VARS	NM_00629	Body		
			EPB41;EPB	NM_00116	3'UTR;3'U	chr1:29447	N_Shore
	rs77940180		MICALCL	NM_03286	5'UTR		
			AHDC1	NM_00102	5'UTR		
rs3209650			LOC28578	NR_02697	Body;Body		
						chr2:13098	Island
			PTPRN2;P	NM_00284	Body;Body;Body		

	rs11529774						
			CAMK2D;	NM_17212	Body;Body;Body;Body;Body;Body		
	rs79407846		FMNL2	NM_05290	Body		
rs78531597							
	rs62327889		SLC39A8	NM_00113	3'UTR		
			VDAC2	NM_00337	Body		
rs61352532	rs59402633		SLC6A19	NM_00100	3'UTR		
rs12254288							
		TRUE	ZNF581;Z	NM_01653	TSS1500;1	chr19:5615	Island
						chr18:5763	Island
	rs28362494		SLC12A7	NM_00659	Body	chr5:10735	S_Shore
			C1orf86;LC	NM_00114	Body;Body	chr1:21210	Island
rs28372931	rs61988513		DCAF4;DC	NM_18134	TSS200;TS	chr14:7339	Island
			THSD7A	NM_01520	Body		
rs4925625							
			C4orf50	NM_20740	3'UTR		
			ZSCAN1	NM_18257	Body	chr19:5855	Island
			THBS4	NM_00324	Body		
rs8078392			EXOC7;EX	NM_00114	Body;Body;Body;Body;Body;Body		
rs76544663			TBC1D16	NM_01902	Body	chr17:7792	N_Shore
rs9261249	rs9261250		NCRNA00	NR_026751	Body		
rs12485489	rs62274237		AADACL2	NM_20736	Body		
			FARS2	NM_00656	Body		
	rs62586104		EGFL6;EG	NM_00116	Body;Body	chrX:13587	S_Shore
			SLC39A11	NM_00115	Body;Body		
			LTB4R2;L	NM_00116	Body;1stEx	chr14:2477	Island
		TRUE	GRIK2;GR	NM_17576	1stExon;1st	chr6:10184	Island
	rs12622009		LOC90784	NR_02698	Body		
			HSD17B10	NM_00103	TSS200;TS	chrX:53461	Island
			MIR886	NR_03058	TSS200	chr5:13541	Island
						chrX:18693	Island
	rs74965504						
rs11147302						chr12:1330	N_Shore
						chr1:14915	Island

		CACNA1C	NM_00112	Body;Body;Body;Body;Body;Body;		
		GK;GK;GK	NM_00112	TSS200;TS	chrX:30670	Island
	rs78653691				chr6:15704	Island
		TRAF3IP2;	NR_02833	Body;5'UTR;1stExon;Body;Body;B		
		CNPY1	NM_00110	Body	chr7:15530	N_Shelf
					chr14:2119	Island
	rs28669852	AFAP1;AF	NM_19859	Body;Body		
		ITPR1;ITP	NM_00222	Body;Body;Body		
rs10280606		LAMB4	NM_00735	Body		
		LOC10010	NR_02724	TSS200	chr13:1991	Island
		CADPS;CA	NM_00371	Body;Body;Body		
		NID2	NM_00736	Body		
	rs12408890	WDR8	NM_01781	Body	chr1:35599	Island
		LOC40093	NR_02703	TSS200	chr22:4648	N_Shore
	rs13383733	C2orf82	NM_20689	TSS200		
					chr7:51838	S_Shelf
	rs72648838	COL23A1	NM_17346	Body		
		HLX	NM_02195	Body	chr1:22105	Island
		CHD7	NM_01778	5'UTR	chr8:61626	N_Shore
					chr4:24317	Island
		DENND2A	NM_01568	Body		
rs78405226		TNS3	NM_02274	Body		
rs7903850		C10orf28	NM_01447	5'UTR		
		GPR115	NM_15383	TSS200		
rs11639369	rs35794319	STRA6;ST	NM_00114	5'UTR;5'UTR;5'UTR;5'UTR;5'UTR		
		NAPSA	NM_00485	Body	chr19:5086	S_Shore
rs2072200		PON3	NM_00094	TSS1500	chr7:95025	Island
					chr4:15566	N_Shore
		KIF20B	NM_01619	Body		
		GPR155;G	NM_15252	Body;Body		
	rs610680					
					chr16:1098	Island
		OTUD7A	NM_13090	Body		
		HDAC4	NM_00603	Body		
		SDHAP3	NR_00326	Body	chr5:15942	Island
rs74857197		PCDHB3	NM_01893	1stExon	chr5:14048	N_Shore
		TEKT5	NM_14467	Body	chr16:1072	S_Shelf

						chrY:24329	S_Shelf
			MKNK2;M	NM_01757	3'UTR;3'U	chr19:2038	N_Shore
		TRUE	AIPL1;AIP	NM_00103	TSS1500;TSS1500;TSS1500		
			ANKRD6	NM_01494	5'UTR		
			MICA	NM_00024	Body		
			CBFA2T3;	NM_17593	5'UTR;Bod	chr16:8899	N_Shelf
			ANKRD26	NR_02655	TSS200		
			MCF2L;M	NM_00111	Body;Body	chr13:1136	S_Shore
	rs11933042					chr4:14141	S_Shore
	rs9261188		NCRNA00	NR_026751	Body		
						chr10:4267	Island
rs9384712			AKD1	NM_00114	Body		
			CHRNA9	NM_01758	TSS1500		
	rs73888297					chr22:4873	Island
	rs77104676		ARHGAP2	NM_01507	Body;Body		
	rs55696928		ODF3L2	NM_18257	TSS1500		
	rs80203576		C6orf221	NM_00101	TSS200	chr6:74073	N_Shore
			FLT4	NM_18292	3'UTR		
			AGBL1	NM_15233	Body		
	rs77304016		FRK	NM_00203	TSS1500		
rs7778889			GLI3	NM_00016	TSS1500	chr7:42276	S_Shore
			PSORS1C1	NM_01406	5'UTR		
rs2647604	rs2647603						
			NTM	NM_00104	Body		
	rs78874169		OR2T10	NM_00100	1stExon		
rs1078792	rs9295885					chr6:30418	Island
						chr10:1261	N_Shore
			FAM70A;F	NM_01793	Body;Body	chrX:11944	N_Shore
			SCNN1B	NM_00033	TSS1500	chr16:2331	Island
	rs12110879		HLA-DRB	NM_00212	Body	chr6:32551	N_Shelf
			KCTD5	NM_01899	Body	chr16:2746	S_Shelf
			DCX;DCX;	NM_17815	Body;Body;Body;Body		
						chr5:12892	S_Shelf
	rs79314686						
			SLC25A33	NM_03231	Body	chr1:95993	S_Shelf
			DLGAP2	NM_00474	Body	chr8:14967	Island
			PCDHA6;P	NM_03184	Body;Body	chr5:14021	N_Shore
						chr12:1151	Island
			IL12RB1	NM_00553	3'UTR		
			SDHAF1	NM_00104	TSS1500	chr19:3648	Island
						chr19:5727	Island

			PFKP	NM_00262	Body		
			HLA-DPB1	NM_00212	Body	chr6:33048	Island
			TIAM1	NM_00325	5'UTR	chr21:3292	N_Shelf
	rs71395332		GALNS	NM_00051	Body	chr16:8890	S_Shore
			ESYT2	NM_02072	Body		
rs77791988	rs71035499					chr11:3224	S_Shore
			AMH	NM_00047	Body	chr19:2250	Island
			SLC22A18	NM_00710	Body;TSS1	chr11:2923	N_Shelf
			EHBP1L1	NM_00109	Body	chr11:6535	Island
						chr5:17720	N_Shore
			AKAP13;A	NM_00720	Body;Body		
			MUC5B	NM_00245	Body	chr11:1247	S_Shore
			GRID1	NM_01755	Body	chr10:8802	Island
			MAP3K5	NM_00592	Body		
						chr7:14013	Island
		TRUE	WDR88	NM_17347	1stExon	chr19:3362	Island
						chr5:58870	S_Shore
			SDHAP2	NR_00326	TSS1500	chr3:19538	Island
			C18orf1;C1	NM_18148	5'UTR;5'UTR		
						chr13:1117	Island
			TTBK1	NM_03253	Body	chr6:43251	N_Shelf
						chr6:30418	Island
	rs2271029		CNTNAP1	NM_00363	Body	chr17:4083	Island
			ELANE	NM_00197	Body	chr19:8528	Island
	rs76605898		B3GNTL1	NM_00100	Body	chr17:8092	N_Shore
rs9261294			RNF39;RN	NM_17076	Body;Body	chr6:30038	S_Shore
			TMSL3;TM	NM_18304	Body;Body	chrX:12993	Island
			VPS52	NM_02255	Body		
rs80267282							
						chr6:29910	N_Shelf
			TSKS	NM_02173	Body	chr19:5024	Island
rs35220957			RBPJL	NM_01427	Body	chr20:4394	Island
	rs28408826		CHID1;CH	NM_00114	Body;Body	chr11:8886	Island
			BIRC3;BIR	NM_18296	5'UTR;5'U	chr11:1021	S_Shelf
	rs34289272						
			HDAC4	NM_00603	Body		
rs35729571			PDE9A;PD	NM_00100	Body;Body	chr21:4410	S_Shelf
	rs74710719		MIR662;M	NR_03038	TSS1500;Body		
	rs11642546		WDR90	NM_14529	Body	chr16:7018	N_Shore
			MYOZ3;M	NM_13337	Body;Body	chr5:15005	N_Shore
						chr16:8659	N_Shelf
			LOC28479	NR_02709	TSS200;Bo	chr20:2512	Island
			IL1RL2	NM_00385	Body		

			NAA10	NM_00349	Body	chrX:15319	Island
rs11823625	rs80198281						
rs62277633	rs1807425		SORCS2	NM_02077	Body		
			ETV1;ETV	NM_00116	Body;Body;Body;Body;Body;Body;		
rs74629957			SDK1;SDK	NR_02781	Body;Body		
			PHKB;ITF	NM_00029	Body;TSS1	chr16:4749	S_Shore
rs62377914			ARSB;ARS	NM_19870	TSS200;1st	chr5:78280	S_Shore
			CACNB2;C	NM_20157	Body;Body;Body;Body;Body;TSS2		
			BCL9L;BC	NM_18255	1stExon;5'U	chr11:1187	Island
	rs1359428		C13orf16	NM_15232	Body	chr13:1119	S_Shore
	rs60918217		COL21A1	NM_03082	Body		
rs34539085			CARD6	NM_03258	1stExon		
			PKHD1;PK	NM_13869	TSS1500;TSS1500		
rs6005095	rs78238497	TRUE	CRYBA4	NM_00188	5'UTR		
			EIF3G	NM_00375	TSS1500	chr19:1023	S_Shore
			TPCN2	NM_13907	Body		
			HOXB2	NM_00214	TSS200	chr17:4662	S_Shore
			ABCA12;A	NM_01565	Body;Body		
	rs78677234					chr17:3844	N_Shelf
	rs75410074						
			LSM5;LSM	NM_00113	3'UTR;Bod	chr7:32529	N_Shelf
						chr11:3375	S_Shelf
rs12995698						chr2:10585	Island
	rs60124064						
	rs79703316		SLC36A3;S	NM_00114	Body;Body		
			IPO9	NM_01808	3'UTR		
rs2455861						chr1:17845	Island
						chr10:1899	S_Shelf
						chr4:13289	Island
			TTTY10	NR_00154	TSS1500		
			SLC23A1;S	NM_15268	Body;Body	chr5:13871	Island
	rs76291322					chr16:7145	N_Shore
	rs72705373		FBLN5	NM_00632	Body	chr14:9241	N_Shelf
			RNF112	NM_00714	TSS200		
		TRUE	RPL21;RPL	NM_00098	5'UTR;Bod	chr13:2782	Island
rs7973399	rs7958490						
			ZFPM1	NM_15381	Body	chr16:8859	Island
			GFOD1	NM_01898	Body		

		SSH1;SSH	NM_00116	Body;Body;Body		
		RYR3	NM_00103	Body		
	rs62122447	ZNF787	NM_00100	Body	chr19:5661	Island
	rs57088661	ASGR2;AS	NM_08091	Body;Body;Body;Body		
		CNKSR2;C	NM_00116	Body;Body	chrX:21391	Island
rs72991430		DIXDC1	NM_00103	Body		
		FLJ44606;F	NM_00116	TSS1500;T	chr5:12640	S_Shore
		DENND2A	NM_01568	Body		
	rs74490142	BACH2;BA	NM_02181	Body;Body		
rs76904026		CYTH1;CY	NM_01745	Body;Body		
					chr8:48676	S_Shore
		PCDHB9	NM_01911	1stExon	chr5:14056	Island
	rs76639551	ZEB2;ZEB	NM_01479	Body;Body		
		MGMT	NM_00241	Body		
		SLC45A4	NM_00108	Body	chr8:14223	N_Shore
rs59553652	rs76720992	CSNK1G2	NM_00131	5'UTR	chr19:1953	N_Shelf
		COX10	NM_00130	TSS1500	chr17:1397	N_Shore
rs78896165		SRRM4	NM_19428	Body	chr12:1195	N_Shore
	rs28732154	BAT3;BAT	NM_00463	Body;Body;Body;Body		
		PMM2	NM_00030	3'UTR		
	rs12912620	TTLL13	NM_00102	Body	chr15:9079	S_Shelf
	rs6911171	UTRN	NM_00712	Body		
		TBCD	NM_00599	Body		
rs78616718		RORA	NM_13426	Body		
		KIFC3;KIF	NM_00555	TSS1500;T	chr16:5783	Island
		DLX5	NM_00522	Body	chr7:96651	Island
rs74060480	rs56176047				chr14:7031	S_Shelf
		OR8A1	NM_00100	TSS1500		
		KDM5D;K	NM_00114	TSS200;TSS200;TSS200		
		FAM65B	NM_01472	Body		
		CLYBL	NM_20680	3'UTR	chr13:1005	Island
		PDHA1	NM_00028	TSS1500	chrX:19361	Island
rs246705		PCDHB6	NM_01893	1stExon	chr5:14053	Island
	rs75332496	FAM188B	NM_03222	TSS1500	chr7:30810	N_Shore
rs4723885		LOC64699	NR_02439	Body	chr7:39649	Island
					chr4:36437	N_Shelf
		GRIK2;GR	NM_00116	Body;Body	chr6:10184	S_Shore
rs888099						

		JAK3	NM_00021	Body	chr19:1795	Island
		OR52B4	NM_00100	TSS200		
		PCDHA2;P	NM_01890	Body;Body	chr5:14018	Island
		CUTA;CU	NM_00101	TSS200;TS	chr6:33385	Island
		VGLL4;VG	NM_01466	Body;Body	chr3:11610	Island
		RSPH10B;	NM_17356	Body;Body		
rs61247158	rs59774758	ODF3L2	NM_18257	Body	chr19:4687	Island
rs66934458	rs56205709	RASA3	NM_00736	Body	chr13:1148	N_Shelf
		LOC10013	NR_02447	TSS200;TSS200		
		HRH1;HR	NM_00109	5'UTR;1stExon		
rs74937732		FLJ44606;	NM_00116	5'UTR;1stE	chr5:12640	Island
					chr12:1221	S_Shelf
		HLA-DRB	NM_00212	Body		
					chr18:7662	S_Shelf
rs9932527	rs7187116				chr16:8914	S_Shore
		WRB;WRB	NM_00462	Body;TSS2	chr21:4076	N_Shore
	rs79581560	TMEM195	NM_00100	Body		
rs11543193		TSPAN11	NM_00108	3'UTR		
					chr8:13651	N_Shore
					chr7:97656	S_Shore
rs8060332	rs58607184	TMPRSS8	NR_02686	TSS200	chr16:2892	Island
rs9705236		TSPAN4;T	NM_00102	TSS1500;T	chr11:8422	Island
		BANK1;B	NM_00112	Body;Body	chr4:10271	S_Shore
rs74471192		C10orf72	NM_00103	Body		
		SPSB4	NM_08086	Body	chr3:14078	S_Shore
		ALDH3B1;	NM_00116	3'UTR;3'U	chr11:6779	N_Shelf
		VWC2L	NM_00108	Body		
rs11545626		ARL4D	NM_00166	Body	chr17:4147	Island
		SDHAP3	NR_00326	Body	chr5:15942	Island
		MGAT5B;	NM_14467	Body;TSS2	chr17:7486	S_Shelf
		ZNF423	NM_01506	Body		
					chr13:2013	Island
	rs60606605				chr17:1928	N_Shelf
		PPAP2C;P	NM_17752	TSS1500;T	chr19:2905	Island
		ESYT2	NM_02072	Body		
					chr22:4949	Island
		ARHGAP6	NM_00612	TSS200;TS	chrX:11682	Island
		LOC10013	NR_02456	TSS1500;T	chr4:12029	Island

						chr12:5436	S_Shelf
			POM121L1	NR_024591	TSS200	chr22:2298	Island
			SCNN1D;S	NM_00113	Body;Body	chr1:12287	N_Shelf
rs35170672							
rs10910196	rs79748833						
			COL1A2	NM_00008	Body		
	rs35795438		DLX3	NM_00522	3'UTR	chr17:4807	N_Shelf
			P4HB	NM_00091	Body	chr17:7981	N_Shore
			AFAP1;AF	NM_00113	3'UTR;3'UTR;Body		
			CDH15	NM_00493	Body	chr16:8925	Island
			CYP2E1	NM_00077	Body	chr10:1353	S_Shore
			SLC39A11	NM_00115	Body;Body		
			MATN4;M	NM_00383	5'UTR;5'U	chr20:4393	Island
rs67396441							
			LOC28583	NR_02697	Body;Body		
			PRKG2	NM_00625	Body		
rs2839204			C21orf57	NM_05818	Body	chr21:4771	N_Shore
			CD8A;CD8	NM_00114	5'UTR;1stE	chr2:87015	Island
			ANKRD58	NM_00110	TSS200	chrX:11889	Island
	rs11728752		ABLIM2;A	NM_03243	Body;Body	chr4:81540	S_Shore
			PIGA;PIGA	NM_00264	TSS200;TS	chrX:15353	Island
			STARD8;S	NM_00114	TSS200;5'U	chrX:67913	Island
		TRUE	PSG4;PSG	NM_21363	Body;Body		
						chr6:31276	N_Shore
			LSP1;LSP1	NM_00101	5'UTR;TSS	chr11:1892	N_Shore
			IGF2;INS-I	NM_00100	TSS200;Body;Body		
	rs13302944		PRKCZ	NM_00274	Body	chr1:19907	S_Shore
rs62242805	rs72862756		SCN5A;SC	NM_00116	Body;Body;Body;Body;Body;Body		
rs75998307							
			FPR3	NM_00203	5'UTR		
rs2242083						chr4:10444	Island
	rs56263556		ZNF208	NM_00715	Body	chr19:2219	Island
			CYP4X1	NM_17803	TSS1500	chr1:47489	N_Shore
			MACF1;M	NM_01209	Body;Body		
	rs75272096						
			GPR1;GPR	NM_00527	5'UTR;5'UTR		
rs11040639	rs1721994					chr11:4991	Island

		CBR1;CBR	NM_00175	1stExon;5'U	chr21:3744	Island
		SH3PXD2A	NM_01463	3'UTR	chr10:1053	N_Shelf
		ZC4H2	NM_01868	TSS1500		
		PCDHB15	NM_01893	1stExon	chr5:14062	N_Shore
		TRIP10	NM_00424	Body	chr19:6746	S_Shore
		SH2D3C;S	NM_00548	Body;5'UT	chr9:13051	Island
					chr15:9688	Island
		FLT4	NM_18292	Body		
		TRIM31	NM_00702	Body		
		SIGLEC5	NM_00383	TSS1500		
		ARMCX2;	NM_17794	TSS200;TSS200		
		EPX	NM_00050	Body	chr17:5627	N_Shore
		TBL1Y;TB	NM_13425	TSS200;TS	chrY:67785	N_Shore
rs6502844		ZNF232	NM_01451	5'UTR	chr17:5019	Island
	rs73726192	HLA-DRB	NM_00212	Body	chr6:32489	S_Shelf
		RNF39;RN	NM_17076	Body;Body	chr6:30038	Island
		HSF5	NM_00108	1stExon	chr17:5656	Island
		FBXW4	NM_02203	Body		
		SDHAP3	NR_00326	TSS1500	chr5:15942	Island
rs3091376	rs5751460	POM121L1	NR_024591	TSS200	chr22:2298	Island
		SLC35E2	NM_18283	5'UTR	chr1:16707	S_Shore
rs55825458		IL4I1;IL4I1	NM_15289	TSS1500;Body		
		BIN1;BIN1	NM_13934	Body;Body;Body;Body;Body;Body;		
		GABBR1;	NM_02190	Body;Body;Body		
rs67522103		SERPINB6	NM_00456	Body		
rs74759312					chr10:1138	S_Shore
	rs2747431					
		CNOT10	NM_01544	Body		
	rs80020503				chr13:2327	Island
rs822532					chr7:14863	Island
	rs2076328	NADK	NM_02301	Body	chr1:16853	S_Shore
		CILP2	NM_15322	Body	chr19:1965	Island
rs78864732		LOC10013	NR_02696	Body		
	rs6954102					
		NLGN4Y;N	NR_02831	Body;TSS1	chrY:16635	N_Shore
	rs73714348				chr8:14364	Island
		GRIK2;GR	NM_17576	TSS1500;T	chr6:10184	N_Shore

	rs73256152						
			SLC39A14;	NM_01535	Body;Body;Body;Body		
	rs55956927		ADAP1	NM_00686	Body	chr7:96598	Island
			ANKRD2;A	NM_02034	Body;Body	chr10:9933	Island
rs76452907	rs55921385					chr7:15562	Island
			ATP9B	NM_19853	Body	chr18:7712	S_Shore
			KCNK3	NM_00224	Body	chr2:26950	Island
rs296365	rs296366		SULT2A1	NM_00316	3'UTR		
	rs12444807						
rs74192474							
rs67729041	rs66612022		COL1A2	NM_00008	Body		
						chr18:1443	N_Shelf
			KDM5D;K	NM_00114	Body;Body;Body		
			NIPA2;NIP	NM_00100	TSS1500;T	chr15:2303	S_Shore
			NEK11;NE	NM_02480	3'UTR;3'UTR		
	rs79367624		GAS8;C16	NM_00148	Body;1stExon;5'UTR;Body		
			COL9A3	NM_00185	TSS1500	chr20:6144	N_Shore
			SLC22A14	NM_00480	TSS1500		
	rs35802101		PSG4;PSG	NM_21363	TSS1500;TSS1500		
			SSX1	NM_00563	Body		
						chr1:28850	Island
			CDK11B;C	NM_03348	Body;Body	chr1:15644	S_Shore
			RPP25;RP	NM_01779	3'UTR;1stE	chr15:7524	N_Shore
						chr1:24780	N_Shore
		TRUE	CLRN3	NM_15231	Body		
						chr15:2467	S_Shore
			TIMP2	NM_00325	Body		
						chr12:9722	N_Shore
	rs79093100						
	rs663254		GIPC2	NM_01765	3'UTR		
rs9295884						chr6:30418	Island
			RPH3AL	NM_00698	TSS1500	chr17:2054	N_Shelf
			PCDHGA1	NM_01891	1stExon;1st	chr5:14071	Island
	rs78626564		EPHA2	NM_00443	Body	chr1:16475	N_Shelf
			SATB2	NM_01526	Body	chr2:20032	Island
			NBAS	NM_01590	Body		

		MAP3K4;M	NM_00672	Body;Body		
					chr2:10275	S_Shore
		SMTN;SM	NM_00693	Body;Body	chr22:3150	N_Shore
					chr12:1331	N_Shore
		PCDHB9	NM_01911	1stExon	chr5:14056	S_Shore
rs558584		CCDC86	NM_02409	TSS1500	chr11:6060	N_Shore
	rs35880313				chr13:1131	N_Shore
		KCTD2	NM_01535	Body		
		TMC3	NM_00108	TSS200		
	rs13406553	DHRS9	NM_00577	TSS1500		
		DCBLD1	NM_17367	TSS1500	chr6:11780	N_Shore
rs58662512					chr22:4645	S_Shelf
		MIR199A1	NR_02958	TSS200;Body;Body;Body;Body		
					chr12:1151	Island
	rs2245293	ABR;ABR	NM_02196	Body;5'UTR		
rs77244310						

PHANTOM	DMR	ENHANCE	HMM_ISL	REGULAT	REGULAT	DHS
			X:103696232-103698055			
		TRUE				
			16:568945-	16:628968-	Unclassifie	TRUE
		TRUE				
			6:31758628-31759271			TRUE
		TRUE				TRUE
		TRUE				
		TRUE				TRUE
	DMR					
	RDMR		12:52376862-52377134			
						TRUE
		TRUE				
			6:169281427-169282428			
			19:61380215-61380289			
		TRUE				TRUE
		TRUE		16:2471205	Unclassifie	TRUE
		TRUE				
			2:242484037-242484266			TRUE
		TRUE	16:84934486-84934669			TRUE
			2:236743838-236743881			
			1:15965836	1:16139180	Unclassifie	TRUE
			4:123072783-123073604			
				16:5121137	Unclassified	
		TRUE				TRUE
			17:76086607-76086958			
			12:131454083-131454778			TRUE
			13:112044797-112045718			
				18:5921873	Unclassified	
			15:20544259-20544679			
			16:359773-360737			
		TRUE				TRUE
		TRUE				TRUE
			12:7407112	12:7578433	Promoter_	TRUE
			16:1009552-1010177			TRUE

			5:13544411	5:13541621	Unclassifie	TRUE
		TRUE				
		TRUE				
0;Body;Body		TRUE				
		TRUE				
			1:9331896-9332398			
			8:1233079-1233850			
		TRUE				
			20:28164609-28165462			
			3:10124751-10125032			
		TRUE				TRUE
		TRUE				TRUE
			1:54594453-54594921			
		TRUE				TRUE
		TRUE				TRUE
			13:112544668-112544788			
		TRUE				
		TRUE				
			6:32659866	6:32552058	Unclassified_Cell_type_specific	
			Y:19697854-19699393			
			X:1291269	X:1292994	Promoter_Associated	
	RDMR					
		TRUE		12:1222316	Promoter_Associated	
		TRUE				TRUE
		TRUE	12:1479506-1480164			TRUE
			17:875707-875826			
		TRUE				
		TRUE				TRUE

	10:26971909-26972111			
	X:1290299	X:1299250	Promoter_A	TRUE
	17:75537362-75537568			
TRUE				
	12:124911655-124912441			
		2:12856783	Promoter_Associated	
	1:215373298-215373391			
	17:670977-671206			
	8:4171050-4171292			
	6:157024951-157025036			TRUE
	5:140543335-140543461			
	16:86796356-86796487			TRUE
TRUE				
	2:231563153-231564304			
TRUE		8:14155487	Unclassifie	TRUE
TRUE	11:6714011	11:6738291	Promoter_Associated	
		22:3807096	Unclassified	
TRUE				TRUE
	8:2008484-2009180			
	19:5555358	19:5086164	Promoter_Associated	
	1:159849178-159849310			
	1:23316569	1:23509857	Promoter_Associated	
TRUE				
	4:190465555-190467725			
	1:245869280-245869790			TRUE
		17:1534006	Unclassified_Cell_type_specific	
	10:1351912	10:1353418	Unclassifie	TRUE
	16:87679790-87679945			
	11:58492569-58492722			
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TRUE				

		1:234981427-234981651			
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DMR		4:15547337	4:15525405	Unclassified	
		1:8300360-	1:8377671-	Unclassified	
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		12:1135938	12:1151096	Unclassified_Cell_type_specific	
		18:7533392	18:7723585	Unclassified_Cell_type_specific	
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	TRUE				
					TRUE
			19:5101726	Unclassifie	TRUE
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DMR					TRUE
	TRUE		2:10501205	Unclassifie	TRUE
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		15:22273811-22274108			
		16:30480212-30480556			
		3:13949146-13949851			
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	TRUE	7:8442594-8442654			
	TRUE				TRUE
		7:139781665-139782089			
		8:2165840-2165959			
		X:100694450-100694687			
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		1:2836655-2837169			
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		10:49018144-49018641			
	TRUE		2:20819931	Unclassifie	TRUE
DMR		2:176644547-176645189			
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		19:1069926	19:1120066	Unclassified_Cell_type_specific	
		17:74187836-74187962			
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		2:1604275-1604340			
		19:4559630	19:4090438	Unclassifie	TRUE
		19:46223671-46223879			
		2:48698290-48698489			
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					TRUE
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	TRUE		6:32222378	Unclassifie	TRUE
	TRUE		10:3894579	Unclassifie	TRUE
		16:86651701-86652023			
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	TRUE				
		16:8769438	16:8916777	Unclassified_Cell_type_specific	
RDMR			6:43736658	Promoter_Associated	
	TRUE				
CDMR					
		16:86173541-86173770			TRUE
		3:19706262	3:19557756	Unclassified	
			12:4976269	Unclassified	
RDMR		19:5959151	19:5489961	Promoter_Associated_Cell_type_specific	
	TRUE				
		1:20747149	1:20940501	Unclassified_Cell_type_specific	
		1:228316886-228317003			
			11:6589971	Unclassifie	TRUE
	TRUE	17:1704949	17:1710846	Promoter_Associated	
		2:869464-869580			
	TRUE				
	TRUE	10:1298389	10:1299478	Promoter_Associated	
	TRUE		6:15671703	Unclassified	

		TRUE	13:1137590	13:1147411	Unclassified_Cell_type_specific	
	RDMR	TRUE				
				4:83955373	Promoter_Associated	
			17:77554730-77555513			TRUE
			5:74943881-74943934			
		TRUE				
		TRUE				
				19:5083637	Promoter_Associated	
			6:26413350	6:26305223	Promoter_Associated_Cell_type_specific	
		TRUE				
			13:110964757-110965305			
low-CpG:45620911-456		TRUE				
				15:8978599	Promoter_Associated	
		TRUE				
		TRUE				
	DMR		1:58814306-58815871			
			10:133915924-133916163			TRUE
		TRUE				
			Y:16076834-16078034			
				17:7895778	Unclassifie	TRUE
			6:142049350-142049489			
		TRUE				
			1:113087432-113087505			
high-CpG:4858321-4858482			10:4858068	10:4867931	Unclassifie	TRUE
		TRUE				
			7:1754218-1754471			
			2:239554242-239554433			
y		TRUE				TRUE
			7:126078-126514			TRUE
			15:98901952-98902653			
		TRUE				TRUE
	DMR		X:106453745-106454142			
			4:191141974-191143118			
	CDMR					
		TRUE				

		TRUE				TRUE
			16:10763509-10764036			
		TRUE				
		TRUE				
				9:13729875	Unclassified	
		TRUE				TRUE
			7:157724753-157725305			
			16:87517609-87517775			
			16:31249988-31251004			
				1:8083829-	Unclassified_Cell_type_specific	
		TRUE				
		TRUE	16:992497-	16:1052731	Unclassifie	TRUE
low-CpG:20788172-207		TRUE				
			1:24616638	1:24810001	Promoter_A	TRUE
		TRUE	6:159280388-159280909			
	DMR		2:234512118-234512656			
		TRUE	6:166180446-166180563			
		TRUE				
	RDMR					
		TRUE		14:3744498	Unclassified_Cell_type_specific	
		TRUE				
		TRUE	1:6008531-6009081			TRUE
			1:49137160-49137483			
	DMR					
	CDMR					
		TRUE				
			1:14501527	1:14655105	Unclassified_Cell_type_specific	
			8:10620625-10621666			
		TRUE	1:27548338	1:27675585	Gene_Associated_Cell_type_specific	
			18:74825910-74826529			
			2:234512118-234512656			
		TRUE	11:6714011	11:6738291	Promoter_Associated	
			12:114528341-114528449			
			16:33390686-33391229			
			17:5391974	17:5656456	Unclassified	

			19:42731376-42732703			
		TRUE				
			14:104363253-104364839			
		TRUE				
			6:32955477-32955824			
low-CpG:70827875-70828160			17:7082807	17:7331603	Gene_Associated_Cell_type_specific	
		TRUE				
	DMR		7:27172191-27173627			
			2:847566-847747			
		TRUE		X:7032302	Promoter_Associated	
	RDMR	TRUE				
		TRUE	18:1193753	18:1194717	Promoter_A	TRUE
		TRUE				
		TRUE				
			14:98682846-98683100			
		TRUE		10:1693306	Unclassified	
			6:30146876	6:30039021	Unclassified_Cell_type_specific	
			21:45061241-45063445			
	RDMR					TRUE
			12:7916632-7917175			
			7:149724594-149726348			
	RDMR					
low-CpG:101740759-101741131			X:1017407	X:1018541	Promoter_A	TRUE
	RDMR		6:31903371	6:31797413	Promoter_Associated	
						TRUE
			16:87517609-87517775			
	DMR	TRUE	1:15967609	1:16140957	NonGene_A	TRUE
				6:32604963	Unclassified_Cell_type_specific	
			5:140455784-140456791			
			X:3956509	X:3968013	Unclassifie	TRUE
	RDMR					
		TRUE		6:16690976	Unclassified_Cell_type_specific	
						TRUE
		TRUE				
		TRUE		7:12949920	Unclassified_Cell_type_specific	

		TRUE				
		TRUE				
high-CpG:47572034-47572233			1:47571999-47572992			
			12:64425408-64425726			
	DMR			19:2426968	Promoter_Associated	
low-CpG:55951362-55951907			X:5595168	X:5593441	Promoter_Associated	
		TRUE				
		TRUE				TRUE
			3:13220677-13221199			
			16:2832519	16:2892264	Promoter_A	TRUE
		TRUE	1:40370964-40371787			
		TRUE				
	RDMR		10:719420-	10:729535-	Unclassifie	TRUE
	RDMR	TRUE				
			16:1333527-1334206			
			5:4154090-4154196			
			3:197194050-197194141			
	RDMR					
			3:197333759-197334072			
		TRUE				TRUE
			5:140222060-140223191			
				17:8016987	Unclassified_Cell_type_specific	
			6:164175441-164176096			
		TRUE	1:17088223	1:17215344	Promoter_A	TRUE
		TRUE				
high-CpG:40724718-40725132			22:4072456	22:4239415	Promoter_A	TRUE
		TRUE	1:45051387	1:45278964	Promoter_A	TRUE
			6:170527545-170528896			
			Y:10088176-10088729			
			19:15428605-15430216			TRUE
			1:16102690	1:16276054	Unclassified_Cell_type_specific	
			16:53920239-53920843			
		TRUE	16:84177475-84177905			
		TRUE				
		TRUE				
		TRUE				

high-CpG:33486114-33486810			6:33485865	6:33377646	Promoter_Associated	
			5:140543532-140544545			
			2:44167424	2:44313758	Unclassified	
			2:240387534-240388257			
		TRUE				
		TRUE				
			22:30928951-30930766			
	DMR	TRUE	9:128415782-128417915			
		TRUE		10:1154657	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
			14:100608872-100608951			
		TRUE				
		TRUE				
			10:118377008-118377466			TRUE
			4:183838618-183838719			
		TRUE				TRUE
			20:61691691-61692497			
		TRUE		22:3759267	Unclassifie	TRUE
			7:56822468-56822994			
		TRUE	14:100244968-100245789			TRUE
			11:126513012-126513121			
		TRUE				
			11:85323379-85324124			
				6:31095254	Unclassified	
			X:1290820	X:1292544	Unclassified	
			14:104766759-104777327			
			5:140533155-140533390			
			2:19413297	2:19549091	Promoter_A	TRUE
		TRUE				
			2:241260182-241261463			
		TRUE				
			16:2807217	16:2866797	Unclassifie	TRUE
		TRUE				
			5:140543335-140543461			
			12:118076047-118076529			TRUE
		TRUE				
			11:1218728-1220416			

high-CpG:149651202-149651531		7:14965092	7:15001985	Promoter_A	TRUE
		5:1909552-1910665			
	TRUE				TRUE
DMR		7:27172191-27173627			
		7:56209901-56210987			
		6:30146876	6:30039021	Unclassified_Cell_type_specific	
		8:14590930	8:14593822	Unclassified_Cell_type_specific	
		2:27740139	2:27885972	Promoter_Associated	
		2:240878887-240879148			
					TRUE
		2:121088475-121088579			
			8:2074812-	Promoter_Associated_Cell_type_specific	
	TRUE		16:2119942	Unclassifie	TRUE
CDMR					
		12:912208-912325			
		1:2874923-2875144			
RDMR		7:25865621-25865743			
		X:122922222-122923182			
		17:7291738	17:7540566	Unclassifie	TRUE
		16:8368070	16:8512344	Unclassified_Cell_type_specific	
	TRUE		21:3857990	Unclassified_Cell_type_specific	
		7:4877518-4877648			
		7:156952553-156953261			
	TRUE				TRUE
	TRUE		21:4017649	Promoter_Associated	
	TRUE				
		2:239590384-239590448			
			22:4057301	Promoter_Associated	
		19:54391524-54391882			
	TRUE				
	TRUE				
		4:9088613-9089054			

			8:14487978	8:14480896	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				TRUE
low-CpG:55269974-55270675						
			2:237986988-237987095			
		TRUE				TRUE
		TRUE				
			16:8641350	16:8785621	Unclassifie	TRUE
		TRUE	17:1704949	17:1710846	Promoter_Associated	
				6:30652289	Promoter_Associated	
			1:3070800-3071206			
			2:176725370-176725963			
			5:140216915-140218043			
		TRUE	12:1218256	12:1232581	Promoter_Associated	
			2:176644547-176645189			
				13:4159309	Promoter_Associated	
				1:20672885	Unclassified	
			7:158395656-158395996			
			17:3718047-3718526			
			3:134985252-134985788			
	RDMR	TRUE	16:71657008-71657131			
			3:49211587-49212481			TRUE
		TRUE				
				20:5278628	Unclassified_Cell_type_specific	
		TRUE		4:24745693	Unclassified_Cell_type_specific	
		TRUE	5:17523115	5:17529863	Unclassified_Cell_type_specific	
			X:37315490-37316849			
		TRUE				
				19:2126474	Promoter_A	TRUE
		TRUE				
	RDMR	TRUE	8:73079763	8:72917248	Unclassified	
			6:30001657	6:29894087	Promoter_Associated	
			8:1418160-	8:1431296-	Unclassified_Cell_type_specific	
			6:30001657	6:29894087	Promoter_Associated	
			16:84968705-84968853			
			Y:9293666-9296814			
	CDMR	TRUE				

		TRUE				
		TRUE				
		TRUE		19:4824593	Promoter_Associated_Cell_type_specific	
			5:3169575-3169811			
			5:140705073-140706075			
		TRUE				TRUE
		TRUE				
0						
high-CpG:33461734-33462266			8:33461773	8:33341954	Promoter_Associated	
	RDMR	TRUE				
	RDMR					
		TRUE				
high-CpG:144881510-144881652			8:14487978	8:14480896	Unclassifie	TRUE
			4:7814512-	4:7763381-	Promoter_A	TRUE
	RDMR		12:113619245-113619773			
		TRUE				TRUE
		TRUE				TRUE
			2:1636469-1636527			TRUE
		TRUE				TRUE
		TRUE				
			13:110079325-110079487			
	RDMR			15:3987575	Unclassified	
			4:1192911-1193178			
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
			6:74119872-74121192			
			6:30335300	6:30226801	Promoter_Associated	
			11:488859-488944			
			6:35841568-35841803			

			17:8191152-8191582			
				9:13070482	Unclassified	
	DMR		4:15547337	4:15525405	Unclassified	
		TRUE				TRUE
	CDMR					
		TRUE				TRUE
			16:14926307-14926467			TRUE
				4:14601837	Promoter_Associated	
			3:75739828-75739956			
			6:101954247-101954458			
		TRUE	11:773645-	11:783587-	Unclassifie	TRUE
			22:2271389	22:2438403	Unclassified_Cell_type_specific	
		TRUE		20:4334334	Unclassifie	TRUE
		TRUE				TRUE
			8:43250370-43250704			
			2:90998272-90999872			
			8:1353066-1353328			
			15:90260861-90260934			
low-CpG:242568433-242568614						
			6:28554754-28554928			
		TRUE				TRUE
			3:19706262	3:19557756	Unclassified	
low-CpG:1651824-1651831						
	RDMR		4:4916948-4917032			
		TRUE				
		TRUE				
			7:985427-985529			
		TRUE				
		TRUE				
		TRUE	9:99109375-99110140			
			14:27803364-27803615			TRUE

		12:131545894-131546177			
		17:7738603	17:7979287	Unclassified_Cell_type_specific	
	TRUE				TRUE
	TRUE				
	TRUE				
	TRUE				TRUE
		20:61909552-61910464			TRUE
		5:140460938-140461126			
		6:28971323	6:28863209	Promoter_Associated	
		8:37124707-37124778			
DMR					
		13:18590636-18590913			
RDMR					
	TRUE		7:94953742	Unclassified_Cell_type_specific	
	TRUE				TRUE
	TRUE	2:53940281-53940994			
					TRUE
		7:105010761-105011086			
		16:85023316-85023461			
CDMR					
			14:9449169	Unclassified_Cell_type_specific	
RDMR			22:3820015	Unclassified_Cell_type_specific	
	TRUE				TRUE
		16:8903397-8903486			
	TRUE		16:1165514	Unclassified_Cell_type_specific	
		1:2110741-	1:2120661-	Promoter_Associated	
		16:86865892-86866064			TRUE
	TRUE				
	TRUE				
	TRUE				
	TRUE				
	TRUE		12:5893417	Unclassified_Cell_type_specific	
			8:14223933	Unclassified_Cell_type_specific	
		5:140460938-140461126			
		3:140207016-140208136			
		1:2110741-	1:2120661-	Promoter_Associated	
			1:899115-8	Unclassified_Cell_type_specific	
					TRUE

		TRUE				TRUE
		TRUE		6:32828471	Unclassifie	TRUE
		TRUE				
		TRUE				
			1:24395091-24395207			
			6:30187118-30187260			
		TRUE				
		TRUE				
			X:9392530-9394487			TRUE
		TRUE				
			6:101003391-101003532			
			17:920371-920559			
						TRUE
high-CpG:71268487-71268667			X:7126717	X:7135121	Unclassifie	TRUE
		TRUE				TRUE
			7:2735074-2735129			
			6:101954247-101954458			
	DMR		19:1269267	19:1283149	Promoter_Associated	
			X:9582625	X:9593922	Promoter_Associated	
		TRUE				TRUE
		TRUE				
		TRUE				
			3:140221263-140222607			
		TRUE		3:12792257	Unclassifie	TRUE
		TRUE				TRUE
high-CpG:20628155-20628346			17:20628177-20628666			TRUE
		TRUE				TRUE
low-CpG:57691272-57691385						

				1:15166559	Gene_Associated_Cell_type_specific	
			1:147478760-147479147			
		TRUE				
	RDMR		16:414431-414530			
	RDMR					
		TRUE				
			8:143657394-143657658			
		TRUE				
			21:45834360-45835538			TRUE
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE	4:15931125	4:15909160	Unclassified_Cell_type_specific	
			1:29061923-29062575			
		TRUE		1:12100445	Unclassifie	TRUE
			6:29756034	6:29648152	Unclassified_Cell_type_specific	
			17:77074036-77074159			
high-CpG:18912347-18913029			X:1891192	X:1900182	Promoter_Associated	
			5:5939614-	5:5886941-	Unclassifie	TRUE
			2:172680872-172681488			
			6:31758628-31759271			TRUE
		TRUE				
			8:111283907-111284460			
	DMR		10:43166274-43166581			
						TRUE
		TRUE				TRUE
		TRUE				
			21:14273780-14276110			
				10:1350528	Unclassified_Cell_type_specific	

high-CpG:152642548-152643122		X:152642116-152643793			
		X:7039011	X:7047374	Promoter_Associated	
	TRUE	10:15395984-15396156			
	TRUE				TRUE
		10:130721263-130721442			
high-CpG:48669455-48669580		3:48668161-48669750			TRUE
		14:9871008	14:9964101	Unclassified_Cell_type_specific	
	TRUE				TRUE
					TRUE
	TRUE				
			4:15438646	Promoter_Associated	
		10:52104506-52104872			
		11:50213790-50214562			
		13:110955733-110955940			
	TRUE				TRUE
		6:37724232	6:37616081	Unclassifie	TRUE
		11:134113808-134114029			
		X:1778814	X:1787855	Unclassifie	TRUE
DMR			19:2426968	Promoter_Associated	
		5:1298490-	5:1245883-	Unclassified_Cell_type_specific	
	TRUE				
			16:9014804	Unclassifie	TRUE
		1:3936272-3937103			
	TRUE				
		1:1134421-	1:1143366-	Unclassified	
		8:1127898-1128090			
	TRUE		2:15280356	Unclassified	
		16:54424008-54424459			
	TRUE				
		5:12643692	5:12640822	Promoter_Associated	
		6:31758628-31759271			TRUE
	TRUE	5:33971926-33974929			TRUE
		7:1921498-1921997			
		5:14069062	5:14071030	NonGene_Associated_Cell_type_specific	
		16:3386419	16:3395627	Unclassified	
RDMR					
		17:1336914	17:1390020	Unclassifie	TRUE

			3:16964957	Unclassified_Cell_type_specific	
	TRUE				TRUE
					TRUE
	TRUE		14:9573174	Unclassifie	TRUE
	TRUE				
	TRUE				
	TRUE				
			7:15041247	Unclassified_Cell_type_specific	
CDMR					
	TRUE				TRUE
		10:131099468-131099634			
		16:54424008-54424459			
		6:53327553-53327664			
	TRUE				
	TRUE				
		6:31758628-31759271			TRUE
	TRUE				TRUE
	TRUE		12:7657743	Unclassifie	TRUE
	TRUE				
		5:41905161	5:41869237	Promoter_A	TRUE
		16:74120585-74121613			
	TRUE				TRUE
			17:1350226	Unclassified_Cell_type_specific	
	TRUE				
		10:134683294-134683373			
		Y:9993394-9995882			
RDMR		5:140510147-140510412			
DMR		16:797343-	16:857066-	Promoter_Associated	
DMR					TRUE
		12:7407112	12:7578433	Promoter_A	TRUE
		19:10608142-10608475			
	TRUE				TRUE
		16:8864135	16:9011399	Unclassifie	TRUE
	TRUE				
	TRUE				

		TRUE				
high-CpG:4	DMR		19:4374734	19:3905561	Unclassified_Cell_type_specific	
	DMR		19:4374734	19:3905561	Unclassified_Cell_type_specific	
	RDMR		1:21912172	1:22105535	Unclassified_Cell_type_specific	
				1:22611120	Promoter_Associated	
		TRUE				TRUE
						TRUE
		TRUE				TRUE
			8:1190061-1190843			
				6:14980558	Promoter_Associated	
			2:48698290-48698489			
		TRUE				
		TRUE				TRUE
		TRUE				
	RDMR					
			8:1352353-1352973			
						TRUE
		TRUE				
		TRUE				
			7:157040922-157041050			
			20:5794750	20:5851445	Promoter_Associated	
		TRUE				TRUE
		TRUE				
			12:9987169-9987420			
		TRUE				
		TRUE		12:5220672	Unclassified_Cell_type_specific	
		TRUE	1:24586928	1:24780263	Unclassified_Cell_type_specific	
		TRUE				TRUE
			2:241483257-241483999			
			21:17906100-17907568			
			10:130169838-130169903			
		TRUE				TRUE
		TRUE				
			6:17018010	6:17033847	Unclassified_Cell_type_specific	

	TRUE				TRUE
	TRUE				
		16:5589121	16:5733323	Promoter_Associated	
low-CpG:66535459-66535968					TRUE
		4:3012371-	4:3042808-	Unclassifie	TRUE
		1:245635916-245636504			
		5:179521007-179521358			
		1:11683842-11684064			TRUE
		11:5915571-5916673			
		2:231563153-231564304			
		12:1312035	12:1326369	Unclassified	
	TRUE				
	TRUE				
	TRUE				TRUE
	TRUE				
	TRUE				
	TRUE	11:967036-967596			
		7:15462861	7:15499803	Promoter_A	TRUE
	TRUE	X:3943276	X:3954780	Unclassifie	TRUE
	TRUE	16:85897103-85897210			TRUE
			7:72722237	Promoter_Associated	
		1:93685860-93687203			
		12:7043585	12:7214800	Unclassified	
		10:124568117-124568601			
	TRUE	4:7895813-7895900			TRUE
	TRUE				
		X:1498170	X:1500669	Unclassified	
		16:85924979-85925325			
					TRUE
low-CpG:40491405-40491505			13:4159309	Promoter_Associated	
	TRUE				
	TRUE				TRUE
	TRUE				
	TRUE				
		16:54352096-54352465			
		6:33046358	6:32938253	Promoter_A	TRUE
	TRUE	5:177480770-177481520			
	TRUE	16:86049026-86049099			TRUE
			17:7400286	Unclassified	

	TRUE				
	TRUE				
	TRUE	10:8600654	10:8601655	Unclassified	
	TRUE	10:661382-661629			TRUE
	TRUE				
	TRUE		15:5252664	Unclassified_Cell_type_specific	
		1:181188404-181189153			
	TRUE				
		16:3553171-3554602			
	TRUE				
		5:140743108-140743439			
		22:1779867	22:1941969	Promoter_Associated	
	TRUE				TRUE
	TRUE				
	TRUE				TRUE
		6:16288897-16289468			
		6:32597721-32598106			
	TRUE				
	TRUE				
		1:15042790	1:15216100	Unclassified	
					TRUE
	TRUE				
		5:2306129-2306261			
	TRUE				TRUE
		3:48673170-48676671			
low-CpG:40492407-40492441					
					TRUE
			8:28174766	Unclassified_Cell_type_specific	
TR	TRUE				
		Y:9273327-9276468			

		TRUE	2:232959406-232961623			
		TRUE				
		TRUE				
		TRUE				TRUE
low-CpG:45620911-45		TRUE				
		TRUE				TRUE
			10:134569986-134570682			
			1:4670706-4672480			TRUE
	DMR	TRUE	8:73079763	8:72917248	Unclassified	
		TRUE				
		TRUE				
		TRUE		16:1405147	Unclassified_Cell_type_specific	
	DMR					
			X:19049688-19051204			TRUE
	DMR			20:1049210	Unclassifie	TRUE
			6:88813982-88814582			
			19:1476003-1476854			
		TRUE				
			19:60427408-60427866			
		TRUE				TRUE
		TRUE	20:5686080	20:5742678	Unclassifie	TRUE
		TRUE	7:51506502-51506886			
	CDMR	TRUE				
		TRUE				
		TRUE				
			1:115627601-115627972			
		TRUE				TRUE
		TRUE		19:1932392	Unclassified_Cell_type_specific	
		TRUE		6:47210252	Unclassifie	TRUE
			13:110079031-110079185			
high-CpG:43626444-43626725			X:43626244-43626729			TRUE
			6:74119872-74121192			
		TRUE				TRUE

high-CpG:2336155-2336354			4:2336137-	4:2365586-	Promoter_A	TRUE
				8:14565794	Unclassified_Cell_type_specific	
		TRUE	17:77225200-77226112			
			1:159615484-159615766			
			16:6624416	16:6768693	Unclassified_Cell_type_specific	
				6:36514594	Promoter_Associated	
		TRUE				
		TRUE	16:63663015-63663216			
		TRUE				
		TRUE				
			6:29963281-29964497			
		TRUE				TRUE
		TRUE		16:2743777	Promoter_A	TRUE
		TRUE				TRUE
			14:80948984-80949129			
			2:97724226	2:98357000	Unclassified	
			1:1218644-	1:1229152-	Unclassified_Cell_type_specific	
			19:1054014	19:1067908	Promoter_Associated	
			18:14737517-14738527			
			7:55484366	7:55516729	Unclassified_Cell_type_specific	
			14:97698959-97699140			
			6:30052410	6:29944009	Unclassified	
			2:202191857-202192202			TRUE
	CDMR			19:1458690	Unclassified_Cell_type_specific	
		TRUE				
			11:1904136-1904468			
			17:1921968	17:1973641	Unclassified	
			8:21961332-21962032			TRUE
		TRUE				
		TRUE				
		TRUE				TRUE
high-CpG:8	DMR		16:8702284	16:8849615	Unclassifie	TRUE
				5:76010566	Unclassified	
			12:123495637-123496063			
						TRUE

		TRUE				
		TRUE				
			17:976144-976703			
low-CpG:45623193-45623284						
	RDMR			20:6190485	Promoter_Associated	
			10:6223443	10:6182425	Unclassifie	TRUE
		TRUE				
			8:38152597	8:38033369	Promoter_Associated	
				7:1976191-	Gene_Associated_Cell_type_specific	
			12:5269462	12:5440863	Unclassified_Cell_type_specific	
		TRUE				TRUE
			10:133831283-133831712			
		TRUE	16:73789677-73789858			
	DMR					
		TRUE				TRUE
			1:146268327-146268471			
		TRUE				
		TRUE	6:33352687	6:33244505	Promoter_A	TRUE
		TRUE				
						TRUE
		TRUE				TRUE
			12:123789398-123789721			TRUE
			13:113982203-113984182			
			X:1290299	X:1299250	Promoter_A	TRUE
				6:15021171	Unclassified_Cell_type_specific	
			13:113815937-113817261			TRUE
		TRUE				
	DMR	TRUE		1:23490797	Promoter_A	TRUE
			13:110272598-110272864			
			1:92187307-92187842			
		TRUE				
		TRUE				TRUE
			8:1459544-1459640			

		20:3322601	20:3376225	Unclassifie	TRUE
	TRUE				
	TRUE	13:100904175-100904481			
	TRUE	19:1407058-1408457			
	TRUE				
		8:41826859-41826897			
	TRUE				
		7:14965092	7:15001985	Promoter_A	TRUE
		8:43250370-43250704			
high-CpG:152890670-152890809		X:1528892	X:1532372	Promoter_Associated	
		6:32740137-32741093			
high-CpG:70390666-70390763		X:7039011	X:7047374	Promoter_Associated	
		1:245870260-245870330			
					TRUE
	TRUE				TRUE
		2:12921078	2:12949373	Unclassified	
		1:145015270-145019201			
	TRUE		11:1033104	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				TRUE
	TRUE				
		19:49552498-49553009			
low-CpG:18296595-18296635					
	TRUE				TRUE
		6:25990231	6:25882232	Unclassified_Cell_type_specific	
high-CpG:56898700-56901058		20:56898137-56901134			
CDMR					
RDMR					
		10:131302609-131302807			
	TRUE				
		16:86146015-86146508			
		16:8856517	16:9003806	Promoter_Associated	
		11:1914070	11:1957728	Unclassified_Cell_type_specific	
		16:45160178-45161124			

			6:30146876-30147422			
			11:678091-678160			
		TRUE				
			12:34438799-34439219			
		TRUE				
high-CpG:87024209-87024827			16:8702284	16:8849615	Unclassifie	TRUE
			1:3907905-3907965			
			10:43166274-43166581			
		TRUE				TRUE
				3:10812534	Unclassifie	TRUE
						TRUE
			12:50759685-50760347			
			5:140517008-140517950			
			19:5494135	19:5024956	Unclassifie	TRUE
	RDMR		5:140481840-140482036			
		TRUE				
			6:30146876	6:30039021	Unclassified_Cell_type_specific	
			5:140461401-140461552			
			6:28554754-28554928			
	RDMR			11:9781200	Promoter_A	TRUE
		TRUE				TRUE
	CDMR		13:3494724	13:3604920	Unclassified_Cell_type_specific	
			7:55484207-55484246			
			X:31194369-31195063			TRUE
		TRUE				
			11:6029148	11:6053430	Unclassified_Cell_type_specific	
			22:15247375-15248168			
		TRUE				
	CDMR					
		TRUE				
			5:178616933-178617265			
			1:205909376-205909873			
			22:44859555-44859953			TRUE
			15:98911653-98916980			
		TRUE				
	DMR					
	CDMR			22:5063091	Promoter_Associated	

	TRUE				
	TRUE				
	TRUE				
	TRUE	7:101342879-101342925			
	TRUE				
	TRUE				
	TRUE				TRUE
					TRUE
		Y:12584321-12585052			
		1:15963548	1:16136865	Promoter_Associated	
		Y:9973136-9976273			
	TRUE				
		15:6030363	15:6251638	Unclassified_Cell_type_specific	
		X:1532789	X:1536256	Promoter_Associated	
	TRUE				TRUE
	TRUE				
	TRUE				
	TRUE		16:7514268	Promoter_A	TRUE
	TRUE				TRUE
		10:7682834	10:7715887	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				
	TRUE	3:15286143	3:15310982	Promoter_A	TRUE
		6:44350915	6:44243254	Unclassifie	TRUE
		12:123505409-123505504			TRUE
		12:1167982	12:1183135	Unclassified	
			6:25882232	Unclassified_Cell_type_specific	
	TRUE		1:23514734	Unclassifie	TRUE
	TRUE				TRUE
CDMR	TRUE	7:27130345-27130623			
		21:43131036-43131361			TRUE
		12:94775848-94776044			
		2:62710469-62711273			
		2:238695394-238695478			
	TRUE				

			17:3795284	17:4070000	Unclassifie	TRUE
		TRUE				TRUE
			16:87865454-87865634			
		TRUE				TRUE
	DMR		19:4374734	19:3905561	Unclassified_Cell_type_specific	
			Y:13525400-13525632			
		TRUE		20:4794041	Promoter_Associated	
						TRUE
			5:140575067-140576014			
			8:49589647	8:49426450	Unclassified	
		TRUE	3:197354390-197354672			TRUE
			4:141610503-141610728			
			16:8808313	16:8955540	Promoter_Associated	
				1:20212963	Promoter_Associated	
low-CpG:131790207-131790302				5:13176227	Promoter_A	TRUE
		TRUE	7:2735268-2735882			
			12:5267480	12:5438870	Unclassifie	TRUE
	RDMR					
		TRUE				
		TRUE				
high-CpG:71268487-71268667			X:7126717	X:7135121	Unclassifie	TRUE
			18:75724121-75725551			
		TRUE				
			6:28691806-28692367			
			Y:2862947-2864321			
			5:1921228-1921360			
	RDMR			16:8884929	Promoter_Associated	
			10:43202507-43203024			
		TRUE				
		TRUE	6:31383697	6:31275659	Promoter_Associated	
			10:5420830	10:5453738	Unclassified_Cell_type_specific	
			12:52662286-52662412			
			18:75609295-75611022			
		TRUE				
			6:30565161	6:30457785	Promoter_Associated	
			19:1021950-1022967			TRUE

		TRUE				TRUE
		TRUE	6:15928038	6:15936041	Unclassified_Cell_type_specific	
low-CpG:45616923-45620319			17:45618098-45618204			
			19:6427603-6428127			TRUE
			1:24616638	1:24810001	Promoter_A	TRUE
	DMR		16:797343-	16:857066-	Promoter_Associated	
			Y:21146854-21147440			
			19:45112900-45113712			
		TRUE				
			Y:2717850-2718354			
		TRUE				
			2:19835797	2:19865050	Unclassified_Cell_type_specific	
	CDMR					
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE				
	RDMR		13:111908421-111908509			
		TRUE		17:7467919	Unclassified_Cell_type_specific	
			6:149819443-149819882			
		TRUE				TRUE
			16:12099723-12099938			
			11:7651315	11:7694753	Unclassifie	TRUE
			17:7532149	17:7770650	Unclassified	
		TRUE				
						TRUE
		TRUE		3:19350544	Unclassifie	TRUE
		TRUE				
high-CpG:32874249-32874279			15:32874149-32874293			
			X:100070280-100070976			
		TRUE				
		TRUE				
			6:28691806-28692367			

	TRUE				TRUE
DMR		4:183299209-183299758			
			22:3078256	Promoter_Associated	
		5:177320194-177320403			
					TRUE
	TRUE				TRUE
		12:1312039	12:1326369	Unclassified	
RDMR					
	TRUE				
	TRUE				
	TRUE				TRUE
					TRUE
	TRUE				
		8:12032292-12032425			
	TRUE				
	TRUE				TRUE
		11:118347497-118348218			
	TRUE				
	TRUE	16:85897103-85897210			TRUE
		X:1067581	X:1068712	Promoter_A	TRUE
		9:13751758	9:13837743	Unclassified_Cell_type_specific	
		16:14287909-14288258			
					TRUE
	TRUE				
		11:650455-650756			
		1:146267690-146268062			
	TRUE				
			6:30652289	Promoter_Associated	
	TRUE		8:14501493	Promoter_Associated	
	TRUE	1:22163326	1:22356664	Unclassifie	TRUE
	TRUE	7:2735268-2735882			
		8:82693479-82693581			

			16:2689363-2689545			
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE				TRUE
Body			8:144739725-144740102			
		TRUE				TRUE
			1:180935814-180935962			
		TRUE				
		TRUE				
		TRUE	17:78564079-78564182			TRUE
			17:4959827-4960719			
		TRUE				
			16:54352096-54352465			
				3:19738498	Unclassified	
		TRUE				
		TRUE				
			1:24616638	1:24810001	Promoter_A	TRUE
		TRUE				
			X:117134262-117135204			TRUE
		TRUE				TRUE
			8:11574947-11576445			
			19:2201561-2205121			
	RDMR					
		TRUE	11:7642778	11:7674972	Unclassifie	TRUE
		TRUE				
	DMR					
			5:166286611-166287056			
			16:87503364-87504191			
			4:788539-788984			
		TRUE				
		TRUE				TRUE
			7:94863327-94864148			
	RDMR					

TRUE				
TRUE				
TRUE				
TRUE				
	7:966520-966876			
	13:18590636-18590913			
	7:4877518-4877648			
TRUE				
TRUE				
TRUE				TRUE
TRUE				
TRUE				
	1:2836655-2837169			
	16:86759041-86759147			TRUE
	3:46593312-46593673			
TRUE				
TRUE				
	1:1122746-1123119			
TRUE		7:94953742	Unclassified_Cell_type_specific	
TRUE				
	2:24136806	2:24171947	Unclassified_Cell_type_specific	
	17:146634-147040			
TRUE		14:7113195	Unclassified_Cell_type_specific	
TRUE	7:44968637	7:45002681	Gene_Asso	TRUE
TRUE				
	16:87575659-87576319			
	10:3128406-3128559			
	10:6223443	10:6182425	Unclassifie	TRUE
TRUE				
TRUE				
	17:68148128-68148894			

			5:37871638-37872038			
		TRUE				TRUE
		TRUE				
			1:215373298-215373391			
			5:812268-8	5:759115-7	Promoter_Associated	
		TRUE		21:4524590	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				TRUE
Body		TRUE				TRUE
				22:2290140	Unclassified	
			16:1662756-1663445			
		TRUE				
		TRUE				TRUE
	CDMR		10:1192822	10:1192920	Unclassified_Cell_type_specific	
		TRUE				
			8:98679639-98679710			
			16:8870996-8871310			
				6:14980558	Promoter_Associated	
			10:124568117-124568601			
		TRUE				TRUE
			7:44130446-44130511			
		TRUE				
	RDMR					
		TRUE				
		TRUE				
			X:19049688-19051204			TRUE
			17:16533561-16534841			TRUE
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
	CDMR					
			22:4485955	22:4648076	Gene_Asso	TRUE
	RDMR					TRUE
		TRUE				

	TRUE				
	TRUE				
RDMR					
			16:1107110	Unclassified	
	TRUE				
		6:116992886-116993085			
	TRUE				
RDMR					TRUE
		6:170396446-170397034			
	TRUE				
		11:28356486-28356639			
		17:17962729-17965569			
		16:2103965-2105062			
	TRUE				TRUE
	TRUE				
RDMR		1:21912172	1:22105535	Unclassified_Cell_type_specific	
	TRUE				TRUE
	TRUE		10:7959592	Unclassifie	TRUE
	TRUE				
	TRUE	16:87412471-87412626			
		3:31469529-31469817			
		12:3818212-3818881			
	TRUE				TRUE
	TRUE		17:7883030	Unclassifie	TRUE
	TRUE				TRUE
		10:131659956-131660208			
	TRUE				
		7:783980-784248			
					TRUE
	TRUE				
		17:78453539-78453803			
	TRUE				
DMR					
	TRUE				
	TRUE		1:8298554-	Unclassifie	TRUE
	TRUE				

				11:7729992	Promoter_Associated_Cell_type_specific	
		TRUE				
			3:127742893-127744324			
		TRUE				TRUE
			19:33909806-33910556			
		TRUE	11:13940491-13942898			
		TRUE				
	RDMR		14:37141499-37141625			
		TRUE	13:99315010-99315041			
			10:134310230-134310469			
low-CpG:2	DMR			19:2426968	Promoter_Associated	
		TRUE				
			16:2689363-2689545			
			19:4117678	19:3648480	Unclassified_Cell_type_specific	
			6:127838005-127839014			
			3:49211587-49212481			TRUE
high-CpG:1022208-1022237			19:1021950-1022967			TRUE
		TRUE				
			17:72423403-72423737			
			11:2373780-2374770			
;3'UTR;3'UTR						
		TRUE				TRUE
		TRUE				
			9:95662932-95663357			
		TRUE	4:183404886-183404938			
		TRUE				TRUE
			6:28691806-28692367			
			19:57144129-57144598			
		TRUE	19:12974371-12974549			
			5:14459533-14459754			TRUE
		TRUE		11:6738291	Promoter_Associated	
		TRUE		17:7531534	Promoter_A	TRUE
						TRUE

		TRUE	13:1124554	13:1134071	Unclassified_Cell_type_specific	
			2:19807170	2:19836354	Promoter_Associated	
		TRUE				TRUE
			7:158405321-158406086			
		TRUE		8:14242706	Unclassified	
				17:7689571	Unclassifie	TRUE
		TRUE				
high-CpG:7202007-7202159			Y:7201522-7203224			
		TRUE		2:10963655	Unclassified_Cell_type_specific	
			5:18057788	5:18064368	Promoter_A	TRUE
			2:96500050	2:97135938	Unclassifie	TRUE
			16:3039294	16:3048563	Promoter_Associated	
			22:4072456	22:4239415	Promoter_A	TRUE
			4:132863643-132874411			
			2:238312494-238312699			
		TRUE				TRUE
	RDMR					
			6:15617263-15617406			
		TRUE				
			12:131513941-131514010			
			4:57756539-57756872			
			2:108988889-108989018			
		TRUE				
		TRUE				
high-CpG:152889815-152891067			X:1528892	X:1532361	Promoter_Associated	
			16:69365734-69365791			
		TRUE				
		TRUE				
	DMR		1:23297488	1:23490797	Promoter_A	TRUE
			4:187197861-187197986			
		TRUE	17:75537843-75537970			
			4:1964415-1964648			
		TRUE				TRUE

	TRUE		2:18906446	Unclassifie	TRUE
RDMR		7:42862748-42863222			
	TRUE				TRUE
		11:58354815-58355069			
	TRUE				
	TRUE		6:32828471	Unclassifie	TRUE
	TRUE				
RDMR		5:140542922-140543132			
		Y:2862947-	Y:2803970-	Promoter_Associated_Cell_type_specific	
					TRUE
	TRUE				
	TRUE				
					TRUE
		15:4328030	15:4549231	Promoter_Associated	
		8:43250768-43251681			
	TRUE				
		15:20472546-20473432			
	TRUE				TRUE
	TRUE		3:72570098	Unclassified_Cell_type_specific	
RDMR					
		14:103463852-103464987			
	TRUE				
		3:12464897	3:12316680	Unclassifie	TRUE
	TRUE				TRUE
		8:2109552-2109752			
			3:18708577	Promoter_A	TRUE
	TRUE				

			2:132301583-132304753			
		TRUE				
			17:15592984-15593853			
		TRUE				
	DMR		3:13894408	3:13921221	Unclassified_Cell_type_specific	
				22:4645113	Unclassified_Cell_type_specific	
				1:8940283-	Promoter_A	TRUE
				1:28573041	Promoter_Associated_Cell_type_specific	
			19:62322014-62322504			
		TRUE				
				5:12640822	Promoter_Associated	
		TRUE				TRUE
			16:781349-781599			
high-CpG:1803163-1803168			19:1802402	19:1851730	Gene_Associated_Cell_type_specific	
		TRUE				TRUE
			11:118347497-118348218			
				2:24096566	Unclassified_Cell_type_specific	
		TRUE		17:3339047	Promoter_A	TRUE
		TRUE		5:90458591	Unclassified	
		TRUE				TRUE
		TRUE				TRUE
		TRUE				
			14:90952908-90953134			
		TRUE				TRUE
		TRUE		1:24085489	Unclassified	
		TRUE				
			Y:21975960-21976252			
			16:1064314-1064392			
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
			3:48285377-48285969			
		TRUE				
	RDMR	TRUE	16:53922249-53923466			
	DMR	TRUE	X:1523298	X:1526763	Unclassifie	TRUE

	TRUE				
		2:2274688-2275078			TRUE
	TRUE				
		7:27112636	7:27146398	Unclassifie	TRUE
			14:1055551	Unclassified_Cell_type_specific	
RDMR					
RDMR					
	TRUE				
	TRUE				
		16:84885038-84885288			
	TRUE		11:1269436	Unclassified	
	TRUE				TRUE
DMR	TRUE	14:9222309	14:9315268	Gene_Associated	
	TRUE				
	TRUE				
	TRUE				TRUE
		10:135327969-135349068			TRUE
	TRUE				TRUE
	TRUE				
		12:129736524-129737489			
	TRUE				
	TRUE				
		10:135193172-135193295			
	TRUE				TRUE
DMR		11:11598435-11600432			
	TRUE				
		16:83077491-83077545			
	TRUE				TRUE
		7:158226624-158226697			
	TRUE				TRUE
	TRUE				
		11:65566571-65567680			
		11:5915571-5916673			
		9:44341918-44342506			

	CDMR					
	DMR		5:17838323	5:17845037	Unclassified	
		TRUE				TRUE
		TRUE				TRUE
			17:77109616-77110886			TRUE
	DMR			19:5564407	Unclassified_Cell_type_specific	
			5:72741666-72741729			
			10:26720588-26721319			
		TRUE				
high-CpG:32320553-32320560			20:3232036	20:3285659	Unclassified_Cell_type_specific	
		TRUE		7:15006729	Promoter_Associated	
			16:8867118	16:9014347	Promoter_Associated	
		TRUE				
		TRUE				
high-CpG:16511100-16511275			17:16510388-16511665			TRUE
		TRUE				TRUE
			17:77554730-77555513			TRUE
		TRUE				
		TRUE				
			6:167709075-167709617			
			6:157024951-157025036			TRUE
						TRUE
			8:10382005	8:10375081	Unclassifie	TRUE
			6:28665649-28666050			
	RDMR					
		TRUE				
			12:129534319-129534640			
		TRUE		14:5052784	Unclassifie	TRUE
	DMR		19:2089787	19:2110573	Unclassified	
		TRUE				
		TRUE	19:6355921	19:5886745	Unclassifie	TRUE
		TRUE				
			14:103621480-103622181			
			16:64994079-64994502			
			17:78128613-78128750			
		TRUE				
			1:2110741-	1:2120661-	Promoter_Associated	
		TRUE				
			4:183838618-183838719			
						TRUE
				19:3478537	Unclassified_Cell_type_specific	
	DMR		19:2201561-2205121			

		TRUE		13:1115218	Unclassified	
		TRUE				TRUE
			17:113233-113291			
				11:6714158	Promoter_Associated	
high-CpG:46643592-46643750			12:4664335	12:4835693	Promoter_Associated	
			4:4188067-4188302			
		TRUE				
			17:4959827	17:5019434	Unclassified_Cell_type_specific	
				19:1888886	Unclassified_Cell_type_specific	
			X:3759130	X:3770633	Promoter_A	TRUE
			7:75983343	7:76144928	Unclassifie	TRUE
		TRUE				
			2:242341224-242342371			
		TRUE	10:1248836	10:1248937	Unclassified_Cell_type_specific	
			1:2256412-	1:2266588-	Unclassifie	TRUE
			X:4863311	X:4874820	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
		TRUE				
	DMR		12:52670831-52671021			
		TRUE				TRUE
	RDMR					
			X:1005497	X:1006627	Promoter_A	TRUE
			16:85301440-85301473			
		TRUE				
		TRUE				
	RDMR		10:719846-	10:729535-	Unclassifie	TRUE
			18:75393037-75393432			TRUE
			8:47648048-47648634			
		TRUE	16:85352837-85352995			
			16:8723373	16:8870523	Promoter_Associated	

	TRUE				TRUE
		17:7784869	17:8025473	Promoter_A	TRUE
	TRUE				TRUE
RDMR	TRUE	8:73079763	8:72917248	Unclassified	
		11:6608306	11:6632663	Unclassifie	TRUE
		16:6515754	16:6660045	Gene_Associated_Cell_type_specific	
			16:869378-	Unclassified_Cell_type_specific	
	TRUE				
		12:1313553	12:1328454	Unclassified_Cell_type_specific	
RDMR		17:35961983-35962222			TRUE
					TRUE
		6:168660620-168661776			
		2:79954809-79954944			
	TRUE		17:7486837	Unclassifie	TRUE
	TRUE				
	TRUE				TRUE
		4:1299140-	4:1308999-	Gene_Associated_Cell_type_specific	
	TRUE	17:56145-57232			
	TRUE				
		6:30146876	6:30039021	Unclassified_Cell_type_specific	
		5:33971926-33974929			
	TRUE				TRUE
	TRUE	6:106541047-106541152			
		16:8751652	16:8898883	Unclassifie	TRUE
		5:140692011-140692726			
	TRUE				TRUE
	TRUE				TRUE
	TRUE	5:2968063-2968305			
high-CpG:17050238-17	TRUE	17:1704949	17:1710846	Promoter_Associated	
		16:8699971	16:8847276	Unclassifie	TRUE
	TRUE	10:7231765	10:7264758	Promoter_Associated	
DMR	TRUE	7:43255207-43255473			
	TRUE	6:42802850	6:42693951	Promoter_Associated	
		Y:20188289-20189188			
	TRUE				TRUE

	TRUE	10:1506980-1507313			
		8:23016342	8:22960212	Unclassifie	TRUE
	TRUE	13:110084970-110085283			TRUE
					TRUE
	TRUE				
	TRUE				
		7:72485870	7:72847767	Unclassified	
			3:14968491	Unclassified_Cell_type_specific	
		6:13968070-13968736			
					TRUE
	TRUE	8:97225950	8:97157132	Unclassifie	TRUE
					TRUE
	TRUE				TRUE
	TRUE				
	TRUE	16:80077545-80078091			
	TRUE		2:19240299	Unclassified_Cell_type_specific	
	TRUE				
DMR			16:4951828	Unclassifie	TRUE
	TRUE				
	TRUE				
			6:32634123	Unclassifie	TRUE
		16:2570393-2570440			TRUE
	TRUE				
	TRUE				
		6:30018182-30019314			
		6:169566319-169567869			
		11:66641728-66644000			
			2:10308935	Unclassified	
			1:19384307	Unclassified_Cell_type_specific	
			4:16589840	Unclassifie	TRUE
		10:6547117	10:6580072	Unclassifie	TRUE
	TRUE				TRUE
	TRUE				
		7:63672852-63672965			
		17:2116695	17:2122620	Promoter_Associated	
	TRUE				
			7:15082029	Gene_Associated	

		TRUE		6:15573912	Unclassified	
high-CpG:49063088-49		TRUE	22:4906099	22:5072108	Unclassified_Cell_type_specific	
			8:9045471-9046812			
			13:23780099-23780951			
		TRUE				
			10:11128131-11128286			
			7:105383476-105383952			
			6:42802850	6:42695456	Promoter_Associated_Cell_type_specific	
			6:30018182-30019314			
			16:2854195	16:2863422	Unclassifie	TRUE
		TRUE				
	RDMR		5:140559654-140559838			
			6:31758628-31759271			TRUE
			12:182853-183533			
			Y:6174065-6175048			
			20:61872487-61873541			
			5:1298490-	5:1245883-	Unclassified_Cell_type_specific	
		TRUE	2:23205575	2:23234728	Unclassified	
		TRUE				
		TRUE				
			8:1892437-1892848			
			18:73092883-73093027			
			7:157768103-157768566			
	RDMR					
		TRUE				
	RDMR					
			X:50228771-50231419			
		TRUE	7:151196528-151196733			
				6:17040439	Unclassifie	TRUE
			4:4278622-4280785			
			6:32597721-32598106			

			11:118347497-118348218			
			10:43821016-43821276			
			6:101953488-101953918			
			17:1899670	17:1954748	Unclassified_Cell_type_specific	
			12:131379030-131379181			
		TRUE				
		TRUE				
				16:1019949	Promoter_Associated	
				21:4536077	Promoter_Associated	
			8:37124707-37124778			
				1:7022332-	Unclassifie	TRUE
	RDMR	TRUE				
			3:47179672	3:47205401	Promoter_Associated	
			16:84586849-84587111			
low-CpG:4	DMR	TRUE				
high-CpG:103297721-103298057			X:1032975	X:1034104	Promoter_Associated	
	CDMR					
	CDMR					
		TRUE				
		TRUE				TRUE
			3:185761583-185763825			
			5:140510514-140510878			
			X:20043986-20045776			TRUE
		TRUE				
			20:3600980	20:3653335	Unclassified_Cell_type_specific	
			6:29756034	6:29648152	Unclassified_Cell_type_specific	
	RDMR	TRUE				
		TRUE				
			16:82524815-82525310			
				11:7729992	Promoter_Associated_Cell_type_specific	
		TRUE		20:4794041	Promoter_Associated	
			16:2842846-2843536			
			1:1876274-1876730			TRUE
	CDMR	TRUE				TRUE
		TRUE				

		7:2045496-2045535			
	TRUE				
		11:3130668-3130734			
	TRUE				
		4:17465862	4:17442201	Unclassified_Cell_type_specific	
	TRUE				
		X:118870542-118871280			
	TRUE				TRUE
		12:131248474-131248848			
		2:242596960-242601502			
			17:7286021	Unclassified	
		22:17365548-17365700			
	TRUE				
			20:6145612	Unclassified_Cell_type_specific	
		4:931966-932075			
		10:43166274-43166581			
		16:8867598	16:9014804	Unclassifie	TRUE
	TRUE				
	TRUE				
		2:241545581-241545649			
		12:5266988	12:5438269	Unclassified	
		12:11591500-11591808			
		4:7487082-7487193			TRUE
CDMR		18:22385283-22385470			
RDMR		16:3170611-3170854			
DMR					
		9:68198989-68200105			
		19:21056822-21057273			
			11:3034391	Promoter_Associated	
			17:7426061	Promoter_Associated	
		6:101953488-101953918			
		1:41122304-41122914			
		6:30146876	6:30039021	Unclassified_Cell_type_specific	
		11:64350766-64351788			
	TRUE				
		16:85210650-85210717			

			13:112582234-112584308			
	RDMR	TRUE	18:11137249-11137905			
		TRUE		6:30781901	Unclassifie	TRUE
		TRUE				
		TRUE	7:156917601-156918338			
			X:139420640-139421248			
		TRUE		16:3188866	Unclassified_Cell_type_specific	
						TRUE
high-CpG:65870189-65870965			16:6587043	16:6731232	Promoter_Associated	
	RDMR					
	DMR		X:101887346-101888193			TRUE
		TRUE				
low-CpG:44083485-44083617				22:4570459	Promoter_Associated_Cell_type_specific	
			Y:21327301-21327921			
		TRUE				
			X:1529379	X:1532845	Promoter_Associated	
		TRUE				TRUE
		TRUE				TRUE
			16:828935-829013			
			13:112678805-112679391			
			16:1433541-1433885			
		TRUE				TRUE
			1:1216966-	1:1226844-	NonGene_Associated	
		TRUE				
			2:242637379-242638530			
		TRUE				TRUE
				1:63249154	Promoter_A	TRUE
		TRUE				
			16:1991606-1991892			
				11:6060782	Unclassifie	TRUE
			3:115438258-115438940			
		TRUE				TRUE
			X:9977833	X:9989119	Unclassifie	TRUE

		16:1068225-1070379			
			6:36409083	Unclassified	
	TRUE				TRUE
	TRUE				
	TRUE				
	TRUE		4:83383286	Gene_Associated	
	TRUE				TRUE
	TRUE				TRUE
	TRUE				
	TRUE				
	TRUE		18:5456520	Unclassified	
	TRUE				
		11:7066709-7068093			
	TRUE				
		19:7843050	19:7936400	Unclassified	
		7:966520-966876			
		13:112044797-112045718			
		10:52104506-52104872			
	TRUE				TRUE
		2:239839541-239839614			
	TRUE				TRUE
		18:75379223-75379816			
		16:3134639	16:3143869	Unclassifie	TRUE
		X:1525171	X:1528639	Promoter_Associated	
	TRUE		1:23463445	Unclassified	
		17:3304309	17:3596910	Promoter_Associated	
		16:87517609-87517775			
		20:207316-	20:259877-	Unclassifie	TRUE
			1:53661271	Unclassified_Cell_type_specific	
DMR		16:797343-	16:857066-	Promoter_Associated	
			1:15630673	Unclassifie	TRUE
	TRUE		2:11009065	Unclassified_Cell_type_specific	
		11:9291680	11:9327531	Promoter_Associated	
	TRUE				TRUE
		1:89762399-89763630			

			11:70827848-70827964			
						TRUE
			8:1776465-	8:1789024-	Unclassified_Cell_type_specific	
				18:4782405	Promoter_Associated	
			4:7351763-7352078			
		TRUE				TRUE
		TRUE	17:7668339	17:7906793	Unclassified	
		TRUE	19:51079168-51082097			
			5:2695995-2696300			
		TRUE				
				11:1847720	Unclassified_Cell_type_specific	
		TRUE				
	RDMR		2:784598-784820			
		TRUE	7:51506502-51506886			
		TRUE	6:846242-846311			
				8:14415829	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
			12:52662286-52662412			
		TRUE				TRUE
		TRUE				
low-CpG:6768866-6769051				12:6898385	Promoter_Associated_Cell_type_specific	
			Y:19697854-19699393			
			X:1687447	X:1696425	Unclassified	
			12:131482196-131483014			
			17:9747457-9747518			
		TRUE				
		TRUE				
			19:61380215-61380289			
			12:7916632-7917175			
				22:4513584	Unclassified_Cell_type_specific	
			X:5336611	X:5334917	Unclassifie	TRUE
		TRUE				TRUE
				19:1531076	Unclassifie	TRUE
			19:564006-	19:613054-	Unclassifie	TRUE
			16:86430794-86431462			
		TRUE				
		TRUE				TRUE
			18:75393037-75393432			TRUE

	TRUE				
	TRUE				
	TRUE				
	TRUE				
		11:69987361-69988166			
		19:862527-864703			
		2:10219842-10219938			TRUE
			7:15471895	Promoter_Associated	
	TRUE				
		2:132826303-132827776			
		5:1647215-	5:1594141-	Unclassified	
	TRUE		22:1767210	Unclassified_Cell_type_specific	
	TRUE				
		6:26705975-26706295			
	TRUE		4:18502114	Unclassifie	TRUE
		14:100765920-100766306			
		16:86942677-86943106			
		19:5555358	19:5086164	Promoter_A	TRUE
		5:1515562-	5:1462557-	Unclassified_Cell_type_specific	
		4:7863548-7864479			
	TRUE	2:1806714-1806798			
			1:43388607	Promoter_A	TRUE
	TRUE				
	TRUE	20:6135515	20:6188462	Unclassified_Cell_type_specific	
	TRUE		4:54554506	Unclassifie	TRUE
	TRUE				
	TRUE				TRUE
		3:44597250-44597870			
	TRUE				
high-CpG:23850494-23850574		14:2384979	14:2477937	Promoter_A	TRUE
		2:66518302-66518513			
	TRUE				TRUE
	TRUE				

		TRUE				
		TRUE				
	DMR					
		TRUE		6:32828471	Unclassifie	TRUE
			11:1411938-1412047			TRUE
		TRUE				TRUE
		TRUE	14:92767777-92768346			TRUE
		TRUE				
			14:2384979	14:2477937	Promoter_Associated	
			14:101491810-101492403			
		TRUE		5:10489934	Unclassified_Cell_type_specific	
			16:2168145-2169420			TRUE
				1:1905045-	Unclassified_Cell_type_specific	
		TRUE				
low-CpG:66535459-66535968						TRUE
		TRUE				
			16:86907152-86907407			TRUE
		TRUE				
		TRUE				TRUE
		TRUE	22:48560032-48560175			
	DMR	TRUE	16:8734866	16:8882190	Unclassified_Cell_type_specific	
				3:9850204-	Promoter_Associated	
		TRUE				
	DMR		X:35847635-35848043			
			14:1034638	14:1043945	Unclassified_Cell_type_specific	
			14:101584647-101584780			
				11:1847720	Unclassified_Cell_type_specific	
	RDMR					
	RDMR					
		TRUE	8:141317755-141317850			TRUE
			5:18060377	5:18067031	Promoter_A	TRUE
		TRUE		2:86092748	Unclassified_Cell_type_specific	
			14:101491810-101492403			
	RDMR	TRUE				TRUE
		TRUE				TRUE

	TRUE		7:13889694	Unclassifie	TRUE
	TRUE				TRUE
		5:140194253-140194696			TRUE
	TRUE				TRUE
					TRUE
		5:140606553-140607551			
		5:140202168-140203355			
		13:113357009-113357511			
		14:75515840-75515927			
	TRUE				TRUE
		7:64532157-64532390			
		11:6029148	11:6053430	Unclassified_Cell_type_specific	
		10:37146970-37147046			
		7:14965092	7:15001985	Promoter_A	TRUE
		1:44341598	1:44569014	Unclassified_Cell_type_specific	
	TRUE				
		11:1978491	11:2021875	Unclassifie	TRUE
		5:1563459-1563685			
	TRUE				
					TRUE
	TRUE	1:6008531-6009081			TRUE
		1:24492651	1:24685920	Unclassifie	TRUE
		5:178255330-178256144			TRUE
			7:15896543	Unclassified_Cell_type_specific	
		14:98795201-98795266			
CDMR			8:14430248	Unclassified_Cell_type_specific	
		2:1637173-1637241			TRUE
	TRUE	13:2316750	13:2426972	Unclassified_Cell_type_specific	
			15:7828678	Unclassified_Cell_type_specific	
		5:140154758-140155185			
RDMR					
		1:2128802-2129313			TRUE
		X:3058070	X:3067064	Promoter_Associated	
		2:1766934-1767295			
		6:25990231	6:25882232	Unclassified_Cell_type_specific	
		7:63680432-63680633			
RDMR		18:27558012-27558481			

			8:145038085-145038969			
		TRUE	7:44071272	7:44104823	Unclassified_Cell_type_specific	
low-CpG:14060861-14060868						
		TRUE	3:15286143	3:15310982	Promoter_A	TRUE
			8:22603167-22609289			
		TRUE		19:1838532	Unclassified	
		TRUE				
		TRUE				
		TRUE		17:7531534	Promoter_A	TRUE
			17:78563038-78563471			
			1:35358919	1:35586503	Unclassified	
				1:16076907	Unclassified_Cell_type_specific	
		TRUE	12:5054401	12:5225758	Unclassified_Cell_type_specific	
	RDMR	TRUE				
		TRUE	12:6940819	12:7069947	Promoter_Associated	
			16:3284907-3285821			
	RDMR	TRUE	15:9468884	15:9688770	Unclassified	
				1:1141523-	Unclassified	
		TRUE				
Body;Body;Body;Body;		TRUE				
		TRUE				
	RDMR		18:490266-491437			
			17:78562801-78562839			
		TRUE	1:12531830-12532404			TRUE
			X:4884459	X:4895762	Promoter_Associated	
		TRUE				TRUE
			11:1868391	11:1872730	Unclassifie	TRUE
	RDMR					
			6:15025078-15025325			
	DMR		1:147120546-147122480			
			4:137535812-137536269			
		TRUE				
			16:1127619-1127891			
			2:238459480-238459662			
		TRUE	7:158035361-158035696			
high-CpG:8	DMR		16:8702284	16:8849615	Unclassifie	TRUE

high-CpG:140195990-140195991			5:140195238-140196330			
			15:24586288-24586368			
		TRUE	1:2326211-2326652			
		TRUE				
			13:99381768-99381906			
			7:63290110-63290261			
			8:61789200-61789841			TRUE
		TRUE				
			16:85023581-85024013			
		TRUE				
		TRUE				TRUE
			12:131814613-131814768			
		TRUE				TRUE
			6:170574045-170574367			
			2:3301290-3301343			
			6:161019998-161020574			
				22:3803224	Unclassifie	TRUE
Body;Body;	DMR	TRUE		12:2749514	Unclassifie	TRUE
		TRUE				
			11:60457635-60458748			
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
			12:44698097-44698426			
		TRUE		2:65527731	Unclassifie	TRUE
			12:7407112	12:7578433	Promoter_A	TRUE
			17:70828078-70828374			
		TRUE	16:2885534	16:2894763	Unclassifie	TRUE
			2:786317-786561			
			1:10962711	1:10982570	Promoter_Associated	
				11:1292455	Unclassified	
			19:1802402	19:1851730	Gene_Associated_Cell_type_specific	
		TRUE				TRUE
		TRUE	7:12117667-12118080			
			6:170320318-170320386			
		TRUE				TRUE

		TRUE		16:1101220	Unclassified	
			1:32513298-32514277			
		TRUE				
high-CpG:40325113-40325219			X:4032468	X:4043971	Promoter_Associated_Cell_type_specific	
			6:30146876-30147422			
			13:111975175-111975333			
		TRUE				
			4:141610503-141610728			
		TRUE				
			4:1388072-1389020			
		TRUE				
		TRUE				
		TRUE				
		TRUE		3:48256958	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
Body;Body		TRUE				
			6:31758628-31759271			TRUE
	CDMR					
			6:66861241-66861534			
		TRUE				
			X:7728137	X:7739487	Promoter_Associated_Cell_type_specific	
		TRUE				TRUE
			12:123396921-123397341			
		TRUE	17:7708051	17:7946635	Unclassified_Cell_type_specific	
		TRUE				TRUE
			17:640106-640303			TRUE
		TRUE				TRUE
			2:96868983	2:97504771	Promoter_Associated	
			5:18019040	5:18025759	Promoter_Associated	
		TRUE				
			10:134522678-134522873			
		TRUE				TRUE
			1:243910446-243910585			
			10:131555818-131555909			
high-CpG:23849959-23		TRUE	14:2384979	14:2477937	Promoter_	TRUE

			16:862035-862176			
high-CpG:18353623-18353678			X:1835273	X:1844361	Promoter_Associated	
		TRUE				
			21:45877524-45878968			
	DMR		20:4336861	20:4393518	Unclassifie	TRUE
		TRUE	7:51507008-51507193			
		TRUE		11:1227273	Unclassifie	TRUE
		TRUE				TRUE
			1:2255728-2256292			TRUE
	RDMR		1:21912172	1:22105535	Unclassified_Cell_type_specific	
		TRUE				
	RDMR		16:53922249-53923466			
				1:19209894	Unclassified	
			6:142451071-142451687			
			5:468419-468926			TRUE
			7:158226624-158226697			
			Y:7201522-7203224			
		TRUE				
			2:139376221-139376865			
		TRUE				
				16:8903590	Unclassified_Cell_type_specific	
			10:133811667-133812089			
			19:21652508-21652856			
			10:134889798-134891072			TRUE
high-CpG:109390586-109391090			12:1093902	12:1109056	Promoter_Associated	
		TRUE				
	DMR					
			16:15397059-15397565			TRUE
00;TSS1500;TSS1500;TSS1500;TSS1500;TSS1500						

			17:4959827-4960719			
			9:13947611	9:14035582	Promoter_Associated	
	RDMR		7:42863313-42863516			
high-CpG:104953158-104953223			X:104952804-104953968			
			16:79524242-79524377			TRUE
		TRUE				TRUE
high-CpG:17665483-17665670			X:1766499	X:1775486	Promoter_Associated	
		TRUE	4:709207-709936			TRUE
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
			4:14738414	4:14716461	Unclassified	
		TRUE				
			17:78492275-78492570			
	RDMR		18:75347293-75348877			TRUE
			16:8702284	16:8849615	Unclassifie	TRUE
			5:1921228-1921360			
		TRUE				TRUE
		TRUE				
	DMR		X:101801594-101801764			TRUE
						TRUE
			11:118347497-118348218			
		TRUE				
		TRUE	6:846242-846311			
	RDMR					
			5:179961262-179961486			
		TRUE				TRUE
		TRUE		1:9778849-	Promoter_A	TRUE
		TRUE		5:17221630	Unclassified_Cell_type_specific	
low-CpG:71182497-71182645			5:71182511	5:71146539	Unclassified	
			5:140516321-140516553			
		TRUE				

		10:121760972-121761407			
		4:188047265-188047919			
	TRUE				
	TRUE				
	TRUE				TRUE
	TRUE				
	TRUE				TRUE
					TRUE
		12:182853-183533			
	TRUE				TRUE
					TRUE
	TRUE				
		7:3101060-	7:3134385-	Promoter_Associated	
	TRUE				
		13:113209435-113209563			
					TRUE
	TRUE				
		1:2097076-	1:2107285-	Unclassified_Cell_type_specific	
	TRUE				
		16:5422305-5422393			
		1:41075951-41076931			
	TRUE				TRUE
			12:5441416	Unclassified_Cell_type_specific	
		5:33971926-33974929			
	TRUE	16:8864135	16:9011399	Unclassifie	TRUE
		2:231763473-231763977			TRUE
		2:1459778-1460638			
		16:87061768-87062172			TRUE
RDMR		2:17266064	2:17295256	Unclassified	
	TRUE		6:15556890	Unclassifie	TRUE
		10:27679004-27679231			
	TRUE				TRUE
high-CpG:144881510-144881652		8:14487978	8:14480896	Unclassifie	TRUE
		21:4567193	21:4684780	Unclassified_Cell_type_specific	

		8:14218167	8:14211254	Unclassified_Cell_type_specific	
		6:6559669-	6:6614106-	Promoter_Associated_Cell_type_specific	
	TRUE				
		11:69066425-69067032			
CDMR					
					TRUE
	TRUE				TRUE
	TRUE		7:11138171	Unclassifie	TRUE
		11:305780-	11:316185-	Unclassified_Cell_type_specific	
	TRUE		3:15310982	Promoter_A	TRUE
		8:14473085	8:14465959	Promoter_Associated	
	TRUE				
	TRUE				TRUE
	TRUE	16:28177954-28178142			
	TRUE				TRUE
	TRUE				TRUE
	TRUE		3:71353876	Promoter_Associated_Cell_type_specific	
		6:30018182-30019314			
		6:29756034	6:29648152	Unclassified_Cell_type_specific	
		3:134985252-134985788			
		14:102028935-102029135			
		15:95997026-95997363			
			19:1660659	Promoter_Associated	
RDMR		16:5287308	16:5431549	Unclassified	
	TRUE				
		16:2788434-2789425			
		17:77554730-77555513			TRUE
RDMR		7:96489900-96490205			
					TRUE
RDMR			15:4073118	Unclassified_Cell_type_specific	
	TRUE				TRUE
		1:246820114-246820193			
	TRUE				
	TRUE				
		1:246921654-246922226			

				1:2981822-	Unclassified_Cell_type_specific	
		TRUE				
			16:833058-833359			
		TRUE				TRUE
		TRUE		6:13948210	Promoter_Associated	
		TRUE				
			16:3182624-3182913			
		TRUE				
			1:40370964-40371787			
				16:1266744	Unclassifie	TRUE
				16:5802852	Promoter_A	TRUE
		TRUE				
			8:2065370-2065770			
			19:5555358	19:5086164	Promoter_A	TRUE
	RDMR		3:61210816	3:61235609	Promoter_A	TRUE
			1:2110741-	1:2120661-	Promoter_Associated	
		TRUE				
		TRUE				
			5:140510514-140510878			
				22:2438403	Unclassified_Cell_type_specific	
	RDMR		4:151722915-151723039			
			6:30187118-30187260			
			4:930644-931149			
			17:78640438-78641204			
			8:969492-969694			
		TRUE				
			2:853889-855091			
;3'UTR;3'UTR						
			19:5059756	19:4590561	Unclassifie	TRUE

	TRUE				
	TRUE				TRUE
	TRUE				TRUE
		19:803661-	19:853008-	Unclassified_Cell_type_specific	
		5:150669786-150670237			
		15:4327990	15:4549231	Promoter_Associated	
	TRUE		16:2743777	Promoter_A	TRUE
	TRUE				
RDMR	TRUE		11:6524645	Unclassifie	TRUE
		13:112044797-112045718			
	TRUE				
	TRUE	4:3361892-3362193			
		16:78249855-78250018			
DMR	TRUE		21:3531983	Promoter_A	TRUE
	TRUE				
		15:76419131-76419326			
		17:7459795	17:7708550	Unclassified	
		X:1008635	X:1012687	Unclassified_Cell_type_specific	
		16:87752657-87755442			
	TRUE				
		7:158501889-158502582			
	TRUE	11:6714011	11:6738291	Promoter_Associated	
		17:5391974	17:5656456	Unclassified	
	TRUE	11:6107934	11:6132224	Unclassifie	TRUE
RDMR					
		10:134184231-134184285			
	TRUE				
	TRUE				
	TRUE		5:11229423	Unclassifie	TRUE
		19:260379-262041			TRUE

RDMR	TRUE	9:21995288	9:22004989	Unclassified	
	TRUE				
	TRUE				
		4:697790-698309			
DMR		16:797343-	16:857066-	Promoter_Associated	
			6:29980416	Unclassifie	TRUE
	TRUE				TRUE
		7:157848494-157849074			
		13:108590495-108591803			
	TRUE				
	TRUE				TRUE
		5:1647215-	5:1594141-	Unclassifie	TRUE
	TRUE				
	TRUE				
		22:4072456	22:4239415	Promoter_	TRUE
		6:1629416-1629583			
	TRUE				
	TRUE		2:11245648	Unclassifie	TRUE
	TRUE				
	TRUE				TRUE
			1:15662625	Promoter_Associated	
		X:3058070	X:3067064	Promoter_Associated	
	TRUE				
	TRUE				TRUE
RDMR			11:7813122	Unclassified	
			16:8897707	Unclassified_Cell_type_specific	
		6:30146876	6:30039021	Unclassified_Cell_type_specific	
	TRUE				TRUE
		10:135122966-135123922			
		8:7066344-7067067			TRUE
		6:1500022-	6:1554396-	Unclassified	
	TRUE				
	TRUE	19:6355921	19:5886745	Unclassifie	TRUE
		10:8228548	10:8229523	Promoter_	TRUE

			17:685619-686127			TRUE
			7:157566580-157566824			
			6:32171573	6:32063883	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
			18:73987320-73987862			
		TRUE	1:25119411-25119510			TRUE
			7:11764137	7:11785412	Unclassifie	TRUE
			11:17206456-17206889			
		TRUE		7:30387618	Promoter_Associated	
		TRUE		20:6233048	Unclassified	
			16:3284907-3285821			
		TRUE				TRUE
			16:906865-907608			
	RDMR					
			2:11032703	2:11096911	NonGene_	TRUE
	RDMR		6:31478935	6:31370048	Promoter_Associated	
			X:8711266-	X:8751090-	Unclassified_Cell_type_specific	
				5:18059323	Unclassified_Cell_type_specific	
		TRUE				
			5:41905161	5:41869237	Promoter_	TRUE
			16:1947391-1947592			
			8:12594138-12594305			
		TRUE	8:10360988	8:10354046	Promoter_	TRUE
			8:10592792-10592898			
			13:112290865-112291143			
		TRUE				
		TRUE				
			19:5394052	19:4924850	Unclassified_Cell_type_specific	
high-CpG:53940607-53		TRUE	2:53940281-53940994			
high-CpG:20628155-20628346			17:20628177-20628666			TRUE
		TRUE	19:12973171-12974155			TRUE
			19:295096-	19:343550-	Promoter_Associated	
		TRUE				
			2:12828548	2:12856783	Promoter_Associated	
		TRUE		2:21918127	Unclassified_Cell_type_specific	
		TRUE				

high-CpG:53139936-53140327			X:5313968	X:5312279	Promoter_Associated	
			7:65607473	7:65971010	Unclassifie	TRUE
			19:62322014-62322504			
			6:169068259-169068645			
			Y:9273327-9276468			
		TRUE				
high-CpG:48669455-48669580			3:48668161-48669750			
			4:141720034-141720186			
			1:2415711-	1:2425223-	Unclassified_Cell_type_specific	
			6:116992886-116993085			
		TRUE				
		TRUE				
		TRUE				
		TRUE	19:5944656-5945161			
			19:42972817-42973503			
low-CpG:45620911-45		TRUE		17:4826647	Unclassified_Cell_type_specific	
			19:51217490-51218424			
		TRUE		6:13429941	Unclassified_Cell_type_specific	
			19:51217490-51218424			
			13:111678238-111678490			
		TRUE	17:78607298-78607384			TRUE
				3:58317740	Promoter_A	TRUE
	CDMR					TRUE
			16:87516521-87517035			TRUE
	RDMR			17:4489845	Unclassifie	TRUE
		TRUE				
			19:4357795	19:3888513	Promoter_Associated	
		TRUE				
			4:133115855-133117899			
		TRUE		11:9543286	Unclassified	
		TRUE	2:706344-706390			
high-CpG:54477068-54477152			20:5447674	20:5504314	Promoter_Associated	
			12:1844001-1845198			
		TRUE	5:66497845	5:66461684	Promoter_A	TRUE
				5:13541621	Unclassifie	TRUE
		TRUE				

		TRUE				
		TRUE		5:34452214	Unclassified_Cell_type_specific	
			6:3237890-3238395			
			11:1848614	11:1891168	Unclassified	
		TRUE	6:31383697	6:31275659	Promoter_Associated	
			12:1901537	12:2031291	Unclassified_Cell_type_specific	
		TRUE		6:37521003	Unclassifie	TRUE
		TRUE	7:51507008-51507193			
	RDMR		4:41574982-41575648			
high-CpG:1647574-1647630			5:1647215-	5:1594141-	Unclassifie	TRUE
	DMR	TRUE	6:42802850	6:42693951	Promoter_Associated	
				2:27712053	Promoter_Associated	
			7:156029297-156029459			
			X:1517497	X:1519988	Promoter_Associated	
		TRUE				
						TRUE
			16:86610226-86610841			
			6:2460291-2460337			
		TRUE				
			17:20684599-20685423			
			5:13863143-13863325			
			22:16911216-16911504			TRUE
			Y:21146854-21147440			
high-CpG:108860553-108860887			4:10886029	4:10864040	Promoter_Associated	
		TRUE				TRUE
	CDMR			7:96652298	Unclassified_Cell_type_specific	
		TRUE				
			6:157024951-157025036			TRUE
			19:19609129-19610168			TRUE
		TRUE				
		TRUE				TRUE
				10:4547425	Unclassified_Cell_type_specific	
		TRUE				
		TRUE	5:399201-399262			
		TRUE				
			13:110860650-110860690			
			1:33544734	1:33772859	Unclassifie	TRUE
			6:169431698-169431905			
		TRUE	17:74623279-74623394			TRUE

	TRUE				TRUE
		5:2440743-2441039			
		1:41122304-41122914			
			2:95786866	Promoter_Associated	
		19:56299023-56299723			
		3:10124751-10125032			
	TRUE				
	TRUE				
					TRUE
CDMR					
	TRUE				
	TRUE				
	TRUE				TRUE
	TRUE				
	TRUE		8:12664973	Unclassifie	TRUE
		5:468419-468926			TRUE
		11:2541019-2541528			
	TRUE				TRUE
DMR		16:359773-	16:420186-	Unclassified	
	TRUE				TRUE
	TRUE	17:77890521-77890615			TRUE
			1:1110981-	Unclassified_Cell_type_specific	
			7:27210758	Unclassified_Cell_type_specific	
	TRUE				
		1:24616638	1:24810001	Promoter_A	TRUE
CDMR					
	TRUE				
		17:7901096	17:7959558	Unclassified	
	TRUE				
		11:3491675-3491782			
		10:132926055-132926135			
	TRUE				
	TRUE				
		5:140569886-140570834			
DMR		4:183299209-183299758			
	TRUE				
		19:2475387-2476578			
		X:1188705	X:1189867	Promoter_Associated	
	TRUE				
	TRUE				

			X:7075253	Promoter_A	TRUE
	TRUE				
	TRUE		3:8704347-	Unclassified	
	TRUE	7:157802820-157802914			
		16:34261532-34262285			
	TRUE				
	TRUE				
		16:8375965	16:8520206	Unclassified_Cell_type_specific	
		8:1352353-1352973			
	TRUE				
CDMR	TRUE				
	TRUE				
		1:22631328	1:22824671	Promoter_Associated	
		5:1298490-	5:1245883-	Unclassified_Cell_type_specific	
			16:1083713	Promoter_Associated	
	TRUE				
		12:122323813-122323871			
	TRUE	5:399201-399262			
RDMR		15:94691602-94691653			
	TRUE	16:876204-	16:936988-	Unclassifie	TRUE
	TRUE	8:48838464-48838608			
	TRUE	8:48838464-48838608			
	TRUE				
		12:68054954-68055822			
	TRUE				
		16:31346393-31347062			TRUE
		X:119017364-119019009			
	TRUE		4:40674903	Promoter_A	TRUE
		8:10382005	8:10375081	Unclassifie	TRUE
		5:140605877-140606072			
	TRUE				
	TRUE		16:1092209	Unclassifie	TRUE

	DMR		1:16877351	1:17004520	Unclassified_Cell_type_specific	
			12:1481777	12:1492653	Promoter_Associated	
		TRUE				TRUE
		TRUE				
			8:1902374-1902484			
				20:5566455	Unclassifie	TRUE
	RDMR	TRUE	6:106541047-106541152			
			6:29963281	6:29855507	Promoter_Associated_Cell_type_specific	
		TRUE				
		TRUE				
		TRUE		6:52217248	Unclassifie	TRUE
		TRUE				
	DMR		16:4807591	16:4951828	Unclassifie	TRUE
		TRUE	1:94333233-94333472			
			19:335009-335437			TRUE
		TRUE				
			17:641730-	17:695136-	Gene_Associated_Cell_type_specific	
		TRUE				
low-CpG:230371855-230372344						
		TRUE				TRUE
			17:1493098	17:1546348	Unclassified_Cell_type_specific	
				1:14780648	Promoter_Associated_Cell_type_specific	
		TRUE				
			6:30146876-30147422			
			12:123151105-123151476			
		TRUE	19:55881374-55882046			
			6:28805742-28805992			
		TRUE	7:100994464-100994954			TRUE
		TRUE	6:29799114	6:29691677	Promoter_A	TRUE
			7:57328345-57328731			
		TRUE				
			17:2779507	17:3077072	Promoter_Associated	
		TRUE				
	RDMR	TRUE	6:106540627-106540959			
			2:176644547-176645189			

		X:13957532-13958230			
		10:126676504-126676753			
		14:7302732	14:7395733	Promoter_Associated	
		11:69943787-69943867			
		19:21056822-21057273			
		16:8379984	16:8524243	Unclassified_Cell_type_specific	
	TRUE				TRUE
RDMR		7:96488014	7:96649922	Unclassified_Cell_type_specific	
		2:23142319	2:23171475	Unclassifie	TRUE
		1:240286910-240287549			
	TRUE				
	TRUE				
		7:156002008-156002141			
	TRUE				
	TRUE				
		Y:18960006-18967102			
DMR	TRUE				TRUE
		16:11174693-11175712			
			1:16490698	Unclassifie	TRUE
	TRUE				TRUE
		21:4654087	21:4771638	Unclassified_Cell_type_specific	
	TRUE				
		9:12264480	9:12360481	NonGene_Associated	
	TRUE				
		16:87694386-87695627			
	TRUE				TRUE
		16:77097455-77097694			
		4:187817679-187818178			
		17:70077444-70077517			TRUE
RDMR					
	TRUE		3:47388500	Unclassifie	TRUE
		19:3141872-3142391			

				2:36824476	Promoter_Associated	
		TRUE				TRUE
		TRUE				
			17:76549665-76549888			
						TRUE
		TRUE				TRUE
high-CpG:4	DMR		19:4374734	19:3905561	Unclassified_Cell_type_specific	
		TRUE	17:7634986	17:7873517	Unclassifie	TRUE
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
		TRUE		10:1001743	Promoter_Associated	
		TRUE				TRUE
			12:2209182-2210061			
			17:3427747	17:3702371	Unclassified	
		TRUE				TRUE
	DMR		X:1492814	X:1495302	Unclassifie	TRUE
		TRUE				
		TRUE				
		TRUE		3:71545445	Unclassified_Cell_type_specific	
		TRUE				
			22:17365548-17365700			
high-CpG:154824631-1		TRUE	4:15482453	4:15460508	Promoter_A	TRUE
		TRUE	7:324396-324823			TRUE
			18:75235239-75235644			
			17:3527755	17:3802338	Promoter_Associated	
			7:158481825-158483260			
			16:8379984	16:8524243	Unclassified_Cell_type_specific	
		TRUE				TRUE
		TRUE				TRUE
			12:129596119-129596232			
		TRUE				
			X:9713457-9715284			TRUE

high-CpG:56606686-56606866			X:5660667	X:5658946	Promoter_Associated_Cell_type_specific	
		TRUE	7:157320895-157320987			
		TRUE				TRUE
			16:83753593-83754007			TRUE
			13:111678238-111678490			
		TRUE		5:14671649	Unclassified_Cell_type_specific	
		TRUE		6:17865880	Unclassifie	TRUE
			16:12525972-12526258			
			7:2928696-2928939			
		TRUE				TRUE
	CDMR		21:4416111	21:4533655	Promoter_Associated	
			12:123789398-123789721			TRUE
		TRUE	4:1036976-1037115			TRUE
	RDMR		X:132945748-132946333			
		TRUE				TRUE
			4:184172054-184172228			
			20:3232036	20:3285659	Unclassified_Cell_type_specific	
	CDMR			21:4533655	Promoter_Associated	
low-CpG:24061717-24061901				19:2426968	Promoter_Associated	
		TRUE				TRUE
		TRUE				
			16:2956075	16:3016087	Unclassified_Cell_type_specific	
		TRUE				TRUE
			4:183299209-183299758			
		TRUE				
	RDMR		4:183300391-183300556			
	RDMR					
		TRUE				TRUE
			1:209718930-209719355			
		TRUE				TRUE
		TRUE				
Body;Body;Body;Body;Body;Body;Body;Body						
	RDMR	TRUE				TRUE
		TRUE	12:123473058-123473131			
		TRUE				
		TRUE				
			1:35358919	1:35586503	Unclassified	

		TRUE				
			1:228316886-228317003			
				20:2492946	Promoter_Associated_Cell_type_specific	
			Y:13525835-13526872			
						TRUE
		TRUE		3:12486018	Unclassified	
		TRUE				
	RDMR					
			12:9446720	12:9594139	Promoter_Associated_Cell_type_specific	
		TRUE				TRUE
			4:2336137-	4:2365586-	Promoter_A	TRUE
high-CpG:56897306-56897703			20:5689685	20:5746385	Promoter_Associated	
			1:24840737	1:24968041	Promoter_Associated_Cell_type_specific	
			6:28691806-28692367			
						TRUE
			12:110104579-110104697			
		TRUE				TRUE
			2:1865061-1865166			
		TRUE				
			13:110861552-110862023			
						TRUE
			10:8228548	10:8229523	Promoter_A	TRUE
			2:112612152-112614875			
			15:21897829-21898105			
Body;Body;Body;Body		TRUE				TRUE
		TRUE				
		TRUE				
	RDMR					
		TRUE				
high-CpG:30817247-30817405			X:3081680	X:3090681	Promoter_Associated	
	RDMR	TRUE				
	DMR		1:205736261-205736726			

	TRUE	7:1919019-	7:1952382-	Unclassifie	TRUE
		21:14273780-14276110			
		16:1879219-1879307			
	TRUE				TRUE
	TRUE	7:36160361-36161014			
	TRUE				
	TRUE				TRUE
RDMR		10:719846-	10:729535-	Unclassifie	TRUE
		2:48698290-48698489			
RDMR			2:11403675	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				
		8:142207391-142208778			
		Y:20188289-20189188			
	TRUE				TRUE
		12:105872769-105873066			
		7:25958137	7:25990129	Promoter_Associated	
	TRUE				
	TRUE		8:16637342	Unclassifie	TRUE
CDMR					
		8:12502643-12503472			
		1:2833966-	1:2844236-	Unclassified_Cell_type_specific	
	TRUE				TRUE
		11:68306808-68307114			
	TRUE				
DMR					
	TRUE				
	TRUE				
	TRUE				TRUE
	TRUE	16:86999710-87000837			TRUE
	TRUE				
			1:11174018	Promoter_Associated_Cell_type_specific	
		7:590867-591217			
	TRUE				
		19:62322014-62322504			
	TRUE	12:100127370-100128269			
	TRUE				

		TRUE				
	CDMR					
				20:4721476	Unclassified	
	CDMR					
		TRUE				
			1:226821657-226823404			
		TRUE		15:5782530	Unclassified_Cell_type_specific	
Body;Body		TRUE				TRUE
			7:137999314-138000282			
high-CpG:23850494-23850574			14:2384979	14:2477937	Promoter_A	TRUE
			8:2020830-	8:2033678-	Unclassifie	TRUE
	RDMR			5:12640822	Promoter_Associated	
			16:86610226-86610841			
			5:25226198-25226865			
			5:140195238-140196330			
		TRUE				
			Y:2862947-2864321			
		TRUE				
	RDMR		7:48096271	7:48128066	Promoter_Associated	
		TRUE				
			16:88173306-88175452			TRUE
						TRUE
high-CpG:87024209-87024827			16:8702284	16:8849615	Unclassifie	TRUE
		TRUE				
		TRUE				
low-CpG:100902942-100903160						
			17:1043352-1043568			
			Y:18967273-18967809			
		TRUE				
high-CpG:19918865-19919101			X:1991844	X:2000834	Promoter_Associated	
		TRUE				
		TRUE				
		TRUE				
		TRUE	X:30236183-30237627			

	TRUE				
		4:188117556-188131610			
			X:7047374	Promoter_Associated	
	TRUE				
	TRUE		7:13435450	Unclassified_Cell_type_specific	
			6:29814895	Unclassifie	TRUE
	TRUE				
		12:31161327-31165315			
		2:23221600	2:23250728	Unclassifie	TRUE
	TRUE				
		2:119780379-119780450			
		7:94863327-94864148			
	TRUE	11:127826872-127827032			
			3:14098758	Promoter_Associated	
	TRUE				TRUE
	TRUE				TRUE
high-CpG:40325113-40325219		X:4032468	X:4043971	Promoter_Associated_Cell_type_specific	
		5:33971926	5:33937484	Unclassified_Cell_type_specific	
	TRUE		8:12561689	Unclassified_Cell_type_specific	
RDMR		22:44859555-44859953			TRUE
	TRUE				TRUE
		19:12237772-12238274			
		9:45622931-45623303			
	TRUE				
		6:31346870	6:31238958	Promoter_Associated	
		15:20472546-20473432			
	TRUE				
	TRUE				
	TRUE		8:68418417	Unclassified	
	TRUE		6:56200754	Unclassified_Cell_type_specific	
	TRUE	6:4023770-4024913			
	TRUE				
		1:115198972-115199456			

	RDMR					
		TRUE				
		TRUE				
		TRUE				
	RDMR	TRUE				
		TRUE				
						TRUE
		TRUE				
			X:149612254-149613323			TRUE
high-CpG:102663050-102663493			14:102662833-102663676			TRUE
	CDMR	TRUE	1:206063625-206063801			TRUE
	DMR					
high-CpG:102096815-102097257			10:1020961	10:1021057	Promoter_Associated	
			7:65607473	7:65971010	Unclassified_Cell_type_specific	
		TRUE		5:13383907	Unclassifie	TRUE
			6:3238561-3238807			
			1:1180386-1180701			
			11:1815028	11:1858538	Unclassified_Cell_type_specific	
			1:6448638-6449057			TRUE
			14:103384882-103384993			
			14:100605184-100605216			
		TRUE				
		TRUE				TRUE
	RDMR					
			2:20732770	2:20870838	Unclassified_Cell_type_specific	
		TRUE				
			1:6946070-	1:7022332-	Unclassifie	TRUE
		TRUE				TRUE
		TRUE				TRUE
		TRUE				
		TRUE				TRUE
			6:30146876-30147422			
		TRUE				TRUE
			12:7672271-7672723			
		TRUE				TRUE
	CDMR					
	DMR		X:1066365	X:1067498	Unclassified_Cell_type_specific	
				5:14070985	NonGene_Associated_Cell_type_specific	
			20:6075980	20:6129013	Gene_Associated_Cell_type_specific	

			19:6090701	19:5621506	Unclassifie	TRUE
		TRUE				TRUE
		TRUE	7:51506502-51506886			
		TRUE	11:127826872-127827032			
			7:157973092-157973258			
high-CpG:2336155-2336354			4:2336137-	4:2365586-	Promoter_A	TRUE
		TRUE				
		TRUE				TRUE
			13:49150420-49150939			
		TRUE				
			6:32659866-32660444			
			12:2209182-2210061			
		TRUE				
		TRUE		2:47053724	Unclassified_Cell_type_specific	
high-CpG:45595889-45596176			X:4559501	X:4571055	Unclassified_Cell_type_specific	
		TRUE				
			12:52670831-52671021			
	DMR		X:101792707-101793695			TRUE
			6:159943849-159944135			
	CDMR					
			19:55653568-55654369			
			2:20732770	2:20870838	Unclassified_Cell_type_specific	
			17:32374657-32374988			
high-CpG:31805554-31806443			6:31805255	6:31696696	Promoter_Associated	
		TRUE				TRUE
			8:143663493-143664313			
		TRUE				
		TRUE				
		TRUE		6:24936899	Unclassified	
			17:74187836-74187962			
		TRUE				
		TRUE				
			1:39752981	1:39981388	Unclassified_Cell_type_specific	
		TRUE				
			13:111678547-111678797			
			2:3652785-3653183			
		TRUE				

				7:15082374	Unclassified_Cell_type_specific	
			3:10124751-10125032			
			13:112032968-112033729			
	RDMR		11:60436884-60437169			
			7:157742880-157743253			
				12:1108873	Promoter_Associated	
	DMR	TRUE	14:7588892	14:7681866	Unclassifie	TRUE
			19:59730038-59730299			
		TRUE				
		TRUE				TRUE
		TRUE	7:157802167-157802580			
			1:2013320-	1:2023570-	Unclassified_Cell_type_specific	
	DMR	TRUE	15:94703711-94705181			TRUE
		TRUE		7:87555911	Unclassified_Cell_type_specific	
		TRUE				TRUE
				14:7644532	Unclassifie	TRUE
		TRUE				
			12:52662286-52662412			
low-CpG:116434145-11		TRUE				
		TRUE				
	RDMR					
			2:176724663-176725225			
	RDMR					TRUE
			4:191141974-191143118			
		TRUE				
	RDMR	TRUE	1:232734082-232734127			
			5:12643692	5:12640822	Promoter_Associated	
		TRUE				
		TRUE				
	CDMR			2:19817453	Promoter_Associated	
		TRUE	17:78564079-78564182			TRUE
		TRUE		15:4026888	Gene_Associated_Cell_type_specific	
			17:139290-139830			
			17:18494258-18494398			
		TRUE	12:1298690	12:1313028	Promoter_A	TRUE
			1:32513298-32514277			
			X:9392530-9394487			

			20:828429-	Unclassified_Cell_type_specific	
RDMR		2:119315620-119315769			
	TRUE				TRUE
		7:4209472-4209557			
		10:135191246-135192212			TRUE
		19:51217490-51218424			
	TRUE				
	TRUE				
	TRUE				
	TRUE	2:26478108	2:26624556	Unclassifie	TRUE
	TRUE				TRUE
		12:5266343	12:5437711	Unclassified_Cell_type_specific	
		7:56209901-56210987			
					TRUE
	TRUE				TRUE
		11:7481703	11:7513875	Unclassified_Cell_type_specific	
	TRUE				TRUE
		X:1485206	X:1487135	Promoter_A	TRUE
DMR			10:1349732	Unclassified_Cell_type_specific	
		5:177365888-177367084			TRUE
	TRUE				
RDMR		12:113619245-113619773			
		6:21869267-21869805			
			1:1555166-	Unclassifie	TRUE
		7:47506024-47506094			
		9:78981891	9:79791844	Promoter_Associated	
		1:6443838-6444506			
	TRUE				TRUE
	TRUE				TRUE
	TRUE	3:75787263-75787751			

		TRUE				
			10:129034200-129034297			
			1:32513298-32514277			
			X:4874324	X:4885850	Promoter_	TRUE
;5'UTR;TSS200				3:11410219	Unclassified	
		TRUE				
			7:55377540-55380490			
			3:49211587-49212481			TRUE
			5:140569886-140570834			
high-CpG:140098928-140099071			X:1400983	X:1402708	Promoter_	TRUE
			7:266289-266810			
		TRUE	12:1298690	12:1313028	Promoter_	TRUE
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
			X:70067331-70067727			
	CDMR					
	RDMR					
		TRUE				
		TRUE				
Body;Body;Body;Body		TRUE				TRUE
			8:142850110-142850288			
		TRUE				TRUE
				6:13924230	Unclassified	
			16:86610226-86610841			
				2:12845312	Unclassifie	TRUE
		TRUE				
		TRUE				
		TRUE				
			2:241230241-241230452			
		TRUE				
			6:79395797-79396295			

RDMR	TRUE				
		6:166776046-166776085			
	TRUE				
		10:7899682-7899777			
		13:18816586-18817215			TRUE
RDMR		4:183300631-183301663			
		10:134184231-134184285			
	TRUE				
	TRUE				
RDMR			5:80595138	Unclassified	
	TRUE				TRUE
		7:157973501-157973547			
	TRUE				
		7:131073360-131073439			
					TRUE
	TRUE				TRUE
		5:1544550-	5:1491578-	Unclassified_Cell_type_specific	
		1:245747809-245748574			
		5:1909552-1910665			
		11:66898529-66898607			
	TRUE				
	TRUE				
		6:169566319-169567869			
RDMR			4:83718165	Unclassified_Cell_type_specific	
	TRUE				
		8:39291177-39291296			
			6:29690709	Promoter_A	TRUE
		14:70092338-70092914			
	TRUE				
DMR					
		1:228559340-228560085			
	TRUE				
		17:4067423	17:4331901	Gene_Asso	TRUE
		Y:21146854-21147440			
	TRUE				TRUE
	TRUE	2:237729897-237730509			TRUE
	TRUE				
		5:140704376-140704573			

			X:34584570-34585886			TRUE
		TRUE				
			5:180018036-180018878			
		TRUE				
			17:78563038-78563471			
			5:180429720-180429833			
			5:178198666-178198784			TRUE
				X:7715069	Promoter_A	TRUE
			4:157339112-157339533			
		TRUE				
			1:40007910	1:40235487	Unclassified_Cell_type_specific	
		TRUE				
			8:142230919-142231244			
low-CpG:46473910-46474044						
	RDMR					
			9:68436916-68438042			
			X:114374373-114374995			
			X:128941100-128946452			
high-CpG:46962370-46963215			X:4696206	X:4707709	Promoter_Associated	
		TRUE	7:52123312-52124009			
	DMR		17:15626944-15627179			
	DMR		6:168244791-168245639			
			7:56572742-56573373			
	CDMR	TRUE	2:22006970	2:22036122	Unclassified	
	RDMR		7:96489900	7:96651951	Unclassified_Cell_type_specific	
			1:19472837-19473529			
				5:43037968	Promoter_Associated	
			6:20140514-20140918			
			6:29756034	6:29648152	Unclassified_Cell_type_specific	
			8:43255246	8:43135848	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
			15:72131939-72132290			
			6:170297418-170297496			

			21:46228537-46228740			
		TRUE				TRUE
		TRUE	15:20475028-20475265			TRUE
		TRUE				
		TRUE				
			8:92640071-92640431			
		TRUE		1:23021997	Unclassifie	TRUE
			5:2695995-2696300			
			19:1802402	19:1851730	Gene_Associated_Cell_type_specific	
			7:94863327-94864148			
			10:135193172-135193295			
high-CpG:53465876-53466404			X:5346555	X:5344866	Promoter_Associated	
			9:138857985-138864431			
		TRUE				
			15:30391988-30395216			
				4:15470687	Unclassified_Cell_type_specific	
		TRUE	10:660579-661214			TRUE
			20:61522997-61523770			
		TRUE	9:71216706	9:72027094	Unclassified	
			1:6946070-	1:7022332-	Unclassifie	TRUE
			7:1947711-1948037			
			21:3496318	21:3604167	Unclassified_Cell_type_specific	
		TRUE				
			5:17996126	5:18002860	Unclassified_Cell_type_specific	
				22:4693484	Unclassified_Cell_type_specific	
	CDMR	TRUE	1:15150011	1:15323318	Unclassified_Cell_type_specific	
			7:12707861	7:12729115	Promoter_Associated	
		TRUE				
			2:13273024	2:13301366	Unclassified	
		TRUE		2:99081176	Promoter_Associated	
			5:140560776-140561785			
			8:144477774-144478159			
			2:24129280	2:24164362	Unclassified	
			12:7051950	12:7223316	Promoter_A	TRUE
		TRUE				TRUE

			6:5029492-5032137			
		TRUE				TRUE
	DMR					
			8:39291177-39291296			
		TRUE		1:20185735	Unclassified_Cell_type_specific	
		TRUE				TRUE
		TRUE		3:4793918-	Unclassified_Cell_type_specific	
			5:17736588	5:17743358	Unclassifie	TRUE
	RDMR		5:13544379	5:13541505	Unclassified_Cell_type_specific	
low-CpG:45616923-45620319			17:45618098-45618204			
	RDMR					
			17:7662531	17:7901110	Unclassifie	TRUE
			13:24217537-24219288			
		TRUE				
			17:7901096	17:7959558	Unclassified	
			11:65950455-65950656			
		TRUE				TRUE
		TRUE				
			8:1314806-1315094			
		TRUE				
						TRUE
				20:6192431	Unclassified_Cell_type_specific	
low-CpG:96725917-96726520						
			X:1005497	X:1006627	Promoter_	TRUE
			10:104825889-104825984			
		TRUE				TRUE
			4:176585920-176586378			
						TRUE
		TRUE				
			12:1315458	12:1330358	Unclassified_Cell_type_specific	
	DMR					
	DMR		X:20043986-20045776			TRUE
				7:27703391	Promoter_Associated	
			4:726485-7	4:735801-7	Unclassified	
		TRUE				

		TRUE				
			1:2874923-2875144			
		TRUE	10:134270126-134270300			
	CDMR					
		TRUE				
			X:67965288-67967183			
		TRUE				
		TRUE				TRUE
			5:14018157	5:14020131	NonGene_Associated_Cell_type_specific	
			6:116354962-116355073			
			5:178141136-178141217			
		TRUE				TRUE
		TRUE	1:226725561-226725872			
						TRUE
			6:30018182-30019314			
			10:134650616-134650732			
		TRUE				
		TRUE	17:78564079-78564182			TRUE
			X:4878745	X:4890023	Promoter_Associated	
			8:43250370-43250704			
			4:2371778-2371868			
			7:157972546-157972653			
		TRUE				
		TRUE	3:49915068	3:49940225	Promoter_A	TRUE
	RDMR		12:113619245-113619773			
		TRUE				
			7:14974998	7:15011782	Unclassified	
		TRUE	10:46503376-46503609			
			5:175978523-175980241			
		TRUE	X:1178416	X:1179574	Unclassifie	TRUE
			14:1009784	14:1019084	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
dy;5'UTR;Body;Body;Body;Body;5'UTR;Body;Body						

		TRUE				
		TRUE		8:13408072	Promoter_Associated_Cell_type_specific	
				6:16763141	Unclassifie	TRUE
			3:139635473-139635818			
	RDMR		7:96489900-96490205			
		TRUE		5:13778491	Unclassified	
			8:2250599-2250778			
	DMR					
		TRUE				
		TRUE				TRUE
			11:58354815-58355069			
			13:67643081-67643361			
	DMR		4:17722382	4:17698662	Promoter_A	TRUE
	DMR		4:15547337	4:15525405	Unclassified	
			3:134985252-134985788			
			6:79395797-79396295			
		TRUE				
			2:23292392	2:23321532	Unclassifie	TRUE
low-CpG:53956487-53956492						
		TRUE				
		TRUE				TRUE
			12:1887290	12:2016983	Unclassifie	TRUE
		TRUE				
				19:4002971	Promoter_Associated	
	CDMR	TRUE				
		TRUE				
				6:32634123	Unclassifie	TRUE
						TRUE
		TRUE				
		TRUE				
			13:111676645-111676964			
			4:1356399-1356827			TRUE
	RDMR		10:719420-719712			TRUE

			6:90653952-90654337			
		TRUE				
		TRUE		15:6375846	Unclassifie	TRUE
		TRUE				
		TRUE				
high-CpG:152389212-152389264			X:1523888	X:1527353	Promoter_Associated	
		TRUE	7:129917408-129917684			
			10:132926439-132926607			
		TRUE	6:31383697	6:31275659	Promoter_Associated	
			6:30526824	6:30419361	Unclassified_Cell_type_specific	
		TRUE				
			6:164012520-164013103			
	RDMR		17:7322334	17:7381558	Promoter_Associated	
	RDMR					
		TRUE				
		TRUE				
			X:1255426	X:1257150	Unclassified	
			8:144922423-144922516			
			19:566708-	19:616758-	Unclassified_Cell_type_specific	
		TRUE				
	DMR		13:2401356	13:2511536	Unclassifie	TRUE
			17:43976708-43977356			TRUE
SS200		TRUE				
		TRUE				TRUE
	DMR		X:1524361	X:1527835	Unclassified_Cell_type_specific	
		TRUE				
			19:564006-565040			TRUE
			7:4099795-4099934			
			11:77584889-77585711			
			2:241704856-241705061			
	DMR		6:17018010	6:17033847	Unclassified_Cell_type_specific	
			6:168660620-168661776			
		TRUE				TRUE
		TRUE		3:16843178	Unclassified	
		TRUE				TRUE

		TRUE				
			15:74270865-74271919			
		TRUE				
				22:4645144	Unclassified_Cell_type_specific	
			15:29142578-29142735			
			19:62322014-62322504			
			15:25270997-25271078			
		TRUE				
high-CpG:4858321-4858482			10:4858068	10:4867931	Unclassified	TRUE
			19:53923985-53924637			TRUE
			2:74989599-74990049			
			6:158000642-158000742			
		TRUE				
		TRUE		1:20528270	Promoter_Associated	
		TRUE				
			6:25990231	6:25882232	Unclassified_Cell_type_specific	
			X:6353168	X:6361485	Promoter_A	TRUE
		TRUE				TRUE
		TRUE				
			19:15428605-15430216			
	DMR			7:50108608	Unclassified	
		TRUE				
		TRUE				TRUE
			6:134478153-134478538			
		TRUE				
		TRUE				
			15:88556848-88557224			
			5:140517008-140517950			
			5:1249151-1249232			
			3:182028813-182029701			
		TRUE				
						TRUE
	RDMR					
Body		TRUE				
						TRUE
			1:3649451-3649536			

	TRUE				
		X:4863939	X:4875429	Promoter_Associated	
			5:14009018	Promoter_Associated	
		10:1073190-1073311			
		6:2460291-2460337			
		14:1049015	14:1058302	Unclassified_Cell_type_specific	
		21:18112895-18113928			
	TRUE	7:15803474	7:15834224	Unclassifie	TRUE
			17:1962722	Unclassifie	TRUE
		1:16877351	1:17004520	Unclassified_Cell_type_specific	
		8:56847891	8:56685337	Promoter_Associated	
	TRUE				
			2:30669584	Promoter_Associated	
		1:156414058-156414447			TRUE
		3:49211587-49212481			TRUE
		X:1528041	X:1531509	Unclassifie	TRUE
	TRUE				
		15:32569637-32570226			
	TRUE				
low-CpG:55098359-55098672					
		10:134261206-134261471			
	TRUE				
	TRUE				TRUE
		X:1527373	X:1530840	Unclassified_Cell_type_specific	
			17:1787504	Promoter_Associated	
		6:166180952-166181037			
	TRUE	17:2833000	17:2886029	Unclassifie	TRUE
RDMR			2:17701594	Unclassified_Cell_type_specific	
		7:155026086-155026213			
					TRUE
		5:1271916-1272874			
		2:24129280	2:24164362	Unclassified	
CDMR					

		TRUE				
			13:112032968-112033729			
			7:1047067-1047681			TRUE
		TRUE	13:113982203-113984182			
	DMR					
		TRUE				
		TRUE		17:7876582	Gene_Asso	TRUE
		TRUE	17:7784869	17:8025473	Promoter_A	TRUE
			13:112700275-112700370			
		TRUE		6:13152049	Promoter_Associated	
		TRUE				
				X:1259542	Unclassified_Cell_type_specific	
		TRUE				
			1:4743829-4743996			
high-CpG:97142598-97143117			2:97142090	2:97778654	Unclassifie	TRUE
			6:30146876-30147422			
		TRUE				
			4:1466150-1466310			
		TRUE	18:12245266-12245396			
		TRUE				
				17:3530235	Unclassified_Cell_type_specific	
	DMR		9:138726021-138727286			
			13:110079325-110079487			
		TRUE		21:4685106	Unclassifie	TRUE
		TRUE		6:422827-4	Unclassifie	TRUE
			12:1887290-1888378			
		TRUE				
			17:19823918-19824447			
			2:89653541-89653604			
		TRUE				
			1:3493951-3494016			TRUE
			8:1300037-1300388			
		TRUE				TRUE
	CDMR					
		TRUE				
			6:30146876-30147422			

	TRUE	1:27548338	1:27675585	Gene_Associated_Cell_type_specific	
		1:19472837-19473529			TRUE
	TRUE				
		1:115199566-115199674			
	TRUE				TRUE
	TRUE				
		8:61789200-61789841			TRUE
	TRUE		5:72683518	Unclassified	
	TRUE				
	TRUE				
			6:29980416	Unclassifie	TRUE
	TRUE	11:4634565	11:4638907	Gene_Asso	TRUE
	TRUE	17:72896864-72897054			TRUE
DMR		12:127316927-127319149			
DMR		10:4350475	10:4418467	Promoter_Associated_Cell_type_specific	
CDMR			5:80488-80	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				
	TRUE		6:10981248	Unclassified_Cell_type_specific	
		22:30928951-30930766			
	TRUE				TRUE
		6:109718104-109719168			
		6:28665649-28666050			
	TRUE				
	TRUE	7:158513171-158513416			TRUE
		5:130371991-130372103			
	TRUE	5:71510833-71511184			TRUE
		5:179521007-179521358			
	TRUE				TRUE
		8:1902374-1902484			
	TRUE				
	TRUE				

		TRUE				
		TRUE				TRUE
		TRUE	11:92703111-92703777			
			14:5048000	14:5141067	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				TRUE
high-CpG:31432543-31432986			6:31431926	6:31324761	Promoter_Associated	
		TRUE		5:17183097	Unclassified_Cell_type_specific	
			5:147679893-147680112			
			3:161652868-161652958			TRUE
		TRUE				
				12:1092472	Unclassifie	TRUE
			11:66898529-66898607			
				6:28091996	Promoter_Associated	
						TRUE
			6:32740137-32741093			
			3:10124751-10125032			
				1:20667749	Unclassifie	TRUE
		TRUE				
		TRUE				
		TRUE				
				1:5526548-	Unclassified_Cell_type_specific	
		TRUE				TRUE
	RDMR	TRUE				
		TRUE				
			6:101953488-101953918			
		TRUE				TRUE
		TRUE				
			1:181188275-181188334			
			12:123375281-123376321			
			1:36462059	1:36688869	Unclassified	
		TRUE	7:2735268-	7:2768986-	Unclassified_Cell_type_specific	
		TRUE	2:232959406-232961623			
			6:42802850	6:42693951	Promoter_Associated	

	TRUE				
	TRUE				
	TRUE				
			1:1361820-	Unclassified	
			6:30042516	Unclassifie	TRUE
	TRUE				
	TRUE				
	TRUE				
		2:238312494-238312699			
		6:30146876	6:30039021	Unclassified_Cell_type_specific	
	TRUE				
		1:2695709-2697026			
RDMR		4:4910563-4911092			
		7:158233989-158234028			
	TRUE				
		2:239684852-239685212			TRUE
	TRUE				
		14:92176017-92176351			
			1:27524266	Unclassifie	TRUE
	TRUE				
CDMR		13:3494724	13:3604920	Unclassified_Cell_type_specific	
	TRUE				
		14:1009784	14:1019084	Unclassified_Cell_type_specific	
	TRUE				
		2:239664344-239664476			
		22:35290280-35291021			
low-CpG:95715823-95716126		11:9571593	11:9607597	Promoter_Associated	
		4:39448119-39449704			
	TRUE	2:121128146-121129113			
		2:869464-869580			
	TRUE				
		5:71749024-71749615			
	TRUE				
		2:23210302	2:23239492	Unclassifie	TRUE
		10:135191246-135192212			
	TRUE				
			4:14601837	Promoter_Associated	

	RDMR		1:215380356-215380602			
			8:1886778-1886965			
		TRUE				
			12:123789398-123789721			TRUE
		TRUE		3:27575259	Promoter_A	TRUE
		TRUE				
			10:7710797-7710860			
			17:146634-147040			
		TRUE				TRUE
				6:32634123	Unclassifie	TRUE
high-CpG:53940607-53		TRUE	2:53940281-53940994			
	DMR		2:19835797	2:19865050	Unclassified_Cell_type_specific	
				1:23024170	Promoter_A	TRUE
				4:47034377	Unclassified	
		TRUE				
		TRUE				TRUE
				X:5334917	Unclassifie	TRUE
	CDMR					TRUE
			6:30526824	6:30418347	Unclassified	
	DMR	TRUE		12:7641408	Unclassified_Cell_type_specific	
		TRUE				TRUE
			13:24109903-24110557			
			6:30146876-30147422			
		TRUE				
		TRUE				TRUE
		TRUE	13:110084970-110085283			TRUE
				19:5054963	Unclassified	
		TRUE				
			17:3761440	17:3814525	Unclassified	
			1:981542-981912			
			6:832641-833102			
			10:43166274-43166581			
		TRUE				
				10:3823604	Promoter_Associated	
			10:27742233-27743384			

		TRUE				
		TRUE				
		TRUE	4:1036976-1037115			TRUE
		TRUE				TRUE
		TRUE				
		TRUE				
				17:2119071	Promoter_A	TRUE
		TRUE				
		TRUE				
	RDMR		1:15042790	1:15216100	Unclassified	
			2:176705722-176705751			
			13:28811887-28812268			
SS200		TRUE				
			10:135122966-135123922			
						TRUE
		TRUE	9:139450448-139450896			
		TRUE				
		TRUE				
			10:135119770-135120351			
		TRUE				
			6:112793983-112795441			
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
		TRUE				TRUE
			19:3983777-3984935			
			7:72451826-72451915			TRUE
		TRUE				TRUE
	RDMR		5:13544359	5:13541505	Unclassified_Cell_type_specific	
		TRUE		5:17232444	Unclassifie	TRUE
			9:131056084-131056193			
			2:865332-865533			
		TRUE		15:4218657	Promoter_A	TRUE
		TRUE	11:132087690-132087893			
			9:136802663-136802832			
			9:12657419	9:12753341	Promoter_Associated	

		TRUE				
			19:3826356	19:3357154	Promoter_Associated	
		TRUE				
						TRUE
			12:52667207-52667281			
	RDMR					TRUE
high-CpG:69426439-69426542			X:6942633	X:6950921	Promoter_Associated	
		TRUE				
		TRUE				
		TRUE				
TSS1500				2:33359167	Unclassifie	TRUE
		TRUE				
			11:2133426-2133619			
			19:5285956-5286320			
			10:1501146-1501278			
			14:80948984-80949129			
		TRUE				
		TRUE				
				6:31587577	Promoter_Associated	
		TRUE		13:1115218	Unclassifie	TRUE
			X:3058070	X:3067064	Promoter_Associated	
			6:85880852-85880975			
		TRUE				
		TRUE				
		TRUE				
R;Body;Body						
		TRUE				
	CDMR	TRUE				
			19:57646274-57646657			
high-CpG:144882358-144882681			8:144879781-144883419			TRUE

	RDMR					
			7:2256075-2256429			
			15:22057220-22057516			
			9:137730665-137732311			
			9:138755108-138755746			
			2:24436133-24437338			
			9:137725884-137726355			
			17:4840939	17:4900651	Promoter_Associated	
				19:1598249	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
	RDMR		10:28070039-28070635			
			Y:22862901-22863191			
		TRUE				
			X:8711266-	X:8751090-	Unclassifie	TRUE
			12:113603150-113603196			
			19:16850362-16850700			
		TRUE		9:72735563	Unclassifie	TRUE
			12:9446489	12:9555122	Unclassified_Cell_type_specific	
			9:38477546-38478450			
			9:13947611	9:14035582	Promoter_A	TRUE
						TRUE
	CDMR			7:55638609	Promoter_A	TRUE
			6:168834624-168834894			
		TRUE				
			9:114874514-114876512			
				17:7770407	Unclassified_Cell_type_specific	
	DMR		19:6364306	19:5895102	Promoter_Associated	
			12:94364936-94365027			
		TRUE				
low-CpG:44857296-44857299						

		TRUE				
			1:1539468-1539682			TRUE
			12:1293876	12:1308239	Unclassified_Cell_type_specific	
			11:5915571-5916673			
			5:225910-226201			
	CDMR		X:1525607	X:1529078	Unclassified_Cell_type_specific	
		TRUE				
			6:30146876	6:30039021	Unclassified_Cell_type_specific	
			9:34799637-34800229			
				1:15419251	Promoter_Associated	
			1:1156434-1158834			
			11:10707392-10707558			
		TRUE				
		TRUE				
		TRUE	1:5986043-5986257			
		TRUE				
high-CpG:152889815-152891067			X:152889	X:1532361	Promoter_Associated	
		TRUE				TRUE
		TRUE				
			12:9987169-9987420			
		TRUE		9:94532158	Unclassified_Cell_type_specific	
				5:32445345	Unclassified	
						TRUE
		TRUE				
			9:136802663-136802832			
	RDMR					
		TRUE				
			X:1528629	X:1532099	Unclassified	
		TRUE				
				17:1021988	Unclassifie	TRUE
			9:133688999-133689630			
				7:15471895	Promoter_	TRUE
				9:11713425	Unclassifie	TRUE
			X:5336611	X:5334917	Unclassifie	TRUE
			19:51217490-51218424			
		TRUE				

		2:130762488-130763022			TRUE
		6:30018182-30019314			
		9:816616-816800			
	TRUE				
	TRUE				TRUE
	TRUE				
	TRUE				
	TRUE				
		19:803661-	19:853008-	Unclassified_Cell_type_specific	
	TRUE		2:24186075	Unclassifie	TRUE
			9:13259673	Promoter_Associated	
		19:17914153-17915733			
		9:138525470-138526628			
RDMR					
	TRUE				
DMR	TRUE				TRUE
			7:230711-2	Unclassified_Cell_type_specific	
		6:127838005-127839014			
	TRUE	21:4360579	21:4478106	Unclassifie	TRUE
		9:129494320-129494553			
			9:35848128	Unclassifie	TRUE
	TRUE				
		11:1638420	11:1681990	Unclassified_Cell_type_specific	
		13:22310250-22310590			
		19:6376393	19:6424683	Promoter_Associated	
			11:6714158	Promoter_Associated	
					TRUE
		X:9392530-9394487			
		19:55425620-55426065			
		12:8608592-8608812			
			X:7715457	Promoter_A	TRUE
		19:1446754	19:1460685	Promoter_Associated	

	TRUE				
	TRUE				TRUE
	TRUE				TRUE
		Y:18181458-18188553			
			9:28596839	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				
	TRUE				
	TRUE				
		11:70102177-70102208			
		7:154884470-154884705			
			21:4383503	Promoter_A	TRUE
	TRUE				
		4:7425483-7425602			
	TRUE				
		2:97015230-97015339			
RDMR		7:42862748-42863222			
	TRUE				TRUE
	TRUE				
		11:6509813	11:6533935	Promoter_Associated	
		19:51109369-51109585			
		17:7844257	17:8084935	Unclassified_Cell_type_specific	
	TRUE				
			14:6798327	Unclassified	
RDMR		4:183300391-183300556			
	TRUE	6:16993170	6:17018939	Unclassified	
			11:1141664	Unclassified_Cell_type_specific	
DMR					TRUE
	TRUE	8:38627215-38627905			
		14:23508510-23509440			
		7:27112636	7:27146398	Unclassifie	TRUE
		16:797343-	16:857066-	Promoter_Associated	
		2:112906490-112907745			
	TRUE				
	TRUE				
		12:44291246-44291436			
	TRUE				TRUE

					TRUE
	TRUE				
	TRUE				
	TRUE				
		19:12856564-12856899			
		13:110733430-110733683			
	TRUE				TRUE
		6:74119872-74121192			
RDMR		2:22737011	2:22766155	Unclassified	
		6:31272827	6:31164733	Promoter_A	TRUE
	TRUE				
	TRUE				TRUE
		19:56021941-56022347			
	TRUE				
	TRUE		10:3568899	Unclassified_Cell_type_specific	
	TRUE	6:168178688-168179417			TRUE
		9:114890846-114892814			TRUE
		19:22592533-22592881			
		7:63135548-63135833			
		3:140245287-140246803			
		22:19354755-19355606			
	TRUE				
		7:75617406	7:75779568	Unclassified_Cell_type_specific	
		14:103765765-103766222			
	TRUE				
			X:7031817	Unclassified	
DMR	TRUE		13:2792733	Unclassified	
			19:5866559	Unclassified	
RDMR			5:12640822	Promoter_Associated	
		21:4571533	21:4689071	Unclassifie	TRUE

			13:110262437-110264460			
				6:31508806	Unclassified	
				1:28417729	Unclassified_Cell_type_specific	
			2:183240-183564			
			5:15003120	5:15005049	Promoter_Associated	
	RDMR		13:22310250-22310590			
		TRUE				TRUE
		TRUE				TRUE
			2:130726040-130726707			TRUE
		TRUE				
		TRUE				TRUE
			9:125834515-125834786			
			7:15695349	7:15726065	Unclassified_Cell_type_specific	
			12:113591583-113591994			
			9:92839076	9:93798621	Unclassified	
		TRUE				
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
			4:133115855-133117899			
			6:159573090-159575387			
		TRUE				
			2:626090-6	2:636378-6	Unclassified	
		TRUE				TRUE
		TRUE				
			14:102043007-102044066			
high-CpG:27195359-27195523			2:27194867	2:27341446	Promoter_A	TRUE
	DMR		21:34753547-34754235			TRUE
		TRUE				
SS200		TRUE				

		TRUE				
		TRUE				
			12:105872769-105873066			
		TRUE				TRUE
		TRUE				TRUE
			5:1353268-1353439			
			9:95662932-95663357			
		TRUE				
			X:1333346	X:1335067	Promoter_Associated	
			5:178510101-178510180			
		TRUE				TRUE
		TRUE				
			1:35358919	1:35586503	Unclassified	
				11:6536267	Unclassifie	TRUE
	CDMR					
		TRUE				
			6:32659866	6:32552058	Unclassified_Cell_type_specific	
		TRUE				
			7:156902292-156902330			
			17:74187836-74187962			
		TRUE		9:13015056	Unclassifie	TRUE
			2:119780379-119780450			
			2:232954225-232954711			
		TRUE	1:53923586-53923674			TRUE
		TRUE	11:6397299	11:6421619	Promoter_Associated	
		TRUE				
			1:15351371	1:15524667	Promoter_Associated	
		TRUE				TRUE
low-CpG:8721746-8721752						
			12:31161327-31165315			

			7:1654340-1655086			TRUE
			2:13273024	2:13301366	Unclassified	
		TRUE				
			X:4697727	X:4709219	Promoter_Associated	
		TRUE				
		TRUE				
			11:71402152-71402326			TRUE
			5:1111848-1114722			
			3:13008029	3:12859766	Unclassified	
			17:74638520-74639220			
		TRUE		10:1297891	Unclassifie	TRUE
	RDMR		12:113586892-113588492			
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
		TRUE				TRUE
			20:43378282-43379069			
	RDMR					
				4:15525405	Unclassified	
			2:20732770-20735202			
			2:1459778-1460638			
			3:14774462	3:14626162	Promoter_Associated	
		TRUE				
		TRUE				
		TRUE	17:7056726	17:7305563	Unclassified	
			10:103323971-103324053			
high-CpG:28225511-28225662			20:2822466	20:2961113	Promoter_A	TRUE
		TRUE				TRUE
			3:56691533	3:56716001	NonGene_Associated	
		TRUE		17:7559833	Unclassifie	TRUE
			5:78567295-78569381			
			X:3058070	X:3067064	Promoter_Associated	

RDMR			17:4827437	Unclassified	
	TRUE	2:53940281-53940994			
		1:150773466-150773569			
	TRUE				
		13:111975175-111975333			
					TRUE
	TRUE				
	TRUE	1:18983446-18983677			
		12:6306806	12:6435567	Gene_Associated_Cell_type_specific	
			1:15423807	Gene_Associated_Cell_type_specific	
					TRUE
			8:10403220	Promoter_Associated	
	TRUE				
	TRUE	2:3676920-	2:3698449-	Unclassified	
	TRUE				
	TRUE				
		14:101624474-101624817			
					TRUE
		4:7786202-7786276			
		2:130762488-130763022			TRUE
		6:35561809-35562331			TRUE
		20:4336861	20:4393518	Unclassifie	TRUE
		6:37724232	6:37616081	Unclassifie	TRUE
		16:87320424-87322542			
		2:24121108	2:24156230	Unclassified_Cell_type_specific	
	TRUE	10:359948-	10:369759-	Unclassifie	TRUE
	TRUE				
		19:3546660-3546977			
	TRUE				TRUE
	TRUE		11:4725527	Unclassified	
	TRUE				TRUE
		2:27226518-27226669			
			16:4525913	Promoter_Associated	
	TRUE				TRUE
			21:4753065	Unclassifie	TRUE
		19:42451390-42487862			
	TRUE	8:800491-800538			
	TRUE				TRUE
	TRUE				
RDMR		7:48096271	7:48128066	Promoter_Associated	

			19:33909806-33910556			
			2:96500050-96500621			TRUE
		TRUE				TRUE
	RDMR		12:1135894	12:1151050	Unclassified_Cell_type_specific	
		TRUE				
			1:3711588-3711757			
			6:49789137-49789351			
	RDMR		9:11486142	9:11582199	NonGene_Associated_Cell_type_specific	
		TRUE				TRUE
		TRUE				
			19:5562282	19:5093114	Unclassifie	TRUE
		TRUE				
		TRUE	13:90625010-90625825			
			17:4426330	17:4690809	Promoter_Associated	
				1:15216100	Unclassified	
			1:2072175-2072366			
		TRUE				TRUE
low-CpG:32575406-32575409						
	RDMR			10:1264341	Gene_Associated_Cell_type_specific	
	RDMR		5:140481840-140482036			
			22:14668248-14668748			
			6:152506478-152506564			
			Y:21146854-21147440			
			1:147946623-147946877			TRUE
			3:13949146	3:13974403	Unclassified_Cell_type_specific	
		TRUE	7:129917408-129917684			
		TRUE	13:111595342-111596108			
			11:1848614	11:1891168	Unclassified	
				3:14160954	Gene_Associated_Cell_type_specific	
		TRUE	10:3158995-3159517			TRUE
			1:245577972-245578109			
	RDMR		4:4910563-4911092			
				19:3036539	Unclassified_Cell_type_specific	
		TRUE				
			5:140146718-140146774			
			19:56021941-56022347			

			5:140236267-140237474			
			17:74015109-74015277			
			1:15932966	1:16060444	Unclassified_Cell_type_specific	
TSS1500				2:33359167	Unclassifie	TRUE
	RDMR		2:66658566	2:66803780	Unclassified	
high-CpG:48669455-48669580			3:48668161-48669750			TRUE
			5:6807902-6808444			
			6:159943526-159943680			
			19:21056822-21057273			
			19:5494135	19:5024956	Unclassifie	TRUE
		TRUE				TRUE
			19:18749033-18749969			
			17:19823918-19824447			
		TRUE				
		TRUE				
		TRUE				TRUE
			1:6448638-6449057			TRUE
			19:1820449	19:1834323	Unclassified	
		TRUE	6:35587410-35588053			
		TRUE				
	DMR		X:73559041-73559693			
			20:4336861	20:4393518	Unclassifie	TRUE
			10:133959745-133959930			
		TRUE				
			17:78220918-78221010			
		TRUE				
			12:7916632-7917175			
			22:2271389	22:2438403	Unclassified_Cell_type_specific	
	RDMR					
			10:29254058-29254368			
						TRUE
			7:157762230-157762776			
		TRUE				
			17:74408674-74408893			
		TRUE				TRUE
			17:78150794-78150908			

			2:1156067-1156333			
		TRUE				
				6:16018229	Promoter_Associated	
		TRUE				
			12:112647129-112647248			
			8:1297587-1298204			
		TRUE				
			7:157422903-157423026			
			Y:19697854-19699393			
			10:88692306-88693270			
		TRUE				
		TRUE		3:14356721	Unclassified	
			12:129622899-129623098			
	RDMR					
high-CpG:23849959-23850497			14:2384979	14:2477937	Promoter_A	TRUE
		TRUE				
			X:21583880-21587146			
			5:140455168-140455333			
		TRUE				TRUE
	CDMR	TRUE		1:20799589	Promoter_A	TRUE
						TRUE
			2:31658798-31660446			
			19:4675653	19:4724412	Promoter_Associated	
			5:12643692	5:12640822	Promoter_Associated	
			10:134954727-134956176			
			6:74119872-74121192			
		TRUE				TRUE
		TRUE				
low-CpG:45624888-45625210						
			14:102757309-102757463			TRUE
		TRUE		7:8029555-	Unclassified_Cell_type_specific	
	RDMR		1:219124087-219124962			
			X:1528720	X:1532182	Gene_Associated	

				1:65889722	Unclassified_Cell_type_specific	
			21:4344680	21:4457376	Unclassified_Cell_type_specific	
		TRUE				
			10:2533497-2534121			
				20:6144715	Unclassified_Cell_type_specific	
			13:18816586-18817215			
		TRUE	14:100609113-100609405			
		TRUE				
			12:128120501-128120607			
		TRUE				TRUE
high-CpG:99137849-99137988			2:99137542	2:99770769	Promoter_Associated	
			7:530384-530443			
high-CpG:32659888-32660014			6:32659866-32660444			
		TRUE				
	RDMR			3:61235609	Promoter_A	TRUE
			7:1986340-	7:2019424-	Unclassifie	TRUE
		TRUE				TRUE
			5:1920959-1921138			
				5:15000584	Unclassified_Cell_type_specific	
			2:1156067-1156333			
		TRUE				
			13:4446128	13:4556302	Promoter_Associated	
		TRUE				
high-CpG:27190661-27		TRUE	7:27190555-27192145			
				8:13102584	Promoter_Associated_Cell_type_specific	
			10:3169691-3169822			TRUE
			6:31346870-31347980			
	DMR		10:8228548	10:8229523	Promoter_A	TRUE
	RDMR		12:52734917-52735181			
				2:30669584	Promoter_Associated	

			6:30001657	6:29894087	Promoter_Associated	
		TRUE				
	DMR		X:78509089-78509412			
			1:1216370-	1:1226844-	NonGene_Associated	
			5:1847925-1848155			TRUE
	DMR		19:5562282	19:5093114	Unclassifie	TRUE
		TRUE				
		TRUE				TRUE
			5:140437735-140437806			
			1:106424943-106425503			
			7:45774639	7:45808101	Promoter_Associated	
	RDMR					
	DMR		X:151556865-151558024			
			22:4783336	22:4944758	Unclassified_Cell_type_specific	
			4:7820764-7820878			
		TRUE				TRUE
		TRUE				
			22:49482487-49483412			
high-CpG:1	DMR		X:149280229-149281104			
			12:129736524-129737489			
			12:8608592-8608812			
		TRUE				
low-CpG:32742410-32742475				6:32634123	Unclassifie	TRUE
			5:4919224-4920544			
			7:152231430-152231856			
			18:75393037-75393432			TRUE
		TRUE		3:14102224	Unclassifie	TRUE
			7:2066195-2066884			
		TRUE				
			19:15694734-15694953			
			11:484906-485156			TRUE
			7:75966935-75967522			

			19:43037598-43038000			
		TRUE				
		TRUE				
			13:24404114-24404341			
	CDMR					
		TRUE				
			15:43190563-43191510			
			1:24586928	1:24780263	Unclassifie	TRUE
	CDMR					
			2:242536017-242536083			
		TRUE	21:45674926-45675474			TRUE
		TRUE				
						TRUE
						TRUE
		TRUE	15:38370386-38371081			
		TRUE				
		TRUE				
	CDMR					
high-CpG:43626444-43626725			X:43626244-43626729			TRUE
		TRUE				
			6:30146876	6:30039021	Unclassified_Cell_type_specific	
		TRUE				
				12:1222650	Gene_Associated_Cell_type_specific	
		TRUE				TRUE
		TRUE				
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
			4:2401607-2402112			TRUE
		TRUE				
			14:102757309-102757463			TRUE
		TRUE				
			6:30528709	6:30420915	Unclassified	
			17:77633694-77633928			
			1:19472837-19473529			TRUE

	TRUE				
		6:30187118-30187260			
	TRUE				
		21:45587642-45587888			
	TRUE				TRUE
		21:45636610-45636995			
	TRUE				
	TRUE				
					TRUE
			11:7033665	Unclassified_Cell_type_specific	
		4:1182053-1182143			
	TRUE				TRUE
		6:29634322-29634449			
CDMR					
					TRUE
			3:11185194	Promoter_Associated	
	TRUE				
	TRUE				
	TRUE				
	TRUE				TRUE
	TRUE				TRUE
	TRUE				
	TRUE				
		4:12909585-12909606			
	TRUE				
RDMR					
			10:9435051	Promoter_Associated	
					TRUE
		2:240232462-240232617			
	TRUE				
	TRUE				
		5:361235-361628			
			11:1339007	Unclassified	

	TRUE				
		10:129837719-129837871			
		5:17842039	5:17848675	Promoter_A	TRUE
DMR	TRUE				TRUE
					TRUE
	TRUE				TRUE
		11:1258155	11:1263099	Unclassified	
		1:19938988	1:20112282	Promoter_Associated	
	TRUE				
	TRUE	15:38055924-38056353			TRUE
	TRUE				TRUE
					TRUE
		5:140155851-140157034			
	TRUE				
			21:4519852	Unclassified_Cell_type_specific	
		3:196054552-196054699			
	TRUE		1:9340143-	Unclassified	
			8:10375081	Unclassifie	TRUE
	TRUE	18:10022142-10022971			
		7:23212101	7:23245124	Gene_Associated	
	TRUE				TRUE
		6:1500022-	6:1554396-	Unclassified	
		18:74775096-74775768			
		8:140995840-140995982			
		10:48447599-48448113			
	TRUE				TRUE
		14:103695069-103695759			
	TRUE	7:12117667	7:12151245	Unclassified_Cell_type_specific	
		10:135228782-135229757			
			13:1070284	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				TRUE
	TRUE				TRUE
		5:140168063-140169188			
		5:75734195	5:75698279	Promoter_A	TRUE
		10:131240867-131241066			
	TRUE				TRUE
		5:140690628-140690710			
	TRUE				TRUE

		TRUE		8:8130586-	Unclassified	
		TRUE				
		TRUE				TRUE
		TRUE				
high-CpG:78216121-78216207			4:78216117	4:77996995	Promoter_Associated	
			11:6091604	11:6115952	Unclassifie	TRUE
			6:22464946-22465071			
			14:101491810-101492403			
		TRUE				TRUE
		TRUE				TRUE
		TRUE				
			6:32740137-32741093			
		TRUE				
			16:10253538-10253934			
			3:140221263-140222607			
	DMR	TRUE				TRUE
			16:54352096-54352465			
	RDMR					
				12:5524765	Unclassified	
	RDMR		11:1488304	11:1492593	Promoter_Associated	
			12:112688329-112688482			TRUE
		TRUE				
			10:3154609-3154845			
			15:98638989-98639117			
		TRUE				
		TRUE	1:91072778-91072881			
		TRUE				TRUE
			12:113603150-113603196			
			3:134985252-134985788			
		TRUE				
high-CpG:172675300-1		TRUE	2:172674374-172676240			
		TRUE				
			10:129837719-129837871			
			2:10219842-10219938			TRUE
			17:37445406-37445888			
			20:33652038-33653681			
				16:3316724	Unclassified	

	TRUE				
		20:3232036	20:3285659	Unclassified_Cell_type_specific	
	TRUE				TRUE
		3:17210838	3:17062541	Unclassified	
	TRUE	5:71510833-71511184			TRUE
		7:75983343	7:76144928	Unclassifie	TRUE
	TRUE				
	TRUE	15:93670981-93671326			
	TRUE				
		12:104984834-104985009			
	TRUE				TRUE
	TRUE		8:20080481	Unclassified	
	TRUE		6:32120376	Promoter_Associated	
	TRUE				
		1:23335826	1:23529146	Unclassified	
	TRUE				
		6:32659866	6:32552058	Unclassified_Cell_type_specific	
low-CpG:45616923-45620319		17:45618098-45618204			
			17:7978752	Unclassified_Cell_type_specific	
	TRUE				
		12:5266988	12:5438269	Unclassified	
	TRUE				
	TRUE				
	TRUE				
RDMR			17:7965173	Promoter_Associated_Cell_type_specific	
	TRUE		12:1158129	Unclassified_Cell_type_specific	
		1:20895554	1:21022416	Promoter_Associated	
		13:112708247-112708397			
		5:2695995-2696300			
		6:29090660-29091243			
	TRUE				
		9:114890846-114892814			
	TRUE		7:12940982	Unclassified_Cell_type_specific	
		6:30146876-30147422			
		5:140533155-140533390			
	TRUE				TRUE

		12:5267480	12:5438870	Unclassifie	TRUE
	TRUE	14:92767777-92768346			TRUE
		7:51048855-51048941			
		3:10124751-10125032			
RDMR		3:53355843	3:53380481	Promoter_Associated	
			5:13541621	Unclassifie	TRUE
	TRUE	7:1542920-1544949			
RDMR					
	TRUE				TRUE
	TRUE	10:134269524-134270027			
		7:157559465-157559852			
		13:1126336	13:1135855	Unclassifie	TRUE
		X:19049688-19051204			
		11:65441684-65441992			
	TRUE				TRUE
		1:7355186-7355285			
			6:10814513	Promoter_Associated	
	TRUE		6:4352280-	Unclassifie	TRUE
	TRUE				
		13:99015793-99016308			
RDMR			11:6352944	Unclassified_Cell_type_specific	
	TRUE				
	TRUE		13:9997450	Unclassified_Cell_type_specific	
	TRUE				
		10:135109074-135110338			
		16:80075431-80075814			
		7:55484366-55484743			
RDMR		12:105875041-105875074			
RDMR					
		11:1038567-1038662			
		2:558162-558519			
	TRUE				
		12:123534312-123534371			
		21:3636406	21:3744189	Unclassified	
	TRUE				

	TRUE				
	TRUE	16:73705909-73707003			
	TRUE				TRUE
	TRUE	13:83351215-83352334			
	TRUE				TRUE
		8:12031844-12032207			
		19:17766500-17767317			TRUE
	TRUE				TRUE
		16:3272474-3274413			
		8:1779956-1780286			TRUE
	TRUE		2:24210107	Unclassifie	TRUE
	TRUE				
		17:78459337-78459529			
		17:113233-113291			
		7:1754218-1754471			
	TRUE				
		22:35823715-35824064			
		3:152661314-152661674			
	TRUE		17:4827257	Unclassified	
		21:4297821	21:4410535	Unclassified_Cell_type_specific	
	TRUE				
		14:102045156-102046652			
		11:6689828	11:6714158	Promoter_Associated	
	TRUE				
DMR		17:4386242	17:4650634	Promoter_Associated_Cell_type_specific	
	TRUE				TRUE
		X:39919184-39921423			TRUE
		15:24662622-24662793			
	TRUE				
		X:4866056	X:4877613	Promoter_Associated	
	TRUE		11:3638390	Unclassified_Cell_type_specific	
			17:7952487	Gene_Associated	
	TRUE	17:7633995	17:7872518	Unclassifie	TRUE
			19:6361204	Promoter_Associated	
	TRUE				TRUE
RDMR		19:5689789	19:5220603	Promoter_A	TRUE

		6:706169-706764			
	TRUE				
		3:42281154-42282600			
		19:5389166	19:4919990	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				TRUE
		2:161213001-161213160			
CDMR		13:3494724	13:3604920	Unclassified_Cell_type_specific	
	TRUE				
		12:5266343	12:5437711	Unclassified_Cell_type_specific	
	TRUE				
		20:42221699-42222800			
		7:51507008-51507193			
		19:63643061-63644062			
	TRUE				TRUE
		20:2678063-2679833			
	TRUE				
	TRUE				TRUE
		10:719189-719260			TRUE
	TRUE				
RDMR		3:75916851-75917451			
		4:7423880-7424012			
		11:991560-991653			
RDMR		5:140568565-140568673			
		14:76110963-76111038			
	TRUE	5:14433305-14433455			
		12:101876089-101876843			
		6:28665649-28666050			
	TRUE				
		2:238312494-238312699			
	TRUE				
		5:140711233-140712211			
			12:7578433	Promoter_Associated	
		7:157844890-157844974			
		5:25226198-25226865			
	TRUE				

RDMR		13:112672867-112673179			
	TRUE		4:17726200	Unclassified	
	TRUE				
		12:1135868	12:1151033	Unclassified_Cell_type_specific	
DMR		11:11598435-11600432			
	TRUE				
		4:110743825-110744479			
	TRUE				
		1:14756066	1:14929445	Unclassifie	TRUE
	TRUE	19:3606801-3606953			TRUE
		2:241210703-241210844			
	TRUE				
high-CpG:30817247-30817405		X:3081680	X:3090681	Promoter_Associated	
	TRUE				TRUE
	TRUE				
high-CpG:161906095-161906122		2:161905748-161906142			
			6:10654655	Promoter_Associated_Cell_type_specific	
	TRUE				
		X:4854467	X:4865951	Promoter_Associated	
		4:2275327-2275585			
		2:1865061-1865166			
	TRUE				
	TRUE		8:41393270	Unclassified	
	TRUE				
		11:390097-	11:400119-	Unclassifie	TRUE
CDMR			6:27521010	Unclassified_Cell_type_specific	
	TRUE				
	TRUE	1:20408553	1:20581881	Unclassified_Cell_type_specific	
	TRUE				TRUE
	TRUE				TRUE
		11:131612606-131612745			
		X:7375057	X:7383383	Promoter_Associated	
		8:37124707-37124778			
		10:130169634-130169698			

high-CpG:129072103-129072607			X:1290713	X:1292440	Promoter_Associated	
low-CpG:2896287-2896296			X:2896133-2896517			
		TRUE				TRUE
			6:27899728-27900365			
			17:22117850-22118335			
	RDMR					
			15:32874149-32874293			
		TRUE				
		TRUE	6:31383697	6:31275659	Promoter_Associated	
			5:13906897	5:13908852	Unclassified_Cell_type_specific	
		TRUE	11:133422036-133422707			TRUE
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
		TRUE				
			17:2998854	17:3296422	Unclassified	
			2:24251131-24252173			
			12:31161327-31165315			
				6:33049468	Unclassified	
		TRUE				
	RDMR					
		TRUE				
		TRUE				
			5:80293015-80293093			
		TRUE		7:94953742	Unclassified_Cell_type_specific	
		TRUE				
						TRUE
	RDMR	TRUE	11:2803508-2803611			TRUE
			7:157743573-157743800			
		TRUE				
		TRUE				
				17:3818297	Gene_Associated	
			X:1001934	X:1003062	Promoter_A	TRUE
		TRUE	6:166179903-166180003			
			5:14003224	5:14005250	Gene_Associated_Cell_type_specific	
			7:753304-753398			

		1:1988507-1988577			
			10:4267348	Unclassifie	TRUE
		14:55302706-55303034			
					TRUE
	TRUE				
		20:60178322-60178580			
	TRUE				
	TRUE				
		7:2730655-2730793			
	TRUE				
		5:11043392	5:11040610	Unclassified_Cell_type_specific	
		5:31832403-31832495			
	TRUE				
	TRUE		17:6151464	Unclassified_Cell_type_specific	
		2:113975957-113976498			TRUE
	TRUE				TRUE
		7:149595207-149595289			
;5'UTR;TSS200;Body;Body;Body;TSS200					
	TRUE	1:91072778-91072881			
		7:64040504-64040692			
high-CpG:39877885-39878287		1:39877598	1:40104740	Unclassifie	TRUE
		5:140168063-140169188			
	TRUE				
	TRUE				
	TRUE				
			8:2081873-	Unclassified_Cell_type_specific	
	TRUE		8:12955285	Unclassified_Cell_type_specific	
	TRUE				
		2:23221600	2:23250728	Unclassifie	TRUE
	TRUE				
	TRUE				
		19:52739282-52740974			
	TRUE				

		TRUE				
			6:170292496-170295015			
			2:768665-768732			
			13:23800293-23800714			
			5:140482992-140483946			
		TRUE				
	DMR	TRUE	7:43255207-43255473			
			3:44777570-44777645			
			6:27590868-27591068			
		TRUE				
			6:14445913	6:14441736	Promoter_Associated	
		TRUE		4:3371177-	Promoter_A	TRUE
		TRUE				
		TRUE				
		TRUE	6:166179903-166180003			
		TRUE		2:21870779	Unclassified_Cell_type_specific	
			2:241338561-241338699			
		TRUE		2:48647472	Unclassified	
		TRUE				
			5:1647215-	5:1594141-	Unclassifie	TRUE
		TRUE	5:71510833-71511184			TRUE
			3:193771919-193771992			
			7:151042321-151042470			
			17:74756858-74757025			
	DMR		3:42922485	3:42947283	Unclassified_Cell_type_specific	
			11:69943787-69943867			
		TRUE				
high-CpG:46503490-46503609			X:4650281	X:4661791	Promoter_A	TRUE
			13:110079031-110079185			
			13:112032968-112033729			
		TRUE				
		TRUE				TRUE
		TRUE		4:14857871	Unclassifie	TRUE
		TRUE				
			6:26232449	6:26123951	Promoter_Associated	
		TRUE				

			7:151054558-151054673			
			X:7023228	X:7031538	Promoter_Associated_Cell_type_specific	
			10:31147972-31148221			
	RDMR		5:14053268	5:14055211	Unclassified	
			17:7673667	17:7912236	Unclassified_Cell_type_specific	
		TRUE		6:14322391	Unclassified	
		TRUE				
				2:30669584	Promoter_A	TRUE
			4:788539-788984			
		TRUE				
			19:18749033-18749969			
low-CpG:26537574-26537741						
		TRUE				
		TRUE				
		TRUE				
			X:4619120	X:4630577	Promoter_Associated_Cell_type_specific	
			19:22491987-22493101			
		TRUE				
			5:140533623-140534821			
high-CpG:20194831-20195196			X:2019330	X:2028501	Promoter_Associated	
				3:17175941	Promoter_Associated	
				7:15810663	Unclassified_Cell_type_specific	
SS200		TRUE				
			Y:14372689-14374399			
	RDMR					
			8:3073828-3073887			
			1:205909376-205909873			
		TRUE				
		TRUE		6:32577685	Unclassifie	TRUE
		TRUE	12:1218256	12:1232581	Promoter_Associated	
				21:4607736	Unclassified_Cell_type_specific	
		TRUE		4:18580112	Unclassified_Cell_type_specific	

			10:132834779-132834899			
			17:75537362-75537568			
	RDMR			5:12640822	Promoter_Associated	
			4:9083998-9086046			
	RDMR			1:22105535	Unclassifie	TRUE
		TRUE				
		TRUE				
	RDMR			1:22105877	Gene_Associated_Cell_type_specific	
		TRUE	7:2694250-	7:2727641-	Unclassifie	TRUE
			2:23292392	2:23321532	Unclassifie	TRUE
			16:84436441-84436647			
		TRUE				
			19:2851365	19:2900360	Promoter_Associated	
		TRUE				
		TRUE				TRUE
		TRUE				
		TRUE				
			1:11003168	1:11023012	Unclassifie	TRUE
						TRUE
			17:76549665-76549888			
			17:22313615-22314516			
			2:98295010-98295357			
		TRUE				TRUE
		TRUE				
			4:57755348-57755531			
		TRUE				
		TRUE				TRUE
		TRUE				TRUE
			6:90653952-90654337			
			19:42731376-42732703			
	RDMR					
				5:13189220	Promoter_Associated	
			10:121136130-121136382			
			5:8674010-8674226			
high-CpG:18912347-18913029			X:1891192	X:1900182	Promoter_Associated	

low-CpG:3150228-3150229						
			5:140209224-140210586			
	RDMR					TRUE
		TRUE				
			4:140420515-140421031			TRUE
				6:29980416	Unclassifie	TRUE
	CDMR		22:4483855	22:4645981	Unclassified_Cell_type_specific	
			19:63258293-63258554			TRUE
	RDMR	TRUE	7:96493380	7:96655715	Unclassified_Cell_type_specific	
			1:115198972-115199456			
		TRUE				
		TRUE	14:100244968-100245789			TRUE
		TRUE				
			5:2258479-2258554			
		TRUE				
low-CpG:85157802-85158071						
		TRUE	5:4994952-	5:4942399-	Unclassifie	TRUE
			11:66898529-66898607			
				17:4486521	Unclassified	
		TRUE				
			Y:15145134-15146481			
		TRUE				TRUE
high-CpG:9069753-9069761			11:9069038	11:9112650	Unclassifie	TRUE
		TRUE				
		TRUE				
			3:49915068	3:49940225	Promoter_A	TRUE
						TRUE
		TRUE	6:166180446-166180563			
		TRUE				
			X:43398975-43400591			
;5'UTR		TRUE				
			20:2580718	20:2632226	Promoter_Associated	
		TRUE				TRUE

		TRUE				TRUE
		TRUE				
			10:3169691-3169822			TRUE
			1:92724308-92725197			
low-CpG:24795428-24795476				10:2475499	Unclassified_Cell_type_specific	
			5:175558597-175559312			TRUE
				10:9433366	Promoter_Associated	
		TRUE				
			17:77752688-77752973			
			6:17057404	6:17073222	Unclassified_Cell_type_specific	
		TRUE				TRUE
			10:134677070-134677370			
			12:11591500-11591808			
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE				
			X:1086667	X:1087796	Promoter_A	TRUE
			12:3433219-3433694			
		TRUE				TRUE
			17:38832807-38833008			
		TRUE		7:92533606	Unclassifie	TRUE
			10:6223443	10:6182425	Unclassifie	TRUE
		TRUE				
			6:90653952-90654337			
		TRUE				
				1:22390407	Promoter_Associated_Cell_type_specific	
		TRUE				TRUE
	RDMR					TRUE
			6:16979656	6:17005411	Unclassifie	TRUE
		TRUE	10:123899289-123899505			TRUE
			6:30187118-30187260			
		TRUE				TRUE
		TRUE				

		TRUE				
			19:5652177	19:5182956	Unclassifie	TRUE
	RDMR					
				5:53812911	Promoter_Associated	
			X:1523888	X:1527353	Promoter_Associated	
		TRUE				
			1:115199566-115199674			
			14:1049015	14:1058302	Unclassifie	TRUE
		TRUE				TRUE
	DMR	TRUE	11:6358476	11:6382778	Unclassified_Cell_type_specific	
		TRUE				
	DMR			14:7737111	Unclassifie	TRUE
	RDMR					
			10:88013014-88013215			
		TRUE				
	RDMR		4:36921646-36923823			
			4:14985268-14985314			
			8:1484139-1485291			
			10:2553740-2555322			
		TRUE				
				13:4159309	Promoter_Associated	
				19:4221043	Unclassifie	TRUE
			11:6689828	11:6714158	Promoter_Associated	
		TRUE				TRUE
						TRUE
			7:14895370	7:14932107	Promoter_A	TRUE
			10:641046-641183			
	RDMR		10:719846-	10:729535-	Unclassifie	TRUE
low-CpG:50977568-50		TRUE				
		TRUE	8:62214562-62215149			TRUE
			4:1466150-1466310			
	RDMR					
		TRUE				

			16:2854195	16:2863422	Unclassified_Cell_type_specific	
		TRUE				TRUE
				12:5440489	Unclassified	
		TRUE				
						TRUE
		TRUE				
	RDMR	TRUE				
			9:13947611	9:14035582	Promoter_Associated	
	DMR		1:14712054	1:14885487	Unclassified_Cell_type_specific	
		TRUE				TRUE
			19:2742600	19:2791603	Gene_Associated_Cell_type_specific	
				14:7601559	Unclassified_Cell_type_specific	
				6:30652289	Promoter_Associated	
			2:24251131-24252173			
		TRUE				TRUE
		TRUE		11:2695151	Unclassified_Cell_type_specific	
			4:132863643-132874411			
			6:30018182-30019314			
			2:2274688-2275078			TRUE
	RDMR			17:4827437	Unclassified	
low-CpG:62697473-62697712			X:62697298-62697679			TRUE
		TRUE	6:4023770-4024913			
			5:5939614-	5:5886941-	Unclassifie	TRUE
			10:130721263-130721442			
	DMR					
			2:98804674	2:99438639	Unclassified	
						TRUE
	DMR					TRUE
			5:13544411	5:13541621	Unclassifie	TRUE
			X:4032468	X:4043971	Promoter_Associated_Cell_type_specific	
		TRUE		14:3562913	Unclassifie	TRUE

		10:118377008-118377466			TRUE
	TRUE				
		18:7096580	18:7283759	Unclassifie	TRUE
RDMR		5:12643692	5:12640822	Promoter_Associated	
	TRUE		17:3339047	Promoter_A	TRUE
	TRUE				TRUE
		5:179980265-179981428			TRUE
	TRUE				TRUE
	TRUE				
	TRUE				TRUE
			6:36409083	Unclassified	
		5:110257630-110257959			
	TRUE				
	TRUE				
		X:24935141-24935636			
			22:1826758	Unclassified	
	TRUE				
	TRUE	8:48838464-48838608			
	TRUE				
		5:720880-7	5:668906-6	Unclassifie	TRUE
DMR		X:5553264	X:5551479	Promoter_Associated	
	TRUE	19:6661685	19:6710633	Unclassified_Cell_type_specific	
		2:153851923-153852075			
	TRUE				
	TRUE				
	TRUE	6:101001729-101001967			
	TRUE	11:69508078-69508240			
					TRUE
		7:75983343	7:76144928	Unclassifie	TRUE
			5:13541621	Unclassifie	TRUE
	TRUE	1:226029724-226029920			TRUE
			19:3626565	Unclassified	
		10:30761950-30762238			
		5:217054-217235			

		TRUE				
		TRUE		6:15299749	Promoter_Associated_Cell_type_specific	
SS200		TRUE				
low-CpG:96592051-965		TRUE				TRUE
			12:1316867	12:1331767	Unclassifie	TRUE
			6:31383697	6:31275659	Promoter_Associated	
		TRUE				
						TRUE
	RDMR					
		TRUE				
		TRUE				TRUE
			19:38314751-38315262			
	DMR					
			12:131888391-131888815			
				11:4694137	Unclassifie	TRUE
		TRUE				
	CDMR					
			2:242637379-242638530			
		TRUE				
			4:17093226	4:17069577	Unclassified	
			14:1049015	14:1058302	Unclassifie	TRUE
			2:10434774	2:10517173	Unclassified_Cell_type_specific	
		TRUE				TRUE
		TRUE	2:17530280	2:17559487	Unclassifie	TRUE
			6:30146876	6:30039021	Unclassified_Cell_type_specific	
		TRUE				
	CDMR		13:83351215-83352334			
			1:11003168	1:11023012	Unclassifie	TRUE
high-CpG:153380652-153380683			7:153380594-153381431			
			10:1506980-1507313			
			14:98927910-98927943			
		TRUE				
		TRUE				TRUE
low-CpG:96592051-965		TRUE				TRUE
	RDMR			11:7813122	Unclassified	
			10:1351922	10:1353424	Unclassifie	TRUE
high-CpG:48545327-48545604			X:4854467	X:4865951	Promoter_Associated	

		TRUE				
			3:198756688-198756775			
		TRUE		10:3481734	Unclassified_Cell_type_specific	
			17:74306067-74306159			
			13:112724830-112725857			TRUE
				5:17678441	Promoter_Associated	
		TRUE				
			6:30018182-30019314			
			6:30146876-30147422			
		TRUE	17:43974025-43974982			TRUE
						TRUE
	CDMR		7:1065569-1066924			
		TRUE				TRUE
		TRUE				
		TRUE	4:19036052	4:19012320	Unclassified	
		TRUE				
			1:1179922-1180108			
				15:3836135	Unclassifie	TRUE
			10:6314879-6315084			
			6:16979656	6:17005411	Unclassifie	TRUE
			7:63680432-63680633			
	DMR		17:5927996	17:6192611	Unclassified	
		TRUE		2:16934651	Promoter_Associated	
			X:133506240-133506914			
			6:30528709	6:30420915	Unclassified	
high-CpG:65525985-65526868			11:6552580	11:6576905	Promoter_Associated	
			6:1500022-	6:1554396-	Unclassified	
			17:75537362-75537568			
			17:46213488-46213876			
		TRUE				TRUE
		TRUE				TRUE
			2:242517652-242518029			
		TRUE				
			20:56159264-56159624			
			6:33968480-33969040			
			12:131892888-131893296			

		7:911133-911361			TRUE
	TRUE				
		20:58975843-58976262			
		7:14965092	7:15001985	Promoter_A	TRUE
		2:23292392	2:23321669	Unclassifie	TRUE
		2:10258007-10258289			
		12:112879814-112879932			
RDMR		17:35961983-35962222			TRUE
		12:123789398-123789721			TRUE
	TRUE	6:110827422-110828273			
	TRUE		8:12042867	Promoter_A	TRUE
		10:135096465-135097138			TRUE
		21:34963183-34965119			
	TRUE		13:1004702	Unclassified_Cell_type_specific	
	TRUE	2:127667834-127667936			
	TRUE		7:73476279	Unclassified	
		7:76462683-76462912			
	TRUE		20:4794041	Promoter_Associated	
		Y:15145134-15146481			
DMR		10:110661667-110662410			
		10:29787251-29787454			
		17:7730773	17:7789365	Promoter_Associated	
					TRUE
		7:139781665-139782089			
		1:41075951-41076931			
		2:24479201-24479591			
	TRUE				
	TRUE				TRUE
					TRUE
	TRUE				
	TRUE				TRUE
		5:554204-555149			
	TRUE				

			19:4226079	19:3756865	Promoter_Associated	
		TRUE				TRUE
		TRUE				TRUE
		TRUE				TRUE
		TRUE				
						TRUE
		TRUE				
				1:24879152	Unclassified_Cell_type_specific	
		TRUE				
			18:75393037-75393432			TRUE
						TRUE
high-CpG:149817740-149817852			X:1498170	X:1500669	Unclassified	
			19:4117678	19:3648480	Unclassified_Cell_type_specific	
high-CpG:4858321-4858482			10:4858068	10:4867931	Unclassifie	TRUE
			X:1057416	X:1058547	Unclassified_Cell_type_specific	
		TRUE	8:129234722-129234785			
ody						
high-CpG:957307-957377			4:956769-9	4:967161-9	Promoter_Associated	
	DMR	TRUE				TRUE
		TRUE				
	RDMR		5:95321676	5:95295112	Promoter_Associated	
			20:61389487-61390059			
		TRUE				
			3:12767608	3:12619431	Promoter_Associated	
	RDMR		17:17568537-17569429			
	CDMR					
		TRUE				TRUE
		TRUE				TRUE
			10:1351912	10:1353418	Unclassifie	TRUE
			14:98682846-98683100			
			1:41599283-41600818			

			6:39379495-39379736			
			18:75271015-75273504			TRUE
	RDMR		9:21995288	9:22004989	Unclassified	
		TRUE				
			11:123445776-123445894			
			X:73429868-73430195			TRUE
		TRUE				
			1:246366878-246367209			
			2:176724663-176725225			
	DMR					
			4:141610503-141610728			
			22:48103386-48103958			
	DMR		X:1343830	X:1345551	Unclassifie	TRUE
			22:23489876-23490210			
		TRUE				
		TRUE				
		TRUE				
			12:7916632-7917175			
			4:57153412-57153774			TRUE
	DMR		6:10828322	6:10720132	Promoter_Associated_Cell_type_specific	
				14:2236218	Unclassified	
		TRUE				
			2:23142319	2:23171475	Unclassifie	TRUE
			10:135128752-135129051			
		TRUE	5:139020929-139021199			TRUE
			4:188221515-188222057			
		TRUE				
			6:29756034-29757072			
		TRUE		12:1168639	Unclassifie	TRUE
			5:140574417-140574683			TRUE
			12:11591500-11591808			
			12:9987169-9987420			
00;TSS200						

		TRUE				
		TRUE	7:94791746	7:94953742	Unclassified_Cell_type_specific	
		TRUE				
			5:74943881-74943934			
		TRUE				
			19:60169266-60169572			
	DMR	TRUE		15:4218657	Promoter_A	TRUE
				6:7106853-	Promoter_Associated	
		TRUE				
		TRUE				
		TRUE				
				10:6183696	Unclassifie	TRUE
			11:2769023	11:2812612	Unclassified_Cell_type_specific	
			2:74211090-74211806			
			14:70092338-70092914			
				12:5611421	Unclassifie	TRUE
			5:76046163	5:76010566	Unclassified	
		TRUE				TRUE
				11:1712730	Unclassified_Cell_type_specific	
		TRUE				
	DMR		X:109925646-109926213			
			17:596727-597409			
Body						
	RDMR		4:183300391-183300556			
						TRUE
		TRUE				
			3:196267281-196268542			
			12:167535-168128			
		TRUE				
			8:145708317-145708459			
	CDMR					
		TRUE				
			1:199883665-199886396			
				18:2200605	Unclassified_Cell_type_specific	
			17:76660050-76660432			TRUE
		TRUE		21:3642087	Promoter_Associated	
		TRUE	8:48838200-48838325			
		TRUE				

		TRUE				
			10:34384336-34384974			
		TRUE				TRUE
		TRUE				
				14:9230181	Unclassified	
		TRUE				
		TRUE				
		TRUE	11:6457158	11:6481487	Unclassifie	TRUE
		TRUE				
			X:1523933	X:1527394	Unclassifie	TRUE
			12:5266988	12:5438269	Unclassified	
high-CpG:149817740-149817852			X:1498170	X:1500669	Unclassified	
			15:21362279-21362541			
		TRUE		11:1021391	Unclassifie	TRUE
			1:159717054-159717132			
	DMR		X:149281427-149284862			TRUE
		TRUE				
			16:3134639	16:3143869	Unclassified_Cell_type_specific	
			9:114879958-114881963			
			13:24217537-24219288			
			7:1079752-	7:1113017-	Unclassifie	TRUE
		TRUE				
		TRUE		2:19886636	Unclassified_Cell_type_specific	
	RDMR		5:140515840-140515957			
		TRUE				TRUE
		TRUE				TRUE
			11:2736546-2736627			
			17:77689797-77690064			
		TRUE				TRUE
	CDMR		20:35963256-35965761			
		TRUE				
		TRUE				
	DMR		X:144707005-144708118			
	CDMR			7:96649922	Unclassified_Cell_type_specific	
			2:238442283-238442396			
			6:142279825-142280029			
high-CpG:23849959-23850497			14:2384979	14:2477937	Promoter_	TRUE

high-CpG:19815370-19815648		X:1981476	X:1990549	Promoter_A	TRUE
					TRUE
	TRUE				
		12:3433219-3433694			TRUE
RDMR					
UTR;1stExon;Body					
	TRUE		6:37617791	Unclassifie	TRUE
	TRUE				TRUE
		X:1290299	X:1299364	Promoter_Associated	
	TRUE	7:102361651-102361762			
		8:52483619-52484751			
	TRUE		14:6978351	Unclassifie	TRUE
		22:44860480-44860688			TRUE
	TRUE				
	TRUE				
		10:135228782-135229757			
		8:1308550-	8:1321062-	Unclassified_Cell_type_specific	
		12:3255012	12:3383655	Unclassified	
	TRUE	17:3397125	17:3671762	Unclassified_Cell_type_specific	
		6:169800047-169800148			
			6:30919983	Unclassified_Cell_type_specific	
	TRUE	X:17583175-17584657			
	TRUE		7:94953742	Unclassified_Cell_type_specific	
		11:119475633-119475724			
		10:27275462-27275688			
		1:2917997-2918575			TRUE
00;TSS1500	TRUE				
	TRUE				
		7:63279448-63281237			
	TRUE				
	TRUE				
DMR		12:182853-183533			TRUE
		7:96485945-96486142			
		10:1241678-1241956			

		TRUE				
			11:6091604	11:6115952	Unclassifie	TRUE
	RDMR					
			18:7577937	18:7767839	NonGene_Associated_Cell_type_specific	
		TRUE				
			7:157751555-157752122			
						TRUE
			19:46009664-46009947			
			15:7688975	15:7910383	Unclassified	
			6:30146876	6:30039021	Unclassified_Cell_type_specific	
			17:8065311	17:8124242	Promoter_A	TRUE
		TRUE	15:38055924-38056353			TRUE
			1:205909376-205909873			
		TRUE	10:68357870-68358056			
		TRUE				
			7:149099665-149101377			
	RDMR	TRUE				TRUE
						TRUE
high-CpG:18353623-18353678			X:1835273	X:1844361	Promoter_Associated	
high-CpG:4858321-4858482			10:4858068	10:4867931	Unclassifie	TRUE
		TRUE				TRUE
			19:63419917-63420931			
		TRUE				
		TRUE				TRUE
			1:2110741-	1:2120661-	Promoter_Associated	
		TRUE	20:2507658	20:2512878	Unclassified_Cell_type_specific	
		TRUE				TRUE
			2:1725201-1725279			TRUE
		TRUE				TRUE
		TRUE				
	DMR	TRUE	8:62214562	8:62051046	Unclassifie	TRUE
		TRUE				
		TRUE	10:3128406-3128559			
			11:1848614	11:1891168	Unclassified	
				7:14308104	Gene_Associated_Cell_type_specific	
				1:22610768	Gene_Asso	TRUE

			19:59730038-59730299			
			12:123346762-123346992			TRUE
		TRUE				TRUE
				12:5439085	Unclassified_Cell_type_specific	
		TRUE	21:4565429	21:4682989	Unclassifie	TRUE
	DMR		X:7126717	X:7135121	Unclassifie	TRUE
		TRUE				
		TRUE				
		TRUE				
			X:3081680	X:3090681	Promoter_Associated	
			7:96488337	7:96650600	Unclassified_Cell_type_specific	
			7:157814865-157815150			
		TRUE				TRUE
	DMR	TRUE		17:4043930	Promoter_Associated	
			6:127838005-127839014			
high-CpG:24947233-24		TRUE	12:2494670	12:2505550	Unclassified	
			Y:7201522-7203224			
			12:52667207-52667281			
			12:5266343	12:5437711	Unclassified_Cell_type_specific	
			1:7045198-7045611			
		TRUE				
		TRUE	6:166179903-166180003			
		TRUE				TRUE
			4:191141974-191143118			
			6:28691806-28692367			
		TRUE				TRUE
		TRUE				
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
		TRUE				TRUE
high-CpG:152565702-152566020			X:152565697-152566913			
			1:24616638	1:24810001	Promoter_Associated	

				1:8959962-	Unclassifie	TRUE
						TRUE
		TRUE				TRUE
			7:157724753-157725305			
				3:9974268-	Promoter_Associated	
			7:158226624-158226697			
		TRUE				
		TRUE				TRUE
		TRUE				
			7:157063222-157063643			
			15:31373466-31373555			
			15:38208295-38208428			
				6:36076869	Gene_Associated_Cell_type_specific	
low-CpG:70827875-70828160				17:7331603	Gene_Associated_Cell_type_specific	
			X:8414541	X:8425875	Promoter_A	TRUE
		TRUE				
		TRUE				
			14:20261387-20261694			
			19:1021950-1022967			
	DMR		2:88845443	2:89064815	Unclassifie	TRUE
			15:38151816-38152291			
		TRUE				
				15:8333194	Unclassifie	TRUE
high-CpG:32755739-32756228			20:3275511	20:3329130	Promoter_Associated	
		TRUE				
		TRUE	2:9153313-9153457			TRUE
			6:27906800-27907406			
			10:112394964-112395003			
			15:29142578-29142735			
						TRUE
		TRUE				
			17:3819034	17:4093670	Unclassified_Cell_type_specific	
		TRUE				
	DMR	TRUE	X:152747214-152749925			
	DMR			17:6734912	Unclassifie	TRUE
			17:78562801-78562839			

	TRUE				TRUE
		3:28919697-28919994			
	TRUE				
		X:150146879-150147105			
		1:20110885-20110960			
					TRUE
	TRUE		10:9570692	Unclassified_Cell_type_specific	
	TRUE				
		2:242491251-242492178			TRUE
		7:157562575-157562847			
		5:17146618	5:17153363	Promoter_A	TRUE
	TRUE	2:3676920-	2:3698449-	Unclassified	
	TRUE				
	TRUE	12:4662216	12:4833563	Unclassifie	TRUE
		6:42802850	6:42695456	Promoter_Associated_Cell_type_specific	
		5:271046-2	5:217629-2	Promoter_Associated	
RDMR		3:55491072-55492537			
	TRUE		11:1266605	Unclassified_Cell_type_specific	
		17:77987705-77987897			
	TRUE	7:15788032	7:15818761	Unclassifie	TRUE
	TRUE		17:7307316	Promoter_A	TRUE
	TRUE		13:3142211	Unclassifie	TRUE
high-CpG:19918865-19919101		X:1991844	X:2000834	Promoter_Associated	
	TRUE				TRUE
	TRUE				
	TRUE				
		5:1909552-1910665			
	TRUE				
		6:30526824	6:30419361	Unclassified_Cell_type_specific	
	TRUE				TRUE
high-CpG:28225511-28225662		20:2822466	20:2961113	Promoter_A	TRUE
		4:930644-931149			
		7:1022123-1023261			
		4:720343-720990			
		17:3427747	17:3702371	Unclassified	
	TRUE				
		11:7120212	11:7152435	Unclassified	

			6:28691806-28692367			
			X:1187103	X:1188259	Promoter_A	TRUE
			8:1387573-1387673			
			11:72731323-72731950			
			6:9507080-9507585			
			7:27174681	7:27207963	Unclassified_Cell_type_specific	
high-CpG:40325113-40325219			X:4032468	X:4043971	Promoter_Associated_Cell_type_specific	
		TRUE				
		TRUE				TRUE
	DMR					
		TRUE				
		TRUE				
		TRUE				TRUE
			3:19706262	3:19557756	Unclassified	
		TRUE	2:239786143-239786235			
		TRUE				
		TRUE				
		TRUE				
			2:74728583-74729057			
		TRUE				
			X:6467098	X:6475430	Promoter_Associated	
		TRUE				
			1:1216966-	1:1226844-	NonGene_Associated	
				20:5219966	Promoter_Associated_Cell_type_specific	
				6:33049468	Unclassified	
			19:57646274-57646657			
			1:22421684	1:22614987	Unclassifie	TRUE
	RDMR			8:12428435	Promoter_Associated_Cell_type_specific	
			8:273841-273886			
			1:27559510-27560330			TRUE
			7:62990927-62991057			
				14:1053993	Unclassified_Cell_type_specific	

		2:785876-786168			
	TRUE				
		17:182607-183090			
high-CpG:138841980-138842354		X:138841098-138843256			TRUE
	TRUE				
	TRUE				
	TRUE				TRUE
DMR					TRUE
		2:23292392	2:23321532	Unclassified_Cell_type_specific	
	TRUE		12:1136528	Unclassifie	TRUE
		6:832641-833102			
	TRUE				
		7:963872-964146			
		4:1192911-1193178			
	TRUE				
		3:56691533	3:56716001	NonGene_Associated	
	TRUE				TRUE
		1:201045468-201045500			
		1:205909376-205909873			
		3:133597963-133598063			
low-CpG:100902942-100903160					
			19:7766576	Unclassified_Cell_type_specific	
		5:11863170	5:11860325	Promoter_Associated	
	TRUE				
		7:63672852-63672965			
		1:3086669-3088504			
	TRUE	19:1407058	19:1455143	Unclassified	
		X:5347782	X:5346113	Promoter_Associated	
		20:58975843-58976262			
		8:7574979-7575663			TRUE
		1:3198648-3199497			
		5:1647215-	5:1594141-	Unclassifie	TRUE
		9:139388302-139388798			
	TRUE				TRUE
	TRUE				
		8:14473045	8:14465959	Promoter_Associated	
	TRUE				
RDMR		2:26057468	2:26204073	Promoter_Associated	
	TRUE				
			X:2185824	Promoter_Associated	

	TRUE	3:19506984	3:19358748	Unclassifie	TRUE
	TRUE				TRUE
			9:91997628	Gene_Associated_Cell_type_specific	
DMR		X:139413290-139416623			
					TRUE
RDMR			8:72917248	Unclassified	
RDMR		1:110553818-110556317			
		19:3546660-3546977			
RDMR	TRUE	12:113608673-113609609			
		6:30187118-30187260			
	TRUE				
	TRUE				
	TRUE				
		9:13943071	9:14031169	Unclassified_Cell_type_specific	
		9:11486353	9:11582461	Unclassified_Cell_type_specific	
RDMR			X:1519988	Promoter_Associated	
		7:143731528-143732029			
		12:7407112	12:7578433	Promoter_A	TRUE
RDMR		1:15042790	1:15216100	Unclassified	
	TRUE				
	TRUE				
		6:1544099-1544401			
		2:236787715-236788295			
	TRUE				
	TRUE				
		7:157040922-157041050			
DMR		X:102204996-102205937			TRUE
	TRUE				TRUE
		8:131069429-131069745			
		10:1350206	10:1351703	Promoter_Associated	
		2:104484979-104485019			
CDMR		13:3494724	13:3604920	Unclassified_Cell_type_specific	
		1:24560367	1:24753695	Unclassified_Cell_type_specific	
	TRUE	17:70568276-70568403			TRUE
		1:147452792-147453248			
					TRUE
	TRUE				

	TRUE	11:13940491-13942898			
DMR		17:7784869	17:8025473	Promoter_A	TRUE
		8:70785639-70786175			
	TRUE				TRUE
		22:17118280-17118545			
		20:23917150-23917414			
	TRUE				
	TRUE				TRUE
			2:11393078	Promoter_Associated_Cell_type_specific	
		19:469862-470886			
	TRUE				TRUE
		8:22188506-22189257			
	TRUE				
		13:80126929-80127419			
		7:37453513	7:37487225	Promoter_A	TRUE
RDMR					
		6:32740137	6:32632265	Unclassified	
		8:1638463-1638636			
		4:38501804-38502104			
	TRUE	1:241651410-241651510			
	TRUE	3:11585138-11585370			TRUE
		3:64522146-64522449			
			12:308499-	Unclassifie	TRUE
		11:1848614	11:1891168	Unclassified	
		5:140461401-140461552			
	TRUE		22:2700627	Unclassifie	TRUE
		13:2477299	13:2587501	Promoter_Associated	
			7:13566113	Promoter_Associated	
		5:140774543-140775229			
		13:113241092-113241279			
	TRUE				TRUE
		4:2401607-2402112			TRUE
			17:100783-	Unclassified_Cell_type_specific	

			19:803661-804624			
		TRUE				
	DMR		16:8723373	16:8870523	Promoter_Associated	
				4:88140405	Promoter_Associated	
				2:24087359	Unclassified	
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE				
						TRUE
	RDMR					
			X:6875240	X:6883556	Unclassifie	TRUE
			6:101953488-101953918			
			7:151184350-151184612			
		TRUE		3:23710232	Unclassified_Cell_type_specific	
			2:1636469-1636527			TRUE
low-CpG:116112827-116112933						
		TRUE	7:1062770-1064945			
		TRUE		13:3073277	Unclassifie	TRUE
		TRUE				
		TRUE				TRUE
		TRUE				
		TRUE				TRUE
			17:3808934	17:4083574	Unclassifie	TRUE
			6:169720073-169720338			
		TRUE		2:23643645	Unclassified_Cell_type_specific	
		TRUE		6:32828471	Unclassifie	TRUE
			5:140692011-140692726			
			7:63197874-63198494			
		TRUE				

		TRUE				
		TRUE				TRUE
			10:133646455-133646588			
low-CpG:13032130-13032221				3:13056540	Promoter_Associated	
			5:140516321-140516553			
	DMR	TRUE		6:13691508	Unclassifie	TRUE
		TRUE				
		TRUE				
		TRUE				
		TRUE				TRUE
	CDMR					
			6:30187118-30187260			
		TRUE	17:75537843-75537970			
						TRUE
			15:99410683-99411468			
		TRUE				
			7:156029868-156029986			
		TRUE				
			7:934964-935104			TRUE
low-CpG:45623193-45623284						
		TRUE		1:14498951	Unclassifie	TRUE
			2:242454426-242454693			
		TRUE				
		TRUE				TRUE
				20:6069236	Unclassified_Cell_type_specific	
		TRUE				
low-CpG:30414789-304		TRUE		17:3339047	Promoter_A	TRUE
	RDMR					
		TRUE				
		TRUE		5:77888050	Unclassified_Cell_type_specific	
			17:19823918-19824447			
			6:28555047-28555115			
	DMR					

		5:140162085-140163180			
		7:1105191-1105603			
		8:10592792-10592898			
		5:1647215-	5:1594141-	Unclassifie	TRUE
		15:4328030	15:4549231	Promoter_Associated	
		1:147429014-147429218			
		2:869464-869580			
	TRUE	1:19853791	1:20027061	Promoter_Associated_Cell_type_specific	
	TRUE				
RDMR	TRUE	19:5689789	19:5220603	Promoter_A	TRUE
	TRUE				
		4:1564434-1565131			
	TRUE				TRUE
		17:74862622-74862744			
		16:20267283-20267953			
	TRUE				TRUE
			6:13819262	NonGene_Associated	
		19:5555358	19:5086164	Promoter_A	TRUE
		2:236338885-236339036			TRUE
		8:1778200-1778355			TRUE
	TRUE				
		2:241260182-241261463			
			3:16016837	Promoter_A	TRUE
		2:89653541-89653604			
high-CpG:46889009-46889446		X:4688863	X:4700359	Promoter_Associated	
	TRUE				
					TRUE
	TRUE		4:6690627-	Promoter_A	TRUE
	TRUE				
		7:100040970-100041563			
		6:27769743	6:27661604	Promoter_A	TRUE
	TRUE				TRUE

				22:2575794	Gene_Associated	
		TRUE				TRUE
		TRUE		11:4802687	Unclassified_Cell_type_specific	
			2:91122000-91122157			
			3:64522146-64522449			
			6:28691806-28692367			
		TRUE				
		TRUE				TRUE
			6:88813982-88814582			
			11:64350766-64351788			
				18:3307687	Promoter_Associated	
			5:140188938-140190113			
		TRUE				
		TRUE				
			10:1394494-1396219			
			18:1293763	18:1294682	Promoter_Associated	
high-CpG:40724718-40725132			22:4072456	22:4239415	Promoter_A	TRUE
	RDMR			5:14055211	Unclassified	
	CDMR		6:1539206-1539630			
			2:233031487-233032158			
		TRUE				
				6:33128418	Unclassified	
		TRUE	5:175493778-175493946			
		TRUE				TRUE
			19:15424555-15425223			
		TRUE				TRUE
	RDMR			15:7251846	Promoter_Associated	
		TRUE		8:10374191	Unclassifie	TRUE
		TRUE				
			3:36960545	3:36985431	Promoter_Associated	
			17:73300799-73301148			
		TRUE				
		TRUE				

		TRUE				
		TRUE		6:16713588	Unclassified_Cell_type_specific	
			10:21501819-21503790			
				13:3068586	Unclassified	
		TRUE	17:7392957	17:7641794	Gene_Associated	
		TRUE				
		TRUE				
			5:18060282	5:18067031	Promoter_Associated	
						TRUE
			17:68148128-68148894			
		TRUE				
		TRUE				
			19:22683551-22684101			
			19:5273928	19:4804820	Unclassified_Cell_type_specific	
			22:44664192-44666286			
		TRUE	7:12117667-12118080			
		TRUE				
			7:2920350-2920485			
high-CpG:27354108-27354214			1:27353982	1:27481112	Promoter_Associated	
Body;Body;Body;Body;		TRUE				
		TRUE				
			13:112783032-112783678			
		TRUE				
			13:100658340-100658497			
		TRUE				TRUE
		TRUE				
		TRUE				TRUE
		TRUE				
		TRUE				TRUE
		TRUE				
			15:6754162	15:6975447	Promoter_Associated	
			6:30001657	6:29894087	Promoter_Associated	
		TRUE				
			1:147422337-147422540			
			5:6487966-6488073			
	CDMR					
		TRUE				

			2:91140387	2:91777278	Unclassifie	TRUE
		TRUE	7:157802820-157802914			
			7:5150455-	7:5182685-	Unclassifie	TRUE
			6:101953488-101953918			
		TRUE				
	RDMR					
		TRUE				
ody						
			19:1327036	19:1340949	Unclassified_Cell_type_specific	
				7:91762807	Promoter_Associated	
		TRUE				TRUE
		TRUE				
		TRUE				
high-CpG:13148870-13149049			20:13148671-13150815			TRUE
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE				
		TRUE		10:3710509	Unclassifie	TRUE
		TRUE				
			12:1135938	12:1151096	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
		TRUE				TRUE
			2:232982211-232982769			
						TRUE
		TRUE				
		TRUE				
	DMR		5:128823240-128824166			TRUE
			X:12065967-12067195			

DMR			6:13520321	Unclassified	
CDMR					
		6:1500022-	6:1554396-	Unclassified	
		8:28230766-28230941			
	TRUE		2:17849945	Unclassified_Cell_type_specific	
	TRUE				
		10:1199912	10:1200011	Unclassified_Cell_type_specific	
		2:2549248-2549326			
			1:63249154	Promoter_A	TRUE
		6:6682050-6682631			
		1:244864675-244865025			
	TRUE				TRUE
					TRUE
		1:22680931	1:22874303	Unclassified_Cell_type_specific	
		1:147452792-147453248			
	TRUE				
	TRUE				
	TRUE	1:2243584-	1:2253667-	Unclassifie	TRUE
CDMR		15:50862711-50862856			
	TRUE				
		12:29433503-29434105			
	TRUE				
			13:4159309	Promoter_Associated	
		1:15967609	1:16140957	NonGene_	TRUE
	TRUE		4:4992371-	Unclassifie	TRUE
		11:7721035	11:7753167	Promoter_Associated	
					TRUE
		6:150317166-150318017			
		7:14965092	7:15001985	Promoter_	TRUE
	TRUE				
	TRUE				
		12:5661600	12:5832962	Promoter_	TRUE
DMR		13:23800293-23800714			
	TRUE				TRUE
	TRUE	17:928217-929248			
		14:64138032-64138401			

			12:127435732-127435964			
		TRUE		17:4303705	Unclassified_Cell_type_specific	
			5:140482992-140483946			
			13:110733430-110733683			
		TRUE				
		TRUE				
		TRUE				
			8:6620373-6620492			
high-CpG:46962370-46963215			X:4696206	X:4707709	Promoter_Associated	
				X:5625826	Unclassifie	TRUE
		TRUE				
		TRUE				
		TRUE				TRUE
00						
			6:101954025-101954110			
high-CpG:7	CDMR		2:72223562-72226253			
			5:28963266-28964394			TRUE
			7:5829266-	7:5862265-	Promoter_Associated	
		TRUE				TRUE
		TRUE				TRUE
			5:12643692	5:12640822	Promoter_Associated	
		TRUE				
			13:43351208-43352505			
			22:4934750	22:5100105	Promoter_Associated	
		TRUE				TRUE
				22:3149810	Unclassifie	TRUE
	RDMR					TRUE
						TRUE
				17:5656630	Gene_Associated_Cell_type_specific	

		TRUE				
			7:15709755	7:15740528	Unclassified_Cell_type_specific	
		TRUE				
high-CpG:7	CDMR		2:72223562-72226253			
			7:63680432-63680633			
			20:56159264-56159624			
			19:22683551-22684101			
		TRUE	3:49730543	3:49756080	Promoter_Associated	
			11:2847136	11:2890760	Unclassified_Cell_type_specific	
			15:99680033-99680235			
		TRUE				
			14:101120126-101120800			TRUE
		TRUE				
		TRUE				
	RDMR					
		TRUE				
		TRUE				TRUE
			1:147422337-147422540			
		TRUE				
		TRUE				
			7:157768103-157768566			
			1:33403558-33403679			
			2:94903675	2:95539782	Unclassified	
		TRUE				TRUE
			7:157724753-157725305			
	RDMR					
			5:14069869	5:14071798	NonGene_	TRUE
		TRUE				
		TRUE				
			7:137999314-138000282			
		TRUE	8:14470647	8:14463507	Promoter_Associated	
		TRUE				
			10:134770320-134770435			
			1:147429014-147429218			
			1:41075951-41076931			

			1:6448638-6449057			TRUE
			X:27791876-27792229			
		TRUE				
		TRUE				
			10:132799279-132799514			
			2:26804049-26804924			
			3:14590404-14591222			
			2:11374992	2:11403381	Unclassified_Cell_type_specific	
			12:131355394-131355649			
Body;Body;Body;Body;		TRUE				
			7:157038420-157038660			
		TRUE				
			13:113793054-113793310			
		TRUE				
	DMR		1:22570190	1:22763530	Unclassifie	TRUE
			1:85854289-85854656			
				3:4344354-	Promoter_Associated	
	CDMR	TRUE	7:1065569-1066924			
		TRUE	11:6714011	11:6738291	Promoter_Associated	
		TRUE				TRUE
Body;Body;Body;Body		TRUE				
	RDMR					
			X:7066941	X:7075253	Promoter_A	TRUE
			1:2874923-2875144			
		TRUE				TRUE
	DMR		19:2201561-2205121			
		TRUE				TRUE
high-CpG:97572605-97573194			2:97572400	2:98206657	Promoter_Associated	
			1:24560367	1:24753695	Unclassified_Cell_type_specific	
low-CpG:47943393-47943398				7:47976840	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
			X:24935141-24935636			
high-CpG:6686502-6686683			5:6685483-	5:6632952-	Promoter_Associated	
	RDMR	TRUE	6:106540627-106540959			

		5:140510514-140510878			
		5:179673298-179673711			TRUE
		6:28769178-28769334			
	TRUE				TRUE
CDMR					
low-CpG:32036741-320	TRUE				TRUE
		1:18681057-18682254			
	TRUE		8:23655948	Unclassifie	TRUE
		14:101624474-101624817			
	TRUE				
Body;Body;Body;Body	TRUE				TRUE
	TRUE				
		7:157851519-157852110			
DMR		7:15709755	7:15740528	Unclassified_Cell_type_specific	
	TRUE	8:22617828-22617905			
		7:15433659	7:15470457	Unclassified	
	TRUE	14:100609113-100609405			
			6:33049468	Unclassifie	TRUE
			6:32634123	Unclassifie	TRUE
	TRUE				
	TRUE				
	TRUE				
		10:1110378-1110667			
		14:43071792-43072182			
		X:125542609-125542988			
	TRUE				TRUE
	TRUE		1:20327572	Promoter_Associated	
		X:1290299	X:1299250	Promoter_Associated	
		12:2209182-2210061			
	TRUE				
		10:1351922	10:1353424	Unclassifie	TRUE
	TRUE	8:141317755-141317850			TRUE
	TRUE				
		6:74119872-74121192			
		14:2373428	14:2466414	Promoter_Associated	
	TRUE				TRUE
low-CpG:10860093-10860218					
	TRUE				

			14:101120126-101120800			TRUE
			14:105963220-105963349			
		TRUE				
			4:187363055-187363137			
			5:589396-590522			TRUE
			14:103841835-103842055			
		TRUE	5:17647635	5:17654356	Unclassifie	TRUE
high-CpG:271357-271476			5:271046-2	5:217629-2	Promoter_Associated	
			7:1108823-1109576			
			5:140606553-140607551			
		TRUE				
		TRUE	3:197354390-197354672			TRUE
		TRUE	17:9069994-9070688			
		TRUE				TRUE
		TRUE				
			8:127637832-127640091			
			20:61522997-61523770			
		TRUE		2:37617441	Unclassifie	TRUE
			10:132928813-132929458			
		TRUE				TRUE
			7:5150455-	7:5182685-	Unclassifie	TRUE
		TRUE				
				13:5148251	Unclassified_Cell_type_specific	
		TRUE				
			6:11251571	6:11240774	Promoter_Associated	
			12:7407112	12:7578433	Promoter_A	TRUE
		TRUE				TRUE
	DMR	TRUE		12:1148513	Unclassified	
			5:140510147-140510412			
		TRUE				
			1:147565200-147565259			
		TRUE				
	DMR			X:1339306	Promoter_Associated	

high-CpG:37960203-37960365			17:3795867	17:4070580	Promoter_Associated	
			13:109887214-109887422			
			15:99405029-99405262			
			4:956769-958049			
		TRUE		6:32828471	Unclassifie	TRUE
			22:23489876-23490210			
		TRUE				
				2:20077540	Promoter_Associated	
			6:88813982-88814582			
	RDMR			1:47901459	Promoter_Associated	
		TRUE				
			3:14214304	3:14066016	Promoter_Associated	
			11:118347497-118348218			
	RDMR					TRUE
			12:130281687-130281727			
			2:201712788-201713129			
			6:30001657	6:29894087	Promoter_Associated	
			11:3210354-3210737			
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				TRUE
		TRUE				
		TRUE				
			6:30146876	6:30039021	Unclassified_Cell_type_specific	
			10:1347602	10:1349101	Unclassified_Cell_type_specific	
		TRUE				
low-CpG:45624888-45625210						
			1:829455-830943			
			6:37037889-37038113			
	RDMR		15:94691709-94692109			
			17:3879327	17:4143737	Promoter_A	TRUE
				22:2922520	Unclassifie	TRUE
			6:30146876-30147422			
		TRUE				
		TRUE				
		TRUE				
			12:1316874	12:1331767	Unclassifie	TRUE

			22:2901484	22:3068548	Promoter_Associated	
		TRUE		17:7486837	Unclassifie	TRUE
			6:10828322	6:10720132	Promoter_Associated_Cell_type_specific	
			15:77976034-77976843			
		TRUE				TRUE
			6:167095865-167095938			
		TRUE	6:170309192-170309742			
				12:1248273	Gene_Associated_Cell_type_specific	
		TRUE	8:59220722	8:59058517	Unclassifie	TRUE
				1:12606835	Unclassified_Cell_type_specific	
			10:27679004-27679231			
			X:7131790	X:7140072	Promoter_Associated	
		TRUE				
				1:16136865	Promoter_Associated	
			2:88364656-88365054			
			1:226957366-226957784			
high-CpG:51688543-51688659			19:51688244-51691087			
		TRUE				
		TRUE	12:2494670	12:2505550	Unclassified	
				1:7762078-	Unclassified_Cell_type_specific	
			4:930644-931149			
			7:56403796-56410557			
		TRUE		2:16005792	Unclassified_Cell_type_specific	
	CDMR	TRUE		17:7948439	Unclassified	
			X:9942469-	X:9982424-	Promoter_Associated	
			8:10382005	8:10375081	Unclassifie	TRUE
		TRUE				TRUE
			17:77599895-77600065			
		TRUE				
			5:140605877-140606072			
		TRUE				
		TRUE				TRUE
			X:6830157	X:6838395	Promoter_Associated	

			X:19049688-19051204			TRUE
			2:206550992-206551338			
		TRUE				
low-CpG:64952070-649		TRUE				
			8:14226161	8:14219152	Gene_Associated	
			Y:9253058-9256190			
00						
		TRUE		6:31104495	Unclassified	
			19:42489115-42489737			
				16:3048473	Promoter_Associated	
			14:100073821-100075434			
		TRUE				TRUE
high-CpG:1	DMR		X:1527472	X:1530953	Unclassifie	TRUE
		TRUE				
			17:212293-212534			
			6:30526824	6:30419361	Unclassified_Cell_type_specific	
		TRUE				TRUE
		TRUE				
			1:18681057-18682254			
		TRUE				
				1:63249154	Promoter_Associated	
		TRUE				
		TRUE	6:170309192-170309742			TRUE
		TRUE				
			6:29756034	6:29648152	Unclassified_Cell_type_specific	
			6:28691806-28692367			
		TRUE		5:16789898	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				
			7:4842412-4842733			
			4:571833-572604			
	RDMR		5:140559654-140559838			
		TRUE				
		TRUE				
				1:20055849	Gene_Associated_Cell_type_specific	
			X:1069050	X:1070188	Unclassified	

			7:157814865-157815150			
		TRUE				
		TRUE	8:48838200-48838325			
		TRUE				TRUE
		TRUE	3:15286143	3:15310982	Promoter_A	TRUE
		TRUE				TRUE
		TRUE				TRUE
			Y:9993394-9995882			
			7:55398320-55398795			
			7:2609719-2609971			
			19:242639-	19:291598-	Unclassified_Cell_type_specific	
	DMR		19:17299896-17301804			
		TRUE				
		TRUE	7:22088931	7:22122064	Promoter_Associated	
	RDMR	TRUE				TRUE
				10:9399860	Unclassifie	TRUE
			12:129824362-129824378			
		TRUE	10:77541884-77542251			
		TRUE				
			10:13039521-13039676			
				6:33041259	Unclassified	
		TRUE		6:17023101	Unclassified	
		TRUE				
			12:9987169-9987420			
			12:8887075-8887246			
low-CpG:37743015-37743401				17:4048941	Unclassified	
	RDMR					
		TRUE				
			19:5458311	19:4989109	Unclassified	
				1:18494232	Promoter_Associated	
			6:30146876-30147422			
		TRUE				TRUE
			21:44666959-44667248			
		TRUE				
	CDMR	TRUE	7:27130345-27130623			

		TRUE				
high-CpG:161906095-161906122			2:161905748-161906142			
		TRUE				TRUE
	DMR		3:42922485	3:42947283	Unclassified_Cell_type_specific	
		TRUE				TRUE
Body;Body;Body;Body;Body;Body;			12:2631085-2631366			
			7:55484366-55484743			
		TRUE				
			17:78507888-78508640			
				17:4080802	Unclassified_Cell_type_specific	
		TRUE	18:1193753	18:1194717	Promoter_A	TRUE
		TRUE				TRUE
			17:7410022	17:7658843	Unclassifie	TRUE
	DMR		10:8228548	10:8229523	Promoter_A	TRUE
		TRUE		21:4410359	Unclassified_Cell_type_specific	
			19:242639-	19:291598-	Unclassified_Cell_type_specific	
		TRUE				
			1:177978482-177980627			
	CDMR	TRUE				
		TRUE				
		TRUE				
			12:97374718-97375133			
				19:6710633	Unclassified_Cell_type_specific	
		TRUE				TRUE
				21:4667524	Unclassifie	TRUE
			2:785876-786168			
		TRUE				
			1:11003168	1:11023012	Unclassifie	TRUE
			1:206059026-206059218			TRUE
			10:124568117-124568601			
		TRUE				
			6:28805742-28805992			
		TRUE				TRUE
			8:206391-206774			
	RDMR					TRUE
low-CpG:10671608-10672092						
			1:3711588-3711757			

			7:15471895	Promoter_A	TRUE
	TRUE	17:7851438	17:8092025	Unclassifie	TRUE
	TRUE		1:23024042	Unclassifie	TRUE
		5:178991944-178992285			
	TRUE				
	TRUE				TRUE
		13:18816586-18817215			TRUE
RDMR	TRUE				
		2:113096178-113096321			
	high-CpG:117364055-117364520	X:1173637	X:1174791	Promoter_Associated	
	TRUE				
		2:91300163-91301017			
	TRUE		8:59698260	Unclassified_Cell_type_specific	
		10:130169634-130169698			
			1:17500620	Unclassified_Cell_type_specific	
	TRUE				
		6:30146876-30147422			
	TRUE	7:2769468-2769503			
		X:1027493	X:1028623	Promoter_Associated_Cell_type_specific	
		17:7856368	17:8097039	Unclassifie	TRUE
		6:44350915	6:44243254	Unclassifie	TRUE
	TRUE				
	TRUE				TRUE
		6:37037889-37038113			
					TRUE
		12:114528341-114528449			
	TRUE				TRUE
		17:7832848	17:8073499	Unclassified_Cell_type_specific	
	TRUE				TRUE
	TRUE	2:23600355-23600814			TRUE
	TRUE				
		10:118377008-118377466			TRUE
	TRUE		11:6738291	Promoter_Associated	
DMR		3:10724276	3:10749243	Unclassifie	TRUE
	TRUE				
		6:28805742-28805992			

TRUE	14:100244968-100245789			TRUE
TRUE	7:101748145-101748928			
TRUE	4:3205066-3205170			
TRUE		5:76034726	Unclassified	
TRUE		19:4933884	Unclassified	
TRUE				
TRUE				
TRUE	1:2218723-2219508			
	6:167509172-167509432			
TRUE				
	6:101953488-101953918			
				TRUE
	14:1009784	14:1019084	Unclassified_Cell_type_specific	
	19:888324-	19:937253-	Gene_Associated	
TRUE				
		18:7411802	Gene_Asso	TRUE
DMR	4:163304462-163305008			
TRUE	6:37725892	6:37617791	Unclassifie	TRUE
	4:7553329-7553866			
		17:7426061	Promoter_Associated	
TRUE				
	13:112032532-112032877			
	7:157768685-157769155			
TRUE				
	3:14517285	3:14368939	Promoter_Associated	
		12:1262018	Unclassified_Cell_type_specific	
	12:123495637-123496063			
high-CpG:129388543-129388696	12:129387699-129390036			
		6:29894087	Promoter_Associated	
TRUE				
		1:18684568	Unclassified_Cell_type_specific	
	3:12570453-12570853			
high-CpG:151963577-151963972	3:15196282	3:15048076	Promoter_Associated	
	12:1887290	12:2016983	Unclassifie	TRUE
TRUE				
TRUE				

TRUE		5:1228095-	Unclassifie	TRUE
TRUE				
TRUE				
	6:28960852-28961093			
TRUE				
TRUE				
TRUE				
TRUE				TRUE
	18:14447811-14450493			
TRUE				
		6:31785399	Unclassified_Cell_type_specific	
TRUE		5:59837269	Unclassified_Cell_type_specific	
TRUE				
				TRUE
		11:1031994	Unclassified_Cell_type_specific	
	11:128317570-128318285			
TRUE				
	11:7066709-7068093			
	13:43869637-43869695			
	2:782198-782365			
TRUE				
	19:4559630	19:4090438	Unclassifie	TRUE
TRUE				
TRUE				
	13:78591759-78592154			
TRUE				
	17:73033777-73034077			
	8:6468990-6469066			
	5:468419-468926			TRUE
	15:29142578-29142735			
	5:140496145-140496332			
	5:1647215-	5:1594141-	Unclassifie	TRUE
		15:6736137	Unclassified_Cell_type_specific	

DMR					TRUE
	TRUE	11:6752065	11:6776428	Gene_Asso	TRUE
			7:1420760-	Unclassified_Cell_type_specific	
		20:207316-	20:259877-	Unclassifie	TRUE
		1:24586928	1:24780263	Unclassifie	TRUE
	TRUE				
	TRUE				TRUE
		17:72750242-72750345			
high-CpG:245869383-2	TRUE	1:24586928	1:24780263	Unclassifie	TRUE
		1:15321286	1:15494615	Promoter_A	TRUE
		7:157188011-157188049			
			13:4732604	Unclassified_Cell_type_specific	
		1:35358919-35359324			
	TRUE				TRUE
		1:148602120-148602154			
DMR		4:155473376-155474030			
	TRUE				
	TRUE				TRUE
			12:4760997	Promoter_Associated_Cell_type_specific	
		3:42702148-42703013			TRUE
	TRUE				
		5:1703877-1704028			
		X:47318385-47319025			
					TRUE
		8:141363354-141363436			
	TRUE				
	TRUE				
	TRUE				TRUE

DMR					
	TRUE				
	TRUE		1:23579610	Unclassifie	TRUE
high-CpG:245869383-2	TRUE	1:24586928	1:24780263	Unclassifie	TRUE
		5:140202168-140203355			
		X:7039011	X:7047374	Promoter_Associated	
	TRUE		4:40266927	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				TRUE
		10:3153489-3153696			
	TRUE				
	TRUE				
		22:16911216-16911504			TRUE
		13:100113201-100113480			
			2:12845312	Unclassifie	TRUE
	TRUE				
			10:1139427	Promoter_Associated_Cell_type_specific	
			7:98976747	Promoter_A	TRUE
DMR		2:23292392	2:23321669	Unclassifie	TRUE
		8:38697906	8:38578551	Unclassified	
		13:109231934-109238221			
		19:419622-419950			
		11:5915571-5916673			
			8:1439471-	Unclassified_Cell_type_specific	
	TRUE	7:15846253	7:15876849	Promoter_Associated	
		17:7079786	17:7328479	Promoter_Associated	
	TRUE				TRUE
	TRUE				
		5:13544411	5:13541621	Unclassifie	TRUE
			12:1080787	Promoter_Associated	
	TRUE				TRUE
					TRUE
	TRUE	10:7682507	10:7715421	Unclassifie	TRUE
	TRUE				TRUE

		TRUE				
			1:98282851-98283206			
		TRUE				
		TRUE	11:1486083-1486395			
		TRUE				
		TRUE				
			17:7767783	17:8008428	Unclassified_Cell_type_specific	
high-CpG:130984912-130985093			X:1309844	X:1311560	Promoter_A	TRUE
		TRUE	5:66497845	5:66461684	Promoter_A	TRUE
		TRUE	10:133408379-133408516			
		TRUE				
			6:31758628-31759271			TRUE
			18:57372432-57372966			
	RDMR	TRUE				TRUE
		TRUE	13:1139461	13:1149280	Unclassifie	TRUE
			22:21316929-21317214			
			8:83516081-83516528			
			17:58097620-58098555			
		TRUE				TRUE
		TRUE				
			5:2440743-2441039			
low-CpG:176723234-176723235						
high-CpG:44325130-44325223			17:4432460	17:4696956	Promoter_Associated	
			22:40854712-40855157			
low-CpG:46966677-46967166						
						TRUE
		TRUE				TRUE
			8:14487978	8:14480896	Unclassifie	TRUE
		TRUE				
			1:15413823-15414068			
		TRUE	1:31052653-31053099			
		TRUE				TRUE
			2:24169676	2:24204811	Promoter_Associated_Cell_type_specific	
		TRUE				
			3:42281154-42282600			
			13:4089985	13:4200234	Unclassified_Cell_type_specific	
		TRUE				
		TRUE				TRUE

	TRUE		5:11254031	Unclassified_Cell_type_specific	
	TRUE				
	TRUE				
	TRUE				
		19:2475387-2476578			TRUE
high-CpG:133421837-133421984		X:1334216	X:1335937	Promoter_Associated	
	TRUE				TRUE
		2:48698290-48698489			
high-CpG:23849959-23850497		14:2384979	14:2477937	Promoter_A	TRUE
Body	TRUE				
		19:295096-	19:343550-	Promoter_Associated	
			15:8333194	Unclassifie	TRUE
	TRUE				
	TRUE				
		1:159615484-159615766			
low-CpG:50281438-50281679					TRUE
			6:32634123	Unclassifie	TRUE
		2:113867818-113869494			
		19:17295234-17295769			TRUE
		3:47372789-47373309			
	TRUE				
					TRUE
	TRUE	3:19860577	3:19712131	Unclassifie	TRUE
		5:177754498-177756463			
		8:14355782	8:14356106	Unclassified_Cell_type_specific	
		2:24129280	2:24164362	Unclassified	
	TRUE				
	TRUE				
	TRUE				
		12:131475906-131476155			
	TRUE				TRUE
	TRUE				
	TRUE				

		TRUE				
			2:239684002-239684558			
	RDMR					
low-CpG:69434498-69434668						
		TRUE				
		TRUE				
		TRUE				TRUE
		TRUE				
		TRUE	17:4386094	17:4439393	Unclassified_Cell_type_specific	
			17:7687322	17:7925873	Promoter_A	TRUE
		TRUE				
		TRUE				
			X:136339735-136340033			
			19:242639-	19:291598-	Unclassified_Cell_type_specific	
		TRUE		3:57969495	Unclassifie	TRUE
		TRUE				
			13:110079031-110079185			
	RDMR	TRUE		2:286759-2	Unclassified_Cell_type_specific	
			6:170574045-170574367			
low-CpG:45616923-45620319			17:45618098-45618204			
	RDMR		3:61210816	3:61235609	Promoter_A	TRUE
			6:16010243	6:16018229	Promoter_Associated	
		TRUE	17:3794782	17:3847716	Unclassifie	TRUE
				1:20212963	Promoter_Associated	
		TRUE				TRUE
	RDMR		10:3813790	10:3823604	Promoter_Associated	
			6:25840672-25840908			
		TRUE				
				1:9335621-	Unclassified	
		TRUE				
		TRUE				
		TRUE				
		TRUE	4:13145945-13146188			
	CDMR					
TR		TRUE				
		TRUE				

			4:7839079-7839264			
			12:126196465-126197152			
		TRUE				TRUE
		TRUE				
high-CpG:1	DMR		X:1527472	X:1530953	Unclassifie	TRUE
	CDMR		X:24931124-24931707			
			X:7367231	X:7375548	Unclassifie	TRUE
		TRUE				TRUE
		TRUE	17:78607581-78608190			TRUE
		TRUE				
	RDMR					
			11:50213790-50214562			
R;5'UTR						
		TRUE				
			13:58295990-58296160			
		TRUE				
			7:15709755	7:15740528	Unclassified_Cell_type_specific	
		TRUE	4:7895813-7895900			TRUE
			13:9894869	13:1001504	Promoter_Associated	
				7:10210755	Unclassifie	TRUE
			8:58334174-58336552			
			2:176724663-176725225			
				2:23234728	Unclassified	
		TRUE				TRUE
		TRUE				
		TRUE				
		TRUE				
			7:55484207	7:55516729	Unclassified_Cell_type_specific	
			1:16036340-16036710			
high-CpG:56898700-56901058			20:56898137-56901134			
			7:65607473	7:65971010	Unclassifie	TRUE
				13:2053128	Promoter_Associated	
				2:42327765	Unclassified	
		TRUE				TRUE

			2:132821167-132821614			TRUE
				X:4374167	Unclassifie	TRUE
			19:2201561-2205121			
			1:176722448-176722898			
			1:181188275-181188334			
			3:12883043	3:12734742	Promoter_Associated_Cell_type_specific	
		TRUE				
high-CpG:92725046-92725073			1:92724308-92725197			
		TRUE				TRUE
			X:1527124	X:1530590	Promoter_Associated	
		TRUE				TRUE
		TRUE				
			2:88845443-88846649			
		TRUE		17:4902098	Promoter_A	TRUE
		TRUE				
		TRUE				
			4:132863643-132874411			
			7:100039577-100040924			
	RDMR		12:118076047-118076529			TRUE
		TRUE				
high-CpG:37315644-37316109			X:37315490-37316849			
			3:140221263-140222607			
		TRUE				TRUE
		TRUE				
			12:131480715-131481101			TRUE
		TRUE				
			12:1481777	12:1492653	Promoter_Associated	
			5:178991944-178992285			
			6:31854774-31855249			
	DMR	TRUE				TRUE
		TRUE				
		TRUE		11:1230958	Unclassified_Cell_type_specific	
		TRUE				
			6:6559404-	6:6614106-	Promoter_Associated_Cell_type_specific	
	DMR					
high-CpG:130703384-130703424			2:130702128-130703653			
			7:157768103-157768566			

			11:3491106-3491333			
		TRUE				
		TRUE				TRUE
		TRUE		8:12527384	Unclassified	
		TRUE				
		TRUE				
		TRUE				
			5:1275775-1275980			
			10:755999-756295			
			19:60845663-60846217			
			18:55787650-55788107			
			5:1128002-1128897			
			1:2110741-	1:2120661-	Promoter_Associated	
			14:7246236	14:7339244	Promoter_Associated	
		TRUE				
	CDMR		6:27629187	6:27521010	Unclassified_Cell_type_specific	
		TRUE				
			1:245577972-245578109			
			19:63245852-63246445			
	RDMR	TRUE		5:79378321	Unclassifie	TRUE
		TRUE	17:75538070-75538586			
		TRUE				
		TRUE				
		TRUE				
		TRUE	X:13497570-13498485			
		TRUE				
high-CpG:23849959-23850497			14:2384979	14:2477937	Promoter_A	TRUE
			6:101953488-101953918			
		TRUE				
			X:5347782	X:5346113	Promoter_Associated	
			5:13544411	5:13541621	Unclassifie	TRUE
		TRUE				
		TRUE				
			X:1860307	X:1869249	Promoter_Associated	
		TRUE		14:2300570	Unclassifie	TRUE
low-CpG:131523594-131524003						
		TRUE				
			1:147422627-147423277			
		TRUE				TRUE

Body;Body;Body;Body;		TRUE		12:2445561	Unclassifie	TRUE
			X:3058070	X:3067064	Promoter_Associated	
		TRUE	6:15708250	6:15704073	Unclassifie	TRUE
ody						
		TRUE				
			7:154992367-154992449			
		TRUE		13:4932341	Unclassifie	TRUE
		TRUE	4:7895813-7895900			TRUE
		TRUE				TRUE
		TRUE				
	DMR			4:33062478	Unclassified_Cell_type_specific	
			13:18816586-18817215			TRUE
		TRUE				
		TRUE				
		TRUE				
			1:3549742-3550949			
						TRUE
			5:177814790-177814864			
	RDMR		1:219124087-219124962			
						TRUE
			4:2401607-2402112			
		TRUE				
		TRUE				TRUE
			10:99901779-99902774			
						TRUE
low-CpG:72281833-722		TRUE				TRUE
			19:5555358	19:5086164	Promoter_A	TRUE
			7:94863327-94864148			
		TRUE				
			4:155882193-155882289			
		TRUE				
		TRUE				
		TRUE				
		TRUE	16:1038591	16:1098370	Unclassifie	TRUE
		TRUE				
		TRUE	2:239808735-239808810			TRUE
			5:1647215-	5:1594141-	Unclassifie	TRUE
			5:140460938-140461126			
				16:1072353	Unclassified_Cell_type_specific	
		TRUE				TRUE

			17:6338476	Unclassified	
	TRUE				
		16:87517894-87517956			
		16:45160178-45161124			
		13:112736114-112736277			
DMR		10:41992545-41993415			
	TRUE				TRUE
		6:26854357-26855375			
	TRUE				
		6:74128853-74130365			
		5:179961262-179961486			
	TRUE				
	TRUE				
		7:42242529-42244622			
			6:31095254	Unclassifie	TRUE
	TRUE				
RDMR					
		6:30526824	6:30419361	Unclassified_Cell_type_specific	
RDMR					
DMR		X:1193278	X:1194427	Unclassified	
		16:2689363-2689545			
	TRUE				
		5:1351761-1351976			
		7:64040504-64040692			
		8:1484139-1485291			
RDMR		12:113586892-113588492			
		19:4117678	19:3648480	Unclassified_Cell_type_specific	
RDMR		19:61968355-61968854			

		10:3128406-3128559			
	TRUE	6:33156288-33156750			
	TRUE		21:3292669	Unclassified	
		16:87435844-87437103			
	TRUE		7:15853303	Gene_Asso	TRUE
	TRUE				TRUE
DMR		19:2201561-2205121			
	TRUE		11:2919715	Unclassified_Cell_type_specific	
					TRUE
					TRUE
	TRUE				
		11:1205496-1205625			
		10:88013014-88013215			
DMR	TRUE		6:13691508	Unclassified	
		7:139781665-139782089			
		19:38314751-38315262			
		3:19686970	3:19538460	Unclassified	
DMR	TRUE		18:1337524	Unclassifie	TRUE
		13:110543554-110543657			
DMR		6:30526824	6:30419361	Unclassified_Cell_type_specific	
		17:38089348-38089793			TRUE
		19:803661-	19:853008-	Unclassified_Cell_type_specific	
	TRUE	17:7851438	17:8092025	Unclassifie	TRUE
		17:7661189	17:7899712	Unclassified	
		19:5494135	19:5024956	Unclassifie	TRUE
		20:43378282-43379069			
		11:878453-878981			
	TRUE				
	TRUE				TRUE
		21:42983104-42983552			
	TRUE				TRUE
			16:701610-	Unclassified	
			5:15005049	Promoter_Associated	
	TRUE	20:25076584-25077610			
	TRUE		2:10284407	Unclassifie	TRUE

high-CpG:152853235-152853858		X:1528531	X:1532001	Promoter_Associated	
		4:7523836-7524209			
Body	TRUE				
RDMR					TRUE
			16:4749571	Promoter_Associated	
0;Body					
	TRUE				TRUE
	TRUE	11:1182862	11:1187810	Unclassifie	TRUE
		13:110778452-110778699			
	TRUE				
	TRUE				
low-CpG:40877217-408	TRUE				
					TRUE
	TRUE				TRUE
					TRUE
	TRUE				
					TRUE
	TRUE				
	TRUE				
		6:159943526-159943680			
	TRUE	2:10521958	2:10585323	Promoter_Associated	
	TRUE				
			5:15067764	Unclassifie	TRUE
	TRUE				TRUE
		1:176722448-176722898			
					TRUE
		4:133115855-133117899			
		5:138741714-138742222			
			16:7145879	Unclassified_Cell_type_specific	
					TRUE
		13:2672336	13:2782495	Unclassifie	TRUE
	TRUE				
		16:8712594	16:8859866	Unclassified_Cell_type_specific	
	TRUE				TRUE

	TRUE				
	TRUE				TRUE
		19:61304024-61304620			
		X:21301768-21303521			
		6:28555047-28555115			
	TRUE				
		5:12643728	5:12640822	Promoter_Associated	
	TRUE				
	TRUE				
		17:74188259-74188399			
	TRUE				
		8:48839411-48840049			
	TRUE				
		5:140548401-140549362			
	TRUE				
		10:131450007-131450091			
	TRUE	8:142300095-142300332			
RDMR		12:118076047-118076529			TRUE
					TRUE
	TRUE				TRUE
	TRUE				
	TRUE				
		17:78440904-78441808			
	TRUE				
CDMR					TRUE
RDMR		7:96489900	7:96651951	Unclassified_Cell_type_specific	
		Y:20366223-20366376			
	TRUE				
		13:99346218-99346880			
		X:1927162	X:1936128	Promoter_Associated	
		16:65566595-65566700			
		5:140511237-140512201			
			7:30810456	Promoter_Associated	
	TRUE	7:39615791	7:39649011	Unclassified	
		6:101954025-101954110			
	TRUE				

		TRUE				TRUE
			5:140162085-140163180			
			6:33493292	6:33385034	Promoter_Associated	
		TRUE	3:11585138-11585370			TRUE
			7:6802867-6803025			
			19:419622-419950			
		TRUE	13:113890599-113890911			
low-CpG:154351087-154351170				7:15471895	Promoter_A	TRUE
		TRUE				TRUE
			5:12643692	5:12640822	Promoter_Associated	

				16:8914777	Unclassified_Cell_type_specific	
	DMR	TRUE				TRUE
				21:4075936	Promoter_Associated	
		TRUE				
		TRUE				TRUE
			8:1352353-1352973			
			7:9733889-9734370			
			16:2832519	16:2892264	Promoter_A	TRUE
			11:832201-	11:842391-	Promoter_Associated	
			4:10293088	4:10271164	Unclassifie	TRUE
		TRUE				
	RDMR					
		TRUE				TRUE
		TRUE				
			17:38832807-38833008			
			5:1647215-	5:1594141-	Unclassified	
		TRUE		17:7486837	Unclassifie	TRUE
			17:76086607-76086958			
			16:48177954-48178061			
			13:1903676	13:2013852	Unclassifie	TRUE

		TRUE				
			22:47884228-47884418			
	DMR		X:11592255-11594177			TRUE
			4:1192911-1193178			
			2:11432482	2:11515001	Unclassifie	TRUE
		TRUE				

				12:5437120	Unclassified_Cell_type_specific	
			22:21316929-21317214			
			1:1216370-	1:1225549-	Unclassified	
	DMR	TRUE				TRUE
		TRUE				
		TRUE				TRUE
			17:77409743-77409968			
			4:7814512-	4:7763381-	Promoter_A	TRUE
			16:8778531	16:8925805	Unclassified_Cell_type_specific	
			10:135193172-135193295			
		TRUE				TRUE
			6:27555425	6:27446282	Promoter_A	TRUE
	DMR		20:4336861	20:4393518	Unclassifie	TRUE
		TRUE				TRUE
				6:29705398	Unclassifie	TRUE
		TRUE				
		TRUE				
			21:4654087	21:4771638	Unclassifie	TRUE
high-CpG:8	DMR	TRUE	2:86869486	2:87017016	Unclassifie	TRUE
			X:1187760	X:1188918	Unclassified_Cell_type_specific	
			X:1526300	X:1535272	Promoter_Associated	
			X:67830113-67830924			TRUE
		TRUE	6:31383697	6:31275659	Promoter_Associated	
				11:1891168	Unclassified	
	RDMR					
			1:1981795-1982277			
		TRUE				
		TRUE				
		TRUE				
		TRUE				TRUE
		TRUE		19:5230177	Unclassifie	TRUE
			4:1034435-	4:1044234-	Unclassified	
			19:21985171-21985462			
				1:39853414	Gene_Asso	TRUE
		TRUE				
			11:49869896-49870911			

high-CpG:36364101-36364201		21:3636406	21:3744189	Unclassified	
	TRUE				
		5:140605877-140606072			
		9:129556283-129557648			
RDMR	TRUE	15:9468884	15:9688770	Unclassified	
		5:17996608	5:18003243	Unclassifie	TRUE
		6:30187118-30187260			
					TRUE
		Y:6838022-6839951			
		17:4959827	17:5019434	Unclassified_Cell_type_specific	
		6:30146876-30147422			
	TRUE				TRUE
		17:5391974	17:5656456	Unclassified	
		5:2222711-2222816			
	TRUE				
		15:99533202-99533391			
		5:1647215-	5:1594141-	Unclassifie	TRUE
		22:21316929-21317214			
		2:231763473-231763977			TRUE
					TRUE
	TRUE		19:5040002	Unclassifie	TRUE
Body;Body;Body;Body	TRUE				TRUE
		6:2903749-2903858			
		6:29756034	6:29648152	Unclassified_Cell_type_specific	
	TRUE				
		7:1681746-1681949			
		13:22168623-22168912			
		7:14826884	7:14863788	Promoter_Associated	
		1:1677285-1677590			
		19:19511515-19513041			
	TRUE				
	TRUE		7:12873136	Unclassified	
CDMR		8:143641580-143642675			
	TRUE		1:85686226	Unclassified_Cell_type_specific	

		16:86918775-86919346			
	TRUE		10:3242843	Unclassifie	TRUE
DMR					TRUE
		8:22321908-22322173			
		7:931943-933249			
		10:99327982-99328347			
		7:155316446-155317226			
	TRUE	18:75227142-75227446			
		2:26804049	2:26951084	Unclassified_Cell_type_specific	
		16:85579864-85580286			
	TRUE				
		12:9446489-9447897			
		6:159943849-159944135			
	TRUE				
		15:20586897-20587004			
			20:6144715	Unclassified_Cell_type_specific	
			19:4371062	Unclassified_Cell_type_specific	
		12:56066316-56066535			
		1:23316569	1:23509857	Promoter_Associated	
		1:2874923-2875144			
		1:1560916-1561665			
CDMR	TRUE				
	TRUE	1:24586928	1:24780263	Unclassifie	TRUE
	TRUE				TRUE
		12:9613296-9614085			
		2:96500050	2:97135938	Unclassifie	TRUE
	TRUE				
		6:30526824	6:30419361	Unclassified_Cell_type_specific	
		5:140692011-140692726			
		1:16345044-16345325			
high-CpG:200028977-200029118		2:20002874	2:20032012	Promoter_A	TRUE
	TRUE				

	TRUE				
			2:10275968	Unclassifie	TRUE
			22:3149875	Unclassifie	TRUE
		12:1316874	12:1331767	Unclassifie	TRUE
		5:140548401-140549362			
	TRUE				TRUE
			11:6060782	Unclassifie	TRUE
		13:112153795-112153964			
		17:70568276-70568403			TRUE
		6:11790933	6:11780255	Unclassified_Cell_type_specific	
CDMR		22:44838554-44839147			
		19:10789078-10789559			TRUE
		12:94364936-94365027			
RDMR		12:113657287-113658815			
		17:1000395-1000574			

Probe_Set_	pvalues	foldchange	qvalues	PCOS1_NS	PCOS2_NS	PCOS3_NS	PCOS1_cal	PCOS2_cal
1552423_at	0.0163131	0.2614745	0.6811878	7.330301	7.4727883	6.968693	P	P
1552485_at	0.0484608	1.6009607	0.5250387	8.054996	8.035363	7.891558	P	P
1552705_at	0.0175385	1.9415474	0.5250387	7.023491	6.836763	6.8384404	P	P
1552928_s_	0.0466583	0.2069989	0.681247	4.787766	4.000419	4.6143303	A	A
1553158_at	0.0447472	2.1389774	0.5250387	7.898601	7.8029003	7.4827538	P	P
1553260_s_	0.0412125	3.0892997	0.5250387	7.248643	6.995845	7.819778	P	P
1553313_s_	0.0395221	2.0303862	0.5250387	7.1298957	7.3865848	7.4995785	P	P
1554003_at	0.041652	0.6261306	0.6838958	9.448131	9.905595	10.050384	P	P
1554549_a_	0.0365403	0.4551223	0.6823972	6.3580823	7.177007	7.040187	A	M
1554591_at	0.0133264	1.8530374	0.5250387	6.791037	7.240494	6.8283834	P	P
1554602_at	0.0120232	0.3662776	0.6811878	7.4412656	8.215548	7.597417	P	P
1554638_at	0.0232398	0.5806234	0.6823972	10.314798	9.816558	10.030833	P	P
1554741_s_	0.0057051	0.5020239	0.6811878	10.038548	10.360643	9.921045	P	P
1554997_a_	0.0184066	0.2279466	0.6811878	5.042042	4.1454773	5.1025953	A	A
1555057_at	0.0235026	1.6058877	0.5250387	7.6245885	7.8072124	7.3091335	P	P
1555106_a_	0.0103636	1.5934121	0.5250387	7.060161	7.3267703	7.1825347	P	P
1555317_at	0.035296	1.8698774	0.5250387	6.6031632	6.6632805	6.444608	P	P
1555761_x_	0.0466602	1.9179505	0.5250387	7.23053	7.989066	7.3791804	M	M
1555847_a_	0.0070406	0.2096997	0.6811878	7.943536	7.616866	7.9010496	P	P
1555867_at	0.0037128	0.5202499	0.6811878	9.072209	9.414868	9.068414	P	P
1555890_at	0.0394671	0.628221	0.6838958	8.202499	7.697035	7.9493647	P	P
1555938_x_	0.0390113	0.4635087	0.6813693	10.938149	10.043646	10.838647	P	P
1555963_x_	0.0084102	0.4729379	0.6811878	7.9296756	8.396959	8.303201	P	P
1556059_s_	0.0374349	0.6512135	0.6823972	8.812412	8.84554	8.99936	P	P
1556095_at	0.0281422	3.0445981	0.5250387	6.5573516	6.9040084	7.7314534	P	P
1556121_at	0.0219945	0.6045627	0.6823972	9.582548	9.892855	9.853554	P	P
1556385_at	0.0309393	0.4144768	0.6813693	8.424359	8.793688	8.097703	P	P
1556420_s_	0.0486682	1.9653525	0.5250387	8.518348	8.228353	7.886216	P	P
1556770_a_	0.0199552	2.5530534	0.5250387	9.66874	9.577423	9.351787	P	P
1556924_at	0.0369926	1.919992	0.5250387	6.0932794	6.682453	6.169352	P	P
1556935_at	0.0109432	1.7973335	0.5250387	7.7961097	8.080832	8.2191105	P	P
1556964_s_	0.0401554	1.6157996	0.5250387	7.619853	8.201013	7.7799063	P	P
1557080_s_	0.026139	2.5879705	0.5250387	7.7535152	7.3863688	8.317156	P	P
1557193_at	0.0273926	2.3156564	0.5250387	8.714109	9.545848	9.215175	P	P
1557384_at	0.0128694	0.635642	0.6823972	8.728761	9.072783	9.063562	P	P
1557403_s_	0.0355201	0.6374343	0.6838958	8.196096	7.798199	7.685096	P	P
1557459_at	0.0028799	0.256814	0.6811878	8.201227	8.744203	8.845011	P	P
1557478_at	0.0358837	1.5482467	0.5250387	9.200047	9.1456375	9.437454	P	P
1557529_at	0.0394734	1.5407566	0.5250387	7.1198215	7.1008697	7.088277	P	P
1557745_at	0.036654	4.3688926	0.5250387	11.470233	9.720607	10.414267	P	P
1558044_s_	0.0227831	0.5699218	0.6823972	8.86262	9.0288515	9.367809	P	P
1558604_a_	0.0163208	0.5624196	0.6813693	8.450794	8.603357	8.238114	P	P
1558685_a_	0.0306709	1.9684798	0.5250387	10.501301	10.07178	10.083475	P	P

1558695_at	0.0419457	1.6219499	0.5250387	10.882811	11.415195	11.26584	P	P
1559005_s_	0.0195346	0.5605751	0.6813693	8.0217085	8.232179	8.441463	P	P
1559332_at	0.0307066	1.8430741	0.5250387	8.338388	8.722948	8.017426	P	P
1559600_at	0.0369454	0.5264713	0.6823972	7.2370877	6.695287	6.990059	A	A
1559922_at	0.0241636	1.8921822	0.5250387	7.790361	7.79436	7.3156157	P	P
1560177_at	0.0111699	0.6598705	0.6813693	6.25276	6.4995303	6.159593	P	P
1560775_at	0.0350397	1.7301956	0.5250387	7.907466	7.6004095	8.264664	P	P
1560813_at	0.0427966	0.6399002	0.6838958	8.893565	9.018685	9.321972	P	P
1560869_a_	0.0280826	0.4898367	0.6813693	5.4033027	5.776533	5.910228	P	P
1561089_at	0.0355436	1.9515635	0.5250387	6.2753386	6.9929667	6.6764774	P	M
1561469_at	0.0161427	0.4836009	0.6811878	5.4913783	5.7341957	5.062725	A	A
1561720_at	0.0463839	1.5292802	0.5250387	6.5215697	6.6360893	6.093981	P	P
1562031_at	0.0251898	2.0387059	0.5250387	10.035525	9.4164915	9.453566	P	P
1562214_at	0.0047379	2.7809679	0.5250387	6.859407	7.4436064	6.9617014	P	P
1562238_at	0.0102089	0.5203108	0.681247	6.253631	6.53929	6.711779	P	P
1562244_at	0.0310958	0.3256779	0.681247	5.9624095	7.269423	6.233321	P	P
1563210_at	0.0407554	1.5910179	0.5250387	7.8431926	8.106699	7.5319233	P	P
1563573_at	0.024393	0.4289124	0.6813693	7.4382863	7.928232	7.963446	P	P
1563601_at	0.0359364	1.9117442	0.5250387	7.4936953	8.17705	8.13005	M	P
1564736_a_	0.0398601	0.5226782	0.6823972	6.690555	7.169871	6.4123545	M	P
1565681_s_	0.0305944	0.6019505	0.6823972	8.8205805	8.432257	8.616394	P	P
1565863_at	0.0075175	2.6426803	0.5250387	8.382335	8.11386	8.406204	P	P
1566446_at	0.0310026	1.9251313	0.5250387	8.169336	8.618197	7.885367	P	P
1566541_at	0.007838	0.4895696	0.6811878	5.6375384	5.641575	5.2810507	A	A
1568627_at	0.0463528	0.658735	0.684602	6.6539545	7.07011	7.1029315	P	P
1568745_at	0.0390465	2.0558875	0.5250387	6.790388	7.618217	6.9147143	P	M
1568768_s_	0.0410523	0.1324555	0.681247	6.4903116	5.438129	6.5318356	P	A
1569147_at	0.0082588	2.5224048	0.5250387	7.5135465	7.5098934	6.9324474	P	P
1569250_at	0.0097074	1.6661151	0.5250387	7.140901	7.126604	7.0175757	P	P
1569318_at	0.0305201	2.3529699	0.5250387	7.1185145	7.3944354	6.790632	P	P
1569499_at	0.0366221	1.6215296	0.5250387	7.5230727	7.463242	7.9713964	P	P
1569520_at	0.0279927	1.7311439	0.5250387	7.2237225	6.994191	6.61074	P	P
1570523_s_	0.0099079	1.5176896	0.5250387	7.673315	7.8352275	7.7827744	P	P
200637_s_a	0.0333854	1.7129965	0.5250387	8.755159	8.693979	8.772566	P	P
200639_s_a	0.0194427	0.5403991	0.6813693	11.981673	12.29703	12.044176	P	P
200767_s_a	0.007352	1.5080988	0.5250387	9.156606	9.462014	9.32273	P	P
200797_s_a	0.0269364	0.3842329	0.681247	12.991613	12.762831	13.414781	P	P
200798_x_	0.0475178	0.16018	0.6813693	10.914559	9.504533	11.007205	P	P
200887_s_a	0.0288597	1.9377012	0.5250387	13.248511	12.754212	12.510877	P	P
200898_s_a	0.0424984	0.5582525	0.6813693	9.299735	9.319233	9.496662	P	P
200969_at	0.0268229	0.5497581	0.681247	11.347869	11.520156	11.509529	P	P
201041_s_a	0.0258391	0.1901887	0.681247	11.873738	11.717037	13.394048	P	P
201160_s_a	0.0375878	0.5929229	0.6823972	13.41706	12.958877	13.200068	P	P
201170_s_a	0.0226371	0.1026576	0.6811878	8.720536	9.025086	9.589547	P	P
201210_at	0.0273967	0.5754671	0.6823972	13.483921	13.167749	13.426336	P	P

201236_s_a	0.0204694	0.1629668	0.6811878	9.801327	9.70158	10.689565	P	P
201243_s_a	0.0278622	0.6364766	0.6813693	11.78805	11.895617	12.199577	P	P
201387_s_a	0.0297539	1.5722947	0.5250387	10.801671	10.913651	11.101145	P	P
201421_s_a	0.0227213	1.5122379	0.5250387	9.280155	9.299141	9.061629	P	P
201473_at	0.0267345	0.1469172	0.6811878	8.655272	8.42076	10.499005	P	P
201566_x_a	0.0348594	0.2663052	0.681247	11.062901	10.534234	10.269673	P	P
201650_at	0.0269747	2.739952	0.5250387	12.153755	12.122625	11.279457	P	P
201830_s_a	0.029232	0.6651609	0.6823972	11.351605	11.155807	10.898989	P	P
201896_s_a	0.0172033	1.5832239	0.5250387	8.394556	8.166626	8.080163	P	P
201903_at	0.0015285	1.6425194	0.5250387	10.099519	10.251433	10.133554	P	P
202014_at	0.0115655	0.3645491	0.6811878	6.7156954	7.465758	6.8333497	A	A
202034_x_a	0.0276115	0.6155941	0.6823972	11.262664	11.031873	11.589029	P	P
202245_at	0.0276029	1.8667663	0.5250387	11.516348	11.216305	11.66854	P	P
202339_at	0.0302926	1.535166	0.5250387	7.5987396	7.5197253	7.1413307	M	P
202409_at	0.0497653	1.5880141	0.5250387	9.179498	9.788175	9.479273	P	P
202411_at	0.0239058	3.4852748	0.5250387	13.358276	13.172221	12.212143	P	P
202445_s_a	0.0174364	0.6119885	0.6823972	7.887212	8.159474	7.778744	P	P
202626_s_a	0.0473476	1.6899839	0.5250387	9.389526	8.833381	8.942456	P	P
202672_s_a	0.0185641	0.0364921	0.6811878	6.243167	5.369506	8.112044	P	A
202702_at	0.0299075	1.6353545	0.5250387	8.637754	8.635931	8.562359	P	P
202746_at	0.0448194	0.5114562	0.6823972	11.911583	12.593572	11.703165	P	P
202765_s_a	0.003639	1.5153896	0.5250387	12.048031	11.83377	11.958053	P	P
202767_at	0.0219089	1.6158983	0.5250387	9.202066	8.714411	8.943329	P	P
202821_s_a	0.0101106	1.6511111	0.5250387	7.498156	7.767016	7.5776134	P	P
202843_at	0.029752	0.2570644	0.6813693	8.34551	7.552567	9.008686	P	P
202859_x_a	0.0331012	0.0666979	0.681247	7.9405174	5.310868	6.213132	P	A
202926_at	0.00994	1.5667533	0.5250387	10.581286	10.342517	10.625896	P	P
202995_s_a	0.033787	0.4421272	0.6813693	9.309802	9.526213	9.725256	P	P
203033_x_a	0.0152201	1.6599479	0.5250387	10.944113	10.674336	11.033313	P	P
203057_s_a	0.0293525	0.6409502	0.6813693	11.231768	11.252678	11.342749	P	P
203093_s_a	0.0388999	1.5333774	0.5250387	8.825675	9.2513	8.795817	P	P
203147_s_a	0.042608	2.2805035	0.5250387	9.039869	9.147494	8.987178	P	P
203153_at	0.0218655	2.9768526	0.5250387	12.063901	12.120482	11.833067	P	P
203204_s_a	0.0495556	1.693085	0.5250387	9.187912	9.795556	9.772409	P	P
203394_s_a	0.0036181	0.2531001	0.6811878	10.440403	10.042666	9.6557865	P	P
203395_s_a	0.0107823	0.4317473	0.6811878	9.894493	9.290803	9.344679	P	P
203409_at	0.0386552	0.6580239	0.6838958	9.341913	9.247506	9.035866	P	P
203563_at	0.0304764	0.523718	0.6823972	6.1970096	6.9520216	6.4242587	P	A
203752_s_a	0.027963	0.2500254	0.6811878	11.881225	12.287705	12.539594	P	P
203882_at	0.0247413	2.1653464	0.5250387	11.54892	11.820997	11.05823	P	P
203910_at	0.0249964	0.578552	0.6823972	11.010338	10.547795	10.852768	P	P
204033_at	0.0420986	1.6328542	0.5250387	7.933669	8.482782	8.015357	P	P
204040_at	0.043011	0.6589206	0.6823972	9.627176	9.430741	9.937712	P	P
204071_s_a	0.016326	0.6632357	0.6823972	10.29182	10.487784	10.449148	P	P
204082_at	0.022974	0.6655402	0.6838958	11.409719	11.84253	11.603793	P	P

204263_s_a	0.0096068	1.6566356	0.5250387	8.558226	8.615686	8.697566	P	P
204325_s_a	0.0193403	1.5705735	0.5250387	7.1135726	6.80552	7.2468467	P	P
204415_at	0.0102851	3.6261243	0.5250387	13.376247	13.039221	12.520865	P	P
204435_at	0.0233643	0.6196815	0.6813693	9.981247	9.918176	10.040378	P	P
204439_at	0.0120621	2.3691988	0.5250387	12.374219	12.069325	11.826047	P	P
204529_s_a	0.0188054	0.2936087	0.6811878	8.447992	8.848757	8.0092125	P	P
204567_s_a	0.0127783	0.6292674	0.6823972	8.676374	8.350383	8.354078	P	P
204621_s_a	0.0088446	0.0279858	0.6811878	7.961774	7.0574718	9.125158	P	A
204622_x_a	0.004497	0.0280302	0.6811878	8.6541605	7.321399	9.197211	P	P
204689_at	0.0439671	2.1276917	0.5250387	8.221571	8.638867	7.656563	P	P
204748_at	0.0315508	0.1512877	0.681247	6.6371064	5.4869	4.98276	P	M
204755_x_a	0.0423753	0.59973	0.6823972	9.731657	9.741344	10.283684	P	P
204793_at	0.0438359	0.6575591	0.684602	11.627929	11.812678	11.346583	P	P
204857_at	0.0355342	1.5353026	0.5250387	7.0629916	7.3594027	6.838818	P	P
204930_s_a	0.0247392	1.8175808	0.5250387	8.345354	8.785896	8.214026	P	P
205090_s_a	0.0212178	2.0389752	0.5250387	7.9236255	8.490101	7.87126	P	P
205200_at	0.0169613	2.8697971	0.5250387	10.895199	10.934051	10.980236	P	P
205249_at	0.0280845	0.1483542	0.681247	8.450779	7.118957	8.982519	P	A
205302_at	0.0134542	0.0773169	0.6811878	7.0910635	5.1888614	6.7979527	P	A
205352_at	0.0258515	0.4927027	0.6811878	8.393324	8.251421	8.388559	P	P
205394_at	0.0367151	2.3527297	0.5250387	6.8434324	6.99628	7.746566	P	P
205450_at	0.007628	0.6245893	0.681247	8.298885	8.542769	8.215493	P	P
205483_s_a	0.0366968	3.9697866	0.5250387	12.753512	12.491248	11.298063	P	P
205512_s_a	0.0145037	1.7713111	0.5250387	9.16492	9.125632	9.566274	P	P
205579_at	0.013632	2.168068	0.5250387	9.620937	9.9400015	9.352064	P	P
205908_s_a	0.0397422	1.8192398	0.5250387	10.074391	9.772189	10.49166	P	P
206012_at	0.0189825	0.1980669	0.6811878	7.67089	9.071198	7.7475185	P	P
206067_s_a	0.0397597	0.5548696	0.681247	11.791114	11.797776	11.796126	P	P
206102_at	0.0254141	1.7427424	0.5250387	8.629861	8.427258	8.859207	P	P
206115_at	0.0293595	0.1234224	0.681247	9.518506	7.7103043	9.763672	P	P
206133_at	0.0323514	1.6242974	0.5250387	12.301624	12.831173	12.675053	P	P
206204_at	0.0420899	2.3324384	0.5250387	11.702656	11.306068	12.374526	P	P
206211_at	0.0075468	0.2570907	0.6811878	6.232087	6.248691	7.143049	P	A
206306_at	0.0368479	1.7093643	0.5250387	6.8305497	6.5262938	7.1629066	P	M
206359_at	0.0415487	0.1006573	0.681247	6.5757174	6.499727	8.006857	A	A
206471_s_a	0.0321868	2.3508583	0.5250387	7.3919163	7.9105644	8.384511	P	P
206493_at	0.0475254	1.7264695	0.5250387	7.763497	7.981562	7.569377	P	P
206515_at	0.0301192	2.7803365	0.5250387	5.993624	6.2469907	5.209479	P	P
206542_s_a	0.0132528	0.6165328	0.6823972	11.898185	12.312291	12.14326	P	P
206544_x_a	0.0195804	0.6437978	0.6823972	11.152475	11.547665	11.466521	P	P
206645_s_a	0.0063224	1.8647267	0.5250387	8.804457	8.493443	8.693845	P	P
206685_at	0.0036209	3.8491914	0.5250387	6.3913417	6.8203073	7.1197996	P	P
206900_x_a	0.0262859	1.7936235	0.5250387	8.402859	8.84316	8.649724	P	P
206954_at	0.0282246	0.5298212	0.6823972	9.059999	9.534493	9.178674	P	P
207056_s_a	0.0234078	0.5631891	0.6823972	7.248912	7.3958035	6.970543	P	P

207177_at	0.0119757	0.3470467	0.6811878	6.438119	7.030487	6.1298146	A	A
207319_s_a	0.0475336	1.6882203	0.5250387	7.658311	8.321974	7.988835	P	P
207574_s_a	0.0023898	0.0532949	0.6811878	8.913122	8.99693	10.112391	P	P
207788_s_a	0.0472625	1.85002	0.5250387	7.111119	7.854914	7.1746836	P	P
208002_s_a	0.0023925	1.7122735	0.5250387	9.576873	9.337781	9.341702	P	P
208078_s_a	0.0317798	0.0429842	0.6811878	9.209627	8.119855	9.699443	P	A
208119_s_a	0.038048	1.9588954	0.5250387	10.106941	10.632741	10.312058	P	P
208729_x_	0.0457125	1.7908982	0.5250387	12.944811	12.514309	12.551895	P	P
208733_at	0.0334627	1.6074839	0.5250387	8.312171	8.784685	8.811574	P	P
208937_s_a	0.026831	0.2850586	0.6811878	10.866137	10.944019	10.776241	P	P
209034_at	0.0411165	0.2678578	0.6813693	11.750481	11.439446	13.09724	P	P
209140_x_	0.0375866	1.5290954	0.5250387	14.183628	13.929086	13.683054	P	P
209193_at	0.049922	0.3520997	0.6823972	9.848334	8.982959	9.406312	P	P
209277_at	0.0307698	0.1727015	0.681247	6.4311805	7.3248286	8.199349	P	M
209278_s_a	0.0153338	0.1382021	0.6811878	7.2440243	9.0195875	8.685257	P	P
209291_at	0.002512	0.3613849	0.6811878	12.451711	12.117324	12.502209	P	P
209292_at	0.0146231	0.4678242	0.6811878	11.127202	11.419792	11.104327	P	P
209304_x_	0.018748	0.0554741	0.6811878	8.727376	8.759385	9.029965	P	P
209305_s_a	0.0108831	0.0488165	0.6811878	7.9398837	7.6917787	8.689539	P	P
209308_s_a	0.0117321	0.5689828	0.6813693	10.055934	9.851268	10.201583	P	P
209399_at	0.0164699	1.5127874	0.5250387	7.7599716	8.060318	7.7438807	P	P
209470_s_a	0.0461957	0.3501441	0.681247	7.61215	7.260164	8.663436	P	P
209501_at	0.0289675	0.6298902	0.6838958	9.723386	10.165802	9.96922	M	A
209529_at	0.0083975	0.1941413	0.6811878	4.5814824	4.806182	5.6045084	A	A
209656_s_a	0.000127	0.625825	0.6811878	11.684235	11.614145	11.723496	P	P
209721_s_a	0.0375424	1.6572443	0.5250387	9.879748	9.454016	9.9625225	P	P
209771_x_	0.0251391	0.1326803	0.6811878	4.7340617	3.3564367	5.6961355	A	A
209774_x_	0.0243247	0.1101068	0.6811878	7.622481	6.88264	7.8670187	P	P
209797_at	0.0122108	1.5283642	0.5250387	10.424426	10.751344	10.454276	P	P
209808_x_	0.0420645	0.4313592	0.6823972	7.960949	8.636012	8.360257	P	P
209883_at	0.0203172	0.5329608	0.6813693	6.0935345	6.477103	6.504152	A	A
209894_at	0.0453339	0.6133037	0.6823972	12.285439	11.624694	11.964486	P	P
209947_at	0.0402396	1.5197314	0.5250387	9.0689	9.2532425	9.293445	P	P
209969_s_a	0.0394616	2.5946496	0.5250387	10.879238	10.438216	9.885998	P	P
210046_s_a	0.0415708	1.5565025	0.5250387	9.75053	9.3392315	9.507505	P	P
210120_s_a	0.0417963	0.5903106	0.6838958	6.667006	7.3076324	7.2206883	A	A
210273_at	0.0258243	2.7918895	0.5250387	7.188447	7.3924575	6.37869	P	P
210517_s_a	0.0093511	0.3986498	0.6811878	12.905745	12.37272	12.398476	P	P
210622_x_	0.0413861	1.5787744	0.5250387	8.347995	8.839785	8.412423	P	M
210695_s_a	0.0313308	1.5824525	0.5250387	9.182419	9.075276	9.394037	P	P
210718_s_a	0.0249296	1.9188138	0.5250387	8.491862	9.004069	8.829379	P	P
211143_x_	0.0264033	0.1257557	0.6811878	7.386122	7.58823	7.6681933	A	A
211734_s_a	0.043111	0.3629986	0.6813693	6.3805227	5.1657977	6.3387585	P	A
211756_at	0.0209588	0.371511	0.6811878	5.13788	6.069415	5.514718	A	A
212143_s_a	0.0453092	0.4887628	0.6823972	11.31259	10.484812	10.408756	P	P

212187_x_	0.0300589	1.9097954	0.5250387	10.175403	9.905005	9.687074	P	P
212189_s_a	0.0308853	1.7075735	0.5250387	10.000138	9.95563	10.070588	P	P
212223_at	0.0101263	0.6293493	0.6813693	10.616644	10.824369	10.742147	P	P
212228_s_a	0.0190346	1.7044164	0.5250387	10.088277	10.021085	10.359101	P	P
212329_at	0.0419291	1.9056695	0.5250387	10.937701	10.466714	11.119597	P	P
212344_at	0.0205937	0.621644	0.6823972	8.691018	8.369192	8.2159605	P	P
212354_at	0.0273487	0.5378476	0.6823972	9.674323	9.203061	9.230229	P	P
212527_at	0.0274917	2.1930985	0.5250387	7.5349336	6.7726707	7.4033628	P	M
212619_at	0.0051212	2.130873	0.5250387	6.5298853	6.7458544	7.0354085	P	P
212641_at	0.0137168	0.6635913	0.6823972	8.737749	9.093589	9.015878	P	P
212724_at	0.0272766	0.5677583	0.6823972	10.767507	10.724814	11.101468	P	P
212732_at	0.0208301	0.1646198	0.6811878	10.57548	9.726089	11.079768	P	P
212837_at	0.0251408	1.5583173	0.5250387	9.749474	10.061588	9.739471	P	P
212843_at	0.0130907	1.7765465	0.5250387	11.623243	11.80719	11.36892	P	P
212927_at	0.0087691	0.6105288	0.6813693	11.022311	10.670215	10.854569	P	P
213006_at	0.0408151	0.1294844	0.6813693	7.9746456	6.3613095	8.934526	P	P
213008_at	0.0351429	1.9604083	0.5250387	7.5690494	7.6474533	8.300085	P	P
213107_at	0.0233816	1.6414469	0.5250387	7.923528	8.351541	8.405735	P	P
213234_at	0.0386503	1.7035113	0.5250387	8.121135	8.570548	8.019931	P	P
213306_at	0.007464	0.4812298	0.6811878	11.022521	10.491002	10.883401	P	P
213310_at	0.0114502	0.6374759	0.6813693	8.585685	8.556261	8.420091	P	P
213326_at	0.0227158	1.5856398	0.5250387	9.627522	9.330163	9.325845	P	P
213854_at	0.0332503	1.9395426	0.5250387	8.389549	9.013133	8.91387	P	P
213959_s_a	0.0221836	1.5192326	0.5250387	8.1761055	7.859743	8.11854	P	P
214040_s_a	0.04071	0.6435321	0.6823972	8.616769	8.237119	8.067799	P	P
214170_x_	0.0428425	1.5391158	0.5250387	10.716389	10.330824	10.795885	P	P
214204_at	0.0101594	0.5842224	0.6811878	6.6795955	7.0911455	6.9076633	P	P
214285_at	0.0398148	2.052526	0.5250387	8.172291	7.471285	8.233552	P	P
214321_at	0.0410326	0.4379542	0.6811878	6.6387777	5.675062	6.156637	P	A
214607_at	0.0414126	2.0777375	0.5250387	8.6555	8.098605	8.885115	P	P
214696_at	0.0309876	0.111251	0.681247	9.854677	7.969485	10.501635	P	P
214741_at	0.0056512	0.5095708	0.6811878	9.529464	9.780574	9.700694	P	P
214805_at	0.027487	0.3607042	0.6813693	9.5388565	10.269036	10.382259	P	P
214873_at	0.0137627	0.5537012	0.6813693	7.3632674	7.351636	7.7838073	P	A
214927_at	0.0005872	2.5039122	0.5250387	7.3140354	7.6412416	7.4888406	P	M
215134_at	0.0487584	1.5283449	0.5250387	7.7247567	7.18437	7.6434774	P	P
215272_at	0.0475414	0.3970457	0.6811878	5.549193	4.7907114	5.8997808	A	A
215279_at	0.0199253	2.1039091	0.5250387	9.490948	10.160263	9.693178	P	P
215293_s_a	0.0182284	1.5378985	0.5250387	9.469076	9.6283	9.209532	P	P
215330_at	0.0106694	0.5704814	0.681247	9.574927	9.45728	9.904787	P	P
215378_at	0.0295351	1.8712998	0.5250387	8.009604	8.300954	8.145874	P	P
215425_at	0.0337982	0.3516154	0.6813693	6.2280684	5.7168894	5.566354	P	A
215506_s_a	0.0265693	0.4217158	0.6813693	11.128034	10.603071	11.269103	P	P
215848_at	0.0304435	1.6473431	0.5250387	7.598084	8.11723	7.805477	P	P
215887_at	0.0431475	1.8301579	0.5250387	8.948257	8.783988	8.587376	P	P

216112_at	0.0191841	1.909839	0.5250387	9.441025	9.988603	9.49638	P	P
216121_at	0.0403448	0.5330749	0.6823972	6.572676	6.9340997	6.5640345	P	P
216142_at	0.0428276	2.1493857	0.5250387	6.99522	7.522701	6.6107464	P	P
216248_s_a	0.00476	0.0256505	0.6811878	8.334181	6.9892945	9.180214	P	P
216282_x_	0.0179438	1.9622208	0.5250387	8.103961	8.712793	8.198659	P	P
216465_at	0.032128	2.8975312	0.5250387	11.582081	10.756382	10.71865	P	P
216565_x_	0.0417955	1.6012732	0.5250387	11.868517	11.590302	11.264424	P	P
216598_s_a	0.0471177	0.4845529	0.6823972	8.550337	7.636466	8.486266	P	P
216766_at	0.0396266	0.4372577	0.6823972	7.0327883	7.9248643	7.886423	A	P
216979_at	0.0354308	0.0899413	0.6811878	6.088841	4.4260335	7.7068825	P	A
217225_x_	0.0058194	1.5144207	0.5250387	11.423519	11.230473	11.513561	P	P
217436_x_	0.0409208	1.5068356	0.5250387	10.616726	10.223223	10.117811	P	P
217499_x_	0.0117358	1.5778013	0.5250387	9.563029	9.6612425	9.638058	P	P
217540_at	0.0089339	1.6716854	0.5250387	7.5811343	7.891914	7.9627748	P	P
217591_at	0.0120025	0.4026691	0.6811878	9.189587	9.225179	9.488617	P	P
217728_at	0.0002722	1.6572912	0.5250387	14.198519	14.107995	14.240562	P	P
217875_s_a	0.0356752	2.1204096	0.5250387	8.579104	8.386434	7.8121777	P	P
217998_at	0.0364932	0.295088	0.681247	7.001629	6.7477484	7.4883614	P	A
217999_s_a	0.0309703	0.173162	0.681247	8.372812	6.6715264	7.3840504	P	M
218077_s_a	0.0165583	1.5020033	0.5250387	8.237844	8.569318	8.22974	P	P
218105_s_a	0.0404354	1.6370562	0.5250387	8.569847	8.766562	8.529915	P	P
218326_s_a	0.0360232	0.5366442	0.681247	10.415395	10.326768	10.434779	P	P
218347_at	0.027096	0.6538331	0.6823972	9.743154	10.098762	9.6380625	P	P
218368_s_a	0.0223985	0.1774928	0.6811878	6.8914213	5.2866173	5.2309384	A	A
218380_at	0.0196224	0.6064186	0.6823972	11.331641	11.468126	10.978014	P	P
218546_at	0.0323554	1.5259411	0.5250387	11.030335	11.521887	11.262381	P	P
218565_at	0.0441677	1.8057974	0.5250387	7.144734	7.906226	7.6578035	P	P
218621_at	0.0244075	1.6329881	0.5250387	8.234784	8.625145	8.256341	P	P
218647_s_a	0.0330274	0.4546694	0.6823972	8.556292	7.8918877	8.815598	P	P
218660_at	0.0156762	1.9848665	0.5250387	9.288067	9.454128	8.866463	P	P
218753_at	0.0490016	1.7346815	0.5250387	9.25152	9.6976795	9.170969	P	P
218834_s_a	0.0059795	2.4042837	0.5250387	9.245466	9.354026	9.051414	P	P
218844_at	0.0323412	1.6253641	0.5250387	9.225178	9.723417	9.419096	P	P
218890_x_	0.0027043	1.6726072	0.5250387	9.218128	9.313419	9.468235	P	P
218940_at	0.044819	0.5432098	0.6823972	9.589996	10.058618	10.403335	P	P
218993_at	0.0090419	1.570173	0.5250387	9.661132	9.876382	9.929838	P	P
219104_at	0.0216243	1.6630701	0.5250387	8.0643215	7.927641	7.971454	P	P
219230_at	0.011746	0.4530017	0.6811878	9.765277	10.141472	10.125202	P	P
219243_at	0.0390042	1.6224192	0.5250387	9.096923	8.903474	8.539213	P	P
219297_at	0.0484984	0.5834692	0.6823972	9.208015	8.83	8.9292145	P	P
219352_at	0.0073336	2.537195	0.5250387	10.673952	10.593119	10.41265	P	P
219371_s_a	0.0231051	0.2894501	0.681247	10.328989	11.000952	11.351132	P	P
219401_at	0.0009982	1.5664393	0.5250387	9.120744	9.197426	9.007084	P	P
219538_at	0.0486938	1.986877	0.5250387	8.445404	9.368272	8.914167	P	P
219691_at	0.0047329	1.6411573	0.5250387	8.4908	8.631833	8.695568	P	P

219786_at	0.0425463	2.2782361	0.5250387	6.703795	7.607807	6.8839817	P	P
219998_at	0.0464825	0.591732	0.6838958	6.691642	6.6377873	7.0135517	A	A
220020_at	0.0221595	2.1038593	0.5250387	7.4146605	7.873804	7.115064	P	P
220027_s_a	0.0212947	1.6146834	0.5250387	9.597866	9.238488	9.179972	P	P
220046_s_a	0.0203074	0.2295891	0.6811878	11.209939	11.051108	11.888211	P	P
220086_at	0.0233242	0.4843566	0.681247	7.751548	7.799486	8.045034	M	A
220140_s_a	0.003995	1.5482318	0.5250387	8.408886	8.666731	8.4815	P	P
220239_at	0.0442966	0.6415598	0.6838958	7.5381627	7.867808	8.110472	P	P
220340_at	0.0046206	1.8377839	0.5250387	8.581231	8.860712	8.89374	P	P
220549_at	0.0140185	0.6242929	0.6823972	6.3679247	6.123877	6.0403285	A	A
220557_s_a	0.0371522	1.9370733	0.5250387	6.8051276	7.5089145	7.166164	P	P
220591_s_a	0.0356332	1.6278842	0.5250387	8.572609	8.956123	9.151966	P	P
220682_s_a	0.0181501	1.6122361	0.5250387	7.2489476	7.3492975	6.918998	P	P
221517_s_a	0.0046139	0.6094796	0.681247	10.171205	10.249301	10.459423	P	P
221584_s_a	0.037223	1.7458936	0.5250387	11.558262	11.632472	11.694175	P	P
221763_at	0.0420804	0.5771704	0.6838958	11.977602	11.380899	12.025839	P	P
221853_s_a	0.0273261	1.6009071	0.5250387	10.835535	10.32839	10.470165	P	P
221978_at	0.0378785	1.6811885	0.5250387	8.806325	8.244604	8.269419	P	P
221998_s_a	0.0189087	1.560295	0.5250387	8.631888	8.968552	8.633987	P	P
222106_at	0.0392391	3.0306604	0.5250387	8.265314	9.1314335	8.029917	P	P
222250_s_a	0.0066409	1.8146749	0.5250387	8.980831	8.678494	9.082972	P	P
222303_at	0.0381636	0.1780936	0.6811878	8.769543	9.3571205	8.740629	P	P
222309_at	0.0430048	0.3476012	0.6813693	6.99809	6.88133	7.794137	P	P
222396_at	0.040517	1.5088125	0.5250387	9.604024	9.452032	9.683566	P	P
222493_s_a	0.001368	2.0026228	0.5250387	8.6875925	8.552205	8.576152	P	P
222599_s_a	0.0056099	1.9404667	0.5250387	8.495669	8.7794695	8.918613	P	P
222854_s_a	0.0001984	1.6330562	0.5250387	9.431101	9.355848	9.301404	P	P
222889_at	0.0288934	1.5374906	0.5250387	8.691982	8.760257	8.585182	P	P
223078_s_a	0.045673	1.7531321	0.5250387	7.205915	7.853286	7.8288183	P	P
223092_at	0.0417144	0.6157735	0.6823972	10.151302	10.429425	10.735223	P	P
223126_s_a	0.0317397	0.6636229	0.6838958	8.582013	8.875371	8.862455	P	P
223218_s_a	0.0488387	0.2016348	0.6811878	10.312506	9.288284	11.529309	P	P
223235_s_a	0.0454318	1.5486758	0.5250387	13.529579	13.032445	13.351946	P	P
223322_at	0.0304698	0.5589759	0.6813693	8.31929	8.1235285	8.055326	P	P
223393_s_a	0.0240343	0.5947829	0.6823972	10.537229	10.849607	10.610964	P	P
223474_at	0.0423198	0.5448375	0.6813693	13.46992	13.343974	13.325995	P	P
223566_s_a	0.0384977	0.5246447	0.6823972	8.270966	8.2416525	8.977139	P	P
223585_x_a	0.0198129	0.641256	0.6823972	6.8985033	6.4912877	6.8747497	P	A
223600_s_a	0.0447758	0.4887685	0.6823972	7.9264584	7.57377	8.0274515	P	A
223623_at	0.0044684	1.9393644	0.5250387	9.348012	9.705952	9.517114	P	P
223674_s_a	0.0383352	0.4947714	0.6823972	6.9975095	6.6273685	7.446299	P	P
223681_s_a	0.0071165	0.5686596	0.6811878	7.8875427	8.192386	8.275939	P	P
223797_at	0.044947	0.5357164	0.6823972	9.544048	9.885016	10.142106	P	P
224061_at	0.0317283	2.0899727	0.5250387	8.903735	8.269489	8.530437	P	P
224496_s_a	0.0229845	0.3614098	0.681247	7.3017106	8.191601	8.103157	P	P

224550_s_a	0.0390505	2.4499215	0.5250387	7.104313	8.002467	8.13867	P	P
224579_at	0.0279915	0.444006	0.6813693	8.91866	9.185015	9.844809	P	P
224611_s_a	0.0486811	1.8081731	0.5250387	8.660293	9.435033	8.866102	P	P
224692_at	0.0313788	0.2941432	0.6811878	10.195817	10.278528	10.783986	P	P
224806_at	0.0272126	1.5445248	0.5250387	10.61012	10.234535	10.678039	P	P
224826_at	0.0475781	0.3855675	0.6823972	10.512595	9.383363	9.9399185	P	P
224852_at	0.036244	1.5275533	0.5250387	10.779483	11.054541	11.143161	P	P
224882_at	0.0170964	1.6418356	0.5250387	10.131631	9.726508	10.141302	P	P
224941_at	0.0017248	0.5779817	0.6811878	6.839908	6.7567244	7.015097	P	A
224997_x_	0.045308	2.7382226	0.5250387	9.593556	8.799725	10.059143	P	P
225018_at	0.0052157	0.6155957	0.681247	8.24069	7.939939	7.9968863	P	P
225048_at	0.0346762	0.433697	0.6823972	11.297881	10.59925	11.474493	P	P
225107_at	0.0406419	0.6175244	0.6813693	11.506474	11.421524	11.943814	P	P
225134_at	0.0231424	0.6201565	0.6823972	7.8736553	8.371425	8.247034	P	A
225213_at	0.0043404	0.6354453	0.6813693	10.976913	11.136128	10.866285	P	P
225220_at	0.048196	0.6513671	0.684602	12.558704	13.117965	12.98647	P	P
225234_at	0.0432186	1.896613	0.5250387	9.356909	9.686998	8.974262	P	P
225345_s_a	0.0406023	1.6596772	0.5250387	8.543898	9.062367	9.1003	P	M
225348_at	0.0227481	1.7358059	0.5250387	10.018847	9.984983	10.342021	P	P
225403_at	0.0039615	1.5696524	0.5250387	10.394598	10.451184	10.256435	P	P
225415_at	0.0292204	1.6245074	0.5250387	11.317616	11.096661	10.840513	P	P
225446_at	0.0446977	0.5335896	0.6823972	9.334436	8.74107	9.434346	P	P
225557_at	0.0361298	0.0862313	0.6811878	7.838752	7.4169755	8.085514	P	P
225730_s_a	0.0430768	1.5718532	0.5250387	9.361966	9.5448065	9.927972	P	P
225767_at	0.0350635	0.0766996	0.681247	6.593673	8.582844	8.728567	P	P
225826_at	0.0207681	1.6539407	0.5250387	9.185949	9.331332	9.568465	P	P
225841_at	0.0192011	1.6583635	0.5250387	9.8368845	10.009287	9.901626	P	P
225871_at	0.004637	0.5901841	0.6811878	9.468829	9.22183	9.1933565	P	P
225931_s_a	0.0195806	1.7349258	0.5250387	9.304458	9.297965	9.286871	P	P
225972_at	0.0081392	0.5960443	0.6813693	9.006555	9.295466	8.986763	P	P
226206_at	0.0498909	0.5668774	0.6838958	8.836283	9.382926	8.850253	P	P
226268_at	0.044801	0.5909853	0.6823972	8.361691	7.956335	8.642605	P	P
226344_at	0.0005647	0.5738645	0.6811878	9.934555	9.96114	9.82077	P	P
226345_at	0.0276293	0.5295382	0.6811878	11.368615	11.280292	11.284557	P	P
226371_at	0.0263288	1.632899	0.5250387	10.302868	10.297513	10.241015	P	P
226429_at	0.001103	2.0662827	0.5250387	9.643129	9.437655	9.337568	P	P
226456_at	0.0411789	1.784438	0.5250387	8.663253	8.86836	8.637392	P	P
226550_at	0.0476989	0.6223057	0.6838958	7.6891227	7.7746773	7.971878	P	P
226561_at	0.0352909	0.5855301	0.6823972	9.775924	9.634276	10.15127	P	P
226650_at	0.0400106	2.1429826	0.5250387	10.460897	11.321192	11.230846	P	P
226657_at	0.0426391	1.6522122	0.5250387	8.654859	8.194742	8.559067	P	P
226767_s_a	0.0026582	1.9209314	0.5250387	9.613707	9.578387	9.909638	P	P
226776_at	0.0264499	0.5958812	0.6823972	8.404292	8.371285	8.134319	P	P
226777_at	0.015579	1.8533399	0.5250387	11.541132	11.105097	11.415916	P	P
226858_at	0.0442653	0.414133	0.6823972	7.8188486	8.540627	8.942226	P	P

226863_at	0.0168146	0.3935869	0.681247	9.277234	8.573856	9.428918	P	P
226886_at	0.0059219	0.598846	0.681247	10.264012	9.906531	10.122348	P	P
226933_s_a	0.0312514	0.3026723	0.681247	9.448625	8.590992	9.24566	P	P
226992_at	0.000183	1.6046469	0.5250387	10.229787	10.162809	10.240952	P	P
227010_at	0.0121304	0.6120833	0.6813693	7.389848	7.114112	7.425933	P	A
227073_at	0.0369274	0.5285933	0.6813693	8.06131	7.901272	8.62903	P	P
227086_at	0.0485282	0.5776108	0.6838958	7.377508	7.9717135	7.2300363	P	P
227099_s_a	0.0341536	0.2335558	0.6813693	12.639163	12.580432	13.731149	P	P
227190_at	0.004993	2.6451068	0.5250387	8.601427	8.596516	8.906352	P	P
227195_at	0.0454394	0.3997508	0.6813693	10.967689	11.365871	10.96428	P	P
227237_x_a	0.0496644	0.4878578	0.6823972	7.3496904	7.428492	8.296629	A	A
227294_at	0.0388431	1.7396851	0.5250387	9.168752	9.452935	9.310533	P	P
227330_x_a	0.0132928	2.2989833	0.5250387	9.793823	9.565694	9.587463	P	P
227339_at	0.0497129	0.2997587	0.6813693	6.047216	7.538296	7.64403	A	A
227444_at	0.0416687	0.5981841	0.6823972	9.587377	9.831782	9.719607	P	P
227506_at	0.0178023	1.5547326	0.5250387	12.335594	12.236568	12.639276	P	P
227529_s_a	0.0003664	0.5208666	0.6811878	11.158432	11.002971	10.992155	P	P
227530_at	0.0011272	0.6663839	0.6811878	12.796562	12.695147	12.629583	P	P
227590_at	0.0450411	1.6178871	0.5250387	8.393746	9.00192	8.586459	P	P
227697_at	0.0384128	0.099742	0.6811878	10.123254	7.749348	10.767796	P	P
227702_at	0.0238857	0.6257128	0.6823972	6.622787	6.2598395	6.373726	P	P
227834_at	0.012871	0.5399954	0.681247	8.302351	7.775706	8.182396	P	P
227936_at	0.016821	0.5522235	0.6813693	7.354584	7.8957973	7.56675	P	A
227940_at	0.0325459	2.2650047	0.5250387	8.384291	8.328932	7.5659494	P	P
227943_at	0.0301576	1.9735917	0.5250387	9.090292	8.319068	8.789635	P	P
227968_at	0.045456	1.5455525	0.5250387	9.562418	9.554437	9.371377	P	P
227971_at	0.0133223	0.4428632	0.6811878	10.960728	11.030148	11.230834	P	P
228092_at	0.0370819	0.472916	0.6823972	7.513254	6.850576	7.286455	P	P
228097_at	0.0235443	0.3427228	0.6811878	6.895728	8.0565605	7.671264	P	P
228108_at	0.0276834	0.5576809	0.6823972	8.417365	7.993189	8.526832	P	P
228175_at	0.0338288	0.5400521	0.6823972	7.987772	8.419693	8.183101	P	P
228235_at	0.037956	2.7378107	0.5250387	11.690578	10.562223	10.683433	P	P
228285_at	0.0210011	6.5182387	0.5250387	7.634965	7.755683	7.3930326	P	P
228325_at	0.0351383	0.1613251	0.681247	8.257231	7.187367	8.840904	P	P
228389_at	0.0387666	0.6424363	0.6823972	7.57649	7.5056744	7.666838	P	M
228457_at	0.0311652	0.5963038	0.6823972	6.4592934	7.051955	6.925994	P	A
228493_at	0.0206661	0.6077167	0.6823972	7.5050135	7.873861	8.004436	P	P
228549_at	0.0146505	0.6525582	0.6823972	9.306355	8.986969	9.125382	P	P
228595_at	0.0386239	1.5646989	0.5250387	8.991464	9.087183	8.921933	P	P
228617_at	0.0329102	1.6281072	0.5250387	13.677876	13.89178	13.364312	P	P
228728_at	0.017706	0.5893628	0.6823972	12.306302	11.971055	12.371437	P	P
228731_at	0.0206887	1.9029864	0.5250387	9.90761	9.76086	10.373181	P	P
228750_at	0.0055581	0.5429544	0.6811878	11.628112	11.297859	11.249693	P	P
228829_at	0.0339335	0.5870091	0.6823972	8.127322	7.5246916	7.959519	P	P
228857_at	0.0286895	0.4142535	0.6813693	8.863372	8.697712	8.271649	P	P

228877_at	0.0182423	2.4251962	0.5250387	7.3243566	7.6986346	8.152292	P	P
228935_at	0.0410687	0.5858886	0.6838958	6.7057123	6.439917	6.9558525	P	A
228964_at	0.0253242	0.4272535	0.6813693	7.6158576	6.93982	7.8340693	P	P
229078_s_a	0.0459013	1.9661533	0.5250387	9.35462	9.520599	9.488154	P	P
229161_at	0.0036529	0.1665418	0.6811878	7.4868526	7.0982833	7.6223474	P	A
229169_at	0.0434565	0.6568209	0.684602	7.840275	7.3250337	7.5824947	P	P
229317_at	0.0167282	0.5904055	0.681247	10.595309	10.343478	10.817325	P	P
229412_at	0.0357626	1.5354543	0.5250387	7.4504485	7.5748973	7.2567997	P	P
229415_at	0.041813	0.3599193	0.6813693	7.422439	8.160264	7.7146497	P	P
229500_at	0.0325922	1.8449112	0.5250387	7.3639793	7.3828535	7.866108	P	P
229549_at	0.0016074	0.5944634	0.6811878	8.3868265	8.552658	8.632343	P	P
229594_at	0.0472132	0.6546582	0.684602	9.78169	9.435794	10.025258	P	P
229748_x_a	0.0096278	1.9295198	0.5250387	9.906721	9.544305	9.9386425	P	P
229764_at	0.0091988	1.9236862	0.5250387	7.5577517	7.565047	7.115492	P	P
229876_at	0.0053572	0.5382965	0.6811878	8.900117	9.074625	8.840001	P	P
229893_at	0.0463453	1.7532114	0.5250387	10.368515	9.687451	9.776142	P	P
229899_s_a	0.044307	0.6392297	0.6823972	8.416152	8.419372	8.584351	P	A
230172_at	0.0138667	1.5574568	0.5250387	10.416473	10.034308	10.193454	P	P
230214_at	0.0288674	1.9737911	0.5250387	8.473816	9.235637	8.966143	P	P
230291_s_a	0.0074451	0.5971492	0.681247	7.715257	7.8032775	7.447548	P	P
230311_s_a	0.0256132	1.8162893	0.5250387	11.33395	10.92794	10.837834	P	P
230404_at	0.0361648	1.6317107	0.5250387	7.0243363	7.075457	7.2673416	P	P
230491_at	0.048614	1.6391662	0.5250387	8.635501	8.655432	8.7918415	P	P
230630_at	0.0281367	2.2377389	0.5250387	6.93361	7.642008	7.2269316	P	P
230757_at	0.025619	0.6056506	0.6823972	8.897681	8.880937	8.652335	P	P
230818_at	0.033306	2.0236735	0.5250387	8.077821	7.9714894	8.484745	P	P
230913_at	0.0414425	0.5697576	0.6838958	8.351589	7.8782344	7.73441	P	P
230954_at	0.0137968	0.6391108	0.6813693	6.599996	6.387334	6.543836	A	A
230962_at	0.042212	0.50159	0.6823972	6.2680283	6.223963	6.760222	P	P
230968_at	0.0126212	2.8155472	0.5250387	7.19052	7.4652042	6.5938363	P	P
231056_at	0.0278594	1.5799328	0.5250387	7.8534946	8.147022	7.7269006	M	M
231067_s_a	0.003027	0.5739181	0.6811878	9.223433	9.391654	9.236152	P	P
231102_at	0.04408	1.5416318	0.5250387	6.26563	6.6722383	6.54977	M	P
231130_at	0.0070837	0.5945915	0.6811878	10.877596	11.026219	10.916527	P	P
231249_at	0.0239685	0.6379079	0.6823972	6.8561482	6.8112483	7.025109	P	A
231597_x_a	0.0149452	0.3397638	0.6811878	4.9883595	5.3324356	5.274194	A	A
231610_at	0.0052334	0.4238544	0.6811878	5.9201593	5.634432	6.212649	P	A
231835_at	0.0462817	1.7372556	0.5250387	8.611558	8.022354	8.371611	P	P
231867_at	0.0289424	0.4468324	0.6813693	6.1430845	6.8197675	6.1102657	A	A
231887_s_a	0.017214	1.718583	0.5250387	8.864862	8.891261	9.327465	P	P
231923_at	0.0317144	0.6532026	0.6813693	9.569191	9.616757	9.251166	P	P
231953_at	0.044036	0.4463185	0.6823972	7.423445	7.0119905	6.8240805	P	P
231999_at	0.0295262	1.5144989	0.5250387	9.998942	10.305149	10.248206	P	P
232017_at	0.0288232	1.9632292	0.5250387	10.779605	10.157186	10.134762	P	P
232044_at	0.048064	0.4711081	0.6813693	8.837901	9.029813	9.234058	P	P

232110_at	0.0013625	1.8159822	0.5250387	6.7689915	6.7236457	6.958907	P	P
232127_at	0.0321515	2.9908044	0.5250387	6.4424734	7.6796412	7.24505	P	P
232280_at	0.0268048	0.552573	0.6813693	7.1718507	7.4865766	7.2596574	P	P
232290_at	0.0387369	0.0961224	0.6811878	5.4934335	6.9350834	6.3393254	A	A
232291_at	0.0319276	0.1994355	0.681247	5.7339935	6.9476333	7.7179236	A	P
232461_at	0.0044433	0.1904077	0.6811878	6.035845	5.877506	6.8812475	M	A
232472_at	0.048551	0.5041518	0.6823972	10.084189	9.216842	9.231328	P	P
232477_at	0.0276979	0.3180001	0.681247	4.433472	4.329263	5.5444164	A	A
232576_at	0.0054071	0.3649387	0.6811878	6.5518255	7.149747	6.9308815	A	A
232621_at	0.006264	1.5765374	0.5250387	7.984203	8.138132	8.289889	P	P
232708_at	0.003913	1.7757626	0.5250387	7.5985913	7.7939277	7.55203	P	P
232807_at	0.0243999	0.6284201	0.6823972	7.1251464	6.9109864	6.7454042	P	P
232811_x_a	0.0448319	0.6291693	0.6838958	6.350098	6.540149	6.916241	P	P
232865_at	0.0475068	0.5728783	0.6813693	10.647132	10.705368	10.595095	P	P
232945_at	0.0351297	2.3008328	0.5250387	7.010054	7.6239886	7.6157107	P	P
233177_s_a	0.0111215	1.9095362	0.5250387	8.145792	8.33262	8.164836	M	P
233193_x_a	0.0014848	1.6584287	0.5250387	9.1002865	9.318182	9.264808	P	P
233223_at	0.0054854	0.1359324	0.6811878	6.515074	5.8538246	6.9683642	A	A
233233_at	0.0107073	0.651988	0.6823972	7.8048086	7.5258846	7.529537	P	P
233666_at	0.0403605	1.9172791	0.5250387	6.1346087	6.050432	5.949142	P	P
233862_at	0.0071098	1.6858213	0.5250387	7.315104	7.6925316	7.4638653	P	P
233932_at	0.0071541	1.564054	0.5250387	7.9649944	7.7991643	8.111647	P	P
233945_at	0.0433125	1.7567456	0.5250387	6.5161357	6.9410377	6.956982	M	P
233970_s_a	0.040401	0.5460399	0.6823972	8.746365	8.487877	9.118371	P	P
234059_at	0.0014034	4.2131192	0.3573948	7.452891	7.576069	7.6043663	P	P
234224_at	0.0360512	1.6714528	0.5250387	9.020086	9.486834	9.130094	P	P
234269_at	0.0074219	2.2683185	0.5250387	7.586267	7.193863	7.599445	P	P
234340_at	0.0256685	1.6503953	0.5250387	7.944702	8.025534	8.348338	P	P
235006_at	0.0455518	1.710069	0.5250387	7.315163	8.015297	7.793706	P	P
235007_at	0.0096394	0.6413968	0.6813693	8.851535	8.68112	8.97879	P	P
235077_at	0.0176408	0.1482967	0.6811878	10.489904	9.822242	11.072016	P	P
235102_x_a	0.0183881	0.0095713	0.6811878	4.428606	6.506485	6.188062	A	A
235153_at	0.0258097	0.5577195	0.6823972	5.528266	6.185296	5.8970847	A	A
235175_at	0.0214171	1.9801933	0.5250387	8.233286	8.771966	8.4724045	P	P
235189_at	0.0423787	1.655661	0.5250387	7.689834	7.8496346	8.096514	P	P
235203_at	0.0126417	0.4923346	0.681247	8.032322	7.501033	7.9294467	P	P
235225_at	0.0245022	2.0123023	0.5250387	7.5054474	7.7283974	7.055989	P	P
235492_at	0.0013339	0.546538	0.6811878	7.4484496	7.3168464	7.4581647	P	A
235559_at	0.0315397	1.6050509	0.5250387	8.233846	8.768414	8.367728	P	P
235592_at	0.0444138	0.0312841	0.6811878	5.919971	7.1961937	4.9114537	A	P
235659_at	0.0415755	1.9529548	0.5250387	7.8442807	7.8335114	7.584437	P	M
235680_at	0.0306664	0.4045615	0.6813693	9.000774	8.121696	8.707651	P	P
235688_s_a	0.0125434	0.5896011	0.681247	6.3393364	6.361035	6.52317	A	A
235736_at	0.0010195	1.8962198	0.5250387	6.8916264	7.1393332	7.1096272	P	P
235739_at	0.0061179	0.1110702	0.6811878	7.946298	7.1391215	8.617057	P	A

235957_at	0.0221591	1.6053707	0.5250387	7.4918504	7.1755614	7.6630797	P	M
236128_at	0.0001896	0.5743939	0.6811878	8.20384	8.114104	8.057536	P	P
236273_at	0.0333297	1.6865189	0.5250387	9.926231	9.527095	9.528082	P	P
236327_at	0.0196062	2.2255794	0.5250387	6.557393	6.7427506	7.288944	P	P
236361_at	0.0421518	0.5781887	0.6838958	7.9395247	8.64891	8.400059	P	P
236577_at	0.0352502	1.9275497	0.5250387	10.620286	9.96787	9.914216	P	P
236665_at	0.0316947	3.236187	0.5250387	6.127555	6.9127297	6.539264	P	P
236685_at	0.0432587	0.2857489	0.6811878	9.250189	9.374268	9.566621	P	P
236907_at	0.0015634	0.2432772	0.6811878	8.549988	8.724785	8.86044	P	P
236918_s_a	0.0438536	0.5610971	0.6813693	7.4621167	7.428312	6.8431582	P	P
236975_at	0.024626	0.244018	0.6811878	7.181939	6.1777363	6.9430904	P	A
237398_at	0.0036025	0.5276282	0.6811878	7.917394	8.227657	7.9943876	P	A
237554_at	0.0300389	1.8334572	0.5250387	7.9835386	8.186733	8.066598	P	P
237561_x_	0.0324229	0.526287	0.6823972	9.668602	9.45302	9.990983	P	P
237627_at	0.030599	0.6300886	0.6823972	7.264232	6.8196564	7.3257446	P	P
237875_at	0.0081407	2.1942577	0.5250387	7.099789	7.6275373	7.1564045	P	P
237917_at	0.0136032	0.4424418	0.681247	5.8446226	5.3676243	5.2344947	P	A
237952_at	0.0365478	2.3972233	0.5250387	5.7572594	6.5411477	5.8141375	P	M
238081_at	0.0108307	0.63457	0.6813693	9.454985	9.240195	9.4833355	P	P
238178_at	0.0272132	0.5778582	0.681247	8.21129	8.337154	8.243244	P	P
238205_at	0.0105213	2.2888389	0.5250387	8.042269	7.737036	7.9434767	P	P
238363_at	0.0035551	2.3061649	0.5250387	6.5825844	7.0093656	6.97666	P	P
238430_x_	0.0075447	1.7031766	0.5250387	10.936367	11.130342	11.216671	P	P
238725_at	0.0378455	0.3232775	0.681247	8.223625	7.9794664	7.552525	A	A
238987_at	0.0028441	0.1683892	0.6811878	8.541809	8.381469	8.943014	P	P
239005_at	0.0336507	1.6145473	0.5250387	8.981283	9.325798	8.77318	P	P
239046_at	0.0361091	1.6607592	0.5250387	7.2595973	7.6726675	7.8489547	P	P
239074_at	0.0382104	2.9754038	0.5250387	7.8298316	8.46181	7.14739	P	P
239133_at	0.0060122	0.6383474	0.681247	9.7409725	9.658182	9.859552	P	P
239163_at	0.0195838	0.6660132	0.6823972	8.734247	9.1091585	9.006571	P	P
239185_at	0.0499399	1.509401	0.5250387	9.446936	9.918958	9.945899	P	P
239247_at	0.022267	2.1464852	0.5250387	8.943117	8.67275	8.159756	P	P
239329_at	0.0458961	0.6447146	0.6823972	9.36057	9.341367	9.19298	P	P
239367_at	0.0493336	1.6283041	0.5250387	7.583323	7.4420786	7.0606403	P	P
239489_at	0.0338003	1.6785761	0.5250387	7.81697	8.419033	8.00943	P	P
239711_at	0.0192603	1.8653847	0.5250387	7.284322	7.6329746	7.326167	P	P
239839_at	0.040897	1.7653368	0.5250387	7.3532195	7.9448605	7.9047313	P	P
239966_at	0.0127937	2.5578585	0.5250387	8.609242	8.669099	8.462363	P	P
240108_at	0.048833	0.5277659	0.6823972	9.777376	9.921042	9.633417	P	P
240236_at	0.003956	0.5541256	0.6811878	8.968989	8.673362	8.858409	P	P
240385_at	0.0240725	0.37586	0.681247	9.866158	10.593048	10.411247	P	P
240391_at	0.0165481	1.5127482	0.5250387	6.719182	6.9765153	6.9311647	P	P
240435_at	0.0229118	2.0407366	0.5250387	7.1103415	7.6962414	7.067339	P	P
240467_at	0.0147841	0.3112048	0.6811878	8.61836	7.9799957	8.458456	P	P
240496_at	0.0049738	0.1933588	0.6811878	5.4633245	4.8160396	5.44868	A	A

240781_x_a	0.0189125	0.63148	0.6813693	5.383103	5.2038245	5.64369	P	A
240806_at	0.0335448	0.5487075	0.6823972	7.571539	8.270872	8.144881	P	P
241210_at	0.0285907	0.580973	0.6823972	6.657066	6.2662635	6.8330812	P	A
241289_at	0.0383131	0.1832321	0.6811878	5.873158	3.7524245	5.2421384	A	A
241302_at	0.0431334	0.3851707	0.6813693	8.996494	7.716797	8.648391	P	P
241347_at	0.0100256	2.5240994	0.5250387	8.850886	9.321007	9.519864	P	P
241366_at	0.0387159	1.6459013	0.5250387	7.5550146	7.079376	7.322399	P	M
241381_at	0.0483265	2.225359	0.5250387	7.57221	6.5197496	7.034905	P	P
241413_at	0.0155887	1.875175	0.5250387	8.689391	8.778441	8.873255	P	P
241487_at	0.0230251	4.511748	0.5250387	8.13486	8.523779	7.0190253	P	P
241534_at	0.041386	2.7152704	0.5250387	6.3437967	6.664009	6.254954	P	M
241722_x_a	0.0309047	0.3458007	0.681247	10.495985	10.619945	11.689263	P	P
241773_at	0.0429136	0.1999957	0.6813693	5.584046	5.5825515	4.2836013	P	A
241780_at	0.0086581	0.5072896	0.6811878	8.324721	8.73798	8.235761	P	P
241832_at	0.0408796	4.3848186	0.5250387	7.961917	9.138571	8.453732	P	P
241866_at	0.0036618	1.736065	0.5250387	6.528088	6.7813854	6.77014	P	M
241892_at	0.0382921	1.5060067	0.5250387	6.231427	6.3129253	6.6821113	P	P
241924_at	0.013741	0.4410992	0.6811878	8.210348	8.713434	7.999982	P	P
241933_at	0.0441326	1.5918301	0.5250387	7.9117675	7.871424	8.100941	P	P
242007_at	0.0282109	1.651355	0.5250387	9.125388	8.638529	8.815176	P	P
242016_at	0.018622	1.5506026	0.5250387	7.648962	8.022011	7.6494503	P	P
242059_at	0.0313834	2.0907213	0.5250387	7.6386123	7.450945	8.186416	P	P
242172_at	0.0447336	0.6644666	0.684602	9.0783615	8.622145	9.103549	P	P
242358_at	0.0131789	0.6583349	0.6823972	9.332509	9.151119	9.501687	P	P
242505_at	0.0196709	0.2571286	0.6811878	7.414349	7.1929464	8.254456	P	P
242558_at	0.0319133	0.5976312	0.6823972	11.075356	11.503382	10.901581	P	P
242625_at	0.0288804	2.6552592	0.5250387	10.252702	10.300523	9.346869	P	P
242657_at	0.0250112	0.2590947	0.6811878	8.779417	8.794291	7.9712543	P	P
242750_at	0.0491473	1.5077682	0.5250387	8.858525	9.119422	8.563083	P	P
242819_at	0.0277459	1.6695632	0.5250387	7.854328	7.9374604	7.981104	P	P
242827_x_a	0.0041852	1.5730152	0.5250387	7.1411543	7.15318	6.971263	P	P
242836_at	0.0302426	0.0111848	0.6811878	7.609735	2.9844184	8.050158	P	A
242868_at	0.0404435	0.493207	0.6823972	9.161632	9.234434	8.391213	P	P
242892_at	0.0458503	0.4206253	0.6823972	6.364059	5.8933296	6.5819416	P	A
242904_x_a	0.0477275	0.1283639	0.6811878	6.4416966	7.1725817	7.060712	P	P
242983_at	0.0310147	1.6492497	0.5250387	9.033925	8.781236	8.710777	P	P
243046_at	0.0272252	0.5427539	0.6823972	10.455603	9.913634	10.569016	P	P
243064_at	0.0257052	1.8631472	0.5250387	7.532082	7.5877204	8.030048	P	P
243117_at	0.0446965	1.574069	0.5250387	7.5931034	7.109562	7.2487955	P	P
243184_at	0.0477439	1.5069874	0.5250387	8.590192	8.853941	9.084718	P	P
243224_at	0.0318202	2.0614898	0.5250387	8.355207	8.722075	8.651028	P	P
243364_at	0.0495136	0.3002911	0.6823972	5.783603	4.5178905	5.369109	A	A
243470_at	0.0103705	1.5965606	0.5250387	7.999428	7.987263	8.143044	P	P
243524_at	0.0352452	1.8188187	0.5250387	7.5886307	8.30969	7.938884	P	P
243558_at	0.0436127	3.266556	0.5250387	7.707686	8.837397	8.365634	P	P

243745_at	0.0340145	1.8671492	0.5250387	9.055051	8.418723	8.40179	P	P
243750_x_	0.0371628	1.7117662	0.5250387	8.241894	7.734585	8.365009	P	P
243802_at	0.0319854	4.4393013	0.5250387	8.06151	7.2020426	8.863948	P	P
243934_at	0.0223254	2.3572119	0.5250387	7.258486	7.3909483	6.615934	P	P
243937_x_	0.0045551	1.5023625	0.5250387	7.5515676	7.3421164	7.5845847	P	M
244033_at	0.0048116	1.5355854	0.5250387	7.607927	7.526325	7.486732	P	P
244370_at	0.0183993	0.3805858	0.6811878	5.680309	5.3535995	5.836949	A	A
244425_at	0.0468271	0.6573399	0.6838958	8.974969	9.304744	8.7192335	P	P
244447_at	0.0029068	0.1973037	0.6811878	8.898327	8.442896	9.3049345	P	A
244470_at	0.0228336	0.407874	0.6813693	7.6488395	8.419875	8.1806965	P	P
244502_at	0.0227069	2.8519186	0.5250387	6.077205	6.8772836	5.9056773	P	P
244546_at	0.0051364	0.1075559	0.6811878	6.4530926	7.1455035	7.830113	P	P
244563_at	0.0311907	0.5334481	0.6813693	6.564871	7.0863314	7.292432	P	P
244597_at	0.0389225	0.586473	0.6823972	8.46631	8.715709	8.4718685	P	P
244654_at	0.0066825	0.4736073	0.6811878	6.853549	6.542449	6.508691	P	A
244662_at	0.0197921	0.6166693	0.6823972	7.4765606	7.387516	7.7143807	P	M
34689_at	0.021924	1.6136912	0.5250387	9.471305	9.534919	9.511936	P	P
36907_at	0.038803	1.5059107	0.5250387	9.564339	9.666998	10.038736	P	P
37028_at	0.041385	0.3894897	0.6823972	7.2732515	8.268279	8.038635	P	P
39313_at	0.0381493	1.5626009	0.5250387	8.583094	8.550657	8.447006	P	P
47069_at	0.0363571	1.6956006	0.5250387	9.095008	8.839827	8.52941	P	P

PCOS3_cal	Control1_N	Control2_N	Control3_N	Control1_ca	Control2_ca	Control3_ca	Gene_Symb	Entrez_Gen
P	9.253506	9.637994	8.518669	P	P	P	ETV3	2117
P	7.5670314	7.354186	6.966571	P	P	P	LACTB	114294
P	6.1918726	5.9627266	5.6250935	P	P	P	DUSP19	142679
A	7.152942	7.153272	5.4732847	P	P	P	TAB3	257397
P	6.4891095	6.116923	7.1329036	A	A	P	C3orf34	84984
P	5.8737435	4.7867055	6.274948	P	A	P	ALS2CR11	151254
P	6.2650185	5.836042	6.734644	A	A	A	SLC5A3	6526
P	10.724832	10.379414	10.362605	P	P	P	RGNEF	64283
P	8.488429	7.6012244	7.870718	P	P	P	WDR20	91833
P	5.7879543	6.316295	6.082276	A	P	A	GDEP	118425
P	8.944287	9.667007	8.992203	P	P	P	RBM8A	9939
P	11.111913	10.841175	10.551444	P	P	P	ZFYVE16	9765
P	11.359384	10.979354	10.964979	P	P	P	FGF7 /// K	2252///3876
P	7.615752	6.6811485	6.212261	P	P	P	PTGS2	5743
P	6.8368664	6.78615	7.0920763	P	P	P	NDUFS4	4724
P	6.3979926	6.7370315	6.4036984	P	P	P	CTDSPL2	51496
P	5.5151453	6.0406313	5.3651586	A	P	P	POLK	51426
P	6.298123	7.05812	6.419812	A	A	P	RBM15	64783
P	10.555088	9.776876	9.761692	P	P	P	LOC28445	284454
P	10.31885	9.968246	10.102823	P	P	P	GNG4	2786
P	8.304838	8.680534	8.8646	P	P	P	OR2A20P /	401428///44
P	11.797905	11.952172	11.520637	P	P	P	VIM	7431
P	9.383355	9.185442	9.335647	P	P	P	B3GNT7	93010
P	9.644204	9.629356	9.205655	P	P	P	SPEN	23013
P	5.1543446	5.152545	6.106201	A	M	P	UNC13C	440279
P	10.781786	10.422761	10.27365	P	P	P	NAP1L1	4673
P	9.231681	10.230602	9.565681	P	P	P		
P	6.751952	7.1363196	7.7216215	A	P	P	YPEL2	388403
P	7.7088423	8.154367	8.569274	P	P	P	FBXL13	222235
P	5.4367642	5.7296314	4.9147534	P	P	P	ALS2CR10	65072
P	7.105203	7.2966046	7.1818833	P	P	P		
P	7.366175	7.060103	7.144127	P	P	P		
P	6.274962	6.630421	6.5662427	P	P	P	ITGBL1	9358
P	7.8625946	7.9146314	8.16377	P	P	P		
P	9.77727	9.426724	9.6268635	P	P	P	ZNF131	7690
P	8.477241	8.813989	8.347341	P	P	P		
P	10.830384	10.710413	10.116317	P	P	P		
P	8.658125	8.326184	8.87227	P	M	P		
P	6.25105	6.704098	6.447122	P	P	P	C12orf51	283450
P	7.708774	8.973547	8.7910385	P	P	P		
P	10.182673	9.607026	9.892501	P	P	P	EXOSC6	118460
P	9.564801	9.090719	9.097882	P	P	P	SSBP2	23635
P	8.808722	9.221665	9.623513	P	P	P	LOC15896	158960

P	10.155999	10.546696	10.756019	P	P	P		
P	8.75634	9.080466	9.336197	P	P	P	CNTLN	54875
P	7.2875	7.3735476	7.8035173	P	P	P		
A	7.4551873	7.9481893	8.2403	P	P	P		
P	6.308174	6.9621887	6.840153	A	P	P	LOC10028	100289210
P	6.8229527	6.8646235	7.0362787	P	P	P	CCDC66	285331
P	7.008368	7.434289	6.9884753	P	P	P		
P	9.539253	9.552756	10.048307	P	P	P		
P	7.163993	6.4498982	6.495847	P	P	P		
P	5.734507	5.5840836	5.8114476	P	A	P		
A	6.3071313	6.6847553	6.4941764	P	P	P		
P	5.610392	6.026427	5.8007746	A	P	P	RECQL5	9400
P	8.75311	8.181205	8.88319	P	P	P	JAK2	3717
P	5.805862	5.636366	5.44256	A	A	A	LOC15117	151171
P	7.4326615	7.707939	7.1800094	P	P	P	USPL1	10208
P	7.7502337	8.355991	8.464516	P	P	P	ZNF578	147660
P	6.8684716	7.2858887	7.330991	A	P	P		
P	8.942289	9.434112	8.533382	P	P	P		
P	6.8543425	6.991413	7.2216988	M	P	P		
P	7.3940444	7.5649223	8.121617	P	P	P	CASP12	120329
P	9.4869375	9.542085	9.005262	P	P	P	DIP2C	22982
P	7.2605715	6.6935725	6.681204	P	P	P		
P	6.91265	7.520159	7.429855	P	P	P		
P	6.497477	6.8337636	6.297462	P	P	P		
P	7.3545775	7.844009	7.427237	P	P	P	SMEK2	57223
P	6.290295	6.2994385	5.6743345	P	M	A	LOC64626	646268
A	9.649489	9.498377	7.477678	P	P	P	LOC10030	100302650
P	5.8120155	6.0008636	6.187934	M	A	P		
M	6.195198	6.3248644	6.5377746	A	A	P	ZNF333	84449
P	5.237203	6.149907	6.1061234	A	P	P	LOC28444	284440
P	6.8584213	7.083827	6.9697537	P	P	P		
P	6.3987494	6.0845933	6.004479	P	P	P		
P	7.0395327	7.3386536	7.0943146	P	P	P	ATG10	83734
P	8.1840515	7.657513	8.003176	P	A	P	PTPRF	5792
P	13.043556	13.244919	12.657477	P	P	P	YWHAZ	7534
P	8.725858	8.613021	8.832108	P	P	P	FAM120A	23196
P	14.768111	14.64018	13.800693	P	P	P	MCL1	4170
P	13.978021	13.299363	11.651623	P	P	P	MCL1	4170
P	11.790129	11.699051	12.208737	P	P	P	STAT1	6772
P	10.389244	10.383916	9.797561	P	P	P	MGEA5	10724
P	12.586701	12.318942	12.010514	P	P	P	SERP1	27230
P	15.437644	15.06909	13.899145	P	P	P	DUSP1	1843
P	14.193844	14.041585	13.567937	P	P	P	CSDA	8531
P	12.837585	12.832418	11.019371	P	P	P	BHLHE40	8553
P	14.203792	14.409425	13.813668	P	P	P	DDX3X	1654

P	13.497124	12.492327	11.728954	P	P	P	BTG2	7832
P	12.676189	12.579628	12.613382	P	P	P	ATP1B1	481
P	10.424753	10.4328	9.969358	P	P	P	UCHL1	7345
P	8.65774	8.369268	8.802588	P	P	P	WDR77	79084
P	12.662972	12.413171	11.544627	P	P	P	JUNB	3726
P	12.56512	13.138799	11.624723	P	P	P	ID2	3398
P	10.641317	10.268042	10.41736	P	P	P	KRT19	3880
P	11.764964	11.618171	11.816093	P	P	P	NET1	10276
P	7.561619	7.5252447	7.583818	P	P	P	PSRC1	84722
P	9.312207	9.491227	9.528638	P	P	P	UQCRC1	7384
A	8.756227	8.635292	8.000043	P	P	P	PPP1R15A	23645
P	12.1442	12.065099	11.807825	P	P	P	RB1CC1	9821
P	10.445307	10.247121	10.94976	P	P	P	LSS	4047
P	6.6616426	6.841661	6.9287353	A	P	P	SYMPK	8189
P	8.690531	8.940948	8.866502	P	P	P	IGF2 /// IN	3481///7239
P	11.089891	10.936946	11.49327	P	P	P	IFI27	3429
P	8.8854685	8.639258	8.414609	P	P	P	NOTCH2	4853
P	8.2765	8.328517	8.350298	P	P	P	LYN	4067
P	12.620092	11.8731	9.538926	P	P	P	ATF3	467
P	7.7215757	7.7904363	8.1574545	P	P	P	TRIM26	7726
P	13.436688	12.913748	12.839971	P	P	P	ITM2A	9452
P	11.261858	11.49182	11.283757	P	P	P	FBN1	2200
P	8.019511	8.358065	8.415657	P	P	P	ACP2	53
P	6.7322	7.120287	6.803099	P	P	P	LPP	4026
P	10.829171	10.533944	9.445966	P	P	P	DNAJB9	4189
P	10.886694	11.605166	8.577393	P	P	P	IL8	3576
P	9.867366	9.936383	9.815859	P	P	P	NBAS	51594
P	10.755044	11.066035	10.161795	P	P	P	FBLN1	2192
P	9.889814	10.19461	10.359057	P	P	P	FH	2271
P	11.697361	12.127245	11.898047	P	P	P	PRDM2	7799
P	8.346894	8.4651985	8.248782	P	P	P	TIMM44	10469
P	7.3053684	7.906171	8.247704	P	P	P	TRIM14	9830
P	9.99211	10.204409	10.937653	P	P	P	IFIT1	3434
P	8.755639	9.011692	8.773244	P	P	P	KDM4A	9682
P	12.098415	12.388786	11.596387	P	P	P	HES1	3280
P	10.662846	11.075233	10.432841	P	P	P	HES1	3280
P	9.943331	9.965117	9.4987755	P	P	P	DDB2	1643
P	7.785765	7.4016056	7.235731	P	P	P	AFAP1	60312
P	14.603512	14.535143	13.325081	P	P	P	JUND	3727
P	10.049276	10.222023	10.802045	P	P	P	IRF9	10379
P	11.865063	11.615778	11.276449	P	P	P	ARHGAP2	9411
P	7.3215857	7.536927	7.5047035	P	P	P	TRIP13	9319
P	10.321402	10.33082	10.190403	P	P	P	RNF144A	9781
P	10.917385	11.210346	10.860696	P	P	P	TOPORS	10210
P	12.408593	12.079711	12.141026	P	P	P	PBX3	5090

P	7.7813277	7.7985387	8.089077	P	P	P	CPT2	1376
P	6.2663	6.578598	6.384583	P	P	P	NF1	4763
P	10.662074	10.913463	11.699297	P	P	P	IFI6	2537
P	10.739498	10.821878	10.422105	P	P	P	NUPL1	9818
P	10.51484	10.718629	11.25209	P	P	P	IFI44L	10964
P	10.362206	10.645022	9.491113	P	P	P	TOX	9760
P	9.287716	9.18504	8.912071	P	P	P	ABCG1	9619
P	14.342167	13.249484	11.604163	P	P	P	NR4A2	4929
P	14.43992	13.776136	12.218487	P	P	P	NR4A2	4929
P	6.7493443	7.27396	7.322975	P	P	P	HHEX	3087
P	9.449159	8.260846	7.3001223	P	P	P	PTGS2	5743
P	10.744213	10.72993	10.560006	P	P	P	HLF	3131
P	12.429248	12.256948	11.904655	P	P	P	GPRASP1	9737
P	6.33361	6.642445	6.460317	P	P	P	MAD1L1	8379
P	7.6872153	7.2482643	7.8266497	P	P	P	BNIP1	662
P	6.9067125	7.1246476	7.2357574	P	P	P	NAGPA	51172
P	9.608474	8.965181	9.586668	P	P	P	CLEC3B	7123
P	12.004566	10.56249	10.081962	P	P	P	EGR2	1959
P	10.352775	10.907747	8.799378	P	P	P	IGFBP1	3484
P	9.708128	9.152931	9.168441	P	P	P	SERPINI1	5274
P	5.399167	6.2953258	6.201957	A	P	P	CHEK1	1111
P	9.141954	8.94969	9.016275	P	P	P	PHKA1	5255
P	10.112723	10.093091	10.665926	P	P	P	ISG15	9636
P	8.268524	8.376286	8.737235	P	P	P	AIFM1	9131
P	8.352758	8.272954	8.911213	P	P	P	HRH1	3269
P	9.174703	9.184298	9.461616	P	P	P	OMD	4958
P	9.691382	10.906837	11.024363	P	P	P	LEFTY2	7044
P	12.626342	12.919364	12.328376	P	P	P	WT1	7490
P	7.498971	8.120791	7.8583536	P	P	P	GINS1	9837
P	13.118128	11.893271	10.956689	P	P	P	EGR3	1960
P	11.687129	12.190956	11.832779	P	P	P	XAF1	54739
P	10.683668	10.15552	10.970036	P	P	P	GRB14	2888
P	8.952551	8.170671	8.469038	P	P	P	SELE	6401
P	5.916975	6.212375	6.124508	P	P	P	RYR3	6263
P	10.301798	11.42252	8.625428	P	P	P	SOCS3	9021
P	6.9560866	6.2243657	6.870585	P	P	P	PLXNC1	10154
P	6.524128	7.252591	7.105831	A	P	A	ITGA2B	3674
P	4.043708	3.9570694	4.9781632	A	A	A	CYP4F3	4051
P	12.925754	12.932588	12.592973	P	P	P	SMARCA2	6595
P	12.156463	12.127947	11.789606	P	P	P	SMARCA2	6595
P	7.7452016	7.825215	7.7398806	P	P	P	NR0B1	190
P	4.5214825	4.6608934	5.286754	A	A	A	HCG4	54435
P	7.3923793	7.9786906	7.9566474	P	P	P	ZNF253	56242
P	10.162153	10.516173	9.798625	P	P	P	WT1-AS	51352
P	8.134931	8.257265	7.677438	P	P	P	SLC4A8	9498

P	8.463076	8.07546	7.684347	P	P	P	PTGFR	5737
P	7.3145375	7.3440394	7.1088595	P	P	P	CDK13	8621
P	13.742663	14.224682	12.677297	P	P	P	GADD45B	4616
P	6.387011	6.806622	6.3632627	P	P	A	SORBS3	10174
P	8.664007	8.492487	8.7717085	P	P	P	ACOT7	11332
P	14.312172	14.032064	11.284317	P	P	P	SIK1	150094
P	8.8693905	9.467949	9.725544	P	P	P	ZNF93	81931
P	11.934367	11.350478	12.134818	P	P	P	HLA-B	3106
P	7.6927867	8.06607	8.112153	P	P	P	RAB2A	5862
P	12.712401	13.0855	12.038791	P	P	P	ID1	3397
P	14.246141	14.692293	13.29365	P	P	P	PNRC1	10957
P	13.44091	13.226203	13.325967	P	P	P	HLA-B	3106
P	11.165722	11.358385	10.049103	P	P	P	PIM1	5292
P	10.195968	10.585134	8.716987	P	P	P	TFPI2	7980
P	11.731709	11.603237	10.364925	P	P	P	TFPI2	7980
P	13.672975	14.137087	13.640592	P	P	P	ID4	3400
P	12.063066	12.149985	12.670585	P	P	P	ID4	3400
P	13.074103	13.660174	11.690833	P	P	P	GADD45B	4616
P	12.706933	13.12326	11.045986	P	P	P	GADD45B	4616
P	10.929219	11.03117	10.570963	P	P	P	BNIP2	663
P	7.089239	7.2185163	7.462162	M	M	P	HLCS	3141
P	9.482651	9.167375	9.7551775	P	P	P	GPM6A	2823
A	10.888769	10.581552	10.375766	P	M	M	CDR2	1039
A	7.6083894	7.4684224	7.1878753	P	P	P	PPAP2C	8612
P	12.306283	12.359633	12.385459	P	P	P	TMEM47	83604
P	8.842633	8.860348	9.38777	P	P	P	IFFO1	25900
M	8.2833185	6.775459	7.95085	P	P	P	CD24	100133941
P	11.303102	10.848934	9.253773	P	P	P	CXCL2	2920
P	10.01696	9.750233	10.032932	P	P	P	CNPY2	10330
P	9.852168	9.761446	8.875002	P	P	P	ING1	3621
P	6.8861847	7.4377604	7.4423227	P	P	P	GLT25D2	23127
P	12.856266	12.611587	12.58193	P	P	P	LEPR	3953
P	8.877961	8.533054	8.352809	P	P	P	UBAP2L	9898
P	8.3050165	9.239638	9.460568	P	P	P	STAT1	6772
P	8.567707	8.932457	9.152693	P	P	P	IDH2	3418
A	7.575655	7.816387	8.113832	P	P	P	RANBP3	8498
M	5.865772	5.7375097	4.933636	A	A	A	PCDH7	5099
P	14.193006	13.963423	13.475914	P	P	P	AKAP12	9590
P	7.644348	7.793555	8.182265	P	P	P	CDK10	8558
P	8.648712	8.752278	8.231856	P	P	P	WWOX	51741
P	7.43124	8.152976	7.876768	P	P	P	ARL17A ///	100294341/
P	11.146337	10.559946	9.454589	P	P	P	NR4A1	3164
P	7.590359	7.9028354	6.8989224	P	P	P	FCER1A	2205
P	6.8486943	7.205588	7.0846596	P	P	P	PTHLH	5744
P	11.411843	12.097515	11.895593	P	P	P	IGFBP3	3486

P	9.388273	8.62516	8.889287	P	P	P	PTGDS	5730
P	9.052974	9.083073	9.526525	P	P	P	COG4	25839
P	11.594904	11.329225	11.247511	P	P	P	IDS	3423
P	9.1148615	9.361524	9.655875	P	P	P	COQ9	57017
P	9.536509	9.776205	10.366249	P	P	P	SCAP	22937
P	8.964618	9.034533	9.346635	P	P	P	SULF1	23213
P	10.056267	10.048876	10.650701	P	P	P	SULF1	23213
P	5.7805524	6.5673604	5.9497046	A	A	P	PPPDE2	27351
P	5.8909216	5.508979	5.655823	P	A	P	TMEM194	23306
P	9.674594	9.403853	9.554706	P	P	P	HIVEP2	3097
P	11.675344	11.980743	11.349145	P	P	P	RND3	390
P	13.490615	13.562284	11.949736	P	P	P	MEG3	55384
P	9.136103	8.997967	9.477282	P	P	P	FAM175B	23172
P	10.864377	10.481243	10.95701	P	P	P	NCAM1	4684
P	11.748146	11.374105	11.557649	P	P	P	SMC5	23137
P	11.495195	11.441738	9.426083	P	P	P	CEBPD	1052
P	6.643091	6.9586287	7.083093	A	P	P	FANCI	55215
P	7.448252	7.7378473	7.369869	P	P	P	TNIK	23043
M	7.4901485	7.4014144	7.570878	M	P	A	KIAA1467	57613
P	12.040528	11.886141	11.66212	P	P	P	MPDZ	8777
P	9.093207	9.365328	9.035613	P	P	P	EIF2C2	27161
P	8.650444	9.039195	8.575803	P	P	P	VAMP1	6843
P	7.8669624	7.7395406	7.9117894	M	A	P	SYNGR1	9145
P	7.2355957	7.4153833	7.6780787	P	P	P	RPGRIP1L	23322
P	8.975642	9.070797	8.828583	P	P	P	GSN	2934
P	9.96685	9.962923	10.085176	P	P	P	FH	2271
P	7.783106	7.572928	7.670187	P	P	P	PACRG	135138
P	7.3720555	6.8538985	6.5284634	P	P	P	FABP3	2170
P	7.5189857	7.309313	7.3668885	P	P	P	NOV	4856
P	6.982756	7.539925	7.9128027	P	P	P	PAK3	5063
P	13.338631	13.349834	11.455262	P	P	P	C17orf91	84981
P	10.884192	10.549493	10.472271	P	P	P	ZNF131	7690
P	11.586279	12.028643	10.914601	P	P	P	EIF4A1	1973
P	8.067313	8.44667	8.54386	M	P	P	LRP5L	91355
P	6.34671	6.066581	6.0576754	P	A	P	ITGBL1	9358
P	7.1252527	6.7927265	6.83191	P	P	P	PI4K2A	55361
A	6.8346086	6.7185106	6.8896055	M	P	P	OGG1	4968
P	8.508044	8.488754	9.119152	P	M	P		
P	8.686097	8.766732	9.002717	P	P	P	PGAP2	27315
P	10.305142	10.581196	10.504079	P	P	P		
P	7.1290627	6.9343705	7.609741	P	P	P		
A	7.2338777	7.921559	6.708171	P	P	P	BTG3	10950
P	12.554194	12.43978	11.678308	P	P	P	DIRAS3	9077
P	7.399894	7.107913	6.847324	P	P	P	SCAPER	49855
P	7.4707847	8.273786	7.8705935	P	P	P	ZNF277	11179

P	8.364749	8.865591	8.900812	P	M	P		
P	7.8970175	7.6898623	7.135504	P	P	P		
P	5.5654	5.7788467	6.4614177	A	A	A		
P	14.454242	13.677567	12.167955	P	P	P	NR4A2	4929
P	7.563496	7.130256	7.4471397	M	P	P	POLR2C	5432
P	9.540966	9.613096	9.46884	P	P	P		
P	10.993162	10.711421	11.023727	P	P	P		
P	9.26438	9.671033	8.949031	P	P	P	CCL2	6347
P	8.622541	9.340438	8.467462	P	P	P		
P	10.605873	10.292885	8.98252	P	P	P	NR4A3	8013
P	10.927966	10.732167	10.715635	P	P	P	NOMO1 ///	23420///283
P	9.912694	9.609848	9.692607	P	P	P	HLA-A ///	13105///3134
P	8.8956175	8.841427	9.136022	P	P	P	OR7E37P	26636
P	7.2599483	6.9807916	6.980642	P	P	P	FAM55C	91775
P	10.528771	10.967794	10.276515	P	P	P		
P	13.541017	13.398259	13.420352	P	P	P	S100A6	6277
P	7.1570263	7.119667	7.343263	P	P	P	PMEPA1	56937
P	9.448498	8.811322	8.017029	P	P	P	PHLDA1	22822
P	10.95007	9.9434805	8.979144	P	P	P	PHLDA1	22822
P	7.7484546	7.9023013	7.640042	P	P	P	ZDHHC3	51304
P	7.914754	7.5720286	8.191517	P	P	P	MRPL4	51073
P	11.227452	10.978777	11.598743	P	P	P	LGR4	55366
P	10.610782	10.346963	10.388404	P	P	P	TYW1	55253
A	9.237179	7.948893	7.964601	P	P	P	TNFRSF12	51330
P	12.18807	11.776358	11.992138	P	P	P	LOC72839	22861///728
P	10.499845	10.59843	10.89869	P	P	P	C1orf115	79762
P	6.8876953	6.864176	6.4614644	P	P	P	C9orf114	51490
P	7.603468	7.7168384	7.7050176	P	P	P	HEMK1	51409
P	9.64039	9.922726	9.161506	P	P	P	YRDC	79693
P	8.408688	8.108163	8.168544	P	P	P	DYSF	8291
P	8.225202	8.99151	8.468118	P	P	P	XKR8	55113
P	8.153907	8.046956	7.614865	M	P	P	TMEM132	54972
P	8.741375	8.7067795	8.857072	P	P	P	ACSF2	80221
P	8.547582	8.562019	8.671772	P	P	P	MRPL35	51318
P	11.123841	11.083879	10.524545	P	P	P	C14orf138	79609
P	8.962067	9.295386	9.248861	P	P	P	RNMTL1	55178
P	7.379159	7.369081	6.982746	P	P	A	RNF141	50862
P	10.77712	11.204825	11.432854	P	P	P	TMEM100	55273
P	8.281775	8.064515	8.144831	P	P	P	GIMAP4	55303
P	10.069497	9.814417	9.353456	P	P	P	WDR44	54521
P	9.00207	9.050227	9.5451565	P	P	P	HERC6	55008
P	13.325137	12.564743	12.045742	P	P	P	KLF2	10365
P	8.376051	8.490891	8.518262	P	P	P	XYLT2	64132
P	7.529551	8.068433	8.217631	P	P	P	WDR5B	54554
P	8.023848	7.711896	7.9284	P	P	P	SAMD9	54809

P	5.3749614	6.402577	5.8359685	A	P	A	MTL5	9633
P	7.6985908	7.747113	7.116402	P	P	P	HSPC159	29094
P	6.2871094	6.685924	6.274816	A	P	P	XPNPEP3	63929
P	8.579172	8.623557	8.769319	P	P	P	RASIP1	54922
P	13.390851	14.176986	12.732668	P	P	P	CCNL1	57018
P	8.622289	9.288217	8.751163	P	P	P	IKZF5	64376
P	7.9131584	7.7531896	8.000488	P	P	P	SNX11	29916
P	8.519286	8.716818	8.213983	P	P	P	KLHL7	55975
P	7.8157125	7.985315	7.915696	P	P	P	GREB1L	80000
P	6.662329	7.082523	6.815091	P	P	P	RAD54B	25788
P	6.252657	5.766307	6.5732813	A	P	M	PACS1	55690
P	8.063821	8.474162	8.051153	P	P	P	EFHC2	80258
P	6.553392	6.651674	6.2494464	P	P	P		
P	10.919883	11.187099	10.914426	P	P	P	MED17	9440
P	10.471086	10.874682	11.067875	P	P	P	KCNMA1	3778
P	12.620776	12.875516	12.293351	P	P	P	JMJD1C	221037
P	10.058877	9.760424	9.808439	P	P	P	NOMO1 ///	23420///283
P	7.464	7.991727	7.6376414	P	P	P	HLA-F	3134
P	8.003037	7.950262	8.349	P	P	P	VRK3	51231
P	6.081855	6.9712644	7.4886937	P	P	P	PRND	23627
P	7.9374347	8.205576	8.037312	P	P	P	INTS7	25896
P	11.441914	12.141703	10.269012	P	P	P		
P	8.4695015	9.459504	8.164657	P	P	P	LOC10050	100506935
P	8.68183	9.050613	9.189949	P	P	P	HN1	51155
P	7.500308	7.54591	7.754757	P	P	P	ZFAND3	60685
P	7.525118	7.8908234	7.9087358	P	P	P	NAV2	89797
P	8.595157	8.642264	8.727998	P	P	P	GEMIN8	54960
P	7.8004074	8.091757	8.253021	P	P	P	DCLRE1B	64858
P	6.6244564	6.9666677	6.9314904	P	P	P	TMOD3	29766
P	11.211772	11.200584	11.056131	P	P	P	ANKH	56172
P	9.130553	9.612464	9.329172	P	P	P	C1orf21	81563
P	13.088724	13.173974	12.577687	P	P	P	NFKBIZ	64332
P	12.681446	12.377762	12.9487	P	P	P	SMOC2	64094
P	8.742943	9.340774	8.874622	P	P	P	RASSF5	83593
P	11.678352	11.406199	11.128517	P	P	P	TSHZ3	57616
P	14.376615	14.473585	13.846982	P	P	P	C14orf4	64207
P	9.622587	9.642211	9.073788	P	P	P	BCOR	54880
P	7.4131856	7.551516	7.2413125	P	P	P	KBTBD2	25948
A	9.310061	8.817578	8.389771	P	P	P	KIAA1683	80726
P	8.80925	8.405502	8.47903	P	P	P	C2orf40	84417
P	8.331366	8.219397	7.5730786	P	P	P	CDC42SE1	56882
P	9.042471	8.797213	8.976526	P	P	P	INADL	10207
P	10.627121	11.1933	10.393045	P	P	P	PRO2852	114224
P	7.31302	7.134969	7.989621	A	P	P	INMT	11185
P	9.89593	9.13403	8.94179	P	P	P	TMEM107	84314

P	6.5097423	6.8668966	6.0880895	P	P	A	MRVI1	10335
P	10.859777	10.218054	10.47423	P	P	P	SLC38A1	81539
P	8.27647	8.316361	7.881334	P	P	P	DNAJC5	80331
P	12.609454	12.382628	11.352717	P	P	P	PPP1R15B	84919
P	9.650534	9.986122	10.015197	P	P	P	TRIM25	7706
P	11.562147	11.765186	10.610909	P	P	P	GPCPD1	56261
P	10.158982	10.282921	10.674593	P	P	P	TTC17	55761
P	9.398946	9.118496	9.358016	P	P	P	ACSS1	84532
P	7.5663767	7.743323	7.681359	P	P	P	PAPPA	5069
P	8.184361	7.7583046	8.353598	P	P	P	H19	283120
P	8.928587	8.705391	8.64572	P	P	P	SPIRE1	56907
P	12.723341	12.453533	11.802392	P	P	P	PHF10	55274
P	12.419865	12.29109	12.299607	P	P	P	HNRNPA2	3181
M	8.887641	9.031994	8.661675	P	P	P	SPRYD3	84926
P	11.751761	11.700757	11.488855	P	P	P	PPTC7	160760
P	13.605044	13.693202	13.238426	P	P	P	SNHG8	100093630
P	8.490051	8.48963	8.351025	P	P	P	CBL	867
P	8.485896	8.106665	7.9280314	P	A	P		
P	9.044217	9.248189	9.631559	P	P	P	SRSF10	10772
P	9.820297	9.555356	9.768676	P	P	P	C9orf23	138716
P	10.190855	10.254684	10.694721	P	P	P	DTX3L	151636
P	10.350183	10.244224	9.62605	P	P	P	BRWD1	54014
P	12.081316	11.359028	9.690906	P	P	P	CSRNP1	64651
P	9.045239	9.15993	8.690715	P	P	P	THUMPD3	25917
P	12.658577	12.109914	9.818682	P	P	P	LOC28480	284801
P	8.682677	8.624185	8.626466	P	A	P	MMAB	326625
P	8.9437	9.396252	9.1885	P	P	P	C1orf59	113802
P	10.069803	10.129934	9.978769	P	P	P	STEAP2	261729
P	8.280503	8.52293	8.674269	P	P	P	RNF213	57674
P	9.958007	9.615013	9.950558	P	P	P	TMEM64	169200
P	10.149431	9.944471	9.403247	P	P	P	MAFK	7975
P	9.127788	9.221877	8.9558525	P	P	P	RAB21	23011
P	10.79936	10.600381	10.717297	P	P	P	ZMAT1	84460
P	12.045571	12.533105	12.052071	P	P	P	ARL5B	221079
P	9.561943	9.347247	9.77853	P	P	P	KDM5A	5927
P	8.337116	8.394179	8.554084	P	P	P	KIAA1704	100507773/
P	7.472861	7.934542	8.179737	P	P	P	C16orf75	116028
P	8.837213	8.294588	8.30191	P	P	P		
P	10.986281	10.468143	10.400375	P	P	P	AGFG1	3267
P	9.514606	10.326393	9.90355	P	P	P	ZFAND2A	90637
P	7.450712	7.6346517	8.108017	P	P	P	C17orf103	256302
P	8.683258	8.679455	8.923274	P	P	P	FAHD1	81889
P	9.1100445	9.272178	8.731073	P	P	P	ENY2	56943
P	10.215766	10.366325	10.78264	P	P	P	ADAM12	8038
P	9.604466	10.269937	9.273872	P	P	P	CSNK1E	1454

P	10.128943	10.423665	10.815874	P	P	P	FAM110C	642273
P	10.981796	10.855505	10.681395	P	P	P	GFPT1	2673
P	10.761612	11.439595	10.069586	P	P	P	ID4	3400
P	9.59437	9.475778	9.515326	P	P	P	NOSTRIN	115677
A	8.224075	7.800187	8.018897	P	P	P		
P	9.20371	9.254561	8.983388	P	P	P	LOC10050	100506904/
P	8.215341	8.642381	8.157806	P	P	P	C22orf39	128977
P	15.545721	15.525395	14.033052	P	P	P	C11orf96	387763
P	7.6120434	7.0034375	7.234932	P	P	P	TMEM37	140738
P	12.176795	12.990467	11.907505	P	P	P	ZNF503	84858
A	8.474406	9.045675	8.806802	M	P	P	ATAD3B	83858
P	8.147361	8.484584	8.835877	P	P	P	ZNF689	115509
P	8.573006	8.654153	8.058923	P	P	P	LOC10013	100132288/
M	9.077964	9.298876	8.399748	P	P	P	RGMB	285704
P	10.597224	10.63303	10.079231	P	P	P	ARMCX4	100131755
P	11.636889	11.818231	11.867356	P	P	P	SLC16A9	220963
P	11.959755	12.05951	11.961121	P	P	P	AKAP12	9590
P	13.240621	13.349608	13.290646	P	P	P	AKAP12	9590
P	7.852369	7.95023	8.149453	P	P	P	C22orf40	150383
P	13.45375	13.875606	12.157852	P	P	P	SOCS3	9021
P	7.378278	6.951857	6.9345765	P	P	P	CYP4X1	260293
P	9.217904	8.833363	8.897146	P	P	P	TXLNB	167838
P	8.750588	8.392933	8.24847	P	P	P	TMEM68	137695
P	6.7726526	6.88533	7.1857553	P	P	P	LOC33980	339803
P	7.4678617	7.7312407	8.091207	P	P	P		
P	8.588841	8.812053	9.154177	P	P	P	PDDC1	347862
P	12.538555	12.251307	11.900985	P	P	P	NRK	203447
P	8.80167	8.027841	7.9842424	P	P	P	CREM	1390
P	9.27881	9.401913	8.718973	P	P	P	MYLIP	29116
P	9.496774	8.87285	9.076908	P	P	P	PPM1L	151742
P	9.2441635	9.311473	8.645616	P	P	P		
P	9.273893	9.392486	10.062167	P	P	P	MGC16121	84848
P	3.913632	5.504453	4.8566027	A	A	P	TDRD9	122402
P	11.323374	11.232179	9.397077	P	P	P	KIAA0146	23514
P	7.9833665	8.476963	8.164594	P	P	P		
P	7.700174	7.6788664	7.3321357	P	P	P	PPM1L	151742
P	8.701552	8.483159	8.38057	P	P	P	LOC10050	100506992
P	9.676244	9.607387	9.97359	P	P	P		
P	8.185226	8.642343	8.190934	P	P	P	HSD17B1	3292
P	12.680472	12.913645	13.2261	P	P	P	XAF1	54739
P	13.231602	12.96772	12.724292	P	P	P	C7orf58	79974
P	8.915259	9.110807	9.280572	P	P	P		
P	12.171409	12.159505	12.492792	P	P	P		
P	8.893448	8.698416	8.3359375	P	P	P	ATF7	11016
P	10.33143	9.866349	9.345981	P	P	P	GNL1	2794

P	6.230551	6.5189767	6.6760516	P	P	P	RGL3	57139
P	7.7657485	7.526161	7.0902467	P	P	P	SLC4A8	9498
P	9.12317	8.621287	8.3624325	P	P	P	PRDM1	639
P	7.980386	8.578259	8.771597	P	P	P	KIAA1704	100507773/
P	10.370725	10.072461	9.414004	P	P	P	IQCG	84223
P	7.910091	8.401097	8.258633	P	P	P	TTC18	118491
P	11.443789	11.231207	11.392101	P	P	P	KPNA5	3841
P	6.4961247	7.0187807	6.8795557	P	P	P	TAF8	129685
P	9.727811	9.349659	8.470574	P	P	P	CYCS	54205
P	6.791946	6.9167624	6.2207866	P	P	P		
P	9.36144	9.286848	9.179554	P	P	P		
P	10.605227	10.291052	10.208956	P	P	P	SPTY2D1	144108
P	8.99921	8.995629	8.534787	P	P	P	LOC10013	100132288
P	6.2929196	6.4010024	6.72183	A	A	A	TPRG1	285386
P	9.681296	9.741231	10.054709	P	P	P	PHKA1	5255
P	8.871754	9.100835	9.465487	P	P	P	FRMD3	257019
P	9.321972	9.1921625	8.799195	P	P	P	NCRNA00	441951
P	9.522394	9.705674	9.516136	P	P	P	IFI27L1	122509
P	8.105993	8.053553	7.627408	P	P	P	MRVI1	10335
P	8.491612	8.284823	8.436611	P	P	P	NFIB	4781
P	10.119118	10.197971	10.246551	P	P	P	PRDM6	93166
P	6.2296367	6.225031	6.741562	P	P	P	FLJ44606	401207
P	7.665956	8.295605	7.917042	P	P	P		
P	6.131976	6.0713053	6.198894	P	P	P	AK4	205
P	9.721305	9.221933	9.6238365	P	P	P		
P	7.451087	6.6366453	7.3226004	P	P	P		
P	8.586825	8.608656	9.192705	P	P	P		
P	7.362364	7.1069746	6.9812703	P	P	P	C20orf112	140688
P	7.89311	7.20624	7.0595055	P	P	P	DCLK1	9201
P	5.927195	5.3543515	5.5603423	P	A	A		
P	7.198073	7.265392	7.3147035	A	A	A	LOC33935	339352
P	9.910993	10.199999	10.13402	P	P	P	AKAP12	9590
P	5.6204457	5.770577	6.190763	A	P	P	CROT	54677
P	11.700578	11.842739	11.512341	P	P	P	FKBP7	51661
P	7.298802	7.755806	7.556487	P	P	P		
A	7.0202713	6.9233446	6.2235246	P	P	P		
M	7.4035935	7.1920023	6.900862	P	P	P	TTBK2	146057
P	7.243975	7.3726287	7.9551044	A	P	P	C1orf93	127281
A	7.4121714	7.1287937	7.996104	P	P	P	ODZ2	57451
P	8.016294	8.404651	8.338114	P	P	P	KIAA1274	27143
P	10.118745	10.093928	10.094159	P	P	P	TMEM150	441027
P	8.411252	8.609604	7.619272	P	P	P	BPTF	2186
P	9.603767	9.808548	9.320283	P	P	P	ANKRD11	29123
P	9.080848	9.757115	9.328305	P	P	P	TJP2	9414
P	10.30682	10.403455	9.52735	P	P	P	RBBP6	5930

P	5.946869	5.822488	6.0976877	A	A	A	GALNT5	11227
P	6.1786523	5.3543167	5.1295686	P	A	A	CLCN5	1184
P	8.077334	8.489049	7.8668537	P	P	P	SLC25A29	123096
A	9.534924	10.642261	7.9309106	P	P	P		
P	9.427721	9.841034	8.390625	P	P	P	MIR17HG	407975
P	8.742592	9.105604	8.195953	P	P	P	AHI1	54806
P	10.567252	10.833871	10.208425	P	P	P		
P	6.8748655	5.912423	6.6485577	P	P	P		
P	8.419532	8.609183	7.952029	P	P	P		
P	7.6361303	7.4757557	7.329966	P	P	P	USP48	84196
P	6.6380453	6.815367	6.995302	M	P	P	GALT	2592
P	7.808067	7.317084	7.649618	P	P	P	FAM131A	131408
P	7.4941907	6.9564376	7.366825	P	P	P	PRICKLE1	144165
P	11.671074	11.552658	11.069455	P	P	P	AFF4	27125
P	5.57347	6.4160666	6.5544286	A	P	P	PUS10	150962
P	7.5420837	7.085232	7.182594	P	A	A	PNKD	25953
P	8.584697	8.461655	8.452494	P	P	P	INTS4	92105
A	9.678847	9.703608	8.515873	P	P	P		
P	8.24132	8.406583	8.061034	P	P	P	LOC10028	100289610
P	5.3958845	5.1720853	4.6599092	P	A	M	TMEM106	54664
P	6.5793757	6.7234464	6.913962	P	P	P		
P	7.274962	7.255863	7.4203277	P	P	P		
P	5.528236	6.208464	6.1832447	A	P	P	UGGT2	55757
P	10.012732	9.674353	9.256538	P	P	P	TRMT6	51605
P	5.4317575	5.6909513	5.2571254	M	P	P		
P	8.092912	8.604303	8.689636	P	P	P		
P	6.285489	6.5694585	5.9492006	A	P	P		
P	7.1225605	7.328427	7.6764436	P	P	P		
P	7.2209363	6.7142873	6.906804	P	P	P	CDKN2AI	91368
P	9.681204	9.365439	9.379778	P	P	P	BBS7	55212
P	13.667475	13.661302	12.087388	P	P	P	MEG3	55384
A	13.539186	12.706216	9.606698	P	P	P		
A	6.9114914	6.4542227	6.807537	P	P	P	RNF183	138065
P	7.26118	7.305931	7.9096313	P	P	P	GBP4	115361
P	6.93433	7.5280743	6.9362206	P	P	P	NARG2	79664
P	9.15799	8.794433	8.568283	P	P	P		
P	6.696446	6.011311	6.548329	P	P	P	SCN2B	6327
P	8.131033	8.368386	8.33199	P	P	P	RNF217	154214
P	7.568729	7.8216395	7.959822	P	P	P	FAM188B	84182
A	11.577506	12.050836	8.159116	P	P	P		
M	7.1465793	6.3132906	6.8013372	P	A	A		
P	10.369841	9.977474	9.359291	P	P	P		
P	7.4036136	7.0559955	7.0262947	P	P	P	TRAF4	9618
P	6.240166	6.1444116	5.987932	P	A	P	LOC10028	100287482
P	11.611267	11.021856	10.827328	P	P	P		

P	6.616348	6.745335	6.9428406	P	P	P	GRIP1	23426
P	8.860175	9.006381	8.908507	P	P	P	ZNF91	7644
P	8.899542	8.5707245	9.215181	P	P	P	NBPF1	55672
P	5.559489	5.443078	6.130127	A	A	P		
P	8.866167	9.437002	9.0856085	P	P	P	GALNTL2	117248
P	8.946204	9.173776	9.581087	P	P	P		
P	4.1124425	5.5349708	4.5797267	A	A	A	CCDC18	343099
P	11.71822	11.23878	10.367831	P	P	P		
P	10.45907	11.034968	10.717998	P	P	P		
P	8.008869	8.125493	8.174994	P	P	P	LRRC34	151827
P	9.42559	8.854154	7.9397593	P	P	P		
P	9.046495	9.10796	8.745058	P	P	P		
P	6.8923397	7.522855	7.1342387	P	P	P		
P	10.796409	10.87198	10.178856	P	P	P		
P	7.5977397	7.86275	7.9737353	P	P	P	LOC10050	100506318
P	5.8449354	6.327589	6.319308	A	A	A		
A	6.3627644	7.0495152	6.547266	P	P	P	NBPF8	728841
P	5.1166425	4.1277905	5.0314565	A	A	A		
P	10.248855	9.873508	10.011409	P	P	P	NCRNA00	404201
P	9.186591	9.189187	8.749783	P	P	P		
P	6.3500776	6.7599096	6.97705	P	P	P	DCAF12L1	139170
P	5.4916697	5.741083	5.7429905	A	P	P		
P	10.268432	10.151408	10.544319	P	P	P	SLFN5	162394
A	9.107245	10.233149	9.052441	P	P	P	IRF1	3659
P	11.156511	11.634442	10.692275	P	P	P	B4GALT1	2683
P	8.20036	8.1943865	8.623539	P	P	P	FLJ39739	388685
P	6.559544	7.0186744	7.021886	P	P	P		
P	5.691807	6.854257	6.2330523	A	A	A	GRAPL	400581
P	10.357073	10.266883	10.567896	P	P	P	CTDSPL2	51496
P	9.6019125	9.682996	9.325945	P	P	P	UBE2B	7320
P	8.994468	9.433513	9.11812	P	P	P	ABCA9	10350
P	7.808471	7.4276266	7.2883887	P	P	P	NCRNA00	401577
P	10.001648	10.134345	9.615615	P	P	P	LOC10050	100507345
P	6.259651	6.8721046	6.8176036	A	P	P	BDNF	627
P	7.0938144	7.341657	7.592135	P	P	P		
P	6.2796674	6.3579955	6.861545	P	P	P	ADAL	161823
P	6.534867	6.985289	7.214527	P	P	P	ZNF555	148254
P	6.82012	7.3497653	7.439598	P	P	P		
P	11.122721	10.371881	10.50153	P	P	P		
P	9.539362	9.617504	9.8903885	P	P	P	STXBP5L	9515
P	12.123674	11.795347	11.102469	P	P	P		
P	6.042919	6.4041605	6.374046	P	A	A	NDUFB2	4708
P	6.366649	6.0928893	6.397122	A	P	P		
P	10.526655	9.987691	9.479694	P	P	P		
A	8.187415	7.216473	7.317285	P	P	P		

P	5.9565434	6.1685314	6.120805	P	P	P	DCUN1D1	54165
P	8.617596	8.9993305	9.024788	P	P	P	RPL15	6138
A	7.645453	7.079783	7.383235	P	P	P		
A	8.071658	7.4806356	7.251261	P	P	P		
P	9.565304	10.316643	9.783124	P	P	P		
P	7.995584	8.032015	7.715624	P	P	A	RNF213	57674
P	6.2912865	6.9325576	6.542174	P	P	P	RBAK	57786
P	5.662746	6.4303803	5.608047	A	P	P	CXorf36	79742
P	7.6247096	8.128792	7.827395	P	P	P		
P	5.2431564	5.475685	6.495881	A	A	P		
P	4.2690687	4.8982253	5.532488	A	A	M	LOC10050	100509088
P	12.783697	12.769198	12.05139	P	P	P		
A	8.098563	7.8380685	6.207833	P	P	P		
P	9.653616	9.373219	9.227198	P	P	P		
P	5.665211	5.5162964	7.399568	A	A	P	FAM98A	25940
P	6.087273	5.8289013	5.7697687	P	P	P	SLC16A7	9194
P	5.5644894	5.868291	6.0251675	A	P	P	NCL	4691
P	9.534074	9.710377	9.286157	P	P	P		
P	7.027634	7.1769233	7.612424	P	P	P	QRSL1	55278
P	7.8332057	8.18187	8.383084	P	P	P		
P	7.0373025	7.1046824	7.299869	P	P	P		
P	6.3461246	6.5576324	7.1577005	P	P	P		
P	9.739237	9.29324	9.555265	P	P	P	MEIS1	4211
P	9.749022	9.954596	10.091817	P	P	P		
P	9.123157	10.315304	9.20053	P	P	P		
P	11.829382	12.180114	11.726808	P	P	P		
P	8.19055	8.381305	9.113956	P	P	P	RSAD2	91543
P	10.785703	10.85398	9.573352	P	P	P		
P	8.26764	8.480252	8.034988	P	P	P	MMAA	166785
P	6.8871036	7.3258157	7.30357	P	P	P		
P	6.3372326	6.5973983	6.362948	P	P	P		
P	14.605348	13.884513	10.829345	P	P	P		
P	10.152091	10.186092	9.570519	P	P	P		
P	7.9892745	7.601345	6.865388	P	P	P		
P	10.102902	10.48958	8.246215	P	P	P		
P	7.80539	8.11129	8.402675	P	P	P		
P	11.366803	11.345868	10.906541	P	P	P		
P	6.5557227	6.663858	7.2037387	A	M	A		
P	6.918249	6.3281064	6.724273	P	A	P		
P	7.9725404	8.2703085	8.504418	P	P	P		
P	7.084738	7.48034	7.9330025	A	A	P		
A	7.5935526	7.119567	6.025867	P	P	P	AUTS2	26053
P	7.286574	7.565617	7.235582	P	P	P		
P	6.9582796	6.895002	7.4248385	P	P	P		
P	5.6226935	6.6924896	7.2508183	A	P	P		

P	7.598093	8.007009	7.6315036	P	P	P		
P	7.5245833	7.1011105	7.4301205	P	P	P	C21orf70	85395
P	6.29595	5.4870844	6.226443	P	A	P	DNAH12	201625
P	5.8033834	5.4454374	6.2918277	A	A	P		
P	6.814377	7.003653	6.9041038	A	P	A	AGAP10 ///	119016///39
P	6.823664	7.0592523	6.8735385	P	P	P	C14orf145	145508
P	7.231717	6.4636226	7.264964	P	P	P	KIAA2022	340533
P	9.607324	9.821288	9.417963	P	P	P		
P	10.709491	11.553719	11.402589	P	P	P		
P	8.989009	9.877443	9.215263	P	P	P	RLIM	51132
P	5.2282166	4.88529	4.2387223	A	P	A		
P	10.847256	10.183214	10.278212	P	P	P	CYCS	54205
P	8.00091	8.051072	7.6773453	P	P	P	QSER1	79832
P	9.6696005	9.137573	9.097249	P	P	P	SPATS2L	26010
M	7.718454	7.9670978	7.429712	P	P	P	MYO1G	64005
P	8.48994	8.136485	8.022289	P	P	P	MBD5	55777
P	8.585575	8.908735	8.928469	A	P	P	TREX1	11277
P	9.047263	9.28231	9.203003	P	P	P	MVK	4598
P	9.574551	9.513462	8.53344	P	P	P	PPP1R15A	23645
P	7.597302	7.9107533	8.100329	P	P	P	WNK1	65125
P	7.754708	8.0188055	8.389403	P	P	P	PRR5	55615

Supplementary Table 2. Differentially expressed genes between normal ovaries and PCOS o

Gene_Onto	Gene_Onto	Gene_Onto	Alignments	Annotation_	Annotation_	Annotation_	Annotation_	Archival_U
0000122 //	0005634 //	0003677 //	chr1:15710	9-Jun-11	This probe set was anno		AF218540(	Hs.352672
	0005739 //	0016787 //	chr15:6341	9-Jun-11	This probe set was anno		AK027808(	Hs.374554
0000188 //	0005737 //	0004721 //	chr2:18394	9-Jun-11	This probe set was anno		BC035000(	Hs.132237
	0005622 //	0005515 //	chrX:30848	9-Jun-11	This probe set was anno		AY331591(	Hs.365565
			chr3:19643	9-Jun-11	This probe	ENST0000(	AY099509(	Hs.334526
			chr2:20235	9-Jun-11	This probe set was anno		BC030659(	Hs.335788
0006020 //	0005886 //	0005215 //	chr21:3546	9-Jun-11	This probe set was anno		ENST0000(	Hs.421196
0021955 //	0005622 //	0003723 //	chr5:73179	9-Jun-11	This probe set was anno		AK129761(	Hs.33254
			chr14:1026	9-Jun-11	This probe set was anno		BC030654(	Hs.283304
				9-Jun-11	This probe set was anno		AI202408,	Hs.420443
0000184 //	0005634 //	0000166 //	chr1:14550	9-Jun-11	This probe	ENST0000(	BC017770(	Hs.351932
0006622 //	0005737 //	0005515 //	chr5:79703	9-Jun-11	This probe set was anno		BC032227(	Hs.83790
0001541 //	0005576 //	0005111 //	chr15:4977	9-Jun-11	This probe set was anno		AY098593(	Hs.121001
0001516 //	0005634 //	0004601 //	chr1:18664	9-Jun-11	This probe set was anno		AY151286(	Hs.196384
0001932 //	0005739 //	0008137 //	chr5:52965	9-Jun-11	This probe	ENST0000(	AB062482(	Hs.374685
		0004721 //	chr15:4471	9-Jun-11	This probe	AK128644	AK291230(	Hs.104336
0006260 //	0005634 //	0000287 //	chr5:74842	9-Jun-11	This probe set was anno		BC014955(	Hs.135756
0001569 //	0005634 //	0000166 //	chr22:4085	9-Jun-11	This probe	AB209680	AF364037(	Hs.433153
			chr19:1394	9-Jun-11	This probe set was anno		AL832183(	Hs.289770
0007165 //	0005834 //	0004871 //	chr1:23571	9-Jun-11	This probe set was anno		ENST0000(	Hs.117183
1295			chr7:14399	9-Jun-11	This probe	AK055549	AK172840(	Hs.406217
0006928 //	0005737 //	0005200 //	chr10:1727	9-Jun-11	This probe set was anno		BC031031(	Hs.375145
0006486 //	0000139 //	0008378 //	chr2:23226	9-Jun-11	This probe	ENST0000(	AK000770(	Hs.299329
0006350 //	0005634 //	0000166 //	chr1:16262	9-Jun-11	This probe set was anno		AF356524(	Hs.433418
0006887 //	0005737 //	0046872 //	chr15:5452	9-Jun-11	This probe set was anno		ENST0000(	Hs.112921
0006260 //	0005634 //	0005515 //	chr12:7643	9-Jun-11	This probe set was anno		ENST0000(	Hs.419776
			chr11:6713	9-Jun-11	This probe set was anno		AK097245(	Hs.352748
	0005634 // nucleus // in		chr17:5740	9-Jun-11	This probe set was anno		AK097253(	Hs.368672
		0005515 //	chr7:10258	9-Jun-11	This probe set was anno		AK021560(	Hs.288720
			chr2:20200	9-Jun-11	This probe set was anno		AB053312(	Hs.191984
			chr6:11255	9-Jun-11	This probe set was anno		AF085839(	Hs.384673
			chrX:10322	9-Jun-11	This probe set was anno		AK091321(	Hs.371436
0007155 //	0005576 //	0004872 //	chr13:1023	9-Jun-11	This probe	AF339779	AK075136(	Hs.382699
			chr18:1279	9-Jun-11	This probe set was anno		AK074657(	Hs.255158
0006350 //	0005622 //	0003676 //	chr5:43122	9-Jun-11	This probe set was anno		AL832081(	Hs.97845
			chr11:1202	9-Jun-11	This probe set was anno		AK094004(	Hs.370704
			chr11:1114	9-Jun-11	This probe set was anno		AA761848,	Hs.407148
			chr7:75081	9-Jun-11	This probe set was anno		AK057787(	Hs.350624
0006464 //	0005622 //	0016874 //	chr12:1126	9-Jun-11	This probe	BC101482	AK091473(	Hs.379848
			chr4:21864	9-Jun-11	This probe set was anno		AK057907(	Hs.350615
0006364 //	0000178 //	0000175 //	chr16:2247	9-Jun-11	This probe	AF126109	AK095542,	Hs.432795
0045449 //	0005634 //	0003677 //	chr5:80710	9-Jun-11	This probe	BX640945	ENST0000(	Hs.290856
			chrX:15365	9-Jun-11	This probe set was anno		BC009467(	Hs.111407

			chr12:1941	9-Jun-11	This probe set was anno		AA235664,	Hs.38348
0007165 //	0005737 //	0000155 //	chr9:17135	9-Jun-11	This probe set was anno		ENST0000(	Hs.210505
			chr2:36773	9-Jun-11	This probe set was anno		BC016339(	Hs.350577
			chr22:2179	9-Jun-11	This probe set was anno		AL831831	Hs.378797
			chr1:11088	9-Jun-11	This probe set was anno		AA206370,	Hs.86248
			chr3:56592	9-Jun-11	This probe s	AK125303	AK095688(	Hs.376219
				9-Jun-11	This probe set was anno		AK057914(	Hs.255363
			chr5:15775	9-Jun-11	This probe set was anno		BC013940	Hs.348325
			chr4:15979	9-Jun-11	This probe set was anno		AF085902(	Hs.271737
			chr5:10195	9-Jun-11	This probe set was anno		BC043160(	Hs.438493
			chr11:7813	9-Jun-11	This probe set was anno		BC039514(	Hs.407574
0006259 //	0005634 //	0000166 //	chr17:7365	9-Jun-11	This probe set was anno		BC042989(	Hs.438441
0000186 //	0005624 //	0000166 //	chr9:50658	9-Jun-11	This probe set was anno		BC043187(	Hs.438487
			chr2:23941	9-Jun-11	This probe set was anno		AK057376	Hs.436178
0006511 // ubiquitin-de		0004221 //	chr13:3119	9-Jun-11	This probe set was anno		AL832776(	Hs.407128
0006355 //	0005622 //	0003676 //	chr19:5295	9-Jun-11	This probe set was anno		AL833487(	Hs.157287
			chr5:65327	9-Jun-11	This probe set was anno		BC038097(	Hs.373425
			chr3:56813	9-Jun-11	This probe set was anno		AL833224	Hs.376891
			chr6:16993	9-Jun-11	This probe set was anno		AL831920	Hs.377048
0006508 //	0005622 //	0004197 //	chr11:1047	9-Jun-11	This probe s	GENSCAN	AF486844(	Hs.367945
0008152 //	0005634 //	0003824 //	chr10:3227	9-Jun-11	This probe s	BC063313 ,	BC048327(	Hs.411370
			chr9:71855	9-Jun-11	This probe set was anno		AF085948,	Hs.167814
			chr13:7448	9-Jun-11	This probe set was anno		AL832616	Hs.335812
			chr2:46288	9-Jun-11	This probe set was anno		AL831856	Hs.377060
	0005634 //	0005488 //	chr2:55843	9-Jun-11	This probe s	ENST0000(	BC045714(	Hs.397694
			chr1:15810	9-Jun-11	This probe s	NR_03394	BC029599(	Hs.57835
			chr2:28112	9-Jun-11	This probe set was anno		NR_02830	Hs.390621
			chr5:68484	9-Jun-11	This probe set was anno		BC039391(	Hs.407606
0006350 //	0005622 //	0003676 //	chr19:1481	9-Jun-11	This probe set was anno		BC064571(	Hs.269952
			chr19:1988	9-Jun-11	This probe s	GENSCAN	BC037856(	Hs.385498
			chr3:14173	9-Jun-11	This probe set was anno		BC025982(	Hs.382227
			chr5:96269	9-Jun-11	This probe set was anno		AK094985(	Hs.382771
0006497 //	0005622 //	0005515 //	chr5:81267	9-Jun-11	This probe set was anno		AF318326(	Hs.436246
0001960 //	0005624 //	0004721 //	chr1:43996	9-Jun-11	This probe s	GENSCAN	AK127475(	Hs.75216
0002553 //	0005625 //	0004497 //	chr10:2342	9-Jun-11	This probe set was anno		BC051814(	Hs.75103
	0005737 //	0003723 //	chr9:96214	9-Jun-11	This probe s	AY450393	AF214737(	Hs.76666
0001709 //	0005634 //	0005515 //	chr1:15054	9-Jun-11	This probe set was anno		BC017197(	Hs.86386
0001709 //	0005634 //	0005515 //	chr1:15054	9-Jun-11	This probe set was anno		AF118124(	Hs.86386
0006350 //	0005634 //	0003677 //	chr2:19183	9-Jun-11	This probe set was anno		ENST0000(	Hs.21486
0006044 //	0005634 //	0003824 //	chr10:1035	9-Jun-11	This probe s	ENST0000(	AF036144(	Hs.5734
0001501 //	0005783 // endoplasmic		chr3:15025	9-Jun-11	This probe set was anno		BC108314(	Hs.76698
0006470 //	0005625 //	0004721 //	chr5:17219	9-Jun-11	This probe s	AK304475	AK298047(	Hs.171695
0000122 //	0005634 //	0003676 //	chr12:1085	9-Jun-11	This probe s	AB209896 .	BC009744(	Hs.1139
0006350 //	0005634 //	0003677 //	chr3:50212	9-Jun-11	This probe set was anno		AB004066(	Hs.171825
0044419 //	0005634 //	0000166 //	chrX:41192	9-Jun-11	This probe s	ENST0000(	AF000982(	Hs.147916

0006281 // DNA repair	0005515 //		chr1:20327	9-Jun-11	This probe set was anno		CR604962(	Hs.75462
0001666 //	0005886 //	0005391 //	chr1:16907	9-Jun-11	This probe	AK316043	ENST0000	Hs.78629
0006511 //	0005622 //	0004197 //	chr4:41259	9-Jun-11	This probe	AB209038	AK054579(	Hs.76118
0000387 //	0005634 //	0005515 //	chr1:11198	9-Jun-11	This probe	ENST0000	BC001679(	Hs.11039
0001570 //	0000785 //	0003677 //	chr19:1290	9-Jun-11	This probe	BT019760	BC004250(	Hs.198951
0000122 //	0000785 //	0005515 //	chr2:88221	9-Jun-11	This probe	AY634687	D13891(11	Hs.180919
0043627 //	0005882 //	0005198 //	chr6:72294	9-Jun-11	This probe	CR591389	BC002539(	Hs.182265
0001558 //	0005622 //	0005085 //	chr10:5494	9-Jun-11	This probe	AK302687	AK294244(	Hs.25155
0001578 //	0000922 //	0005515 //	chr1:10982	9-Jun-11	This probe	AK289593	AF223000(	Hs.77550
0006119 //	0005739 //	0003824 //	chr3:48636	9-Jun-11	This probe	ENST0000	AK300694(	Hs.119251
0006417 //	0005783 //	0005515 //	chr19:4937	9-Jun-11	This probe set was anno		AK296668(	Hs.76556
0000045 //	0000407 //	0005515 //	chr8:53535	9-Jun-11	This probe set was anno		AB059622(	Hs.50421
0006694 //	0005783 //	0000250 //	chr21:4760	9-Jun-11	This probe set was anno		AK092334(	Hs.93199
0006397 //	0005634 //	0005488 //	chr19:4631	9-Jun-11	This probe set was anno		AB209024(	Hs.107019
0000165 //	0005576 //	0005158 //	chr11:2150	9-Jun-11	This probe	AY971350	NM_00112	Hs.251664
0006915 //	0005739 // mitochondri		chr14:9457	9-Jun-11	This probe	BT006781	AK289535(	Hs.278613
0001709 //	0005634 //	0003706 //	chr1:12045	9-Jun-11	This probe set was anno		AF315356(	Hs.8121
0006468 //	0005634 //	0000166 //	chr8:56792	9-Jun-11	This probe	BC126456	AK290494(	Hs.80887
0006094 //	0005634 //	0003677 //	chr1:21278	9-Jun-11	This probe set was anno		AB209032(	Hs.460
	0005622 //	0003677 //	chr6:30152	9-Jun-11	This probe set was anno		AK096996(	Hs.1287
	0016020 //	0005515 //	chrX:78615	9-Jun-11	This probe	AK303238	AY359051(	Hs.17109
0001501 //	0001527 //	0005201 //	chr15:4870	9-Jun-11	This probe set was anno		BC146854(	Hs.750
0001501 //	0005764 //	0001784 //	chr11:4726	9-Jun-11	This probe	AK301860	AK298122(	Hs.75589
0007155 //	0005634 //	0005515 //	chr3:18793	9-Jun-11	This probe	U29116 // g	AK302959(	Hs.180398
0006457 //	0005634 //	0005515 //	chr7:10821	9-Jun-11	This probe	ENST0000	AB026908(	Hs.6790
0001525 //	0005576 //	0005125 //	chr4:74606	9-Jun-11	This probe set was anno		BC013615(	Hs.624
			chr2:15307	9-Jun-11	This probe	AK126995	AF056195(	Hs.15430
0044419 //	0005576 //	0005201 //	chr22:4589	9-Jun-11	This probe	AK128725	AF126110(	Hs.79732
0006099 //	0005737 //	0003824 //	chr1:24166	9-Jun-11	This probe	BT009839	M15502(11	Hs.75653
0006350 //	0005622 //	0003676 //	chr1:14057	9-Jun-11	This probe set was anno		CR612351(	Hs.26719
0006626 //	0005739 //	0000166 //	chr19:7991	9-Jun-11	This probe	CR627419	AF026030(	Hs.123178
	0005622 //	0008270 //	chr9:10084	9-Jun-11	This probe	AK303366	AF220131(	Hs.179703
	0005737 //	0005488 //	chr10:9115	9-Jun-11	This probe	BT006667	AK308688(	Hs.20315
0006350 //	0005634 //	0003676 //	chr1:44115	9-Jun-11	This probe	AK300039	AK294596(	Hs.155983
0000122 //	0005634 //	0003677 //	chr3:19385	9-Jun-11	This probe set was anno		AK300482(	Hs.250666
0000122 //	0005634 //	0003677 //	chr3:19385	9-Jun-11	This probe	CR541843	AF264785(	Hs.250666
0000209 //	0005634 //	0003677 //	chr11:4723	9-Jun-11	This probe	BT007139	AK091640(	Hs.77602
0009966 //	0005737 //	0003779 //	chr4:77604	9-Jun-11	This probe set was anno		AF188700(	Hs.80306
0002076 //	0000785 //	0003677 //	chr19:1839	9-Jun-11	This probe set was anno		ENST0000	Hs.2780
0000209 //	0005622 //	0003677 //	chr14:2463	9-Jun-11	This probe	AK295467	BC035716(	Hs.1706
0007165 //	0005622 //	0005096 //	chr1:94638	9-Jun-11	This probe set was anno		ENST0000	Hs.70983
0000239 //	0001673 //	0000166 //	chr5:89306	9-Jun-11	This probe	ENST0000	BC000404(	Hs.6566
	0005794 //	0005515 //	chr2:70576	9-Jun-11	This probe set was anno		ENST0000	Hs.78894
0006350 //	0005634 //	0003677 //	chr9:32540	9-Jun-11	This probe	GENSCAN	AB045732(	Hs.179982
0002087 //	0005634 //	0003677 //	chr9:12850	9-Jun-11	This probe	AJ420602 /	AK092148(	Hs.294101

0006629 //	0005739 //	0004095 //	chr1:53662	9-Jun-11	This probe set was anno		BC002445(	Hs.274336
0000165 //	0005622 //	0005096 //	chr17:2942	9-Jun-11	This probe	BX648717	M82814(11	Hs.93207
0001836 //	0005739 //	0005515 //	chr1:27992	9-Jun-11	This probe	BT006850	BC011601(	Hs.265827
0006810 //	0005634 //	0005487 //	chr13:2587	9-Jun-11	This probe	ENST0000	AB007870(	Hs.55075
0006955 //	0005737 // cytoplasm //		chr1:79086	9-Jun-11	This probe	AK316232	AB000115(	Hs.75470
	0005634 //	0003677 //	chr8:59717	9-Jun-11	This probe	AK302331	AB018351(	Hs.184297
0006810 //	0000139 //	0000166 //	chr21:4363	9-Jun-11	This probe	AK298491	AF323660(	Hs.10237
0006350 //	0005634 //	0003677 //	chr2:15718	9-Jun-11	This probe	AK291456	BC009288(	Hs.82120
0006350 //	0005634 //	0003677 //	chr2:15718	9-Jun-11	This probe set was anno		ENST0000	Hs.82120
0000122 //	0005634 //	0003677 //	chr10:9444	9-Jun-11	This probe	BC014336	L16499(11)	Hs.118651
0001516 //	0005634 //	0004601 //	chr1:18664	9-Jun-11	This probe set was anno		ENST0000	Hs.196384
0006350 //	0005634 //	0003677 //	chr17:5334	9-Jun-11	This probe	AF035305	BC036093(	Hs.250692
	0005737 //	0005488 //	chrX:10190	9-Jun-11	This probe	GENSCAN	BC114552(	Hs.113082
0000089 //	0000775 //	0005515 //	chr7:18554	9-Jun-11	This probe	AK310481	AF083811(	Hs.7345
0006810 //	0005635 //	0005515 //	chr5:17257	9-Jun-11	This probe set was anno		AF083957(	Hs.77572
0005975 //	0005794 //	0003944 //	chr16:5074	9-Jun-11	This probe set was anno		AF052111(	Hs.21334
0001501 //	0005576 //	0005488 //	chr3:45067	9-Jun-11	This probe set was anno		BC011024(	Hs.65424
0006350 //	0005622 //	0003676 //	chr10:6457	9-Jun-11	This probe	BC035625	J04076(11)	Hs.1395
0001558 //	0005576 //	0005520 //	chr7:45928	9-Jun-11	This probe	M20841 //	BC035263(	Hs.102122
0007417 //	0005576 //	0004867 //	chr3:16745	9-Jun-11	This probe	GENSCAN	AK290082(	Hs.78589
0000077 //	0000781 //	0000166 //	chr11:1254	9-Jun-11	This probe	AK293143	AF016582(	Hs.20295
0005975 //	0005737 //	0003824 //	chrX:71800	9-Jun-11	This probe	BC104944	AK123357(	Hs.2393
0007267 //	0005576 //	0005515 //	chr1:94887	9-Jun-11	This probe set was anno		AY168648(	Hs.833
0006309 //	0005625 //	0003677 //	chrX:12926	9-Jun-11	This probe set was anno		AF100928(	Hs.18720
0006954 //	0005886 //	0004871 //	chr3:11300	9-Jun-11	This probe	BC060802	ENST0000	Hs.1570
0007155 //	0005576 //	0005515 //	chr9:95176	9-Jun-11	This probe set was anno		AB000114(	Hs.94070
0007179 //	0005576 //	0005125 //	chr1:22612	9-Jun-11	This probe	AK094077	AF081513(	Hs.25195
0000122 //	0005622 //	0003676 //	chr11:3240	9-Jun-11	This probe set was anno		BC032861(	Hs.1145
0001833 //	0005634 //	0005515 //	chr20:2538	9-Jun-11	This probe set was anno		ENST0000	Hs.36232
0006350 //	0005622 //	0003676 //	chr8:22545	9-Jun-11	This probe set was anno		ENST0000	Hs.74088
0006915 //	0005634 //	0008270 //	chr17:6659	9-Jun-11	This probe	AK290276	AK292710(	Hs.139262
0007165 //	0000139 //	0004872 //	chr2:16534	9-Jun-11	This probe	AK074599	AK301961(	Hs.83070
0002092 //	0005615 //	0004888 //	chr1:16969	9-Jun-11	This probe set was anno		BC142677(	Hs.89546
0006810 //	0016020 //	0004872 //	chr15:3360	9-Jun-11	This probe set was anno		AB001025(	Hs.9349
0001666 //	0005737 //	0004860 //	chr17:7635	9-Jun-11	This probe set was anno		AB004904,	Hs.296176
0007155 //	0005622 //	0004872 //	chr12:9454	9-Jun-11	This probe	AK093735	AB208934(	Hs.286229
0007155 //	0005886 //	0004872 //	chr17:4244	9-Jun-11	This probe	AB209552	BC117443(	Hs.785
0006691 //	0005783 //	0004497 //	chr19:1575	9-Jun-11	This probe set was anno		AB002454(	Hs.106242
0006338 //	0005634 //	0000166 //	chr9:20290	9-Jun-11	This probe	ENST0000	AK094076(	Hs.198296
0006338 //	0005634 //	0000166 //	chr9:20290	9-Jun-11	This probe	AK308941	AK094076(	Hs.198296
0000122 //	0005624 //	0003677 //	chrX:30322	9-Jun-11	This probe	GENSCAN	BC011564(	Hs.268490
			chr6:29758	9-Jun-11	This probe set was anno		NR_00213	Hs.60856
0006350 //	0005622 //	0003676 //	chr19:1998	9-Jun-11	This probe	AB209550	AK074757(	Hs.137582
0008283 // cell proliferation // non-t			chr11:3245	9-Jun-11	This probe	NR_02392	M60614(11	Hs.251573
0006810 //	0016020 //	0005215 //	chr12:5181	9-Jun-11	This probe set was anno		AB018282(	Hs.132136

0007165 //	0005576 //	0004871 //	chr1:78956	9-Jun-11	This probe	NM_00095	AF004021(	Hs.89418
0006468 // protein phos		0000166 //	chr7:39991	9-Jun-11	This probe	ENST0000	AB058694(	Hs.59498
0000185 // activation of		0005515 //	chr19:2476	9-Jun-11	This probe	GENSCAN	AF087853(	Hs.110571
0000122 //	0005634 //	0005200 //	chr8:22423	9-Jun-11	This probe	ENST0000	AF037261(	Hs.33787
0006629 //	0005737 //	0000062 //	chr1:63243	9-Jun-11	This probe	BT006888	AB074415(	Hs.8679
0000122 //	0005622 //	0000166 //	chr10:3160	9-Jun-11	This probe set was anno		AB047786(	Hs.900025
0006350 //	0005622 //	0003676 //	chr19:2004	9-Jun-11	This probe set was anno		AK295921(	Hs.900178
0002223 //	0005615 //	0005515 //	chr6:29795	9-Jun-11	This probe	AY007140	AF026218(	Hs.77961
0006810 //	0000139 //	0000166 //	chr8:61429	9-Jun-11	This probe set was anno		ENST0000	Hs.78305
0000122 //	0005625 //	0005515 //	chr20:3019	9-Jun-11	This probe set was anno		AK291152(	Hs.75424
0006350 //	0005634 //	0005515 //	chr6:89793	9-Jun-11	This probe	U03105 // g	AF279899(	Hs.75969
0002223 //	0005615 //	0005515 //	chr6:31321	9-Jun-11	This probe	AF016641	AK124160(	Hs.77961
0006468 //	0005634 //	0000166 //	chr6:37138	9-Jun-11	This probe	DQ022562	M24779(11	Hs.81170
0007596 //	0005576 //	0004867 //	chr7:93514	9-Jun-11	This probe	D29992 // g	AK129833(	Hs.295944
0007596 //	0005576 //	0004867 //	chr7:93515	9-Jun-11	This probe set was anno		AK129833(	Hs.295944
0000082 //	0005634 //	0003714 //	chr6:19837	9-Jun-11	This probe set was anno		BC014941(	Hs.34853
0000082 //	0005634 //	0003714 //	chr6:19837	9-Jun-11	This probe set was anno		AJ420553(	Hs.34853
0000185 // activation of		0005515 //	chr19:2476	9-Jun-11	This probe	AF090950	AF087853(	Hs.110571
0000185 // activation of		0005515 //	chr19:2476	9-Jun-11	This probe	AY615270	AF078077(	Hs.110571
0006915 //	0005635 //	0005096 //	chr15:5995	9-Jun-11	This probe	ENST0000	BC002461(	Hs.155596
0006464 //	0000785 //	0000166 //	chr21:3812	9-Jun-11	This probe set was anno		D87328(11	Hs.79375
	0009986 //	0005262 //	chr4:17655	9-Jun-11	This probe set was anno		BC022508(	Hs.75819
	0005634 //	0005515 //	chr16:2235	9-Jun-11	This probe set was anno		BC017503(	Hs.75124
	0005886 //	0003824 //	chr19:2813	9-Jun-11	This probe set was anno		AB209696(	Hs.24879
	0005886 // plasma mem		chrX:34645	9-Jun-11	This probe set was anno		BC039242(	Hs.8769
	0005882 // intermediate		chr12:6648	9-Jun-11	This probe set was anno		AK000710(	Hs.46659
0001666 //	0005886 //	0004871 //	chrY:21152	9-Jun-11	This probe	M58664 //	AK125531(	Hs.286124
0006935 //	0005576 //	0005125 //	chr4:74962	9-Jun-11	This probe	BC011976	BC015753(	Hs.75765
	0005783 //	0005515 //	chr12:5670	9-Jun-11	This probe	AF186113	BC001027(	Hs.8752
0007049 //	0005634 //	0005515 //	chr13:1113	9-Jun-11	This probe	AF044076	AB024401(	Hs.46700
0009103 //	0005783 //	0016740 //	chr1:18390	9-Jun-11	This probe set was anno		AF288389(	Hs.106794
0001525 //	0005576 //	0004872 //	chr1:66031	9-Jun-11	This probe set was anno		ENST0000	Hs.226627
		0005515 //	chr1:15419	9-Jun-11	This probe	ENST0000	AJ243669(	Hs.8127
0006350 //	0005634 //	0003677 //	chr2:19184	9-Jun-11	This probe set was anno		AK096686(	Hs.21486
0005975 //	0005739 //	0000287 //	chr15:9062	9-Jun-11	This probe	AK316388	AK299987(	Hs.5337
0006810 //	0005634 //	0005515 //	chr19:5917	9-Jun-11	This probe set was anno		BC004349(	Hs.176657
0007155 //	0005886 //	0005509 //	chr4:30722	9-Jun-11	This probe	ENST0000	AB006757(	Hs.34073
0006605 //	0005737 //	0005515 //	chr6:15164	9-Jun-11	This probe set was anno		AB003476(	Hs.788
0006468 // protein phos		0000166 //	chr16:8975	9-Jun-11	This probe	L33264 // g	AB209829(	Hs.77313
0001649 //	0005634 //	0003824 //	chr16:7819	9-Jun-11	This probe	AK290438	AF211943(	Hs.279790
0006810 //	0005794 //	0000166 //	chr17:4437	9-Jun-11	This probe set was anno		NM_01663	Hs.321170
0006350 //	0005634 //	0003677 //	chr12:5244	9-Jun-11	This probe	L13740 // g	D49728(11	Hs.1119
0000187 //	0005886 //	0004872 //	chr1:15927	9-Jun-11	This probe set was anno		BC005912(	Hs.900757
0001501 //	0005576 //	0005179 //	chr12:2811	9-Jun-11	This probe set was anno		BC005961(	Hs.900797
0001558 //	0005576 //	0005515 //	chr7:45951	9-Jun-11	This probe set was anno		BC000013(	Hs.77326

0001516 //	0005576 //	0004667 //	chr9:13987	9-Jun-11	This probe	ENST0000	AY026356(	Hs.8272
0006810 //	0000139 //	0005515 //	chr16:7051	9-Jun-11	This probe	AK293235	AB088369(	Hs.108779
0008152 //	0005764 //	0003824 //	chrX:14856	9-Jun-11	This probe	BC037845	ENST0000	Hs.303154
0006744 //	0005739 //	0003677 //	chr16:5748	9-Jun-11	This probe set was anno		AL136884(	Hs.4288
0001666 //	0000139 //	0005515 //	chr3:47455	9-Jun-11	This probe	GENSCAN	AK091005(	Hs.78442
0006915 //	0005615 //	0003824 //	chr8:70414	9-Jun-11	This probe set was anno		AF545571(	Hs.70823
0006915 //	0005615 //	0003824 //	chr8:70414	9-Jun-11	This probe set was anno		AF545571(	Hs.70823
			chr22:4199	9-Jun-11	This probe	ENST0000	AF038183(	Hs.12421
	0016020 //	membrane //	chr12:5744	9-Jun-11	This probe set was anno		ENST0000	Hs.14912
0006350 //	0005622 //	0003676 //	chr6:14307	9-Jun-11	This probe	GENSCAN	ENST0000	Hs.75063
0007155 //	0000139 //	0000166 //	chr2:15132	9-Jun-11	This probe set was anno		BC012513(	Hs.6838
			chr14:1012	9-Jun-11	This probe set was anno		AF052114	Hs.112844
	0070552 //	0005515 //	chr10:1264	9-Jun-11	This probe set was anno		BC008999(	Hs.82324
0007155 //	0005576 //	extracellular	chr11:1131	9-Jun-11	This probe set was anno		ENST0000	Hs.167988
0006281 //	0005634 //	0000166 //	chr9:72873	9-Jun-11	This probe set was anno		BC034441(	Hs.103283
0006350 //	0005634 //	0003677 //	chr8:48648	9-Jun-11	This probe set was anno		BC094715,	Hs.76722
0006281 //	0005634 //	0005515 //	chr15:8983	9-Jun-11	This probe	GENSCAN	AB058697(	Hs.80961
0006468 //	0005634 //	0000166 //	chr3:17077	9-Jun-11	This probe set was anno		ENST0000	Hs.170204
	0016020 //	membrane //	chr12:1321	9-Jun-11	This probe set was anno		BC039267(	Hs.6189
0007155 //	0005886 //	0005515 //	chr9:13105	9-Jun-11	This probe set was anno		AB210041(	Hs.169378
0006350 //	0000932 //	0000340 //	chr8:14153	9-Jun-11	This probe set was anno		BC054491(	Hs.324504
0016192 //	0005739 //	0005515 //	chr12:6571	9-Jun-11	This probe set was anno		BC023286(	Hs.20021
0006605 //	0005887 //	integral to pl	chr22:3976	9-Jun-11	This probe set was anno		ENST0000	Hs.6139
0001701 //	0005737 //	0031870 //	chr16:5363	9-Jun-11	This probe	BC136433	AK093307(	Hs.12328
0006915 //	0005576 //	0003779 //	chr9:12403	9-Jun-11	This probe	AK304629	AK096280(	Hs.290070
0006099 //	0005737 //	0003824 //	chr1:24166	9-Jun-11	This probe	BT009839	BC003108(	Hs.75653
	0005739 //	mitochondri	chr6:16348	9-Jun-11	This probe	ENST0000	AF546872(	Hs.307438
0006631 //	0005737 //	0005215 //	chr1:31838	9-Jun-11	This probe	BC007021	NM_00410	Hs.49881
0001558 //	0005576 //	0005520 //	chr8:12043	9-Jun-11	This probe	AY082381	NM_00251	Hs.235935
0006468 //	protein phos	0000166 //	chrX:11033	9-Jun-11	This probe	BC143544	ENST0000	Hs.152663
			chr17:1615	9-Jun-11	This probe set was anno		BX648321(	Hs.29206
0006350 //	0005622 //	0003676 //	chr5:43121	9-Jun-11	This probe set was anno		AK299315(	Hs.78743
0006412 //	0005829 //	0000166 //	chr17:7478	9-Jun-11	This probe	AK303599	U79273(11	Hs.239483
0006898 //	0005615 //	0005515 //	chr22:2574	9-Jun-11	This probe	BC137460	ENST0000	Hs.272317
0007155 //	0005576 //	0004872 //	chr13:1023	9-Jun-11	This probe	AK075136	AK075136	Hs.311054
0006661 //	0005737 //	0000166 //	chr10:9943	9-Jun-11	This probe set was anno		ENST0000	Hs.25300
0006281 //	0005634 //	0003677 //	chr3:98216	9-Jun-11	This probe	AF060509	ENST0000	Hs.158196
			chr10:2975	9-Jun-11	This probe	BX648589	AK092850(	Hs.100841
0006506 //	0000139 //	0004872 //	chr11:3842	9-Jun-11	This probe	ENST0000	AF159615(	Hs.133968
			chr7:13075	9-Jun-11	This probe set was anno		AA515614,	Hs.226103
			chr5:13992	9-Jun-11	This probe set was anno		AK024213(	Hs.287627
0006979 //	0005737 //	cytoplasm //	chr21:1896	9-Jun-11	This probe set was anno		AL049332(	Hs.77311
0000079 //	0005886 //	0000166 //	chr1:68511	9-Jun-11	This probe	CR541870	AK021882(	Hs.194695
	0005622 //	0008270 //	chr15:7667	9-Jun-11	This probe set was anno		AB040887(	Hs.285848
0006350 //	0005622 //	0003676 //	chr7:11184	9-Jun-11	This probe	ENST0000	AK027128(	Hs.288982

			chr1:89280	9-Jun-11	This probe	AK092835	AK023600(	Hs.301390
			chr2:20469	9-Jun-11	This probe set was anno		AL080106	
			chr15:6848	9-Jun-11	This probe set was anno		GENSCAN0000004378	
0006350 //	0005634 //	0003677 //	chr2:15718	9-Jun-11	This probe set was anno		ENST0000	Hs.82120
0006350 //	0005634 //	0003677 //	chr16:5749	9-Jun-11	This probe	AK300124	BC000409,	Hs.79402
			chrX:99919	9-Jun-11	This probe set was anno		AL110206	Hs.306339
			chr1:25451	9-Jun-11	This probe	NR_00159	ENST00000413189(11)	
0001666 //	0005576 //	0001664 //	chr17:3258	9-Jun-11	This probe	BT007329	BC009716(	Hs.303649
			chr2:45905	9-Jun-11	This probe set was anno		AK025152(	Hs.306773
0001707 //	0005634 //	0003677 //	chr9:10258	9-Jun-11	This probe	BX649089	ENST0000	Hs.80561
820///40805	0005783 //	0004180 //	chr16:1497	9-Jun-11	This probe	BC028389	AL512687(	Hs.227823
0002474 //	0000139 //	0005515 //	chr6:29974	9-Jun-11	This probe	AY007140	ENST0000	Hs.85242
			chr13:4201	9-Jun-11	This probe	AF073924	NR_00216	Hs.332964
	0005576 // extracellular		chr3:10154	9-Jun-11	This probe set was anno		ENST0000	Hs.293253
			chr3:17007	9-Jun-11	This probe set was anno		AW105461	Hs.272108
0007165 //	0001726 //	0005509 //	chr1:15350	9-Jun-11	This probe	BT006965	BC001431(	Hs.275243
0030521 //	0005886 //	0050699 //	chr20:5622	9-Jun-11	This probe	ENST0000	AF224278(	Hs.83883
0006915 //	0005634 //	0005515 //	chr12:7642	9-Jun-11	This probe set was anno		AK304224,	Hs.82101
0006915 //	0005634 //	0005515 //	chr12:7642	9-Jun-11	This probe set was anno		ENST0000	Hs.82101
0006605 //	0000139 //	0008270 //	chr3:44966	9-Jun-11	This probe	AF441791	AF247703(	Hs.14896
0006412 //	0005622 //	0003735 //	chr19:1036	9-Jun-11	This probe	GENSCAN	AB049635(	Hs.279652
0007165 //	0005886 //	0004871 //	chr11:2738	9-Jun-11	This probe set was anno		AF257182(	Hs.160271
0008033 // tRNA proces		0000166 //	chr7:66461	9-Jun-11	This probe	BC068520	BC015591(	Hs.16277
0001525 //	0001726 //	0004872 //	chr16:3070	9-Jun-11	This probe set was anno		AB035480(	Hs.10086
0006915 //	0005622 //	0000166 //	chr17:5402	9-Jun-11	This probe	CR620726	AK057464(	Hs.7212
	0016020 // membrane //		chr1:22086	9-Jun-11	This probe set was anno		AK125403(	Hs.103395
			chr9:13158	9-Jun-11	This probe	AK303563	BC010579(	Hs.224137
0006306 //	0005739 //	0003676 //	chr3:50608	9-Jun-11	This probe	BX537562	AF172244(	Hs.46907
0051051 //	0005739 // mitochondri		chr1:38268	9-Jun-11	This probe	AK090770	AK129676(	Hs.46736
	0005886 // plasma mem		chr2:71680	9-Jun-11	This probe	DQ267935	AF075575(	Hs.143897
	0016020 // membrane //		chr1:28293	9-Jun-11	This probe	AK124529	AK054909(	Hs.55024
	0000139 // Golgi memb		chr11:6069	9-Jun-11	This probe	GENSCAN	BC114569(	Hs.118552
0006629 //	0005739 //	0000166 //	chr17:4850	9-Jun-11	This probe	ENST0000	AK294205(	Hs.288959
0006412 //	0005622 //	0003735 //	chr10:7628	9-Jun-11	This probe	ENST0000	BC020651(	Hs.93814
			chr14:5057	9-Jun-11	This probe	NM_02455	AK129564(	Hs.13056
0006396 //	0005739 //	0003723 //	chr17:6855	9-Jun-11	This probe	GENSCAN	BC011550(	Hs.182729
0006355 // regulation of		0003677 //	chr11:1053	9-Jun-11	This probe	BT006662	AF214680(	Hs.44685
	0016020 // membrane //		chr17:5379	9-Jun-11	This probe	BC010128	ENST0000	Hs.173233
		0000166 //	chr7:15026	9-Jun-11	This probe	AK301441	ENST0000	Hs.30822
0030334 //	0005737 //	0017137 //	chrX:11753	9-Jun-11	This probe	AK304432	BC028697(	Hs.98510
0006464 //	0005622 //	0016874 //	chr4:89345	9-Jun-11	This probe set was anno		AF336798(	Hs.179669
0006350 //	0005622 //	0003676 //	chr19:1643	9-Jun-11	This probe set was anno		AF134053(	Hs.107740
0006024 //	0000139 //	0008375 //	chr17:4842	9-Jun-11	This probe set was anno		AJ277442(	Hs.32117
			chr3:12213	9-Jun-11	This probe	CR457279	BC043494(	Hs.142395
	0005737 // cytoplasm //		chr7:92729	9-Jun-11	This probe set was anno		AF445355(	Hs.65641

0006875 //	0005625 //	0046872 //	chr11:6847	9-Jun-11	This probe set was anno		BC064579(	Hs.121378
	0005622 //	0005529 //	chr2:64681	9-Jun-11	This probe	AK092165	BC036082(	Hs.114771
0009987 //	0005739 //	0004177 //	chr22:4125	9-Jun-11	This probe	BX648018	AL834310(	Hs.182061
0007165 //	0005737 // cytoplasm //		chr19:4922	9-Jun-11	This probe	GENSCAN	AK123179(	Hs.233955
0006350 //	0005634 // nucleus // in		chr3:15686	9-Jun-11	This probe	AF367476	AF180920(	Hs.4859
0006350 //	0005622 //	0003676 //	chr10:1247	9-Jun-11	This probe set was anno		AF230808(	Hs.20631
0006810 // transport // i		0005515 //	chr17:4618	9-Jun-11	This probe set was anno		AF121861(	Hs.15827
0007601 //	0005634 //	0005515 //	chr7:23145	9-Jun-11	This probe	ENST0000	AF111113(	Hs.26481
	0016020 // membrane //		chr18:1903	9-Jun-11	This probe set was anno		AK293321(	Hs.278850
0000724 //	0005634 //	0000166 //	chr8:95444	9-Jun-11	This probe set was anno		AF007866(	Hs.241384
0000042 //	0005794 //	0005515 //	chr11:6599	9-Jun-11	This probe	AY320283	BC010096(	Hs.260150
		0005509 //	chrX:44007	9-Jun-11	This probe	GENSCAN	AK026254(	Hs.301143
	0005737 //	0003779 //	chr2:46844	9-Jun-11	This probe	AK291298	AF123320(11)	
0006350 //	0005634 //	0003712 //	chr11:9351	9-Jun-11	This probe	GENSCAN	AF105421(	Hs.22630
0001666 //	0005783 //	0003779 //	chr10:7864	9-Jun-11	This probe	BC137115	ENST0000	Hs.89463
0006350 //	0005622 //	0005515 //	chr10:6492	9-Jun-11	This probe	BC143722	AK123507(	Hs.6685
820///40805	0005783 //	0004180 //	chr16:1638	9-Jun-11	This probe	BC028389	AL512687(	Hs.322466
0002474 //	0016020 //	0032393 //	chr6:29693	9-Jun-11	This probe	GQ141863	AK125274,	Hs.110309
0006468 //	0005634 //	0000166 //	chr19:5048	9-Jun-11	This probe set was anno		AB031052(	Hs.98289
0006878 //	0005886 //	0005507 //	chr20:4705	9-Jun-11	This probe set was anno		AF086354(	Hs.121281
0016180 //	0005634 //	0005488 //	chr1:21211	9-Jun-11	This probe	GENSCAN	AK297225(	Hs.48604
			chr21:4018	9-Jun-11	This probe set was anno		AY216265(11)	
			chr6:24710	9-Jun-11	This probe set was anno		XR_10868	Hs.292998
	0005634 // nucleus // in		chr17:7313	9-Jun-11	This probe	ENST0000	AF060925(	Hs.109706
		0003677 //	chr6:37787	9-Jun-11	This probe	AK310757	BC031481(	Hs.6120
0007399 //	0005634 //	0000166 //	chr11:2007	9-Jun-11	This probe set was anno		AB063115(	Hs.23467
0000387 //	0005634 //	0005515 //	chrX:14026	9-Jun-11	This probe	DQ224033	AK125062(	Hs.44423
0000075 //	0000781 //	0004518 //	chr1:11444	9-Jun-11	This probe set was anno		BC029687(	Hs.115660
	0005737 //	0003779 //	chr15:5212	9-Jun-11	This probe	GENSCAN	AF177171(	Hs.22826
0001501 //	0005886 //	0005315 //	chr5:14708	9-Jun-11	This probe set was anno		AY358503(	Hs.168640
			chr1:18435	9-Jun-11	This probe set was anno		AF312864(	Hs.12532
0006350 //	0005634 // nucleus // in		chr3:10156	9-Jun-11	This probe set was anno		AB037925(	Hs.301183
0010811 //	0005576 //	0005509 //	chr6:16884	9-Jun-11	This probe set was anno		AB014730(	Hs.22209
0006915 //	0005737 //	0005515 //	chr1:20668	9-Jun-11	This probe	GENSCAN	AB209145(	Hs.238730
0001656 //	0005622 //	0003677 //	chr19:3176	9-Jun-11	This probe set was anno		ENST0000	Hs.278436
	0005634 // nucleus // no		chr14:7749	9-Jun-11	This probe	AF075110	BC108292(	Hs.179260
0000122 //	0005634 //	0003714 //	chrX:39911	9-Jun-11	This probe	ENST0000	AF317391(	Hs.130732
		0005515 //	chr7:32909	9-Jun-11	This probe	BC047107	AB040922(	Hs.20237
	0005739 // mitochondri		chr19:1836	9-Jun-11	This probe	ENST0000	AB051470(	Hs.166852
	0005576 // extracellular		chr2:10668	9-Jun-11	This probe	ENST0000	AF325503(	Hs.43125
0006909 //	0005737 //	0005095 //	chr1:15102	9-Jun-11	This probe set was anno		AF187845(	Hs.22065
0023034 //	0005737 //	0005515 //	chr1:62274	9-Jun-11	This probe set was anno		AB044807(	Hs.321197
			chr9:34186	9-Jun-11	This probe set was anno		AF130079(	Hs.23368
	0005737 //	0008168 //	chr7:30791	9-Jun-11	This probe set was anno		AF128846(	Hs.204038
	0016020 // membrane //		chr17:8076	9-Jun-11	This probe	AK127891	ENST0000	Hs.900978

	0005737 // cytoplasm //		chr11:1059	9-Jun-11	This probe	AK301296	AF081249(	Hs.251385
0006810 //	0005624 //	0005283 //	chr12:4657	9-Jun-11	This probe set was anno		ENST0000	Hs.193063
0006457 //	0016020 //	0031072 //	chr20:6255	9-Jun-11	This probe set was anno		AK074041(	Hs.165563
0006417 //	0000164 //	0004722 //	chr1:20437	9-Jun-11	This probe	AY007107	BC065280(	Hs.17448
0009615 //	0005634 //	0003700 //	chr17:5496	9-Jun-11	This probe	BC038247	ENST0000	Hs.10362
0005975 // carbohydrat		0003824 //	chr20:5410	9-Jun-11	This probe set was anno		AL833069(	Hs.171917
		0005488 //	chr11:4342	9-Jun-11	This probe	AK021517	AK023161(	Hs.17283
0006085 //	0005739 //	0000166 //	chr20:2498	9-Jun-11	This probe set was anno		AK125058(	Hs.7218
0007565 //	0005576 //	0004175 //	chr9:11916	9-Jun-11	This probe set was anno		AY189937(	Hs.250655
			chr11:2016	9-Jun-11	This probe	BC106079	BC063626(	Hs.279525
0006810 //	0005737 //	0003779 //	chr18:1244	9-Jun-11	This probe	BC016825	AB032961(	Hs.16758
0006350 //	0005634 //	0005515 //	chr6:17010	9-Jun-11	This probe set was anno		AJ420510(	Hs.7759
0000398 //	0005634 //	0000166 //	chr7:26229	9-Jun-11	This probe set was anno		BX537494(	Hs.232400
0008285 //	0005886 //	0004721 //	chr12:5345	9-Jun-11	This probe	BC136312	ENST0000	Hs.62119
	0005739 //	0003824 //	chr12:1109	9-Jun-11	This probe set was anno		AK098051(	Hs.13854
			chr4:11919	9-Jun-11	This probe	NR_03401	BC017993(	Hs.296141
0007166 //	0005634 //	0003700 //	chr11:1191	9-Jun-11	This probe set was anno		ENST0000	Hs.90960
			chr8:12451	9-Jun-11	This probe set was anno		AK125888(	Hs.6630
0000244 //	0005634 //	0000166 //	chr1:24290	9-Jun-11	This probe set was anno		AF419331(	Hs.288038
		0003676 //	chr9:34610	9-Jun-11	This probe	GENSCAN	BC032136(	Hs.278242
0006974 //	0005634 //	0004842 //	chr3:12229	9-Jun-11	This probe set was anno		BX648267(	Hs.16331
0006350 //	0005634 // nucleus // in		chr21:4066	9-Jun-11	This probe set was anno		AL109785(	Hs.119155
0006350 //	0005634 //	0003677 //	chr3:39183	9-Jun-11	This probe	AB063301	AB053121(	Hs.6607
		0003723 //	chr3:94047	9-Jun-11	This probe	ENST0000	BC001622(	Hs.30488
			chr20:2618	9-Jun-11	This probe	GENSCAN	BC036544	Hs.155364
0009236 //	0005739 //	0000166 //	chr12:1099	9-Jun-11	This probe	GENSCAN	AK295211(	Hs.12106
			chr1:10919	9-Jun-11	This probe	ENST0000	BC012198(	Hs.7962
0006810 //	0005768 //	0003824 //	chr7:89864	9-Jun-11	This probe set was anno		AF455138(	Hs.118258
		0000166 //	chr17:7833	9-Jun-11	This probe set was anno		AL161961(	Hs.17767
	0016020 // membrane //		chr8:91634	9-Jun-11	This probe set was anno		ENST0000	Hs.88594
0006350 //	0005634 //	0003677 //	chr7:15810	9-Jun-11	This probe	AK092414	BC012777(	Hs.11607
0006810 //	0000139 //	0000166 //	chr12:7218	9-Jun-11	This probe set was anno		AB075482(	Hs.154697
	0005622 //	0003676 //	chrX:10113	9-Jun-11	This probe	BC152470	ENST0000	Hs.296317
0007264 //	0005622 //	0000166 //	chr10:1896	9-Jun-11	This probe set was anno		ENST0000	Hs.25362
0006350 //	0005622 //	0003677 //	chr12:3892	9-Jun-11	This probe set was anno		ENST0000	Hs.6567
//55425			chr13:4556	9-Jun-11	This probe set was anno		AJ420573(	Hs.283709
0006260 //	0005634 //	0003677 //	chr16:1143	9-Jun-11	This probe set was anno		BC013040(	Hs.77448
			chrX:46458	9-Jun-11	This probe set was anno		BC090942(	Hs.91389
0001675 //	0005634 //	0003677 //	chr2:22842	9-Jun-11	This probe set was anno		NM_00113	Hs.108082
	0005634 //	0008270 //	chr7:11925	9-Jun-11	This probe	AK123998	AK290170(	Hs.116567
			chr17:2114	9-Jun-11	This probe set was anno		NM_15291	Hs.14478
0008152 //	0005739 //	0003824 //	chr16:1876	9-Jun-11	This probe	BC063017	ENST0000	Hs.322482
0006350 //	0000124 //	0003713 //	chr8:11035	9-Jun-11	This probe set was anno		NM_00119	Hs.44243
0006508 //	0005576 //	0004222 //	chr10:1277	9-Jun-11	This probe set was anno		ENST0000	Hs.8895
0006281 //	0005634 //	0000166 //	chr22:3869	9-Jun-11	This probe	ENST0000	CR618521(	Hs.5722

	0000922 // spindle pole		chr2:38813	9-Jun-11	This probe set was anno		AL137761(	Hs.8379
0002063 //	0005737 //	0004360 //	chr2:69546	9-Jun-11	This probe set was anno		NM_00205	Hs.13396
0000082 //	0005634 //	0003714 //	chr6:19839	9-Jun-11	This probe	BC014941	AI075961,	Hs.34853
0006897 //	0005634 //	0003677 //	chr2:16965	9-Jun-11	This probe	ENST0000	AK123698(	Hs.10260
			chr7:12338	9-Jun-11	This probe set was anno		BC067285(	Hs.182469
0000187 //	0005634 //	0000166 //	chr2:12805	9-Jun-11	This probe	AK093893	XR_11238	Hs.300511
			chr22:1943	9-Jun-11	This probe	BC062599	AK095271(	Hs.119960
			chr11:4396	9-Jun-11	This probe set was anno		NM_00114	Hs.127824
0006810 //	0016020 //	0005216 //	chr2:12019	9-Jun-11	This probe set was anno		BC046362(	Hs.26216
0006350 //	0005622 //	0003676 //	chr10:7715	9-Jun-11	This probe	AK127647	BC011625(	Hs.182740
0051301 // cell division		0000166 //	chr1:14310	9-Jun-11	This probe	AK092833	AB033099(	Hs.23413
0006350 //	0005622 //	0003676 //	chr16:3061	9-Jun-11	This probe set was anno		AL834299(	Hs.8184
0000226 //	0005634 // nucleus // in		chr21:9907	9-Jun-11	This probe	AK097438	AK096952(	Hs.103441
0007155 //	0005793 //	0042802 //	chr5:98128	9-Jun-11	This probe	GENSCAN	BC067736(	Hs.108972
	0016020 //	0005488 //	chrX:10074	9-Jun-11	This probe	GENSCAN	AY726601(	Hs.69705
0006810 //	0005886 //	0015293 //	chr10:6141	9-Jun-11	This probe set was anno		ENST0000	Hs.238927
0006605 //	0005737 //	0005515 //	chr6:15167	9-Jun-11	This probe set was anno		ENST0000	Hs.38022
0006605 //	0005737 //	0005515 //	chr6:15167	9-Jun-11	This probe set was anno		ENST0000	Hs.38022
			chr22:4663	9-Jun-11	This probe	CR456415	AK127072(	Hs.108358
0001666 //	0005737 //	0004860 //	chr17:7635	9-Jun-11	This probe	AK025416	BC060858(	Hs.311405
0055114 //	0005783 //	0004497 //	chr1:47515	9-Jun-11	This probe set was anno		AK091806(	Hs.26040
	0005737 //	0003824 //	chr6:13956	9-Jun-11	This probe set was anno		AL832322(	Hs.85428
0008152 //	0016020 //	0008415 //	chr8:56674	9-Jun-11	This probe	NM_15241	BC020835(	Hs.280858
			chr2:61368	9-Jun-11	This probe	ENST0000	BC008254(	Hs.252433
			chr1:14981	9-Jun-11	This probe	BX648801	AA682568,	Hs.25933
	0005576 // extracellular		chr11:7672	9-Jun-11	This probe	BC110868	AK128653(	Hs.298262
0006468 // protein phos		0000166 //	chrX:10520	9-Jun-11	This probe set was anno		BX538345(	Hs.30643
0006006 //	0005634 //	0003677 //	chr10:3541	9-Jun-11	This probe	ENST0000	BC017117(	Hs.155924
0006928 //	0005622 //	0004842 //	chr6:16146	9-Jun-11	This probe set was anno		AF006003,	Hs.20072
0000165 //	0005789 //	0003824 //	chr3:16079	9-Jun-11	This probe set was anno		ENST0000	Hs.19339
			chr12:5190	9-Jun-11	This probe set was anno		AK124576(	Hs.4749
			chrX:13367	9-Jun-11	This probe	ENST0000	NR_02460	Hs.108785
0007126 //	0005634 //	0000166 //	chr14:1044	9-Jun-11	This probe	BC128057	BC042804(	Hs.21454
			chr8:48648	9-Jun-11	This probe	ENST0000	U00948	Hs.278634
			chr12:2719	9-Jun-11	This probe set was anno		BC056670	Hs.184156
0000165 //	0005789 //	0003824 //	chr3:16079	9-Jun-11	This probe set was anno		ENST0000	Hs.12731
			chrX:11905	9-Jun-11	This probe set was anno		XR_10978	Hs.184993
			chr1:22602	9-Jun-11	This probe set was anno		ENST00000424332	
0006694 //	0005737 //	0003824 //	chr17:4070	9-Jun-11	This probe	AK127832	BC037415(	Hs.85279
0006915 //	0005634 //	0008270 //	chr17:6678	9-Jun-11	This probe	AK128092	BX649188(	Hs.154993
	0005783 // endoplasmic		chr7:12091	9-Jun-11	This probe	AK124845	AL832619(	Hs.24144
			chr11:1065	9-Jun-11	This probe set was anno		AK001875(	Hs.24321
			chr8:12138	9-Jun-11	This probe set was anno		AI377111,	Hs.28625
0006350 //	0005622 //	0003676 //	chr12:5393	9-Jun-11	This probe	AK302907	BC042363(	Hs.55888
0002456 //	0005615 //	0000166 //	chr6:30509	9-Jun-11	This probe set was anno		ENST0000	Hs.117406

0007165 //	0005622 //	0005085 //	chr19:1150	9-Jun-11	This probe s	BC101756	AK096811(	Hs.127826
0006810 //	0016020 //	0005215 //	chr12:5190	9-Jun-11	This probe set was anno		AK093005(	Hs.215937
0000122 //	0005622 //	0003676 //	chr6:10655	9-Jun-11	This probe set was anno		AY198414(	Hs.289088
//55425			chr13:4560	9-Jun-11	This probe s	AK001308	AJ420573(	Hs.283709
			chr3:19763	9-Jun-11	This probe s	ENST0000(	AK095570(	Hs.110041
		0005488 //	chr10:7501	9-Jun-11	This probe s	AF435958	AF435959(	Hs.110667
0006606 //	0005634 //	0005488 //	chr6:11705	9-Jun-11	This probe set was anno		ENST0000(	Hs.32615
0001833 //	0005634 //	0003677 //	chr6:42018	9-Jun-11	This probe s	AF465841	BC033728(	Hs.306088
0006309 //	0000159 //	0004722 //	chr7:25158	9-Jun-11	This probe set was anno		NM_01894	Hs.157301
			chr4:42069	9-Jun-11	This probe set was anno		ENST00000509683(11)	
			chr7:12841	9-Jun-11	This probe set was anno		AI422778,	Hs.7753
			chr11:1862	9-Jun-11	This probe s	BC056261	AF086471(	Hs.44425
0000226 //	0005874 // microtubule		chr21:9907	9-Jun-11	This probe s	AK097438	AK096952(	Hs.103441
	0005737 // cytoplasm //		chr3:18895	9-Jun-11	This probe s	ENST0000(	AK123232(	Hs.127780
0005975 //	0005737 //	0003824 //	chrX:71798	9-Jun-11	This probe set was anno		ENST0000(	Hs.296095
	0005737 //	0005488 //	chr9:85859	9-Jun-11	This probe set was anno		BX647549(	Hs.55501
			chr20:4790	9-Jun-11	This probe set was anno		AK124175(	Hs.284158
	0016020 // membrane //		chr14:9456	9-Jun-11	This probe s	BC015423	CR625015(	Hs.19414
	0005737 // cytoplasm //		chr11:1059	9-Jun-11	This probe s	AK304702	ENST0000(	Hs.158047
0006260 //	0005622 //	0003677 //	chr9:14083	9-Jun-11	This probe s	NM_00559	AI205868,	Hs.326416
0006350 //	0005622 //	0003676 //	chr5:12242	9-Jun-11	This probe set was anno		ENST0000(	Hs.135118
0006810 // transport // inferred from			chr5:12638	9-Jun-11	This probe set was anno		NM_00116	Hs.49573
			chr12:1491	9-Jun-11	This probe set was anno		BX649153(	Hs.79953
0006139 //	0005737 //	0000166 //	chr1:65694	9-Jun-11	This probe set was anno		ENST0000(	Hs.292805
			chr5:13168	9-Jun-11	This probe set was anno		AK126749(11)	
			chr2:97538	9-Jun-11	This probe set was anno		AI871280,	Hs.17910
			chr21:4372	9-Jun-11	This probe set was anno		AF086547	Hs.59525
			chr20:3105	9-Jun-11	This probe set was anno		AK097804(	Hs.126373
0001764 //	0005887 //	0000166 //	chr13:3634	9-Jun-11	This probe set was anno		ENST0000(	Hs.129997
			chr7:19041	9-Jun-11	This probe set was anno		CR622072(	Hs.12549
0008033 // tRNA proces		0005524 //	chr19:5209	9-Jun-11	This probe s	AK291173	XM_00311	Hs.148425
0006605 //	0005737 //	0005515 //	chr6:15167	9-Jun-11	This probe s	NM_14449	AI267615,	Hs.38022
0006091 //	0005625 //	0008415 //	chr7:86988	9-Jun-11	This probe set was anno		BC051874(	Hs.130909
0006457 //	0005783 //	0003755 //	chr2:17932	9-Jun-11	This probe set was anno		ENST0000(	Hs.50745
			chr1:43919	9-Jun-11	This probe set was anno		ENST00000444386	
				9-Jun-11	This probe set was anno		AI371550,	Hs.154173
0006468 //	0005882 //	0000166 //	chr15:4303	9-Jun-11	This probe s	NM_17350	BE045720,	Hs.125836
	0005737 // cytoplasm //		chr1:25200	9-Jun-11	This probe s	BC032051	AF425266(	Hs.23765
0007165 //	0016020 //	0004180 //	chr5:16762	9-Jun-11	This probe set was anno		ENST0000(	Hs.173560
			chr10:7228	9-Jun-11	This probe set was anno		ENST0000(	Hs.300646
	0016020 //	0008430 //	chr4:83404	9-Jun-11	This probe set was anno		AK023055(	Hs.199647
0000122 //	0005634 //	0005515 //	chr17:6590	9-Jun-11	This probe set was anno		AK027184(	Hs.99872
0001701 //	0005634 // nucleus // in		chr16:8934	9-Jun-11	This probe s	GENSCAN	AY373756(	Hs.22116
0010033 //	0005634 //	0004385 //	chr9:71862	9-Jun-11	This probe set was anno		AF489824(	Hs.289005
0016567 //	0000151 //	0003676 //	chr16:2456	9-Jun-11	This probe s	AY072922	AK023612(	Hs.145629

0006024 //	0000139 //	0004653 //	chr2:15816	9-Jun-11	This probe set was anno		ENST0000	Hs.168830
0006810 //	0000139 //	0000166 //	chrX:49857	9-Jun-11	This probe set was anno		ENST0000	Hs.166486
0006810 //	0005739 //	0005215 //	chr14:1007	9-Jun-11	This probe	BC142945 /	AK022257(	Hs.179647
			chr12:1305	9-Jun-11	This probe set was anno		AK024522(	Hs.194101
	0016020 // membrane //		chr13:9200	9-Jun-11	This probe set was anno		AB176707(	Hs.24115
	0005737 // cytoplasm //		chr6:13581	9-Jun-11	This probe set was anno		BX648311(	Hs.273294
			chr3:17188	9-Jun-11	This probe set was anno		AK022461(	Hs.287528
			chr11:3311	9-Jun-11	This probe set was anno		AK027139(11)	
			chr6:15516	9-Jun-11	This probe set was anno		AK021581(	Hs.170264
0006511 //	0005634 //	0004221 //	chr1:22012	9-Jun-11	This probe set was anno		AK000110(	Hs.178518
0005975 //	0005625 //	0003824 //	chr9:34646	9-Jun-11	This probe	AK300070	AK096137(	Hs.75641
	0005576 // extracellular		chr3:18405	9-Jun-11	This probe	ENST0000	AK024378(	Hs.141660
0006606 //	0005634 //	0005515 //	chr12:4285	9-Jun-11	This probe	AF038184 /	AK096233(	Hs.229084
0006350 //	0005634 //	0003700 //	chr5:13222	9-Jun-11	This probe set was anno		AB209547(	Hs.231967
0001522 // pseudouridin		0003723 //	chr2:61192	9-Jun-11	This probe set was anno		AA748843,	Hs.293914
	0005634 //	0004416 //	chr2:21913	9-Jun-11	This probe set was anno		AK309308(	Hs.100747
0016180 //	0005634 //	0005488 //	chr11:7768	9-Jun-11	This probe	BC082256 /	AK000455(	Hs.14632
			chr6:11218	9-Jun-11	This probe set was anno		GQ497714(9)	
			chr12:6508	9-Jun-11	This probe set was anno		AA303392,	Hs.272415
	0016020 // membrane //		chr7:12271	9-Jun-11	This probe set was anno		AK001834	Hs.3542
			chr2:62295	9-Jun-11	This probe	BC071802 /	AV730766,	Hs.274510
			chr21:2932	9-Jun-11	This probe set was anno		AL109791(	Hs.241559
0006486 //	0005783 //	0003980 //	chr13:9652	9-Jun-11	This probe set was anno		AK021547(	Hs.22983
0006413 //	0005634 //	0003743 //	chr20:5918	9-Jun-11	This probe set was anno		AB032979(	Hs.128791
			chr3:98301	9-Jun-11	This probe set was anno		AK022155(	Hs.296697
			chr3:61863	9-Jun-11	This probe set was anno		AL137541	Hs.306471
			chrX:13799	9-Jun-11	This probe set was anno		AK000019(	Hs.306375
			chr20:3378	9-Jun-11	This probe set was anno		AK021431(	Hs.235543
			chr5:13373	9-Jun-11	This probe set was anno		BC008293(	Hs.293659
0001947 //	0005737 //	0005515 //	chr4:12274	9-Jun-11	This probe	ENST0000	ENST0000	Hs.136182
			chr14:1013	9-Jun-11	This probe set was anno		AK098378	Hs.53112
			chr17:1896	9-Jun-11	This probe set was anno		AV743330,	Hs.331099
	0016020 //	0005515 //	chr9:11605	9-Jun-11	This probe	AK091940	BC013036(	Hs.211374
	0005737 //	0000166 //	chr1:89646	9-Jun-11	This probe	NM_05294	ENST0000	Hs.138360
	0005634 //	0004872 //	chr15:6074	9-Jun-11	This probe	ENST0000	AF502591(	Hs.145704
			chr17:7983	9-Jun-11	This probe set was anno		AK098016(	Hs.21108
0006810 //	0001518 //	0005216 //	chr11:1180	9-Jun-11	This probe set was anno		NM_00458	Hs.12714
0042787 //	0016020 //	0004842 //	chr6:12540	9-Jun-11	This probe	BC026087 /	AK093417(	Hs.307526
			chr7:30895	9-Jun-11	This probe	AK304075	AK090826(	Hs.143810
			chr5:95243	9-Jun-11	This probe set was anno		AK093529(	Hs.100636
			chr2:96914	9-Jun-11	This probe set was anno		AW008077	Hs.164303
			chr17:4051	9-Jun-11	This probe set was anno		AI914925,	Hs.222240
0006915 //	0005634 //	0003677 //	chr17:2707	9-Jun-11	This probe set was anno		ENST0000	Hs.35437
			chr7:12914	9-Jun-11	This probe	AF086124 /	BC050400(	Hs.178144
			chr2:15718	9-Jun-11	This probe set was anno		F32182,AV	Hs.165258

0007399 //	0005783 //	0003713 //	chr12:6674	9-Jun-11	This probe set was anno		ENST0000	Hs.107708
0006350 //	0005622 //	0003676 //	chr19:2354	9-Jun-11	This probe set was anno		ENST0000	Hs.183950
	0005737 // cytoplasm //		chr1:16931	9-Jun-11	This probe set was anno		AK123260	Hs.247677
			chr1:11171	9-Jun-11	This probe set was anno		AA767373	
	0000139 //	0004653 //	chr3:16264	9-Jun-11	This probe	AY358443	AK094780	Hs.63163
			chr5:12252	9-Jun-11	This probe set was anno		AA425940,	Hs.98506
			chr1:93646	9-Jun-11	This probe	ENST0000	ENST0000	Hs.126389
			chr6:14325	9-Jun-11	This probe set was anno		H15073,A	Hs.151124
			chr8:10173	9-Jun-11	This probe set was anno		AK098572	Hs.144923
		0005515 //	chr3:16951	9-Jun-11	This probe	ENST0000	AK130856	Hs.120277
			chr13:2773	9-Jun-11	This probe set was anno		AW103126	Hs.244583
			chr11:1202	9-Jun-11	This probe set was anno		R82611,R3	Hs.24598
			chr2:15872	9-Jun-11	This probe set was anno		AI700646,	Hs.202259
			chr19:1619	9-Jun-11	This probe	ENST0000	AV738306,	Hs.293379
			chr2:54311	9-Jun-11	This probe set was anno		XR_11232	Hs.170427
			chr5:17155	9-Jun-11	This probe set was anno		BE501281	
	0005737 // cytoplasm //		chr1:14529	9-Jun-11	This probe set was anno		BC071723	Hs.47142
			chr7:13765	9-Jun-11	This probe set was anno		AA033987	
			chr4:85929	9-Jun-11	This probe set was anno		AY250185	Hs.46730
			chr1:56956	9-Jun-11	This probe set was anno		AW474391	Hs.264433
			chrX:12568	9-Jun-11	This probe set was anno		BC035674	Hs.120403
			chr11:3448	9-Jun-11	This probe set was anno		N66025,AI	Hs.141604
0030154 //	0005634 //	0000166 //	chr17:3359	9-Jun-11	This probe	AY319652	AL832814	Hs.133526
0006350 //	0005634 //	0003677 //	chr5:13181	9-Jun-11	This probe set was anno		ENST0000	Hs.180559
0002064 //	0000138 //	0003831 //	chr9:33165	9-Jun-11	This probe set was anno		CR605922	Hs.176725
			chr1:14790	9-Jun-11	This probe set was anno		AI248270,	Hs.193620
				9-Jun-11	This probe set was anno		BF194846,	Hs.290165
		0005515 //	chr17:1906	9-Jun-11	This probe set was anno		BC060883	Hs.87636
		0004721 //	chr15:4482	9-Jun-11	This probe set was anno		ENST0000	Hs.125882
0000209 //	0000785 //	0000166 //	chr5:13372	9-Jun-11	This probe set was anno		BC005979,	Hs.165681
0006810 //	0005739 //	0000166 //	chr17:6701	9-Jun-11	This probe set was anno		AF423307	Hs.154009
			chrY:25263	9-Jun-11	This probe set was anno		AI277292,	Hs.192756
			chr12:7218	9-Jun-11	This probe set was anno		XR_11466	Hs.167028
0001657 //	0005576 //	0005102 //	chr11:2767	9-Jun-11	This probe set was anno		AY054392	Hs.146442
			chr5:15870	9-Jun-11	This probe set was anno		BE674693,	Hs.190447
0008033 // tRNA proces		0004000 //	chr15:4364	9-Jun-11	This probe set was anno		BC075857	Hs.161274
0006350 //	0005622 //	0003676 //	chr19:2857	9-Jun-11	This probe set was anno		ENST0000	Hs.121682
			chr5:88121	9-Jun-11	This probe set was anno		AW971469	Hs.178398
			chr1:19532	9-Jun-11	This probe set was anno		AI287539,	Hs.148078
0006810 //	0005737 // cytoplasm //		chr3:12114	9-Jun-11	This probe set was anno		ENST0000	Hs.25131
			chr18:1977	9-Jun-11	This probe set was anno		BF002339	
0006120 //	0005739 //	0008137 //	chr7:14042	9-Jun-11	This probe	ENST0000	ENST0000	Hs.188521
			chr15:5850	9-Jun-11	This probe set was anno		AK095426	Hs.145411
				9-Jun-11	This probe set was anno		AA947873	
			chr7:15080	9-Jun-11	This probe set was anno		AW593848	Hs.195048

	0000151 //	0005515 //	chr3:18265	9-Jun-11	This probe set was anno		ENST0000	Hs.260282
0006412 //	0005622 //	0003723 //	chr3:23965	9-Jun-11	This probe set was anno		AK055501(	Hs.134772
			chr17:3112	9-Jun-11	This probe set was anno		AI435335,	Hs.270036
			chr4:14859	9-Jun-11	This probe set was anno		AA702111	
			chr5:40984	9-Jun-11	This probe set was anno		AI758238,	Hs.196556
		0000166 //	chr17:7823	9-Jun-11	This probe	AK093793	ENST0000	Hs.189284
0006350 //	0005622 //	0003676 //	chr7:51069	9-Jun-11	This probe set was anno		ENST0000	Hs.54811
	0005576 // extracellular		chrX:45007	9-Jun-11	This probe set was anno		ENST0000	Hs.267442
			chr15:5937	9-Jun-11	This probe set was anno		T98940,AA	Hs.110067
			chr16:5676	9-Jun-11	This probe set was anno		BC037791(	Hs.283396
			chr18:5533	9-Jun-11	This probe	BC065760	XR_11178	Hs.145225
			chr1:15054	9-Jun-11	This probe set was anno		AA633838,	Hs.160999
			chr9:11370	9-Jun-11	This probe set was anno		AI679236,	Hs.43057
			chr16:6501	9-Jun-11	This probe set was anno		AI473366,	Hs.56071
			chr2:33813	9-Jun-11	This probe set was anno		AK096187(	Hs.211648
0006810 //	0005624 //	0005477 //	chr12:6017	9-Jun-11	This probe set was anno		BC030693,	Hs.170504
0001525 //	0005634 //	0000166 //	chr2:23231	9-Jun-11	This probe set was anno		ENST0000	Hs.253767
			chrX:15335	9-Jun-11	This probe set was anno		ENST00000495474	
0006412 // translation //		0000166 //	chr6:10711	9-Jun-11	This probe set was anno		ENST0000	Hs.152346
			chr6:14611	9-Jun-11	This probe set was anno		AB073353(	Hs.174257
			chr19:3749	9-Jun-11	This probe set was anno		AI478965,	Hs.270293
			chr12:2282	9-Jun-11	This probe set was anno		N68640,H4	Hs.152940
0001525 //	0005634 //	0003677 //	chr2:66793	9-Jun-11	This probe	AF088018	N50458,AA	Hs.191349
			chr12:2609	9-Jun-11	This probe set was anno		AK090817(	Hs.233382
			chr3:69522	9-Jun-11	This probe set was anno		AW873245	Hs.152155
			chr3:41255	9-Jun-11	This probe set was anno		AK127399(	Hs.162459
0001503 //	0005783 //	0003824 //	chr2:70375	9-Jun-11	This probe set was anno		AF442151(	Hs.271530
			chr17:3860	9-Jun-11	This probe set was anno		R08865,AV	Hs.177170
	0005739 //	0000166 //	chr4:14657	9-Jun-11	This probe set was anno		ENST0000	Hs.117747
			chr7:93595	9-Jun-11	This probe set was anno		AA001150	
			chr5:11864	9-Jun-11	This probe set was anno		AA806368,	Hs.272159
			chr3:14161	9-Jun-11	This probe set was anno		AI469200,	Hs.171941
			chr2:46529	9-Jun-11	This probe set was anno		H84651,AA	Hs.307559
			chr2:23919	9-Jun-11	This probe set was anno		AA004689	
			chr8:29940	9-Jun-11	This probe set was anno		GENSCAN0000000545	
			chr22:3184	9-Jun-11	This probe set was anno		AA580649,	Hs.207300
			chr4:10372	9-Jun-11	This probe set was anno		BC024228(	Hs.270366
			chr13:2801	9-Jun-11	This probe set was anno		AA704984,	Hs.194300
			chr10:1337	9-Jun-11	This probe set was anno		AL038973,	Hs.144873
			chr15:3008	9-Jun-11	This probe set was anno		AW173166	
			chr7:15543	9-Jun-11	This probe set was anno		AK091942(	Hs.87856
			chr7:69364	9-Jun-11	This probe set was anno		AF326917,	Hs.167236
				9-Jun-11	This probe set was anno		AW206536	
				9-Jun-11	This probe set was anno		AF075018(	Hs.153800
			chr1:23627	9-Jun-11	This probe set was anno		BE767796,	Hs.44392

			chrX:15853	9-Jun-11	This probe set was anno		AW291889	Hs.121592
			chr21:4635	9-Jun-11	This probe	AF391114	AF391113(	Hs.126522
0001539 //	0005737 //	0000166 //	chr3:57327	9-Jun-11	This probe set was anno		AK128592(	Hs.201378
			chr22:5097	9-Jun-11	This probe set was anno		AI990895,	Hs.232280
0032312 // regulation of		0000166 //	chr10:5174	9-Jun-11	This probe	BC032492	ENST0000	Hs.314437
			chr14:8096	9-Jun-11	This probe set was anno		ENST0000	Hs.216593
0006139 // nucleobase,		0000166 //	chrX:73953	9-Jun-11	This probe set was anno		AY563507(	Hs.66035
			chr14:7423	9-Jun-11	This probe set was anno		AW573027	
			chr8:10366	9-Jun-11	This probe set was anno		AA922146,	Hs.255609
0006350 //	0005634 //	0003714 //	chrX:73833	9-Jun-11	This probe set was anno		BF063235,	Hs.163432
			chr1:23146	9-Jun-11	This probe set was anno		AK095163	Hs.163222
0006309 //	0000159 //	0004722 //	chr7:25159	9-Jun-11	This probe set was anno		NM_01894	Hs.205711
			chr11:3299	9-Jun-11	This probe set was anno		ENST0000	Hs.193338
	0043234 // protein com		chr2:20123	9-Jun-11	This probe set was anno		AW957847	Hs.269548
	0005886 //	0000166 //	chr7:45008	9-Jun-11	This probe	AK074135	AK074050(	Hs.283365
	0005634 //	0003677 //	chr2:14927	9-Jun-11	This probe set was anno		ENST0000	Hs.291812
0006260 //	0005634 //	0003676 //	chr3:48507	9-Jun-11	This probe	ENST0000	AF151105(	Hs.23595
0006694 //	0005737 //	0000166 //	chr12:1100	9-Jun-11	This probe	AK293130	AK023087(	Hs.75138
0006417 //	0005783 //	0005515 //	chr19:4937	9-Jun-11	This probe set was anno		AK296668(	Hs.76556
0003084 //	0005576 //	0000166 //	chr12:9893	9-Jun-11	This probe set was anno		DQ925670	Hs.239895
0007049 // cell cycle // inferred fron			chr22:4513	9-Jun-11	This probe	AK291564	BC016921(	Hs.79601

varies

Chromosom	Chromosom	Chromosom	Chromosom	Chromosom	Chromosom	EC	Ensembl	Gene_Title
chr1q21-q2	157108266	chr1	84.14	157102938	-		ENSG0000	ets variant
chr15q22.1	63422025	chr15	86.16	63414026	+		ENSG0000	lactamase,
chr2q32.1	183964720	chr2	77.15	183942943	+	EC:3.1.3.16	ENSG0000	dual specifi
chrXp21.2	30877797	chrX	96.26	30848450	-		ENSG0000	TGF-beta a
chr3q29	196439095	chr3	69.31	196433920	-		ENSG0000	chromosom
chr2q33.1	202483898	chr2	99.34	202352247	-		ENSG0000	amyotrophi
chr21q22.1	35469654	chr21	99.95	35467497	+		ENSG0000	solute carri
chr5q13.2	73207522	chr5	98.47	73179604	+		ENSG0000	190 kDa gu
chr14q32.3	102681339	chr14	94.85	102606211	+			WD repeat
chr4q21.1	NA		NA	NA				Gene differ
chr1q12	145508998	chr1	98.33	145507636	+		ENSG0000	RNA bindi
chr5q14	79748252	chr5	89.04	79703867	+		ENSG0000	zinc finger,
chr15q21.2	49777632	chr15	62.45	49775347	+		ENSG0000	fibroblast g
chr1q25.2-	186649519	chr1	97.36	186642025	-	EC:1.14.99.	ENSG0000	prostagland
chr5q11.1	52968051	chr5	85.42	52965869	+			NADH deh
chr15q15.3-	44816455	chr15	95.15	44719990	+	EC:3.1.3.-	ENSG0000	CTD (carbo
chr5q13	74878773	chr5	65.79	74842833	+	EC:2.7.7.7	ENSG0000	polymerase
chr1p13	40948193	chr22	50.33	40859223	-			RNA bindi
chr19p13.1	13947102	chr19	47.2	13945329	-			hypothetica
chr1q42.3	235713342	chr1	54.95	235711032	-		ENSG0000	guanine nuc
chr7q35	143996399	chr7	72.69	143993370	+		ENSG0000	olfactory re
chr10p13	17279591	chr10	94.9	17278584	+			vimentin
chr2q37.1	232264809	chr2	42.09	232263066	+		ENSG0000	UDP-GlcN
chr1p36	16266640	chr1	95.59	16262481	+		ENSG0000	spen homol
chr15q21.3	54920803	chr15	98.68	54527227	+		ENSG0000	unc-13 hom
chr12q21.2	76440267	chr12	99.69	76438669	-		ENSG0000	nucleosome
	67138578	chr11	98.18	67136401	-			
chr17q22	57433664	chr17	87.49	57409036	+			yippee-like
chr7q22.1	102583784	chr7	95.86	102582337	+			F-box and l
chr2q33	202018647	chr2	88.26	202005006	-		ENSG0000	amyotrophi
	112555959	chr6	96.68	112555375	-			
	103227408	chrX	70.81	103225825	+			
chr13q33	102370265	chr13	79.02	102369197	+		ENSG0000	integrin, bet
	12792061	chr18	88.03	12790115	-			
chr5p12-p1	43125131	chr5	71.87	43122190	+		ENSG0000	Zinc finger
	120216412	chr11	71.2	120213701	+			
	111477674	chr11	82.38	111473612	+			
	75082548	chr7	37.2	75081243	+		ENSG00000228720 ///	
chr12q24.1	112711575	chr12	93.89	112687360	-	EC:6.3.2.-	ENSG0000	chromosom
	21866945	chr4	99.46	21864898	-			
chr16q22.1	22476662	chr16	30.04	22474267	+	EC:3.1.13.-		exosome co
chr5q14.1	80711708	chr5	48.54	80710582	-		ENSG0000	single-stran
chrXq28	153656825	chrX	19.87	153656462	-			hypothetica

	19419262	chr12	26.67	19418892	+			
chr9p22.2	17299239	chr9	85.12	17135037	+		ENSG0000	centlein, ce
	36775157	chr2	88.68	36773933	-			
	21794246	chr22	69.23	21791858	+			
chr1p13.3	110880722	chr1	89.33	110880026	-			Hypothetica
chr3p14.3	56605012	chr3	53.08	56592872	+			coiled-coil
	NA		NA	NA				
	15777382	chr5	83.74	15775819	+			
	159794306	chr4	63.86	159793905	-			
	10196301	chr5	6.71	10195298	-			
	78140882	chr11	51.63	78135272	-		ENSG00000251323	
chr17q25	73654247	chr17	17.09	73652556	-	EC:3.6.4.12		RecQ prote
chr9p24	5068158	chr9	78.23	5065804	+	EC:2.7.10.2		Janus kinas
chr2q37.3	239463695	chr2	84.4	239419052	-		ENSG0000	hypothetica
chr13q12-q	31226092	chr13	65.83	31192087	+			ubiquitin sp
chr19q13.4	52962089	chr19	53.22	52956834	+			Zinc finger
	65327847	chr5	32.12	65327129	+			
	56817289	chr3	51.82	56813522	-			
	169938352	chr6	51.63	169934883	-			
chr11q22.3	104769397	chr11	99.57	104757416	-		ENSG0000	caspase 12
chr10p15.3	324787	chr10	97.8	322711	-		ENSG0000	DIP2 disco-
	71855693	chr9	13.7	71855142	+			
	74494758	chr13	79.7	74489850	-			
	46291419	chr2	60.44	46288635	+			
chr2p16.1	55844846	chr2	95.59	55843286	-			SMEK hom
chr1q23.1	158102985	chr1	66.55	158101833	-			hCG16547
chr2p23	28113955	chr2	91.42	28112513	-			hypothetica
	68485310	chr5	66.69	68484110	-			
chr19p13	14818053	chr19	61.89	14815724	+			zinc finger
chr19p13.1	19887226	chr19	78.02	19884689	-			hypothetica
	141734014	chr3	12.2	141733172	-			
	96270869	chr5	52.41	96269784	-		ENSG00000247121	
chr5q14.1	81354425	chr5	66.97	81267975	+		ENSG0000	ATG10 aut
chr1p34	44089337	chr1	94.81	43996546	+	EC:3.1.3.48	ENSG0000	protein tyro
chr8q23.1	23428597	chr10	79	23425839	+		ENSG0000	tyrosine 3-n
chr9q22.31	96326771	chr9	99.13	96214172	+		ENSG0000	family with
chr1q21	150552247	chr1	98.7	150547032	-		ENSG0000	myeloid cel
chr1q21	150552055	chr1	99.01	150548543	-		ENSG0000	myeloid cel
chr2q32.2	191878405	chr2	98.93	191833875	-		ENSG0000	signal trans
chr10q24.1-	103578175	chr10	98.57	103544206	-	EC:2.3.1.48	ENSG0000	meningiom
chr3q25.1	150264301	chr3	98.44	150259786	-		ENSG0000	stress-assoc
chr5q34	172198203	chr5	99.95	172195101	-	EC:3.1.3.16	ENSG0000	dual specifi
chr12p13.1	10875953	chr12	90.13	10851688	-		ENSG0000	cold shock
chr3p26	5026861	chr3	96.65	5021207	+		ENSG0000	basic helix-
chrXp11.3-	41209441	chrX	95.77	41192650	+	EC:3.6.4.13	ENSG0000	DEAD (As

chr1q32	203278727	chr1	98.71	203274663	+		ENSG0000	BTG family
chr1q24	169101954	chr1	95.34	169076003	+		ENSG0000	ATPase, Na
chr4p14	41270441	chr4	96.06	41259129	+	EC:3.4.19.1	ENSG0000	ubiquitin ca
chr1p13.2	111991851	chr1	97.94	111982895	-		ENSG0000	WD repeat
chr19p13.2	12904129	chr19	98.27	12902332	+		ENSG0000	jun B proto-
chr2p25	8824368	chr2	97.24	8822197	+			inhibitor of
chr17q21.2	72295736	chr6	90.29	72294394	+		ENSG0000	keratin 19
chr10p15	5499674	chr10	98.03	5494395	+		ENSG0000	neuroepithe
chr1p13.3	109825747	chr1	67.23	109822189	-		ENSG0000	proline/seri
chr3p21.3	48647470	chr3	99.95	48636435	-	EC:1.10.2.2	ENSG0000	ubiquinol-c
chr19q13.2	49379314	chr19	99.57	49375677	+		ENSG0000	protein pho
chr8q11	53626983	chr8	96.45	53535018	-		ENSG0000	RB1-induci
chr21q22.3	47648676	chr21	94.91	47609038	-	EC:5.4.99.7	ENSG0000	lanosterol s
chr19q13.3	46366367	chr19	99.35	46318721	-		ENSG0000	symplekin
chr11p15.5	2160002	chr11	78.23	2150346	-		ENSG0000	insulin-like
chr14q32	94583032	chr14	96.15	94577975	+		ENSG0000	interferon,
chr1p13-p1	120612032	chr1	99.86	120454177	-		ENSG0000	notch 2
chr8q13	56923131	chr8	98.3	56792371	+	EC:2.7.10.2	ENSG0000	v-yes-1 Ya
chr1q32.3	212794099	chr1	99.27	212782112	+		ENSG0000	activating t
chr6p21.3	30173001	chr6	79.39	30152232	-		ENSG0000	tripartite m
chrXq13.3-	78623047	chrX	94.39	78615880	-		ENSG0000	integral me
chr15q21.1	48937985	chr15	98.56	48701510	-		ENSG0000	fibrillin 1
chr11p11.2|	47270363	chr11	99.95	47260852	-	EC:3.1.3.2	ENSG0000	acid phosph
chr3q28	188596567	chr3	92.91	187930720	+		ENSG0000	LIM domai
chr7q31|14	108215294	chr7	100	108210355	+		ENSG0000	DnaJ (Hsp4
chr4q13-q2	74609431	chr4	70.71	74606301	+		ENSG0000	interleukin
chr2p24	15701432	chr2	99.33	15307040	-		ENSG0000	neuroblasto
chr22q13.3	45996563	chr22	99.66	45898855	+		ENSG0000	fibulin 1
chr1q42.1	241680617	chr1	94.54	241661086	-	EC:4.2.1.2		fumarate hy
chr1p36.21	14114799	chr1	96.79	14057521	+	EC:2.1.1.43	ENSG0000	PR domain
chr19p13.3-	8008566	chr19	99.32	7991994	-		ENSG0000	translocase
chr9q22.33	100881594	chr9	80.89	100846511	-		ENSG0000	tripartite m
chr10q23.3	91163610	chr10	99.82	91152405	+		ENSG0000	interferon-i
chr1p34.1	44170150	chr1	97.57	44115823	+	EC:1.14.11.	ENSG0000	lysine (K)-s
chr3q28-q2	193856396	chr3	92.36	193853705	+		ENSG0000	hairy and e
chr3q28-q2	193856396	chr3	96.26	193853933	+		ENSG0000	hairy and e
chr11p12-p	47260763	chr11	99.89	47236512	+		ENSG0000	damage-spe
chr4p16	7873805	chr4	98.78	7760440	-		ENSG0000	actin filame
chr19p13.2	18392468	chr19	81.54	18390569	-		ENSG0000	jun D proto-
chr14q11.2	24635772	chr14	96.53	24631349	+		ENSG0000	interferon r
chr1p22.1	94703121	chr1	98.43	94638170	-		ENSG0000	Rho GTPas
chr5p15.33	918070	chr5	98.64	893068	+		ENSG0000	thyroid hor
chr2p25.2	7184224	chr2	93.61	7057616	+		ENSG0000	ring finger
chr9p21	32550819	chr9	97.94	32540823	-		ENSG0000	topoisomer
chr9q33.3	128729368	chr9	99.96	128509732	+		ENSG0000	pre-B-cell l

chr1p32	53679444	chr1	94.41	53662514	+	EC:2.3.1.21	ENSG0000	carnitine pa
chr17q11.2	29701464	chr17	98.09	29422116	+		ENSG0000	neurofibron
chr1p35	27998708	chr1	76.46	27992580	-		ENSG0000	interferon,
chr13q12.1	25910478	chr13	98.22	25875768	+		ENSG0000	nucleoporin
chr1p31.1	79108069	chr1	88.1	79086148	+		ENSG0000	interferon-i
chr8q12.1	60031767	chr8	98.36	59717976	-		ENSG0000	thymocyte
chr21q22.3	43717352	chr21	98.19	43639378	+		ENSG0000	ATP-bindin
chr2q22-q2	157189212	chr2	98.27	157180950	-		ENSG0000	nuclear rece
chr2q22-q2	157189183	chr2	98.45	157180950	-		ENSG0000	nuclear rece
chr10q23.3	94455388	chr10	92.41	94449717	+			hematopoie
chr1q25.2-c	186649556	chr1	97.42	186640968	-	EC:1.14.99.	ENSG0000	prostagland
chr17q22	53400888	chr17	97.1	53342526	+		ENSG0000	hepatic leuk
chrXq22.1	101913378	chrX	99.96	101906441	+		ENSG0000	G protein-c
chr7p22	2270273	chr7	93.25	1855433	-		ENSG0000	MAD1 mitc
chr5q33-q3	172591344	chr5	99.68	172571539	+		ENSG0000	BCL2/aden
chr16p13.3	5083915	chr16	99.63	5074846	-	EC:3.1.4.45	ENSG0000	N-acetylglu
chr3p22-p2	45077562	chr3	92.22	45067769	+		ENSG0000	C-type lecti
chr10q21.1	64576127	chr10	99.56	64571756	-			early growtl
chr7p13-p1	45933259	chr7	97.95	45928086	+		ENSG0000	insulin-like
chr3q26.1	167543356	chr3	100	167453548	+		ENSG0000	serpin pepti
chr11q24.2	125525571	chr11	99.23	125496642	+	EC:2.7.11.1	ENSG0000	CHK1 chec
chrXq12-q1	71933917	chrX	99.72	71800480	-	EC:2.7.11.1	ENSG0000	phosphoryla
chr1p36.33	949919	chr1	99.37	948878	+		ENSG0000	ISG15 ubiq
chrXq26.1	129299672	chrX	99.95	129263509	-		ENSG0000	apoptosis-i
chr3p25	11304415	chr3	74.01	11300686	+		ENSG0000	histamine re
chr9q22.31	95186560	chr9	99.47	95176537	-		ENSG0000	osteomodul
chr1q42.1	226128873	chr1	92.1	226124305	-		ENSG0000	left-right de
chr11p13	32457077	chr11	95.15	32409323	-		ENSG0000	Wilms tumc
chr20p11.2	25427957	chr20	43.04	25388362	+		ENSG0000	GINS comp
chr8p23-p2	22550815	chr8	90.46	22545238	-		ENSG0000	early growtl
chr17p13.1	6676908	chr17	78.13	6659397	+		ENSG0000	XIAP assoc
chr2q22-q2	165478358	chr2	93.56	165349332	-		ENSG0000	growth fact
chr1q22-q2	169703179	chr1	98.41	169691781	-		ENSG0000	selectin E
chr15q14-q	34158302	chr15	99.72	33603176	+		ENSG0000	ryanodine r
chr17q25.3	76355282	chr17	96.97	76353006	-		ENSG0000	suppressor
chr12q23.3	94699225	chr12	97.72	94542498	+		ENSG0000	plexin C1
chr17q21.3	42466873	chr17	99.94	42449549	-		ENSG0000	integrin, alp
chr19p13.2	16205358	chr19	41.54	15751706	+	EC:1.14.13.30		cytochrome
chr9p22.3	2193555	chr9	89.11	2029018	+		ENSG0000	SWI/SNF r
chr9p22.3	2192990	chr9	89.21	2029018	+		ENSG0000	SWI/SNF r
chrXp21.3	30327480	chrX	96.62	30322463	-		ENSG0000	nuclear rece
chr6p21.3	29760850	chr6	97.49	29758815	-			HLA compl
chr19p13.1	20003939	chr19	87.71	19989288	+		ENSG0000	zinc finger
chr11p13	32461618	chr11	84.24	32459474	+			WT1 antise
chr12q13.1	51891648	chr12	96.64	51818756	+		ENSG0000	solute carri

chr1p31.1	79004217	chr1	98.9	78956842	+		ENSG0000	prostagland
chr7p13	40132622	chr7	96.94	39991318	+	EC:2.7.11.2	ENSG0000	cyclin-depe
chr19p13.3	2478255	chr19	97.77	2476256	+		ENSG0000	growth arre
chr8p21.3	22432263	chr8	96.41	22423190	+		ENSG0000	sorbin and S
chr1p36	6453438	chr1	94.44	6324331	-	EC:3.1.2.2	ENSG0000	acyl-CoA th
chr21q22.3	31816308	chr10	62.89	31608160	+	EC:2.7.11.1	ENSG0000	salt-inducib
chr19p12	20240650	chr19	65.01	20044681	+			zinc finger
chr6p21.3	29913064	chr6	91.18	29795626	+		ENSG0000	major histoc
chr8q12.1	61536203	chr8	97.29	61429522	+		ENSG0000	RAB2A, m
chr20q11	30193921	chr20	95.09	30193169	+		ENSG0000	inhibitor of
chr6q15	89794481	chr6	99.45	89793751	+			proline-rich
chr6p21.3	31325022	chr6	96.54	31321896	-		ENSG0000	major histoc
chr6p21.2	37143160	chr6	96.4	37138063	+	EC:2.7.11.1		pim-1 oncog
chr7q22	93520203	chr7	97.94	93514721	-		ENSG0000	tissue factor
chr7q22	93520028	chr7	99.9	93515898	-		ENSG0000	tissue factor
chr6p22.3	19842428	chr6	96.66	19837617	+		ENSG0000	inhibitor of
chr6p22-p2	19842428	chr6	96.66	19837617	+			Inhibitor of
chr19p13.3	2478257	chr19	98.4	2476134	+		ENSG0000	growth arre
chr19p13.3	2477664	chr19	100	2476256	+		ENSG0000	growth arre
chr15q22.2	59981518	chr15	98.84	59955063	-		ENSG0000	BCL2/aden
chr21q22.1|	38334473	chr21	93.6	38123492	-	EC:6.3.4.10	ENSG0000	holocarboxy
chr4q34	176733472	chr4	98.99	176554601	-		ENSG0000	glycoprotei
chr16p12.3	22385797	chr16	99.03	22357256	-		ENSG0000	cerebellar d
chr19p13	291379	chr19	100	281371	-	EC:3.1.3.4	ENSG0000	phosphatidi
chrXp11.4	34675155	chrX	95.03	34645201	-		ENSG0000	transmembr
chr12p13.3	6660135	chr12	98.31	6648721	-		ENSG0000	intermediat
chr6q21	21154962	chrY	85.81	21152525	-			CD24 mole
chr4q21	74964892	chr4	95.02	74962800	-		ENSG0000	chemokine
chr12q15	56709817	chr12	96.24	56708283	-			canopy 2 ho
chr13q34	111373420	chr13	96.37	111367328	+		ENSG0000	inhibitor of
chr1q25	184006863	chr1	99.67	183904970	-	EC:2.4.1.50	ENSG0000	glycosyltran
chr1p31	66101110	chr1	99.6	66031248	+		ENSG0000	leptin recep
chr1q21.3	154243328	chr1	98.61	154197557	+		ENSG0000	ubiquitin as
chr2q32.2	191878894	chr2	98.98	191840367	-		ENSG0000	signal trans
chr15q26.1	90633860	chr15	88.6	90627215	-	EC:1.1.1.42	ENSG0000	isocitrate de
chr19p13.3	5978102	chr19	94.71	5917014	-		ENSG0000	RAN bindi
chr4p15	31144728	chr4	96.14	30722191	+		ENSG0000	protocadher
chr6q24-q2	151677908	chr6	99.97	151646822	+		ENSG0000	A kinase (P
chr16q24	89762244	chr16	99.68	89753106	+	EC:2.7.11.2	ENSG0000	cyclin-depe
chr16q23.3-	79246376	chr16	98.92	78198123	+	EC:1.1.1.-		WW domai
chr17q21.3	44439068	chr17	48.68	44376504	-		ENSG0000	ADP-ribosy
chr12q13	52453285	chr12	93.63	52445248	+			nuclear rece
chr1q23	159277991	chr1	93.1	159272125	+		ENSG0000	Fc fragment
chr12p12.1-	28123001	chr12	79	28115262	-		ENSG0000	parathyroid
chr7p13-p1	45960871	chr7	95.26	45951844	-		ENSG0000	insulin-like

chr9q34.2-	139876193	chr9	81.04	139871956	+	EC:5.3.99.2	ENSG0000	prostagland
chr16q22.1	70557448	chr16	96.73	70514471	-		ENSG0000	component
chrXq28	148563243	chrX	66.83	148560299	-	EC:3.1.6.13	ENSG0000	iduronate 2-
chr16q21	57495179	chr16	93.52	57481386	+		ENSG0000	coenzyme
chr3p21.31	47517412	chr3	98.2	47455199	-		ENSG0000	SREBF cha
chr8q13.1	70573147	chr8	98.84	70414108	+		ENSG0000	sulfatase 1
chr8q13.1	70573147	chr8	98.84	70414108	+		ENSG0000	sulfatase 1
chr22q13.2	42017004	chr22	91.38	41993896	-		ENSG0000	PPPDE pep
chr12q13.3	57472516	chr12	98.27	57449425	-		ENSG0000	transmembr
chr6q23-q2	143158184	chr6	99.15	143072605	-		ENSG0000	human imm
chr2q23.3	151344168	chr2	97.13	151324711	-		ENSG0000	Rho family
chr14q32	101313845	chr14	85.19	101292456	+		ENSG0000	maternally
chr10q26.1	126525236	chr10	98.56	126490384	+		ENSG0000	family with
chr11q23.1	113148620	chr11	94.51	113103514	+	EC:2.7.11.1	ENSG0000	neural cell
chr9q21.12	72969786	chr9	93.08	72873939	+		ENSG0000	structural m
chr8p11.2-	48650235	chr8	96.86	48648641	-		ENSG0000	CCAAT/en
chr15q26.1	89860954	chr15	97.61	89836171	+		ENSG0000	Fanconi ane
chr3q26.31	171177852	chr3	97.85	170779129	-	EC:2.7.11.1	ENSG0000	TRAF2 and
chr12p13.1	13236383	chr12	91.67	13214546	+		ENSG0000	KIAA1467
chr9p23	13126725	chr9	97.75	13105705	-		ENSG0000	multiple PD
chr8q24	141536259	chr8	96.21	141532461	-			Eukaryotic
chr12p	6573150	chr12	96.51	6571405	-		ENSG0000	vesicle-asso
chr22q13.1	39774386	chr22	77.12	39760174	+		ENSG0000	synaptogyri
chr16q12.2	53721867	chr16	99.91	53634599	-		ENSG0000	RPGRIP1-
chr9q33	124074770	chr9	90.1	124030345	+		ENSG0000	gelsolin
chr1q42.1	241663891	chr1	73.33	241660856	-	EC:4.2.1.2	ENSG0000	fumarate hy
chr6q26	163736346	chr6	98.1	163483318	+		ENSG0000	PARK2 co-
chr1p33-p3	31845923	chr1	98.66	31838306	-			fatty acid bi
chr8q24.1	120436678	chr8	93.44	120435196	+			nephroblast
chrXq23	110464176	chrX	95.73	110339599	+	EC:2.7.11.1	ENSG0000	p21 protein
chr17p13.3	1619494	chr17	66.75	1615082	-		ENSG0000	chromosom
chr5p12	43175821	chr5	94.73	43121657	+		ENSG0000	zinc finger
chr17p13	7479502	chr17	79.05	7478063	+	EC:3.6.4.13		Eukaryotic
chr22q11.2	25758524	chr22	97.31	25747311	-		ENSG0000	low density
chr13q33	102371131	chr13	84.95	102359118	+		ENSG0000	integrin, bet
chr10q24	99436321	chr10	85.21	99433856	+	EC:2.7.1.67	ENSG0000	phosphatidy
chr3p26.2	9829941	chr3	81.42	9821650	+	EC:4.2.99.1	ENSG0000	8-oxoguani
	29753202	chr10	89.63	29751873	+			
chr11p15.5	3847580	chr11	93.3	3842564	+		ENSG0000	post-GPI at
	130757545	chr7	43.78	130756033	-			
	139926260	chr5	43.65	139923854	+			
chr21q21.1	18967321	chr21	82.6	18963578	+			BTG family
chr1p31	68513384	chr1	100	68511823	-		ENSG0000	DIRAS fam
chr15q24	77197744	chr15	94.29	76672023	-		ENSG0000	S-phase cyc
chr7q31.1	111928974	chr7	49.71	111846756	+		ENSG0000	zinc finger

	89282776	chr1	29.71	89280812	+			
	20471983	chr2	66.26	20469816	-			
0	68489688	chr15	83.56	68486740	-			
chr2q22-q2	157189041	chr2	97.76	157180968	-		ENSG0000	nuclear rece
chr16q13-q	57507849	chr16	98.64	57496596	+	EC:2.7.7.6	ENSG0000	polymerase
	99921411	chrX	71.35	99919228	-			
,ENST0000	25451945	chr1	100	25451543	-		ENSG00000233419	
chr17q11.2	32584176	chr17	97.58	32582337	+		ENSG0000	chemokine
	45908427	chr2	81.61	45905419	+			
chr9q22	102596341	chr9	88.02	102584178	+		ENSG0000	nuclear rece
chr16p12.3	14990014	chr16	90.17	14973914	+		ENSG0000	NODAL mo
chr6p21.3 /	29977148	chr6	99.55	29974373	+		ENSG0000	major histo
chr13q14.1	42017480	chr13	62.66	42016914	+		ENSG0000	olfactory re
chr3q12.3	101544770	chr3	66.28	101542975	+		ENSG0000	family with
	170077386	chr3	50	170076805	+			
chr1q21	153508503	chr1	99.36	153507075	-		ENSG0000	S100 calciu
chr20q13.3	56285616	chr20	93.16	56226835	-		ENSG0000	prostate tra
chr12q15	76425681	chr12	82.86	76420598	-		ENSG0000	pleckstrin h
chr12q15	76425681	chr12	82.86	76420598	-		ENSG0000	pleckstrin h
chr3p21.31	45017657	chr3	96.71	44966337	-		ENSG0000	zinc finger,
chr19p13.2	10370715	chr19	98.31	10362679	+		ENSG0000	mitochondr
chr11p14-p	27494293	chr11	97.89	27387509	-		ENSG0000	leucine-rich
chr7q11.21	66704500	chr7	99.55	66461824	+		ENSG0000	tRNA-yW s
chr16p13.3	3072381	chr16	96.69	3070359	+		ENSG0000	tumor necro
chr17p13.2	5404305	chr17	91.42	5402747	-		ENSG0000	hypothetica
chr1q41	220872493	chr1	96.88	220863707	+		ENSG0000	chromosom
chr9q34.11	131592100	chr9	84.03	131581931	-		ENSG0000	chromosom
chr3p21.3	50622258	chr3	83.02	50608358	+		ENSG0000	HemK meth
chr1p34.3	38272890	chr1	80.11	38268616	-		ENSG0000	yrdC domai
chr2p13.3	71913892	chr2	99.15	71680759	+		ENSG0000	dysferlin, li
chr1p35.3	28294604	chr1	95.5	28293248	+			XK, Kell bl
chr11q12.2	60704630	chr11	97.21	60691945	+		ENSG0000	transmembr
chr17q21.3	48552192	chr17	95.37	48503612	+	EC:6.2.1.-	ENSG0000	acyl-CoA sy
chr2p11.2	76288057	chr10	90.19	76287339	+		ENSG0000	mitochondr
chr14q21.3	50583297	chr14	99.72	50575355	-			chromosom
chr17p13.3	695738	chr17	100	685592	+	EC:2.1.1.-	ENSG0000	RNA methy
chr11p15.4	10562734	chr11	97.01	10536289	-		ENSG0000	ring finger
chr17q22	53800142	chr17	99.94	53796989	-		ENSG0000	transmembr
chr7q36.1	150271040	chr7	96.37	150264495	+		ENSG0000	GTPase, IM
chrXq24	117583921	chrX	99.96	117530980	+		ENSG0000	WD repeat
chr4q22.1	89364248	chr4	72.49	89345027	+		ENSG0000	hect domain
chr19p13.1	16438337	chr19	84.34	16435650	+		ENSG0000	Kruppel-lik
chr17q21.3	48438512	chr17	98.49	48423392	+	EC:2.4.2.26	ENSG0000	xylosyltrans
chr3q21.1	122134610	chr3	82.49	122132874	-		ENSG0000	WD repeat
chr7q21.2	92732549	chr7	85.39	92729164	-		ENSG0000	sterile alpha

chr11q13.2-	68517895	chr11	96.63	68474912	-		ENSG0000	metallothio
chr2p14	64685792	chr2	95.63	64681661	+		ENSG0000	galectin-rel
chr22q13.2	41323596	chr22	88.97	41253101	+	EC:3.4.11.9	ENSG0000	X-prolyl am
chr19q13.3	49232338	chr19	97.19	49223842	-		ENSG0000	Ras interact
chr3q25.31	156877936	chr3	98.46	156865590	-		ENSG0000	cyclin L1
chr10q26	124768311	chr10	93.11	124753198	-		ENSG0000	IKAROS fa
chr17q21.3	46200105	chr17	98.89	46184946	+		ENSG0000	sorting nexi
chr7p15.3	23165662	chr7	75.73	23145487	+		ENSG0000	kelch-like 7
chr18q11.2	19088676	chr18	99.79	19031059	+		ENSG0000	growth regu
chr8q22.1	95449132	chr8	100	95444174	-		ENSG0000	RAD54 hon
chr11q13.1-	66012215	chr11	99.94	65998346	+		ENSG0000	phosphofuri
chrXp11.3	44202911	chrX	98.87	44007962	-		ENSG0000	EF-hand do
	46852137	chr2	47.58	46844408	-			
chr11q14	93545571	chr11	98.54	93517467	+		ENSG0000	mediator co
chr10q22.3	79397291	chr10	96.26	78644637	-		ENSG0000	potassium l
chr10q21.3	64967801	chr10	98.77	64926980	-		ENSG0000	jumonji dor
chr16p12.3	16388657	chr16	65.07	16386034	+		ENSG0000	NODAL mo
chr6p21.3	29694301	chr6	91.49	29693711	+		ENSG0000	major histo
chr19q13	50498177	chr19	60.06	50484889	-	EC:2.7.11.1	ENSG0000	vaccinia rel
chr20pter-p	4709106	chr20	78.5	4705143	+		ENSG0000	prion protei
chr1p36.13-	212208862	chr1	91.54	212114697	-		ENSG0000	integrator c
	40183124	chr21	85.21	40182385	+			
	24710415	chr6	55.49	24710112	-			hypothetica
chr17q25.1	73132211	chr17	99.77	73131345	-		ENSG0000	hematologic
chr6pter-p2	38122397	chr6	96.94	37787632	+		ENSG0000	zinc finger,
chr11p15.1	20143145	chr11	96.77	20077248	+	EC:3.6.4.12	ENSG0000	neuron navi
chrXp22.2	14048011	chrX	89.6	14026398	-		ENSG0000	gem (nucle
chr1p13.2	114456706	chr1	84.45	114447978	+		ENSG0000	DNA cross-
chr15q21.1-	52201287	chr15	99.56	52121863	+		ENSG0000	tropomodul
chr5p15.1	14871781	chr5	89.53	14708956	-		ENSG0000	ankylosis, p
chr1q25	184598153	chr1	90.67	184356209	+		ENSG0000	chromosom
chr3p12-q1	101579865	chr3	90.49	101568424	+		ENSG0000	nuclear fact
chr6q27	169068671	chr6	99.86	168842030	+		ENSG0000	SPARC rela
chr1q32.1	206762606	chr1	98.54	206680878	+		ENSG0000	Ras associa
chr19q12	31770175	chr19	97.44	31765852	-		ENSG0000	teashirt zinc
chr14q24.3	77494366	chr14	87.13	77490885	-		ENSG0000	chromosom
chrXp11.4	39956656	chrX	99.56	39911070	-		ENSG0000	BCL6 corep
chr7p14.3	32919284	chr7	97.16	32909698	-		ENSG0000	kelch repea
chr19p13.1	18385235	chr19	99.68	18367908	-		ENSG0000	KIAA1683
chr2q12.2	106694608	chr2	99.87	106682112	+		ENSG0000	chromosom
chr1q21.3	151032050	chr1	89.74	151024589	-		ENSG0000	CDC42 sma
chr1p31.3	62629174	chr1	95.79	62274144	+		ENSG0000	InaD-like (I
	34188019	chr9	56.19	34186266	+			hypothetica
chr7p15.1	30796290	chr7	43.18	30791750	+	EC:2.1.1.49	ENSG0000	indolethyla
chr17p13.1	8079673	chr17	86.72	8076559	-		ENSG0000	transmembr

chr11p15	10715161	chr11	99.69	10597870	-		ENSG0000	murine retr
chr12q13.1	46581581	chr12	90.92	46576837	-		ENSG0000	solute carri
chr20q13.3	62567368	chr20	95.18	62559692	+		ENSG0000	DnaJ (Hsp4
chr1q32.1	204381191	chr1	92.99	204372514	-		ENSG0000	protein pho
chr17q23.2	54968522	chr17	74.47	54965311	-	EC:6.3.2.19	ENSG0000	tripartite m
chr20p12.3	5591664	chr20	87.2	5410779	-		ENSG0000	glycerophos
chr11p11.2	43516481	chr11	98.24	43425652	+		ENSG0000	tetratricope
chr20p11.2	25004277	chr20	98.47	24986872	-	EC:6.2.1.1	ENSG0000	acyl-CoA s
chr9q33.2	119164153	chr9	88.82	119160611	+	EC:3.4.24.7	ENSG0000	pregnancy-
chr11p15.5	2017653	chr11	83.78	2016405	-		ENSG0000	H19, impri
chr18p11.2	12546905	chr18	92.38	12446299	-		ENSG0000	spire homol
chr6q27|Xq	170109463	chr6	97.65	170107131	-		ENSG0000	PHD finger
chr7p15	26231735	chr7	98.18	26229269	-		ENSG0000	heterogene
chr12q13.1	53473175	chr12	96.37	53458100	-	EC:2.7.1.11	ENSG0000	SPRY dom
chr12q24.1	110972991	chr12	99.81	110970884	-	EC:3.1.3.16		PTC7 prote
chr4q26	119200978	chr4	82.87	119199911	+		ENSG0000	small nucle
chr11q23.3	119178857	chr11	93.5	119175481	+		ENSG0000	Cas-Br-M (
	124513595	chr8	95.72	124510128	-		ENSG00000156804	
chr1p36.11	24294965	chr1	82.37	24290836	-		ENSG0000	serine/argin
chr9p13.3	34612053	chr9	92.93	34610492	-		ENSG0000	chromosom
chr3q21.1	122294047	chr3	68.46	122292847	+		ENSG0000	deltex 3-lik
chr21q22.2	40670456	chr21	88.72	40668364	-		ENSG0000	bromodoma
chr3p22	39185062	chr3	96.51	39183345	-		ENSG0000	cysteine-se
chr3p25.3	9427389	chr3	86.36	9404735	+		ENSG0000	THUMP do
chr20p11.1	26190500	chr20	56.13	26189271	-		ENSG0000	hypothetica
chr12q24	110011327	chr12	95	109994385	-	EC:2.5.1.17	ENSG0000	methylmalo
chr1p13.3	109203691	chr1	98.26	109190918	-		ENSG0000	chromosom
chr7q21	89866997	chr7	87.09	89864222	+		ENSG0000	six transme
chr17q25.3	78369112	chr17	96.9	78337500	+		ENSG0000	ring finger
chr8q21.3	91637416	chr8	98.01	91634227	-		ENSG0000	transmemb
chr7p22.3	1582677	chr7	97.48	1581091	+		ENSG0000	v-maf musc
chr12q21.1	72183975	chr12	99.09	72181999	+			RAB21, me
chrXq21	101142053	chrX	89.53	101137262	-		ENSG0000	zinc finger,
chr10p12.3	18970568	chr10	96.84	18967034	+		ENSG0000	ADP-ribosy
chr12p11	393179	chr12	92.48	389222	-		ENSG0000	lysine (K)-s
chr13q13-q	45607742	chr13	89.16	45563670	+		ENSG0000	KIAA1704
chr16p13.1	11445617	chr16	85.68	11439305	+		ENSG0000	chromosom
	46461495	chrX	95.81	46458686	-			
chr2q36.3	228425930	chr2	97.41	228424577	+			ArfGAP wi
chr7p22.3	1199777	chr7	97.16	1192542	-		ENSG0000	zinc finger,
chr17p11.2	21145139	chr17	76.07	21142182	-		ENSG0000	chromosom
chr16p13.3	1878275	chr16	78.13	1876971	+	EC:3.-.-.-	ENSG0000	fumarylacet
chr8q23.1	110358181	chr8	60.03	110355877	+		ENSG0000	enhancer of
chr10q26.3	127702777	chr10	97.31	127700959	-		ENSG0000	ADAM met
chr22q13.1	38693117	chr22	66.42	38692211	-	EC:2.7.11.1	ENSG0000	casein kina

chr2p25.3	42283	chr2	91.94	38813	-		ENSG0000	family with
chr2p13	69548588	chr2	79.52	69546913	-	EC:2.6.1.16		glutamine--
chr6p22-p2	19840057	chr6	93.03	19839443	-			Inhibitor of
chr2q31.1	169721565	chr2	97.02	169659127	+		ENSG0000	nitric oxide
	123391038	chr7	77.82	123389101	+			
chr2q14.3	128059252	chr2	95.06	128057965	-	EC:2.7.11.2	ENSG0000	hypothetica
chr22q11.2	19435605	chr22	89.41	19430372	-			chromosom
chr11p11.2	43965428	chr11	90.14	43964591	+			chromosom
chr2q14.2	120196080	chr2	93.01	120194863	+		ENSG0000	transmembr
chr10q22.2	77158910	chr10	91.02	77157915	-		ENSG0000	zinc finger
chr1p36.33	1431581	chr1	90.43	1431014	+		ENSG0000	ATPase fan
chr16p11.2	30614583	chr16	92.52	30613878	-		ENSG0000	zinc finger
chr21p11.2	9968580	chr21	91.97	9907192	-		ENSG0000	hypothetica
chr5q15	98131617	chr5	92.16	98128564	+		ENSG0000	RGM doma
chrXq22.1	100750794	chrX	84.86	100749345	+		ENSG0000	armadillo re
chr10q21.2	61413729	chr10	87.07	61410522	-		ENSG0000	solute carrie
chr6q24-q2	151679671	chr6	83.78	151678864	+		ENSG0000	A kinase (P
chr6q24-q2	151679671	chr6	83.78	151678864	+		ENSG0000	A kinase (P
chr22q13.3	46641045	chr22	95.12	46639910	-		ENSG0000	chromosom
chr17q25.3	76353327	chr17	88.84	76352858	-		ENSG0000	suppressor
chr1p33	47516422	chr1	72.54	47515862	+	EC:1.14.14.	ENSG0000	cytochrome
chr6q24.1	139562797	chr6	94.74	139561200	-		ENSG0000	taxilin beta
chr8q12.1	56685937	chr8	84.07	56674759	-		ENSG0000	transmembr
chr2p15	61372085	chr2	41.15	61368731	-			hypothetica
	149818282	chr1	44.74	149816569	+			
chr11p15.5	767695	chr11	71.49	767227	-		ENSG0000	Parkinson d
chrXq22.3	105202601	chrX	97.99	105201774	+	EC:2.7.11.1	ENSG0000	Nik related
chr10p11.2	35468775	chr10	98.18	35415925	+		ENSG0000	cAMP respo
chr6p23-p2	16147098	chr6	98.72	16146020	+	EC:6.3.2.-	ENSG0000	myosin regu
chr3q26.1	160796692	chr3	98.95	160795658	+	EC:3.1.3.16	ENSG0000	protein pho
	51909547	chr12	89.82	51905763	+			
chrXq26.3	133680662	chrX	91.68	133677366	-		ENSG0000	hypothetica
chr14q32.3	104519002	chr14	97.97	104498392	+	EC:3.6.4.13	ENSG0000	tudor domai
chr8q11.21	48648698	chr8	96.35	48648195	-			KIAA0146
	27191883	chr12	31.6	27190794	+			
chr3q26.1	160793799	chr3	99.13	160792420	+	EC:3.1.3.16	ENSG0000	protein pho
	119055863	chrX	93.19	119054634	-		ENSG0000	hypothetica
	226029044	chr1	39.22	226028250	-		ENSG00000242861	
chr17q11-q	40704911	chr17	72.04	40704454	-	EC:1.1.1.62		hydroxyster
chr17p13.1	6678966	chr17	30.51	6678427	+		ENSG0000	XIAP assoc
chr7q31.31	120937498	chr7	97.31	120911340	+		ENSG0000	chromosom
	106549381	chr11	95.8	106545662	-			
	121385811	chr8	89.64	121385108	+			
chr12q13	54020178	chr12	94.96	53936673	-			activating tr
chr6p21.3	30509925	chr6	46.77	30509153	-		ENSG0000	guanine nuc

chr19p13.2	11508238	chr19	79.77	11504735	-		ENSG0000	ral guanine
chr12q13.1	51902975	chr12	72.52	51901761	+		ENSG0000	solute carrie
chr6q21	106557809	chr6	95.34	106557173	+		ENSG0000	PR domain
chr13q13-q	45606398	chr13	96.57	45605920	+		ENSG0000	KIAA1704
chr3q29	197633698	chr3	26.59	197632928	-			IQ motif co
chr10q22.2	75037079	chr10	96.94	75013519	-		ENSG0000	tetratricope
chr6q22.1	117056803	chr6	92.52	117056036	+		ENSG0000	karyopherin
chr6p21.1	42025524	chr6	81.26	42018261	+		ENSG0000	TAF8 RNA
chr7p15.3	25158886	chr7	79.77	25158274	-			cytochrome
	42080916	chr4	81.6	42069150	+		ENSG00000014824	
	128413476	chr7	87.11	128412580	+			
chr11p15.1	18628767	chr11	63	18627947	-		ENSG0000	SPT2, Supp
chr21p11.2	9966378	chr21	93.85	9907188	-		ENSG0000	hypothetica
chr3q28	189038850	chr3	95.9	188956610	+		ENSG0000	tumor prote
chrXq12-q1	71799128	chrX	93.94	71798663	-	EC:2.7.11.1	ENSG0000	phosphoryla
chr9q21.32	85860466	chr9	81.69	85859536	-		ENSG0000	FERM dom
chr20q13.1	47905793	chr20	83.27	47905018	+			non-protein
chr14q32.1	94569055	chr14	98.02	94568560	+			interferon,
chr11p15	10597872	chr11	97.41	10597306	-		ENSG0000	murine retro
chr9p24.1	14083478	chr9	89.98	14083024	+			Nuclear fac
chr5q23.2	122523696	chr5	91.66	122424812	+	EC:2.1.1.43	ENSG0000	PR domain
chr5q23.2	126387588	chr5	97.36	126386997	-			glutaredoxi
	14915925	chr12	35.63	14915434	-			
chr1p31.3	65695219	chr1	20.78	65694769	+	EC:2.7.4.3	ENSG0000	adenylate ki
	131681562	chr5	51.52	131680830	-			
	97539100	chr2	75.8	97538107	+			
	43724498	chr21	90.22	43724008	+			
chr20q11.1	31071213	chr20	62.73	31052583	-		ENSG0000	chromosom
chr13q13	36343672	chr13	99.44	36342788	-	EC:2.7.11.1	ENSG0000	doublecorti
	19042039	chr7	97.21	19041411	+			
chr19q13.4	52105044	chr19	87.32	52097860	+		ENSG0000	putative AT
chr6q24-q2	151679337	chr6	96.33	151678865	-			A kinase (P
chr7q21.1	86989370	chr7	86.24	86988899	+	EC:2.3.1.13	ENSG0000	carnitine O-
chr2q31.2	179328873	chr2	93.47	179328392	-	EC:5.2.1.8	ENSG0000	FK506 bind
	43919917	chr1	89.57	43919455	+		ENSG00000229348	
	NA		NA	NA				
chr15q15.2	43037412	chr15	98.53	43036808	+	EC:2.7.11.1		Tau tubulin
chr1p36.32	2522906	chr1	85.3	2520032	+		ENSG0000	chromosom
chr5q34	167691161	chr5	98.22	167626067	+		ENSG0000	odz, odd Oz
chr10q22.1	72328205	chr10	94.73	72289668	+		ENSG0000	KIAA1274
chr4q21.22	83417303	chr4	85.32	83404959	-			transmembr
chr17q24.3	65956490	chr17	95.82	65908074	+			bromodoma
chr16q24.3	89350150	chr16	96.56	89348386	-		ENSG0000	ankyrin rep
chr9q13-q2	71863975	chr9	98.78	71862092	+		ENSG0000	tight junctio
chr16p12.2	24566259	chr16	99.28	24564313	+			retinoblasto

chr2q24.1	158171038	chr2	73.79	158168818	+	EC:2.4.1.41	ENSG0000	UDP-N-ace
chrXp11.23	49863886	chrX	100	49857619	+		ENSG0000	chloride cha
chr14q32.2	100771757	chr14	78.13	100768716	-			Solute carri
	13054730	chr12	63.16	13052678	+			
chr13q31.3	92006831	chr13	87.68	92004088	+		ENSG0000	MIR17 host
chr6q23.3	135812288	chr6	69.14	135811597	-			Abelson hel
	171891446	chr3	90.98	171889804	+			
	33114650	chr11	66.89	33112412	+			
	155163338	chr6	52.57	155162159	+			
chr1p36.12	22031108	chr1	54.1	22012547	-	EC:3.4.19.1	ENSG0000	ubiquitin sp
chr9p13	34649339	chr9	83.92	34646702	+	EC:2.7.7.12	ENSG0000	galactose-1-
chr3q27.1	184060910	chr3	58.56	184057246	+			family with
chr12q12	42852181	chr12	70.54	42850558	-			Prickle hom
chr5q31	132228812	chr5	80.06	132227508	-		ENSG0000	AF4/FMR2
chr2p16.1	61194583	chr2	95.88	61192810	-			Pseudourid
chr2q35	219211512	chr2	81.85	219135269	+		ENSG0000	paroxysmal
chr11q14.1	77705699	chr11	62.57	77688952	-			integrator c
	11220085	chr6	91.11	11218595	-			
chr12q14.2-	65090664	chr12	95.64	65089970	+			Similar to n
chr7p21.3	12273303	chr7	98.21	12271073	-			transmembr
	62297569	chr2	44.14	62295757	+			
	29329576	chr21	95.56	29327484	-			
chr13q32.1	96547502	chr13	81.18	96529155	-		ENSG0000	UDP-gluco
chr20p12.3	5931123	chr20	100	5918509	-		ENSG0000	tRNA meth
	98303174	chr3	76.59	98301393	-			
	61866296	chr3	49.19	61863581	+			
	137991886	chrX	66.37	137990570	-			
	33790905	chr20	8.5	33789549	-			
chr5q31.1	133747586	chr5	62.76	133737837	-		ENSG0000	CDKN2A i
chr4q27	122749350	chr4	83.33	122745595	-		ENSG0000	Bardet-Bie
chr14q32	101316565	chr14	82.56	101315424	+			maternally
	18967449	chr17	52.78	18966936	-			
chr9q32	116061145	chr9	97.71	116059373	-		ENSG0000	ring finger
chr1p22.2	89648115	chr1	28.95	89646846	-		ENSG0000	guanylate b
chr15q22.2	60771344	chr15	97.12	60747527	-		ENSG0000	NMDA rec
	79837343	chr17	30.43	79836305	-			
chr11q23	118035290	chr11	97.73	118033524	-			sodium cha
chr6q22.31	125404865	chr6	98.83	125404019	+		ENSG0000	ring finger
chr7p14.3	30932001	chr7	97.77	30895057	+		ENSG0000	family with
	95243547	chr5	82.8	95243000	-			
	96914832	chr2	93.36	96914252	-			
	40516556	chr17	85.76	40515649	-			
chr17q11-q	27077976	chr17	75.58	27077517	+		ENSG0000	TNF recept
chr7q32.1	129152757	chr7	97.79	129142625	+		ENSG0000	hypothetica
	157185685	chr2	93.62	157185089	-			

chr12q14.3	66741723	chr12	85.78	66741105	-		ENSG0000	glutamate r
chr19p12	23541207	chr19	70.52	23540495	-		ENSG0000	zinc finger
chr1p36.13	16932373	chr1	17.84	16931911	-		ENSG0000	neuroblasto
	111711030	chr1	50.81	111710435	+			
chr3p25.1	16269450	chr3	99.73	16264117	+	EC:2.4.1.41	ENSG0000	UDP-N-ace
	122529959	chr5	97.35	122529482	+			
chr1p22.1	93672689	chr1	99.65	93646315	+		ENSG0000	coiled-coil
	143258435	chr6	77.54	143257980	-			
	101732108	chr8	100	101731630	-			
chr3q26.2	169514584	chr3	97.59	169511266	-		ENSG0000	leucine rich
	27739723	chr13	83.9	27739206	-			
	120296469	chr11	50.42	120295999	+			
	158724628	chr2	39.05	158724154	-			
	16193822	chr19	21.74	16193045	+			
	54312205	chr2	17.41	54311734	+		ENSG0000	hypothetica
	171559804	chr5	90.81	171559356	-			
chr1q21.1	145294875	chr1	50.79	145294450	+			neuroblasto
	137655552	chr7	100	137655093	-			
chr4q21.3	85929905	chr4	95.19	85929323	+		ENSG0000	non-protein
	56957120	chr1	35.56	56956665	-			
chrXq25	125683810	chrX	60.26	125683367	-		ENSG0000	DDB1 and
	34482637	chr11	47.17	34482018	-			
chr17q12	33594754	chr17	76.24	33593350	+		ENSG0000	schlafen fa
chr5q31.1	131817793	chr5	59.14	131817301	-		ENSG0000	interferon r
chr9p13	33166102	chr9	69.41	33165098	-	EC:2.4.1.22 /// EC:2.4.1		UDP-Gal:b
chr1q21.1	147903295	chr1	46.04	147902030	-			Hypothetica
	NA		NA	NA				
chr17p11.2	19065586	chr17	67.79	19064719	+			GRB2-relat
chr15q15.3-	44821235	chr15	64.44	44820648	+	EC:3.1.3.-	ENSG0000	CTD (carbo
chr5q31.1	133724461	chr5	83.68	133723826	+	EC:6.3.2.19	ENSG0000	ubiquitin-c
chr17q24.2	67020496	chr17	96.26	67016551	-		ENSG0000	ATP-bindin
chrXp22.33	2526946	chrY	97.09	2526365	+			Non-protei
	72184540	chr12	98.64	72183816	+			hypothetica
chr11p13	27677009	chr11	67.07	27676443	-		ENSG0000	brain-derive
	158708869	chr5	98.16	158708389	+			
chr15q15.3	43641612	chr15	73.61	43641174	+	EC:3.5.4.-	ENSG0000	adenosine d
chr19p13.3	2857692	chr19	74.34	2857287	+		ENSG0000	zinc finger
	88121874	chr5	97.47	88121096	-			
	19532553	chr1	100	19532145	-			
chr3q13.33	121143607	chr3	95.11	121143257	+		ENSG0000	syntaxin bi
	19774031	chr18	100	19773571	+			
chr7q34	140422041	chr7	100	140421414	+	EC:1.6.5.3 /	ENSG0000	NADH deh
	58506332	chr15	46.83	58505739	-			
	NA		NA	NA				
	150802212	chr7	69.5	150801896	+			

chr3q26.3	182657904	chr3	69.09	182657547	-	ENSG0000	DCN1, defe
chr3p24.2	23965864	chr3	52.63	23965394	+		Ribosomal
	31122846	chr17	48.66	31122446	-		
	148599875	chr4	50.41	148599392	-		
	40984740	chr5	98.26	40984287	+		
chr17q25.3	78252709	chr17	96.25	78237367	+	ENSG0000	ring finger
chr7p22.1	5107657	chr7	7.73	5106904	+	ENSG0000	RB-associat
chrXp11.3	45008608	chrX	94	45007962	-	ENSG0000	chromosom
	59375342	chr15	49.69	59374875	+		
	56762629	chr16	55.35	56762214	-		
	55336415	chr18	90.38	55335983	+		hypothetica
	150545335	chr1	46.36	150544803	-		
	113702596	chr9	97.34	113702193	-		
	65018968	chr16	66.49	65018599	-		
chr2p22.3	33814386	chr2	97.84	33813979	-	ENSG0000	family with
chr12q13	60175738	chr12	95.3	60175118	+	ENSG0000	solute carrie
chr2q37.1	232318987	chr2	84.72	232318241	-	ENSG0000	nucleolin
	153353922	chrX	88.66	153353204	-	ENSG00000169057	
chr6q21	107116287	chr6	68.36	107115667	+	ENSG0000	glutaminyl-
	146115166	chr6	86.78	146114638	-		
	37493673	chr19	40.13	37493217	+		
	22822384	chr12	79.1	22821383	+		
chr2p14-p1	66793942	chr2	96.92	66793373	+		Meis home
	26098247	chr12	32.39	26097788	-	ENSG00000246695	
	69522488	chr3	92.29	69522104	-		
	41255898	chr3	78.7	41255048	+		
chr2p25.2	7038125	chr2	48.07	7037593	+	ENSG0000	radical S-ad
	38602563	chr17	61.15	38601923	+		
chr4q31.21	146579848	chr4	52.66	146579196	+	ENSG0000	methylmalo
	93596393	chr7	36.91	93595929	-		
	118648440	chr5	55.99	118648067	+		
	141611493	chr3	34.04	141610954	+		
	46529871	chr2	98.5	46529345	+		
	239190887	chr2	8.93	239190150	-		
5	29940977	chr8	67.02	29940609	+		
	31848333	chr22	81.3	31847666	-		
	103727459	chr4	39.54	103726644	-		
	28013310	chr13	37.67	28012646	-		
	133785112	chr10	100	133784705	+		
	30081784	chr15	55.68	30081329	-		
	155435081	chr7	60.65	155434466	-		
chr7q11.22	69755772	chr7	98.92	69364394	+	ENSG0000	autism susc
	NA		NA	NA			
	NA		NA	NA			
	23628744	chr1	82.23	23627868	-		

	15854047	chrX	57.06	15853726	-			
chr21q22.3	46396887	chr21	91.36	46359958	+		ENSG0000	chromosom
chr3p14.3	57330943	chr3	99.6	57327727	-		ENSG0000	dynein, axo
	50971407	chr22	44.81	50970993	+			
chr10q11.2	51742294	chr10	97.34	51741817	+		ENSG0000	ArfGAP wi
chr14q31.1	80963270	chr14	98.9	80962820	-		ENSG0000	chromosom
chrXq13.3	73953749	chrX	94.74	73953405	-		ENSG0000	KIAA2022
	74237090	chr14	89.83	74236628	-			
	103665220	chr8	96.53	103664718	-			
chrXq13-q2	73833964	chrX	98.77	73833483	-			Ring finger
	231467581	chr1	34.91	231466911	-			
chr7p15.3	25159646	chr7	66.97	25159210	-			cytochrome
chr11p13	32998843	chr11	99.45	32998112	+		ENSG0000	glutamine a
chr2q33.1	201237993	chr2	35.6	201237424	+			Spermatoge
chr7p13-p1	45008968	chr7	45.76	45008118	-		ENSG0000	myosin IG
chr2q23.1	149274261	chr2	98.47	149273549	+		ENSG0000	methyl-Cp
chr3p21.31	48509044	chr3	95	48507344	+	EC:3.1.11.2	ENSG0000	three prime
chr12q24	110035068	chr12	68.55	110013872	+	EC:2.7.1.36	ENSG0000	mevalonate
chr19q13.2	49379315	chr19	96.47	49375697	+		ENSG0000	protein pho
chr12p13.3	1011148	chr12	91.96	989373	+	EC:2.7.11.1		WNK lysin
chr22q13	45133561	chr22	76.37	45133086	+		ENSG0000	proline rich

GeneChip_	Genome_V	GO.Avadis.	InterPro	OMIM	Pathway	RefSeq_Pro	RefSeq_Tra	Representat
Human Ger	February 2	GO:0000122|GO:00063		164873		NP_001138	NM_00114	NM_00524
Human Ger	February 2	GO:0005739|GO:00167		608440		NP_116246	NM_03285	NM_17184
Human Ger	February 2	GO:0000188|GO:00064		611437		NP_001135	NM_00114	BC035000
Human Ger	February 2	GO:0005622|GO:00058		300480		NP_690000	NM_15278	NM_15278
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_116287	NM_03289	AY099509
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_001161	NM_00116	NM_15252
Human Ger	February 2	GO:0006020|GO:00068		600444		NP_008864	NM_00693	NM_00693
Human Ger	February 2	GO:0021955|GO:00301		612790		NP_001073	NM_00108	BC012946
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_653175	NM_14457	BC030654
Human Ger	February 2009 (Genome Reference			609717			NR_02655	BC020934
Human Ger	February 2	GO:0000184|GO:00063		605313		NP_005096	NM_00510	BC017770
Human Ger	February 2	GO:0006622|GO:00071		608880		NP_001098	NM_00110	BC032227
Human Ger	February 2	GO:0001541|GO:00066		148180		NP_002000	NM_00200	AF523265
Human Ger	February 2	GO:0001516|GO:00015		600262	Eicosanoid_	NP_000954	NM_00096	AY151286
Human Ger	February 2	GO:0001932|GO:00061		252010 /// 2	Electron_T	NP_002486	NM_00249	AB062482
Human Ger	February 2	GO:0004721|GO:0016787|GO:0016791				NP_057480	NM_01639	BC035744
Human Ger	February 2	GO:0006260|GO:00062		605650		NP_057302	NM_01621	BC014955
Human Ger	February 2	GO:0001569|GO:00072		606077		NP_073605	NM_02276	AF364037
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_03651	BU617052
Human Ger	February 2	GO:0007165|GO:00071		604388	Calcium_re	NP_001092	NM_00109	BM666010
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_00215	BC040701
Human Ger	February 2	GO:0006928|GO:00444		193060		NP_003371	NM_00338	AI520969
Human Ger	February 2	GO:0006486|GO:0000139|GO:0005794|GO:001				NP_660279	NM_14523	CA503291
Human Ger	February 2	GO:0006350|GO:00063		613484		NP_055816	NM_01500	BM992098
Human Ger	February 2	GO:0006887|GO:0007268|GO:0023034|GO:000				NP_001074	NM_00108	AL834407
Human Ger	February 2	GO:0006260|GO:00063		164060		NP_004528	NM_00453	AK021751
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BQ028191
Human Ger	February 2	GO:0005634|GO:00057		609723		NP_001005	NM_00100	AK097253
Human Ger	February 2	GO:0005515		609080		NP_001104	NM_00111	AK021560
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AB053312
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AF085839
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AW418647
Human Ger	February 2	GO:0007155|GO:00071		604234		NP_004782	NM_00479	AI753143
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI085450
Human Ger	February 2	GO:0006350|GO:00063		604073		NP_003423	NM_00343	AL832081
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AW104813
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL831884
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BM977131
Human Ger	February 2	GO:0006464|GO:0005622|GO:0016020|GO:001				NP_001103	NM_00110	AK091473
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BE551038
Human Ger	February 2	GO:0006364|GO:00063		606490		NP_478126	NM_05821	BF692729
Human Ger	February 2	GO:0045449|GO:00056		607389		NP_036578	NM_01244	AL536899
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BC009467

Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AF085937
Human Ger	February 20	GO:0007165|GO:00057		611870		NP_001107	NM_00111	AK098502
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BC016339
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL831831
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AF086464
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_001012	NM_00101	BF035734
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AV703843
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BF692592
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AF085902
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BC043160
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BC039514
Human Ger	February 20	GO:0006259|GO:00062		603781		NP_001003	NM_00100	BC042989
Human Ger	February 20	GO:0000186|GO:00064		147796 /// 187950 /// 25		NP_004963	NM_00497	BC043187
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						XR_108382	AK057376
Human Ger	February 20	GO:0006511|GO:0004221				NP_005791	NM_00580	AL832776
Human Ger	February 20	GO:0006355|GO:0045449|GO:0005622|GO:000				NP_001093	NM_00109	AL833487
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BC038097
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL833224
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL831920
Human Ger	February 20	GO:000650	IPR011600	608633		NP_001177	NM_00119	AF486845
Human Ger	February 20	GO:0008152|GO:00056		611380		NP_055789	NM_01497	N42910
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AF085948
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL832616
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL831856
Human Ger	February 20	GO:0005634|GO:00057		610352		NP_001116	NM_00112	BC032531
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_03394	BC029599
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_02830	AW080339
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BE891071
Human Ger	February 20	GO:0006350|GO:00063		611811		NP_115809	NM_03243	BC040378
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_02695	BC037856
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BC025982
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BC019347
Human Ger	February 20	GO:0006497|GO:00064		610800		NP_001124	NM_00113	AF318326
Human Ger	February 20	GO:0001960|GO:00064		179590		NP_002831	NM_00284	AI762627
Human Ger	February 20	GO:0002553|GO:00066		601288		NP_001129	NM_00113	NM_00340
Human Ger	February 20	GO:0005737|GO:00058		612265		NP_055427	NM_01461	NM_01461
Human Ger	February 20	GO:0001709|GO:00069		159552	Apoptosis_	NP_001184	NM_00119	AI275690
Human Ger	February 20	GO:0001709|GO:00069		159552	Apoptosis_	NP_001184	NM_00119	NM_02196
Human Ger	February 20	GO:0006350|GO:00063		209950 /// 600555		NP_009330	NM_00731	NM_00731
Human Ger	February 20	GO:0006044|GO:00065		604039		NP_001135	NM_00114	AK002091
Human Ger	February 20	GO:0001501|GO:0006006|GO:0006464|GO:000				NP_055260	NM_01444	BG107676
Human Ger	February 20	GO:000647	IPR000242	600714		NP_004408	NM_00441	NM_00441
Human Ger	February 20	GO:0000122|GO:00001		603437		NP_001138	NM_00114	AL556190
Human Ger	February 20	GO:0006350|GO:00063		604256		NP_003661	NM_00367	NM_00367
Human Ger	February 20	GO:0044419|GO:00056		300160		NP_001180	NM_00119	NM_00135

Human Ge	February 2	GO:0006281|GO:00063	601597		NP_006754	NM_00676	NM_00676
Human Ge	February 2	GO:0001666|GO:00067	145500 /// 1	Calcium_re	NP_001668	NM_00167	NM_00167
Human Ge	February 2	GO:0006511|GO:00165	168600 /// 191342		NP_004172	NM_00418	NM_00418
Human Ge	February 2	GO:0000387|GO:00063	611734		NP_077007	NM_02410	NM_02410
Human Ge	February 2	GO:0001570|GO:00016	165161		NP_002220	NM_00222	NM_00222
Human Ge	February 2	GO:0000122|GO:00031	600386		NP_002157	NM_00216	D13891
Human Ge	February 2	GO:0043627|GO:00444	148020		NP_002267	NM_00227	NM_00227
Human Ge	February 2	GO:0001558|GO:00069	606450		NP_001040	NM_00104	NM_00586
Human Ge	February 2	GO:0001578|GO:00015	613126		NP_001005	NM_00100	BC001425
Human Ge	February 2	GO:0006119|GO:00061	191328	Electron_T	NP_003356	NM_00336	NM_00336
Human Ge	February 2	GO:0006417|GO:00069	611048		NP_055145	NM_01433	NM_01433
Human Ge	February 2	GO:0000045|GO:00018	114480 /// 606837		NP_001077	NM_00108	NM_01478
Human Ge	February 2	GO:0006694|GO:00066	600909	Cholesterol	NP_001001	NM_00100	AW084510
Human Ge	February 2	GO:0006397|GO:00071	602388		NP_004810	NM_00481	NM_00481
Human Ge	February 2	GO:0000165|GO:00015	147470		NP_000603	NM_00061	X07868
Human Ge	February 2	GO:0006915|GO:00069	600009		NP_001123	NM_00113	NM_00553
Human Ge	February 2	GO:0001709|GO:00017	600275 /// 610205		NP_077719	NM_02440	NM_02440
Human Ge	February 2	GO:0006468|GO:00064	165120		NP_001104	NM_00111	NM_00235
Human Ge	February 2	GO:0006094|GO:00063	603148	Hypertroph	NP_001025	NM_00103	NM_00167
Human Ge	February 2	GO:0005622|GO:00057	600830		NP_003440	NM_00344	NM_00344
Human Ge	February 2	GO:0016020|GO:00160	300222		NP_001165	NM_00117	AL021786
Human Ge	February 2	GO:0001501|GO:00018	129600 /// 134797 /// 15		NP_000129	NM_00013	AI264196
Human Ge	February 2	GO:0001501|GO:00070	171650		NP_001124	NM_00113	NM_00161
Human Ge	February 2	GO:0007155|GO:00056	600700 /// 601626		NP_001161	NM_00116	AL044018
Human Ge	February 2	GO:0006457|GO:00056	602634		NP_036460	NM_01232	NM_01232
Human Ge	February 2	GO:0001525|GO:00069	146930		NP_000575	NM_00058	NM_00058
Human Ge	February 2009 (Genome Reference		608025		NP_056993	NM_01590	NM_01590
Human Ge	February 2	GO:0044419|GO:00055	135820 /// 608180		NP_001987	NM_00199	NM_00648
Human Ge	February 2	GO:0006099|GO:00061	136850 /// 1	Krebs-TCA	NP_000134	NM_00014	NM_00014
Human Ge	February 2	GO:0006350|GO:00063	601196		NP_001007	NM_00100	AV724783
Human Ge	February 2	GO:0006626|GO:00068	605058		NP_006342	NM_00635	NM_00635
Human Ge	February 2	GO:0005622|GO:00057	606556		NP_055603	NM_01478	BE962483
Human Ge	February 2	GO:0005737|GO:00054	147690		NP_001539	NM_00154	NM_00154
Human Ge	February 2	GO:0006350|GO:00165	609764		NP_055478	NM_01466	BC002558
Human Ge	February 2	GO:0000122|GO:00017	139605		NP_005515	NM_00552	BE973687
Human Ge	February 2	GO:0000122|GO:00017	139605		NP_005515	NM_00552	NM_00552
Human Ge	February 2	GO:000020 IPR001680	278740 /// 600811		NP_000098	NM_00010	NM_00010
Human Ge	February 2	GO:0009966|GO:00057	608252		NP_001128	NM_00113	NM_02163
Human Ge	February 2	GO:000207 IPR011700	165162	Hypertroph	NP_005345	NM_00535	NM_00535
Human Ge	February 2	GO:0000209|GO:00063	147574		NP_006075	NM_00608	NM_00608
Human Ge	February 2	GO:0007165|GO:00072	610496		NP_004806	NM_00481	NM_00481
Human Ge	February 2	GO:0000239|GO:00015	604507		NP_001159	NM_00116	NM_00423
Human Ge	February 2	GO:000579 IPR001841 // Zinc finger, RING-typ			NP_055561	NM_01474	NM_01474
Human Ge	February 2	GO:0006350|GO:00065	609507 /// 609923		NP_001182	NM_00119	NM_00580
Human Ge	February 2	GO:000208 IPR005542	176312		NP_001128	NM_00113	NM_00619

Human Ger	February 20	GO:0006629|GO:00066		255110 /// 6	Fatty_Acid_	NP_000089	NM_00009	M58581
Human Ger	February 20	GO:0000165|GO:00016		162200 /// 162210 /// 19		NP_000258	NM_00026	NM_00026
Human Ger	February 20	GO:0001836|GO:00069		147572		NP_002029	NM_00203	NM_02287
Human Ger	February 20	GO:0006810|GO:00069		607615		NP_001008	NM_00100	NM_01477
Human Ger	February 20	GO:0006955|GO:0005737				NP_006811	NM_00682	NM_00682
Human Ger	February 20	GO:0005634|GO:00036		606863		NP_055544	NM_01472	AI961231
Human Ger	February 20	GO:0006810|GO:00068		603076		NP_004906	NM_00491	NM_00491
Human Ger	February 20	GO:0006350|GO:00063		168600 /// 6	Nuclear_Re	NP_006177	NM_00618	AI935096
Human Ger	February 20	GO:0006350|GO:00063		168600 /// 6	Nuclear_Re	NP_006177	NM_00618	NM_00618
Human Ger	February 20	GO:0000122|GO:00015		604420		NP_002720	NM_00272	NM_00152
Human Ger	February 20	GO:0001516|GO:00015		600262	Eicosanoid_	NP_000954	NM_00096	NM_00096
Human Ger	February 20	GO:0006350|GO:00063		142385		NP_002117	NM_00212	M95585
Human Ger	February 20	GO:0005737|GO:00054		300417		NP_001092	NM_00109	NM_01471
Human Ger	February 20	GO:0000089|GO:00000		176807 /// 6	Cell_cycle_	NP_001013	NM_00101	NM_00355
Human Ger	February 20	GO:0006810|GO:00069		603291		NP_001196	NM_00120	NM_01397
Human Ger	February 20	GO:0005975|GO:00064		607985		NP_057340	NM_01625	NM_01625
Human Ger	February 20	GO:0001501|GO:00015		187520		NP_003269	NM_00327	NM_00327
Human Ger	February 20	GO:0006350|GO:00063		129010 /// 145900 /// 60		NP_000390	NM_00039	NM_00039
Human Ger	February 20	GO:0001558|GO:00071		146730	Smooth_m	NP_000587	NM_00059	NM_00059
Human Ger	February 20	GO:000741	IPR000215	602445 /// 604218		NP_001116	NM_00112	NM_00502
Human Ger	February 20	GO:000007	IPR001245	603078	Cell_cycle_	NP_001107	NM_00111	NM_00127
Human Ger	February 20	GO:0005975|GO:00059		300559 /// 3	Glycogen_	NP_001116	NM_00112	NM_00263
Human Ger	February 20	GO:0007267|GO:00096		147571		NP_005092	NM_00510	NM_00510
Human Ger	February 20	GO:000630	IPR013027	300169 /// 300816		NP_001124	NM_00113	NM_00420
Human Ger	February 20	GO:0006954|GO:00071		600167	GPCRDB_	NP_000852	NM_00086	NM_00086
Human Ger	February 20	GO:0007155|GO:0005576|GO:0005578|GO:000				NP_005005	NM_00501	NM_00501
Human Ger	February 20	GO:0007179|GO:00072		601877		NP_001165	NM_00117	NM_00324
Human Ger	February 20	GO:0000122|GO:00015		136680 /// 194070 /// 19		NP_000369	NM_00037	NM_02442
Human Ger	February 20	GO:0001833|GO:00062		610608		NP_066545	NM_02106	NM_02106
Human Ger	February 20	GO:0006350|GO:00072		602419		NP_004421	NM_00443	NM_00443
Human Ger	February 20	GO:0006915|GO:00056		606717		NP_059993	NM_01752	NM_01752
Human Ger	February 20	GO:0007165|GO:00071		601524		NP_004481	NM_00449	NM_00449
Human Ger	February 20	GO:000209	IPR013111	131210 /// 145500 /// 16		NP_000441	NM_00045	NM_00045
Human Ger	February 20	GO:0006810|GO:00068		180903	Calcium_re	NP_001027	NM_00103	NM_00103
Human Ger	February 20	GO:0001666|GO:00019		604176 /// 605805		NP_003946	NM_00395	BG035761
Human Ger	February 20	GO:0007155|GO:00071		604259		NP_005752	NM_00576	NM_00576
Human Ger	February 20	GO:0007155|GO:00071		273800 /// 6	Integrin-me	NP_000410	NM_00041	NM_00041
Human Ger	February 20	GO:0006691|GO:00551		601270		NP_000887	NM_00089	NM_00089
Human Ger	February 20	GO:000633	IPR001487	600014		NP_003061	NM_00307	AV725365
Human Ger	February 20	GO:000633	IPR001487	600014		NP_003061	NM_00307	NM_00307
Human Ger	February 20	GO:0000122|GO:00063		300018 /// 3	Nuclear_Re	NP_000466	NM_00047	NM_00047
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_00213	NM_01898
Human Ger	February 20	GO:0006350|GO:00063		606954		NP_066385	NM_02104	NM_02104
Human Ger	February 20	GO:0008283		607899			NR_02392	NM_01585
Human Ger	February 20	GO:0006810|GO:00068		605024		NP_001035	NM_00103	NM_00485

Human Ger	February 2	GO:0007165|GO:00071	600563	GPCRDB_	NP_000950	NM_00095	NM_00095
Human Ger	February 2	GO:000646 IPR001245	603309		NP_003709	NM_00371	NM_00371
Human Ger	February 2	GO:0000185|GO:00001	604948		NP_056490	NM_01567	NM_01567
Human Ger	February 2	GO:0000122|GO:00069	610795		NP_001018	NM_00101	NM_00577
Human Ger	February 2	GO:0006629|GO:00090	602587		NP_009205	NM_00727	NM_00727
Human Ger	February 2	GO:0000122|GO:00001	605705	Hypertroph	NP_775490	NM_17335	NM_03075
Human Ger	February 2	GO:0006350|GO:00063	603975		NP_112495	NM_03121	NM_03121
Human Ger	February 2	GO:0002223|GO:00024	106300 /// 1	Proteasome	NP_005505	NM_00551	D83043
Human Ger	February 2	GO:0006810|GO:00068	179509		NP_002856	NM_00286	AW301641
Human Ger	February 2	GO:0000122|GO:00015	600349		NP_002156	NM_00216	D13889
Human Ger	February 2	GO:0006350|GO:00454	606714		NP_006804	NM_00681	AF279899
Human Ger	February 2	GO:0002223|GO:00024	106300 /// 1	Proteasome	NP_005505	NM_00551	L42024
Human Ger	February 2	GO:0006468|GO:00064	164960		NP_002639	NM_00264	M24779
Human Ger	February 2	GO:0007596|GO:00055	600033		NP_006519	NM_00652	AL574096
Human Ger	February 2	GO:0007596|GO:00055	600033		NP_006519	NM_00652	L27624
Human Ger	February 2	GO:0000082|GO:00063	600581		NP_001537	NM_00154	AW157094
Human Ger	February 2	GO:0000082|GO:00063	600581		NP_001537	NM_00154	AL022726
Human Ger	February 2	GO:0000185|GO:00001	604948		NP_056490	NM_01567	AF087853
Human Ger	February 2	GO:0000185|GO:00001	604948		NP_056490	NM_01567	AF078077
Human Ger	February 2	GO:0006915|GO:00069	603292		NP_004321	NM_00433	BC002461
Human Ger	February 2	GO:0006464|GO:00082	253270 /// 609018		NP_000402	NM_00041	D87328
Human Ger	February 2	GO:0009986|GO:00160	601275		NP_005268	NM_00527	D49958
Human Ger	February 2	GO:0005634|GO:00057	117340		NP_001793	NM_00180	AL582414
Human Ger	February 2	GO:0005886|GO:00160	607126		NP_003703	NM_00371	AF047760
Human Ger	February 2	GO:0005886|GO:00059	300698		NP_113630	NM_03144	AL136550
Human Ger	February 2	GO:000588 IPR001664	610495		NP_001034	NM_00103	BC002857
Human Ger	February 2	GO:0001666|GO:00017	126200 /// 600074		NP_037362	NM_01323	AA761181
Human Ger	February 2	GO:0006935|GO:00069	139110		NP_002080	NM_00208	M57731
Human Ger	February 2	GO:0005783|GO:00058	605861		NP_001177	NM_00119	BC001027
Human Ger	February 2	GO:0007049|GO:00082	275355 /// 601566		NP_005528	NM_00553	AW193656
Human Ger	February 2	GO:0009103|GO:0005783|GO:0005788|GO:001			NP_055916	NM_01510	AF288389
Human Ger	February 2	GO:0001525|GO:00015	601007		NP_001003	NM_00100	U50748
Human Ger	February 2	GO:0005515			NP_001120	NM_00112	BC003170
Human Ger	February 2	GO:0006350|GO:00063	209950 /// 600555		NP_009330	NM_00731	BC002704
Human Ger	February 2	GO:0005975|GO:00060	147650	Krebs-TCA	NP_002159	NM_00216	U52144
Human Ger	February 2	GO:0006810|GO:00150	603327		NP_003615	NM_00362	BC004349
Human Ger	February 2	GO:0007155|GO:00071	602988		NP_001166	NM_00117	AB006757
Human Ger	February 2	GO:0006605|GO:00071	604698	G_Protein_	NP_005091	NM_00510	AB003476
Human Ger	February 2	GO:000646 IPR001245	603464		NP_001092	NM_00109	AF153430
Human Ger	February 2	GO:0001649|GO:00069	133239 /// 605131		NP_057457	NM_01637	U13395
Human Ger	February 2	GO:0006810|GO:0015031|GO:0016192|GO:000			NP_001107	NM_00111	AF119889
Human Ger	February 2	GO:0006350|GO:00063	139139	Nuclear_Re	NP_002126	NM_00213	D49728
Human Ger	February 2	GO:0000187|GO:00018	147140		NP_001992	NM_00200	BC005912
Human Ger	February 2	GO:0001501|GO:00015	168470 /// 613382		NP_002811	NM_00282	BC005961
Human Ger	February 2	GO:0001558|GO:00016	146732	Smooth_mu	NP_000589	NM_00059	BF340228

Human Ger	February 20	GO:0001516|GO:00015	176803	Eicosanoid_	NP_000945	NM_00095	NM_00095
Human Ger	February 20	GO:0006810|GO:00068	606976 /// 613489		NP_001182	NM_00119	AK022874
Human Ger	February 20	GO:0008152|GO:00057	300823 /// 309900		NP_000193	NM_00020	AI926544
Human Ger	February 20	GO:0006744|GO:00454	607426 /// 612837		NP_064708	NM_02031	AC004382
Human Ger	February 20	GO:0001666|GO:00066	601510		NP_036367	NM_01223	D83782
Human Ger	February 20	GO:000691 IPR000917	610012		NP_001121	NM_00112	AW043713
Human Ger	February 20	GO:0006915|GO:00081	610012		NP_001121	NM_00112	BE500977
Human Ger	February 2009 (Genome Reference Consortium GRCh37)				NP_056519	NM_01570	BF057059
Human Ger	February 20	GO:0016020|GO:0016021|GO:0016021			NP_001124	NM_00113	AW205215
Human Ger	February 20	GO:0006350|GO:00063	143054		NP_006725	NM_00673	AL023584
Human Ger	February 20	GO:000715 IPR013753	602924		NP_005159	NM_00516	BG054844
Human Ger	February 2009 (Genome Reference		605636			NR_00276	AI950273
Human Ger	February 20	GO:0070552|GO:00055	611144		NP_115558	NM_03218	D63877
Human Ger	February 20	GO:000715 IPR013162	116930		NP_000606	NM_00061	AA126505
Human Ger	February 20	GO:0006281|GO:00063	609386		NP_055925	NM_01511	AB011166
Human Ger	February 20	GO:0006350|GO:00063	116898		NP_005186	NM_00519	AV655640
Human Ger	February 20	GO:0006281|GO:00069	608053 /// 609053 /// 61		NP_001106	NM_00111	BG403615
Human Ger	February 20	GO:0006468|GO:00064	610005		NP_001155	NM_00116	R59093
Human Ger	February 20	GO:0016020|GO:0016021			NP_065904	NM_02085	AB040900
Human Ger	February 20	GO:0007155|GO:00444	603785		NP_003820	NM_00382	AA917899
Human Ger	February 20	GO:0006350|GO:00064	606229		NP_001158	NM_00116	AI613483
Human Ger	February 20	GO:0016192|GO:00057	185880		NP_055046	NM_01423	AU150319
Human Ger	February 20	GO:0006605|GO:00481	603925		NP_004702	NM_00471	BF511590
Human Ger	February 20	GO:0001701|GO:00018	216360 /// 610937 /// 61		NP_001121	NM_00112	BF515597
Human Ger	February 20	GO:0006915|GO:00075	105120 /// 137350		NP_000168	NM_00017	BE675337
Human Ger	February 20	GO:0006099|GO:00061	136850 /// 1	Krebs-TCA	NP_000134	NM_00014	AA669797
Human Ger	February 20	GO:0005739	607572 /// 608427		NP_001073	NM_00108	BF224076
Human Ger	February 20	GO:0006631|GO:00066	134651		NP_004093	NM_00410	AI041520
Human Ger	February 20	GO:0001558|GO:00055	164958		NP_002505	NM_00251	BF440025
Human Ger	February 20	GO:0006468|GO:00072	300142 /// 3	G13_Signal	NP_001121	NM_00112	AW085556
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NR_02850	AF070569
Human Ger	February 20	GO:0006350|GO:00063	604073		NP_003423	NM_00343	AW968301
Human Ger	February 20	GO:0006412|GO:00311	602641		NP_001407	NM_00141	U79273
Human Ger	February 20	GO:0006898|GO:0007568|GO:0010165|GO:001			NP_001129	NM_00113	AL137651
Human Ger	February 20	GO:000715 IPR006209	604234		NP_004782	NM_00479	AL359052
Human Ger	February 20	GO:0006661|GO:00081	609763		NP_060895	NM_01842	H84390
Human Ger	February 20	GO:0006281|GO:00062	144700 /// 601982		NP_002533	NM_00254	R59977
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AF035278
Human Ger	February 20	GO:0006506|GO:0006506|GO:0006916|GO:000			NP_001138	NM_00114	AL049261
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AL049991
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AU148255
Human Ger	February 20	GO:0006979|GO:00082	605674		NP_001124	NM_00113	AL049332
Human Ger	February 20	GO:0000079|GO:00063	605193		NP_004666	NM_00467	AK021882
Human Ger	February 20	GO:0005622|GO:00056	611611		NP_001139	NM_00114	AW139369
Human Ger	February 20	GO:0006350|GO:00063	605465		NP_068834	NM_02199	AK027128

Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AU157200
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL080106
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL137403
Human Ger	February 20	GO:0006350|GO:00063		168600 /// 6	Nuclear_Re	NP_006177	NM_00618	S77154
Human Ger	February 20	GO:0006350|GO:00063		180663	RNA_trans	NP_116558	NM_03294	AJ224143
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL110206
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL121994
Human Ger	February 20	GO:0001666|GO:00019		158105 /// 182940 /// 60		NP_002973	NM_00298	S69738
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AK025152
Human Ger	February 20	GO:0001707|GO:00063		600542 /// 6	Hypertroph	NP_008912	NM_00698	X89894
Human Ger	February 20	GO:0005783|GO:00057		609157 /// 609158 /// 60		NP_001004	NM_00100	AL512687
Human Ger	February 20	GO:000247	IPR013151	106300 /// 1	Proteasome	NP_001091	NM_00109	M80469
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_00216	AW874308
Human Ger	February 20	GO:0005576				NP_001127	NM_00113	AA721025
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BF725121
Human Ger	February 20	GO:0007165|GO:00074		114110	Prostagland	NP_055439	NM_01462	NM_01462
Human Ger	February 20	GO:0030521|GO:00058		606564		NP_064567	NM_02018	NM_02018
Human Ger	February 20	GO:0006915|GO:00069		605335		NP_031376	NM_00735	NM_00735
Human Ger	February 20	GO:0006915|GO:00069		605335		NP_031376	NM_00735	NM_00735
Human Ger	February 20	GO:0006605|GO:0018345|GO:0000139|GO:000				NP_001128	NM_00113	BE542551
Human Ger	February 20	GO:0006412|GO:00056		611823		NP_057040	NM_01595	NM_01595
Human Ger	February 20	GO:000716	IPR000276	181500 /// 606666		NP_060960	NM_01849	NM_01849
Human Ger	February 20	GO:0008033|GO:00551		611243		NP_060734	NM_01826	NM_01826
Human Ger	February 20	GO:0001525|GO:00069		605914		NP_057723	NM_01663	NM_01663
Human Ger	February 20	GO:0006915|GO:00069		606579 /// 606636		NP_001028	NM_00103	NM_02173
Human Ger	February 20	GO:0016020|GO:0016021				NP_078985	NM_02470	NM_02470
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_057474	NM_01639	BG223334
Human Ger	February 20	GO:0006306|GO:0006479|GO:0032259|GO:000				NP_057257	NM_01617	NM_01617
Human Ger	February 20	GO:0051051|GO:00057		612276		NP_078916	NM_02464	NM_02464
Human Ger	February 20	GO:0005886|GO:00058		253601 /// 254130 /// 60		NP_001123	NM_00113	NM_00349
Human Ger	February 20	GO:0016020|GO:0016021				NP_060523	NM_01805	NM_01805
Human Ger	February 20	GO:0000139|GO:0005783|GO:0005789|GO:000				NP_060340	NM_01787	NM_01787
Human Ger	February 20	GO:0006629|GO:00066		610465		NP_079425	NM_02514	NM_02514
Human Ger	February 20	GO:0006412|GO:00064		611841		NP_057706	NM_01662	NM_01662
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_001035	NM_00104	NM_02455
Human Ger	February 20	GO:0006396|GO:00057		612600		NP_060616	NM_01814	NM_01814
Human Ger	February 20	GO:0006355|GO:0003677|GO:0005515|GO:000				NP_057506	NM_01642	NM_01642
Human Ger	February 20	GO:0016020|GO:0016021				NP_001093	NM_00109	NM_01828
Human Ger	February 20	GO:0000166|GO:00055		608087		NP_060796	NM_01832	NM_01832
Human Ger	February 20	GO:0030334|GO:0005737|GO:0005768|GO:000				NP_001171	NM_00118	NM_01904
Human Ger	February 20	GO:0006464|GO:00056		609249		NP_001158	NM_00116	NM_01791
Human Ger	February 20	GO:0006350|GO:00327		602016		NP_057354	NM_01627	NM_01627
Human Ger	February 20	GO:0006024|GO:00001		264800 /// 608125		NP_071450	NM_02216	NM_02216
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_061942	NM_01906	NM_01906
Human Ger	February 20	GO:0005737		610455 /// 610456		NP_001180	NM_00119	NM_01765

Human Ger	February 2	GO:0006875|GO:00072		604374		NP_001034	NM_00103	NM_00492
Human Ger	February 2	GO:0005622|GO:0005529				NP_054900	NM_01418	NM_01418
Human Ger	February 2	GO:0009987|GO:00057		613553		NP_071381	NM_02209	NM_02209
Human Ger	February 2	GO:0007165|GO:00057		609623		NP_060275	NM_01780	NM_01780
Human Ger	February 2	GO:000635	IPR006671	613384		NP_064703	NM_02030	NM_02030
Human Ger	February 2	GO:0006350|GO:00454		606238		NP_071911	NM_02246	NM_02246
Human Ger	February 2	GO:0006810|GO:0007154|GO:0015031|GO:000				NP_037455	NM_01332	NM_01332
Human Ger	February 2	GO:0007601|GO:00508		611119 /// 612943		NP_001026	NM_00103	NM_01884
Human Ger	February 2	GO:0016020|GO:0016021				NP_001136	NM_00114	NM_02493
Human Ger	February 2	GO:0000724|GO:00007		604289		NP_036547	NM_01241	NM_00655
Human Ger	February 2	GO:0000042|GO:00444		607492		NP_060496	NM_01802	NM_01802
Human Ger	February 2	GO:0005509		300817		NP_079460	NM_02518	NM_02518
Human Ger	February 2	GO:0005737|GO:0005737|GO:0005856|GO:0003779|GO:0005515						NM_01599
Human Ger	February 2	GO:0006350|GO:00063		603810		NP_004259	NM_00426	AF105421
Human Ger	February 2	GO:0001666|GO:00016		600150 /// 609446		NP_001014	NM_00101	U11058
Human Ger	February 2	GO:0006350|GO:00063		604503		NP_004232	NM_00424	AI694023
Human Ger	February 2	GO:0005783|GO:00057		609157 /// 609158 /// 60		NP_001004	NM_00100	N39536
Human Ger	February 2	GO:0002474|GO:00069		143110	Proteasome	NP_001091	NM_00109	BE138825
Human Ger	February 2	GO:0006468|GO:0032516|GO:0070373|GO:000				NP_001020	NM_00102	BF062886
Human Ger	February 2	GO:0006878|GO:00512		604263		NP_036541	NM_01240	AL133396
Human Ger	February 2	GO:0016180|GO:00056		611350		NP_056249	NM_01543	AK001363
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AV700891
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						XR_10868	AW972292
Human Ger	February 2	GO:0005634				NP_001002	NM_00100	AF060925
Human Ger	February 2	GO:0003677|GO:00082		607455		NP_068762	NM_02194	AW303359
Human Ger	February 2	GO:0007399|GO:00056		607026		NP_001104	NM_00111	AU137607
Human Ger	February 2	GO:0000387|GO:0006397|GO:0008380|GO:000				NP_001035	NM_00104	AA044921
Human Ger	February 2	GO:000007	IPR001279	609683		NP_073747	NM_02283	AI703304
Human Ger	February 2	GO:0005737|GO:00057		605112		NP_055362	NM_01454	AF177171
Human Ger	February 2	GO:0001501|GO:00068		118600 /// 123000 /// 60		NP_473368	NM_05402	AA854943
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_110433	NM_03080	AI159874
Human Ger	February 2	GO:0006350|GO:00069		608004		NP_001005	NM_00100	AB037925
Human Ger	February 2	GO:0010811|GO:00301		607223		NP_001159	NM_00116	AB014737
Human Ger	February 2	GO:0006915|GO:00071		607020		NP_872604	NM_18266	BC004270
Human Ger	February 2	GO:0001656|GO:0001657|GO:0001701|GO:000				NP_065907	NM_02085	AL136805
Human Ger	February 2	GO:0005634|GO:00056		611720		NP_078772	NM_02449	AI932310
Human Ger	February 2	GO:0000122|GO:00004		300166 /// 300485		NP_001116	NM_00112	AF317391
Human Ger	February 2	GO:0005515				NP_056298	NM_01548	AF151831
Human Ger	February 2	GO:000573	IPR011700 // Basic leucine zipper //			NP_001138	NM_00114	AL136867
Human Ger	February 2	GO:0005576|GO:00056		611752		NP_115787	NM_03241	AF325503
Human Ger	February 2	GO:000690	IPR000095 // PAK-box/P21-Rho-bi			NP_001033	NM_00103	AF286592
Human Ger	February 2	GO:0023034|GO:00057		603199		NP_795352	NM_17687	AB044807
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						XR_10893	AF130079
Human Ger	February 2	GO:0005737|GO:00081		604854		NP_006765	NM_00677	AF128846
Human Ger	February 2	GO:0016020|GO:0016021				NP_115730	NM_03235	BC006292

Human Ger	February 2	GO:0005737|GO:00057		604673		NP_001092	NM_00109	AF081250
Human Ger	February 2	GO:0006810|GO:00068		608490		NP_001070	NM_00107	BF247552
Human Ger	February 2	GO:0006457|GO:00435		611203		NP_079495	NM_02521	AL118506
Human Ger	February 2	GO:0006417|GO:00069		613257		NP_116222	NM_03283	BF796046
Human Ger	February 2	GO:0009615|GO:00332		600453		NP_005073	NM_00508	BE563152
Human Ger	February 2	GO:000597	IPR002044 // Glycoside hydrolase,			NP_062539	NM_01959	AK001947
Human Ger	February 2	GO:0005488				NP_060729	NM_01825	BE964325
Human Ger	February 2	GO:0006085|GO:0006085|GO:0008152|GO:000				NP_115890	NM_03250	AL035661
Human Ger	February 2	GO:0007565|GO:00075		176385		NP_002572	NM_00258	BF107618
Human Ger	February 2009 (Genome Reference			103280 /// 130650 /// 180860 /// 194			NR_00219	AL575306
Human Ger	February 2	GO:0006810|GO:00057		609216		NP_001122	NM_00112	BF512188
Human Ger	February 2	GO:0006350|GO:00073		613069		NP_060758	NM_01828	AI818048
Human Ger	February 2	GO:0000398|GO:00063		600124	mRNA_pro	NP_002128	NM_00213	AI963008
Human Ger	February 2	GO:0008285|GO:0005886|GO:0005925|GO:000				NP_116229	NM_03284	AF131774
Human Ger	February 2	GO:0005739|GO:00038		609668		NP_644812	NM_13928	AW300598
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_00358	BF340290
Human Ger	February 2	GO:0007166|GO:00071		165360		NP_005179	NM_00518	AV710415
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AU155376
Human Ger	February 2	GO:0000244|GO:00003		605221	mRNA_pro	NP_001177	NM_00119	AI954700
Human Ger	February 2	GO:0003676				NP_680544	NM_14817	AL528391
Human Ger	February 2	GO:0006974|GO:00069		613143		NP_612144	NM_13828	AA577672
Human Ger	February 2	GO:0006350|GO:0045449|GO:0005634|GO:000				NP_001007	NM_00100	AI638279
Human Ger	February 2	GO:0006350|GO:00063		606458		NP_149016	NM_03302	AI091372
Human Ger	February 2	GO:000372	IPR000241 // Putative RNA methyl			NP_001107	NM_00111	AI921788
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					XP_001714	XM_00171	AI825833
Human Ger	February 2	GO:0009236|GO:00057		251110 /// 607568		NP_443077	NM_05284	AV702487
Human Ger	February 2009 (Genome Reference			612178		NP_001096	NM_00110	BE502436
Human Ger	February 2	GO:000681	IPR013130	605094		NP_001035	NM_00104	BF680588
Human Ger	February 2	GO:0000166|GO:0005515|GO:0008270|GO:001				NP_065965	NM_02091	AI954660
Human Ger	February 2	GO:0016020|GO:0016021				NP_001008	NM_00100	AA524005
Human Ger	February 2	GO:0006350|GO:00063		600197		NP_002351	NM_00236	BG231691
Human Ger	February 2	GO:0006810|GO:00072		612398		NP_055814	NM_01499	AI309554
Human Ger	February 2	GO:000562	IPR007087 // Zinc finger, C2H2-typ			NP_001011	NM_00101	AI741051
Human Ger	February 2	GO:000726	IPR013753	608909		NP_848930	NM_17881	AW270158
Human Ger	February 2	GO:0006350|GO:00063		180202		NP_001036	NM_00104	AI672662
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_061029	NM_01855	BE218238
Human Ger	February 2	GO:0006260|GO:00056		612426		NP_689521	NM_15230	AW138157
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI672159
Human Ger	February 2	GO:0001675|GO:00064		600862		NP_001128	NM_00113	BE551849
Human Ger	February 2	GO:0005634|GO:00057		610699		NP_872297	NM_18249	AI984061
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_690878	NM_15291	H27948
Human Ger	February 2	GO:0008152|GO:0005739|GO:0005739|GO:000				NP_001018	NM_00101	AI341467
Human Ger	February 2	GO:0006350|GO:0006810|GO:0016568|GO:001				NP_001180	NM_00119	BF433516
Human Ger	February 2	GO:000650	IPR013111	602714		NP_003465	NM_00347	AA147933
Human Ger	February 2	GO:0006281|GO:00064		600863	Wnt_signal	NP_001885	NM_00189	T51255

Human Ger	February 2(	GO:0000922|GO:00057		611395		NP_001071	NM_00107	AI674565
Human Ger	February 2(	GO:0002063|GO:00059		138292		NP_002047	NM_00205	AF131846
Human Ger	February 2(	GO:0000082|GO:00063		600581		NP_001537	NM_00154	AV646610
Human Ger	February 2(	GO:000689	IPR000861	607496		NP_001034	NM_00103	AK002203
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BF438330
Human Ger	February 2(	GO:0000187|GO:00064		609487	MAPK_Ca	NP_006600	NM_00660	N50665
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_001159	NM_00116	AA194312
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_001138	NM_00114	AW276078
Human Ger	February 2(	GO:0006810|GO:0006811|GO:0006816|GO:001				NP_899063	NM_18324	N93191
Human Ger	February 2(	GO:0006350|GO:0045449|GO:0005622|GO:000				NP_116161	NM_03277	AA603467
Human Ger	February 2(	GO:005130	IPR011703	612317		NP_114127	NM_03192	AW593303
Human Ger	February 2(	GO:0006350|GO:0006355|GO:0045449|GO:000				NP_612456	NM_13844	AI474448
Human Ger	February 2(	GO:000022	IPR000435 // Tektin // 1.2E-28 /// IF			NP_001028	NM_00103	AA811509
Human Ger	February 2(	GO:0007155|GO:00071		612687		NP_001012	NM_00101	BE206621
Human Ger	February 2(	GO:0016020|GO:0016021|GO:0005488					NR_028407	AW519141
Human Ger	February 2(	GO:0006810|GO:0046415|GO:0055085|GO:000				NP_919274	NM_19429	BG401568
Human Ger	February 2(	GO:0006605|GO:00071		604698	G_Protein_	NP_005091	NM_00510	BF511276
Human Ger	February 2(	GO:0006605|GO:00071		604698	G_Protein_	NP_005091	NM_00510	BF511276
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_997210	NM_20732	BE501980
Human Ger	February 2(	GO:0001666|GO:00019		604176 /// 605805		NP_003946	NM_00395	AI244908
Human Ger	February 2(	GO:0055114|GO:0005783|GO:0005789|GO:000				NP_828847	NM_17803	AA557324
Human Ger	February 2(	GO:0005737|GO:00038		611438		NP_694967	NM_15323	AL589605
Human Ger	February 2(	GO:0008152|GO:0016020|GO:0016021|GO:000				NP_689630	NM_15241	AI671172
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_036496	N90774
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI798680
Human Ger	February 2(	GO:000557	IPR002818 // ThiJ/PfpI // 6.5E-4			NP_872418	NM_18261	AI139988
Human Ger	February 2(	GO:0006468|GO:00001		300791		NP_940867	NM_19846	AI653107
Human Ger	February 2(	GO:0006006|GO:00063		123812		NP_001872	NM_00188	AL552470
Human Ger	February 2(	GO:0006928|GO:00073		610082		NP_037394	NM_01326	AW292746
Human Ger	February 2(	GO:0000165|GO:00064		611931		NP_640338	NM_13924	AW274846
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AL137310
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_024607	BE048571
Human Ger	February 2(	GO:0007126|GO:0007140|GO:0007140|GO:000				NP_694591	NM_15304	AI989706
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_001073	NM_00108	AI363213
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BF197118
Human Ger	February 2(	GO:0000165|GO:00064		611931		NP_640338	NM_13924	AI590190
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						XR_10978	T87628
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI491983
Human Ger	February 2(	GO:0006694|GO:00067		109684	Steroid_Bic	NP_000404	NM_00041	AA894611
Human Ger	February 2(	GO:0006915|GO:00056		606717		NP_059993	NM_01752	AA142842
Human Ger	February 2(	GO:0005783				NP_001099	NM_00110	BF724137
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AW236803
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI693516
Human Ger	February 2(	GO:0006350|GO:00063		606371		NP_001123	NM_00113	AI279868
Human Ger	February 2(	GO:0002456|GO:00069		143024		NP_005266	NM_00527	AA775731

Human Ger	February 20	GO:000716	IPR001895 // Guanine-nucleotide di			NP_001030	NM_00103	AI379517
Human Ger	February 20	GO:0006810|GO:00068		605024		NP_001035	NM_00103	AI570494
Human Ger	February 20	GO:000012	IPR001214	603423		NP_001189	NM_00119	AI692659
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_061029	NM_01855	AI073486
Human Ger	February 2009 (Genome Reference			612477		NP_001127	NM_00113	BF055127
Human Ger	February 20	GO:0005488				NP_660153	NM_14517	AW024437
Human Ger	February 20	GO:0006606|GO:00066		604545		NP_002260	NM_00226	BG231980
Human Ger	February 20	GO:0001833|GO:00063		609514		NP_612639	NM_13857	AA641254
Human Ger	February 20	GO:0006309|GO:00068		123970 /// 6	Apoptosis /	NP_061820	NM_01894	BF593856
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI609256
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AA868461
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_919261	NM_19428	AI890299
Human Ger	February 20	GO:000022	IPR000435 // Tektin // 1.3E-25 /// IF			NP_001028	NM_00103	AI380156
Human Ger	February 20	GO:0005737				NP_940887	NM_19848	AW629527
Human Ger	February 20	GO:0005975|GO:00059		300559 /// 3	Glycogen_N	NP_001116	NM_00112	BE503584
Human Ger	February 20	GO:0005737|GO:00058		607619		NP_777598	NM_17493	BF589413
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						NR_00360	AI625235
Human Ger	February 20	GO:0016020|GO:00160		611320		NP_660292	NM_14524	AL039706
Human Ger	February 20	GO:0005737|GO:00057		604673		NP_001092	NM_00109	AL044056
Human Ger	February 20	GO:0006260|GO:00063		600728		NP_001177	NM_00119	T90642
Human Ger	February 20	GO:000635	IPR001214 // Nuclear protein SET /			NP_001129	NM_00113	AF272898
Human Ger	February 20	GO:0006810|GO:0022900				NP_001157	NM_00116	AI418538
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BF111884
Human Ger	February 20	GO:0006139|GO:00091		103030		NP_001005	NM_00100	AI566130
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AA195276
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI360054
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BE674309
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_542183	NM_08061	AL034550
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AW953794
Human Ger	February 20	GO:000803	IPR011063 // PP-loop // 9.4E-5			XP_003118	XM_00311	AI479923
Human Ger	February 20	GO:0006605|GO:00071		604698	G_Protein_	NP_005091	NM_00510	BF114967
Human Ger	February 20	GO:0006091|GO:00066		606090		NP_001137	NM_00114	BE674103
Human Ger	February 20	GO:0006457|GO:00057		607062		NP_001128	NM_00113	AA683602
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							BE676062
Human Ger	February 2009 (Genome Reference Consortium GRCh37)							AI371550
Human Ger	February 20	GO:0006468|GO:00082		604432 /// 611695		NP_775771	NM_17350	BF433088
Human Ger	February 20	GO:0005737|GO:0005829				NP_001182	NM_00119	AL359575
Human Ger	February 20	GO:0007165|GO:00160		610119		NP_001116	NM_00112	AB032953
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_055246	NM_01443	AB033100
Human Ger	February 20	GO:0016020|GO:0016021|GO:0008430				NP_001073	NM_00108	AU152102
Human Ger	February 20	GO:0000122|GO:00018		601819		NP_004450	NM_00445	AK027184
Human Ger	February 20	GO:0001701|GO:00018		611192		NP_037407	NM_01327	AF130076
Human Ger	February 20	GO:001003	IPR001452	607709 /// 607748		NP_001163	NM_00117	AK025185
Human Ger	February 20	GO:0016567|GO:00001		600938		NP_008841	NM_00691	AI657019

Human Ger	February 2	GO:0006024|GO:0000139|GO:0005794|GO:001			NP_055383	NM_01456	AK022198
Human Ger	February 2	GO:0006810|GO:00068	300008 /// 300009 /// 30		NP_000075	NM_00008	AK021494
Human Ger	February 2	GO:0006810|GO:0006844|GO:0055085|GO:000			NP_001034	NM_00103	AK022257
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						BE815259
Human Ger	February 2	GO:0016020|GO:00160	609415			NR_02734	AA256157
Human Ger	February 2	GO:0005737|GO:00058	608629 /// 608894		NP_001128	NM_00113	AI962891
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AK022461
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AK027139
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AU144570
Human Ger	February 2	GO:0006511|GO:0005634|GO:0005737|GO:000			NP_001027	NM_00103	AK000110
Human Ger	February 2	GO:0005975|GO:00060	230400 /// 6	GPCRDB_	NP_000146	NM_00015	AA453223
Human Ger	February 2	GO:0005576			NP_001164	NM_00117	AU158601
Human Ger	February 2	GO:0006606|GO:00164	608500 /// 612437		NP_001138	NM_00114	AU145382
Human Ger	February 2	GO:0006350|GO:00063	604417		NP_055238	NM_01442	N59653
Human Ger	February 2	GO:0001522|GO:00080	612787		NP_653310	NM_14470	BF514791
Human Ger	February 2	GO:0005634|GO:00057	118800 /// 609023		NP_001070	NM_00107	AB033010
Human Ger	February 2	GO:0016180|GO:00056	611348		NP_291025	NM_03354	AK000455
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AK000850
Human Ger	February 2009 (Genome Reference Consortium GRCh37)				XP_002343	XM_00234	BE540060
Human Ger	February 2	GO:0016020|GO:00160	613413		NP_001127	NM_00113	AK001834
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AL049975
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AL109791
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Human Ger	February 2	GO:0006413|GO:0006446|GO:0008033|GO:000			NP_057023	NM_01593	AB032979
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AU147174
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AL137541
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AK000019
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AK021431
Human Ger	February 2009 (Genome Reference Consortium GRCh37)				NP_542387	NM_08065	AL571598
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Human Ger	February 2009 (Genome Reference		605636			NR_00276	BF956762
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AI684439
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Human Ger	February 2	GO:0005737|GO:00001	612466		NP_443173	NM_05294	BG260886
Human Ger	February 2	GO:0005634|GO:00048	610835		NP_001018	NM_00101	BE780502
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AA398756
Human Ger	February 2	GO:0006810|GO:00068	601327		NP_004579	NM_00458	AA447729
Human Ger	February 2	GO:004278	IPR002867 // Zinc finger, C6HC-ty		NP_689766	NM_15255	AI888256
Human Ger	February 2009 (Genome Reference Consortium GRCh37)				NP_115598	NM_03222	AI539542
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AW960145
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AI742077
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AI914925
Human Ger	February 2	GO:0006915|GO:00071	602464		NP_004286	NM_00429	AI992283
Human Ger	February 2009 (Genome Reference Consortium GRCh37)				NP_001182	NM_00119	BF000047
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AA523939

Human Ger	February 20	GO:0007399|GO:00081	604597		NP_001171	NM_00117	BE672408
Human Ger	February 20	GO:0006350|GO:00063	603971		NP_003421	NM_00343	AI672373
Human Ger	February 20	GO:0005737	610501		NP_060410	NM_01794	AW269499
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AA767373
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AI860775
Human Ger	February 2009 (Genome Reference Consortium GRCh37)				NP_996769	NM_20688	BF056459
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Human Ger	February 20	GO:0005515			NP_001166	NM_00117	AW975772
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AV736334
Human Ger	February 2009 (Genome Reference Consortium GRCh37)					XR_10998	BE669493
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						BE501281
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AA033987
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)				NP_848565	NM_17847	AW572906
Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AW015521
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Human Ger	February 20	GO:0002064|GO:00025	137060 /// 607091		NP_001488	NM_00149	AL574435
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Human Ger	February 20	GO:0004721|GO:0016787|GO:0016791			NP_057480	NM_01639	AW169159
Human Ger	February 20	GO:0000209|GO:00016	179095		NP_003328	NM_00333	AW364833
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)					XR_11032	AI308862
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AA947873
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AI654048
Human Ger	February 20	GO:000016 IPR007581 // Endonuclease V // 1.6			NP_065965	NM_02091	AA936632
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)				NP_056290	NM_01547	AI864271
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AW976631
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AW362945
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)						AW292974
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Human Ger	February 2009 (Genome Reference Consortium GRCh37)					NP_001070	NM_00107	BG026723
Human Ger	February 20	GO:0043234				NP_001093	NM_00110	AA701247
Human Ger	February 20	GO:0005886|GO:00160		613445		NP_149043	NM_03305	BE646398
Human Ger	February 20	GO:0005634|GO:00036		156200 /// 611472		NP_060798	NM_01832	AA651772
Human Ger	February 20	GO:000626	IPR013520	152700 /// 192315 /// 22		NP_057465	NM_01638	AJ243797
Human Ger	February 20	GO:0006694|GO:00066		251170 /// 2	Cholesterol	NP_000422	NM_00043	M88468
Human Ger	February 20	GO:0006417|GO:00069		611048		NP_055145	NM_01433	U83981
Human Ger	February 20	GO:0003084|GO:00064		145260 /// 201300 /// 60		NP_001171	NM_00118	AB002342
Human Ger	February 20	GO:0007049		609406		NP_001017	NM_00101	AA533284

Sequence_S	Sequence_T	Species_Sci	SwissProt	Target_Des	Trans_Mem	Transcript_	Transcript_	Unigene_Cl
GenBank	Consensus	Homo sapie	B4E3M7 ///	gb:NM_005240.1 /DB_		AF218540 /	Hs2.352672	full length
GenBank	Consensus	Homo sapie	P83111	gb:NM_171846.1 /DB_		AK027808	Hs2.374554	full length
GenBank	Consensus	Homo sapie	Q8WTR2	gb:BC035000.1 /DB_X		BC035000 /	Hs2.132237	full length
GenBank	Consensus	Homo sapie	A6ND79 ///	gb:NM_152787.1 /DB_		AY331591	Hs2.365565	full length
GenBank	Consensus	Homo sapie	Q96LK0	gb:AY099509.1 /DB_X		AY099509	Hs2.334526	full length
GenBank	Consensus	Homo sapie	C9IZH7 ///	gb:NM_152525.1 /DB_		AL832221 /	Hs2.335788	full length
GenBank	Consensus	Homo sapie	P53794	gb:NM_006	GENSCAN	ENST0000	Hs2.421196.1	
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GenBank	Consensus	Homo sapie	B3KPG5 ///	gb:BC030654.1 /DB_X		AK130824	Hs2.283304	full length
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GenBank	Consensus	Homo sapie	Q8WWE9 /	gb:BC017770.1 /DB_X		BC017770 /	Hs2.351932	full length
GenBank	Consensus	Homo sapie	B3KXA7 //	gb:BC032227.1 /DB_X		BC032227 /	Hs2.83790.	full length
GenBank	Consensus	Homo sapie	P21781 ///	gb:AF523265.1 /DB_X		AF523265 /	Hs2.121001	full length
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GenBank	Consensus	Homo sapie	O43181 ///	gb:AB062482.1 /DB_X		AB062482	Hs2.374685	full length
GenBank	Consensus	Homo sapie	Q05D32	gb:BC035744.1 /DB_X		AK291230	Hs2.104336	full length
GenBank	Consensus	Homo sapie	Q59G18 ///	gb:BC014955.1 /DB_X		BC014955 /	Hs2.135756	full length
GenBank	Consensus	Homo sapie	A1A693 ///	gb:AF364037.1 /DB_X		AF364037 /	Hs2.433153	full length
GenBank	Consensus	Homo sapiens		gb:BU617052 /DB_XR		AL832183 /	Hs2.289770.1	
GenBank	Consensus	Homo sapie	B1APZ0 ///	gb:BM666010 /DB_XR		ENST0000	Hs2.117183	full length
GenBank	Consensus	Homo sapiens		gb:BC040701.1 /DB_X		AK172840	Hs2.406217.1	
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GenBank	Consensus	Homo sapie	B4DF98 ///	gb:AL834407.1 /DB_X		ENST0000	Hs2.112921	full length
GenBank	Consensus	Homo sapie	B3KNT8 ///	gb:AK021751.1 /DB_X		ENST0000	Hs2.419776	full length
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GenBank	Consensus	Homo sapie	Q96QA6	gb:AK097253.1 /DB_X		AK097253	Hs2.368672	full length
GenBank	Consensus	Homo sapie	C9J565 ///	gb:AK021560.1 /DB_X		AK021560	Hs2.288720	full length
GenBank	Consensus	Homo sapiens		gb:AB053312.1 /DB_X		AB053312	Hs2.191984.1	
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GenBank	Consensus	Homo sapie	B3KQ42 ///	gb:AL832081.1 /DB_X		AL832081 /	Hs2.97845.	full length
GenBank	Consensus	Homo sapiens		gb:AW104813 /DB_XR		AK094004	Hs2.370704.1	
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GenBank	Consensus	Homo sapie	C9JLM8 ///	gb:BM977131 /DB_XR		AK057787	Hs2.350624.1	
GenBank	Consensus	Homo sapie	B7ZKU4 ///	gb:AK091473.1 /DB_X		AK091473	Hs2.379848	full length
GenBank	Consensus	Homo sapiens		gb:BE551038 /DB_XR		AK057907	Hs2.350615.1	
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GenBank	Consensus	Homo sapie	A6ND70 ///	gb:AL536899 /DB_XR		CR608789 /	Hs2.290856	full length
GenBank	Consensus	Homo sapie	Q96GH2	gb:BC009467.1 /DB_X		BC009467 /	Hs2.111407.1	

GenBank	Consensus s	Homo sapiens		gb:AF085937.1 /DB_XI		AA235664	Hs2.38348.1	
GenBank	Consensus s	Homo sapie	B1AMC8 //	gb:AK098502.1 /DB_X		ENST0000(	Hs2.210505	full length
GenBank	Consensus s	Homo sapiens		gb:BC016339.1 /DB_X		BC016339 /	Hs2.350577.1	
GenBank	Consensus s	Homo sapiens		gb:AL831831.1 /DB_X		AL831831 /	Hs2.378797.1	
GenBank	Consensus s	Homo sapiens		gb:AF086464.1 /DB_XI		AA206370	Hs2.86248.1	
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GenBank	Consensus s	Homo sapiens		gb:BF692592 /DB_XRI		BC013940 /	Hs2.348325.1	
GenBank	Consensus s	Homo sapiens		gb:AF085902.1 /DB_XI		AF085902 /	Hs2.271737.1	
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GenBank	Consensus s	Homo sapiens		gb:BC039514.1 /DB_X		BC039514 /	Hs2.407574.1	
GenBank	Consensus s	Homo sapie	A5YM55 //	gb:BC042989.1 /DB_X		BC042989 /	Hs2.438441	full length
GenBank	Consensus s	Homo sapie	A8K910 ///	gb:BC043187.1 /DB_X		BC043187 /	Hs2.438487	full length
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GenBank	Consensus s	Homo sapie	A8K1B1 ///	gb:AL832776.1 /DB_X		AL832776 /	Hs2.407128	full length
GenBank	Consensus s	Homo sapie	B4DR51 ///	gb:AL833487.1 /DB_X		AL833487 /	Hs2.157287	full length
GenBank	Consensus s	Homo sapiens		gb:BC038097.1 /DB_X		BC038097 /	Hs2.373425.1	
GenBank	Consensus s	Homo sapiens		gb:AL833224.1 /DB_X		AL833224 /	Hs2.376891.1	
GenBank	Consensus s	Homo sapiens		gb:AL831920.1 /DB_X		AL831920 /	Hs2.377048.1	
GenBank	Consensus s	Homo sapie	Q6UXS9	gb:AF486845.1 /DB_XI		AF486844 /	Hs2.367945	full length
GenBank	Consensus s	Homo sapie	B3KWX2 /	gb:N42910 /DB_XREF=		BC048327 /	Hs2.411370	full length
GenBank	Consensus s	Homo sapiens		gb:AF085948.1 /DB_XI		AF085948 /	Hs2.167814.1	
GenBank	Consensus s	Homo sapiens		gb:AL832616.1 /DB_X		AL832616 /	Hs2.335812.1	
GenBank	Consensus s	Homo sapiens		gb:AL831856.1 /DB_X		AL831856 /	Hs2.377060.1	
GenBank	Consensus s	Homo sapie	B4DKA9 //	gb:BC032531.1 /DB_X		BC045714 /	Hs2.397694	full length
GenBank	Consensus s	Homo sapiens		gb:BC029599.1 /DB_X		BC029599 /	Hs2.57835.1	
GenBank	Consensus s	Homo sapiens		gb:AW080339 /DB_XR		NR_028308	Hs2.390621.1	
GenBank	Consensus s	Homo sapiens		gb:BE891071 /DB_XRI		BC039391 /	Hs2.407606.1	
GenBank	Consensus s	Homo sapie	B3KSN8 ///	gb:BC040378.1 /DB_X		BC040378 /	Hs2.269952	full length
GenBank	Consensus s	Homo sapie	A8K0U2	gb:BC037856.1 /DB_X		BC037856 /	Hs2.385498	full length
GenBank	Consensus s	Homo sapiens		gb:BC025982.1 /DB_X		BC025982 /	Hs2.382227.1	
GenBank	Consensus s	Homo sapiens		gb:BC019347.1 /DB_X		AK094985	Hs2.382771.1	
GenBank	Consensus s	Homo sapie	Q9H0Y0	gb:AF318326.1 /DB_XI		AF318326 /	Hs2.436246	full length
GenBank	Consensus s	Homo sapie	A2A437 ///	gb:AI76262	ENSP0000(	AK127475	Hs.75216.0	full length
GenBank	Exemplar s	Homo sapie	B0AZS6 ///	gb:NM_003406.1 /DB_		BC051814 /	g4507952	full length
GenBank	Exemplar s	Homo sapie	Q6STG1 ///	gb:NM_014612.1 /DB_		AF214737 /	g8922113	full length
GenBank	Consensus s	Homo sapie	B4DG83 ///	gb:AI27569	NP_001184	BC017197 /	Hs.86386.0	full length
GenBank	Exemplar s	Homo sapie	B4DG83 ///	gb:NM_021	NP_001184	AF118124 /	g11386164	full length
GenBank	Exemplar s	Homo sapie	A5D905 ///	gb:NM_007315.1 /DB_		ENST0000(	g6274551	full length
GenBank	Consensus s	Homo sapie	B3KMK2 //	gb:AK002091.1 /DB_X		AF036144 /	Hs.5734.0	full length
GenBank	Consensus s	Homo sapie	C9JSB0 ///	gb:BG1076	ENSP0000(	BC108314 /	Hs.76698.0	full length
GenBank	Exemplar s	Homo sapie	B4DNT2 //	gb:NM_004417.2 /DB_		AK127679	g7108342	full length
GenBank	Consensus s	Homo sapie	P16989 /// (	gb:AL556190 /DB_XRI		BC009744 /	Hs.1139.0	full length
GenBank	Exemplar s	Homo sapie	B4DDI4 ///	gb:NM_003670.1 /DB_		AB004066 /	g4503298	full length
GenBank	Exemplar s	Homo sapie	A8K538 ///	gb:NM_001356.2 /DB_		AF000982 /	g13514812	full length

GenBank	Exemplar s	Homo sapie	P78543	gb:NM_006763.1 /DB_		CR604962	g5802987	full length
GenBank	Exemplar s	Homo sapie	A3KLL5 ///	gb:NM_001	ENSP0000	ENST0000	g4502276	full length
GenBank	Exemplar s	Homo sapie	A6NKP9 //	gb:NM_004181.1 /DB_		AK054579	g4759283	full length
GenBank	Exemplar s	Homo sapie	B4DJP0 ///	gb:NM_024102.1 /DB_		BC001679	g13129109	full length
GenBank	Exemplar s	Homo sapie	P17275 ///	gb:NM_002229.1 /DB_		BC004250	g4504808	full length
GenBank	Exemplar s	Homo sapie	Q02363 ///	gb:D13891.1 /DB_XRE		D13891 //	g464183	full length
GenBank	Exemplar s	Homo sapie	B4DE59 ///	gb:NM_002276.1 /DB_		AK293479	g4504916	full length
GenBank	Exemplar s	Homo sapie	B4DFS9 ///	gb:NM_005863.1 /DB_		AK294244	g5031938	full length
GenBank	Exemplar s	Homo sapie	A8K0M8 //	gb:BC001425.1 /DB_X		AF223000	g12655140	full length
GenBank	Exemplar s	Homo sapie	B4DUL5 //	gb:NM_003365.1 /DB_		AK300694	g4507840	full length
GenBank	Exemplar s	Homo sapie	B4DKQ3 //	gb:NM_014330.2 /DB_		AK296668	g9790902	full length
GenBank	Exemplar s	Homo sapie	A8K6N4 ///	gb:NM_014781.1 /DB_		AB059622	g7661991	full length
GenBank	Consensus	Homo sapie	B2R694 ///	gb:AW084510 /DB_XR		AK092334	Hs.93199.0	full length
GenBank	Exemplar s	Homo sapie	B7Z6F7 ///	gb:NM_004819.1 /DB_		AB209024	g4759195	full length
GenBank	Consensus	Homo sapie	A6XGL2 //	gb:X07868 /DB_XREF		ENST0000	Hs.251664.	full length
GenBank	Exemplar s	Homo sapie	A8K0H0 ///	gb:NM_005	ENSP0000	AK289535	g5031780	full length
GenBank	Exemplar s	Homo sapie	B5MCT1 //	gb:NM_024	ENSP0000	AF315356	g13249343	full length
GenBank	Exemplar s	Homo sapie	A8K379 ///	gb:NM_002350.1 /DB_		AK290494	g4505054	full length
GenBank	Exemplar s	Homo sapie	P18847 ///	gb:NM_001674.1 /DB_		AB209032	g4502262	full length
GenBank	Exemplar s	Homo sapie	A2AE48 ///	gb:NM_003449.1 /DB_		AK096996	g4508004	full length
GenBank	Consensus	Homo sapie	B4E062 ///	gb:AL0217	ENSP0000	AY359051	Hs.17109.0	full length
GenBank	Consensus	Homo sapie	B4E3I6 ///	gb:AI264196 /DB_XRE		BC146854	Hs.750.0	full length
GenBank	Exemplar s	Homo sapie	B7Z4Z2 ///	gb:NM_001	ENSP0000	AK298122	g4557009	full length
GenBank	Consensus	Homo sapie	B7Z871 ///	gb:AL044018 /DB_XR		AK302959	Hs.180398.	full length
GenBank	Exemplar s	Homo sapie	O95037 ///	gb:NM_012	ENSP0000	AB026908	g9558754	full length
GenBank	Exemplar s	Homo sapie	C9J4T6 ///	gb:NM_00	ENSP0000	BC013615	g10834977	full length
GenBank	Exemplar s	Homo sapie	A2RRP1 ///	gb:NM_015909.1 /DB_		AF056195	g7706239	full length
GenBank	Exemplar s	Homo sapie	B1AHM4 /	gb:NM_006486.1 /DB_		AF126110	g5922008	full length
GenBank	Exemplar s	Homo sapie	B1ANK7 //	gb:NM_000143.1 /DB_		M15502 //	g4503716	full length
GenBank	Consensus	Homo sapie	A8MW16 /	gb:AV7247	ENSP0000	CR612351	Hs.26719.0	full length
GenBank	Exemplar s	Homo sapie	O43615 ///	gb:NM_006351.1 /DB_		AF026030	g5454123	full length
GenBank	Consensus	Homo sapie	B4E0G2 ///	gb:BE962483 /DB_XR		AF220131	Hs.179703.	full length
GenBank	Exemplar s	Homo sapie	B3KS50 ///	gb:NM_001548.1 /DB_		AK308688	g4504584	full length
GenBank	Exemplar s	Homo sapie	B4DGH3 //	gb:BC0025	GENSCAN	AK294596	g12803466	full length
GenBank	Consensus	Homo sapie	B4DU36 ///	gb:BE973687 /DB_XR		AK300482	Hs.250666.	full length
GenBank	Exemplar s	Homo sapie	B4DU36 ///	gb:NM_005524.2 /DB_		AF264785	g8400709	full length
GenBank	Exemplar s	Homo sapie	Q92466	gb:NM_000107.1 /DB_		AK091640	g4557514	full length
GenBank	Exemplar s	Homo sapie	B4DMU2 /	gb:NM_021638.1 /DB_		AF188700	g11056013	full length
GenBank	Exemplar s	Homo sapie	P17535	gb:NM_005354.2 /DB_		ENST0000	g10938013	full length
GenBank	Exemplar s	Homo sapie	A0A962 ///	gb:NM_006084.1 /DB_		AK074144	g5174474	full length
GenBank	Exemplar s	Homo sapie	Q52LW3	gb:NM_004815.1 /DB_		ENST0000	g4758881	full length
GenBank	Exemplar s	Homo sapie	C9K0T3 ///	gb:NM_004237.1 /DB_		BC000404	g11321606	full length
GenBank	Exemplar s	Homo sapie	B4DEZ0 ///	gb:NM_014	ENSP0000	ENST0000	g7661955	full length
GenBank	Exemplar s	Homo sapie	Q9NS56	gb:NM_005802.1 /DB_		AB045732	g5032190	full length
GenBank	Exemplar s	Homo sapie	B7Z4A9 ///	gb:NM_006195.1 /DB_		AK092148	g5453851	full length

GenBank	Exemplar s	Homo sapie	P23786 ///	gb:M58581.1 /DB_XRE		BC002445	g180988	full length
GenBank	Exemplar s	Homo sapie	A8K1M1 //	gb:NM_000267.1 /DB_		ENST0000	g4557792	full length
GenBank	Exemplar s	Homo sapie	P09912 ///	gb:NM_02	ENSP0000	BC011601	g13259549	full length
GenBank	Exemplar s	Homo sapie	A6NI12 ///	gb:NM_014778.1 /DB_		AB007870	g7662097	full length
GenBank	Exemplar s	Homo sapie	A4PB31 ///	gb:NM_006820.1 /DB_		AB000115	g5803026	full length
GenBank	Consensus	Homo sapie	B3KM29 //	gb:AI961231 /DB_XRE		AB018351	Hs.184297.	full length
GenBank	Exemplar s	Homo sapie	A8K7Y7 ///	gb:NM_00	ENSP0000	AF323660	g8051574	full length
GenBank	Consensus	Homo sapie	B7Z5U7 ///	gb:AI935096 /DB_XRE		BC009288	Hs.82120.0	full length
GenBank	Exemplar s	Homo sapie	B7Z5U7 ///	gb:NM_006186.1 /DB_		ENST0000	g5453821	full length
GenBank	Exemplar s	Homo sapie	B1AQ17 ///	gb:NM_001529.1 /DB_		L16499 // H	g10835016	full length
GenBank	Exemplar s	Homo sapie	P35354 ///	gb:NM_000963.1 /DB_		ENST0000	g4506264	full length
GenBank	Exemplar s	Homo sapie	A8K1X8 ///	gb:M95585.1 /DB_XRE		BC036093	g184223	full length
GenBank	Exemplar s	Homo sapie	Q5JY77	gb:NM_014710.1 /DB_		BC114552	g7662129	full length
GenBank	Exemplar s	Homo sapie	A4D218 ///	gb:NM_003550.1 /DB_		AF083811	g4505064	full length
GenBank	Exemplar s	Homo sapie	D3DQM3 /	gb:NM_01	ENSP0000	AF083957	g7524349	full length
GenBank	Exemplar s	Homo sapie	B4DZG9 //	gb:NM_01	ENSP0000	AF052111	g7705908	full length
GenBank	Exemplar s	Homo sapie	B2R582 ///	gb:NM_003278.1 /DB_		BC011024	g4507556	full length
GenBank	Exemplar s	Homo sapie	B4DL38 ///	gb:NM_000399.2 /DB_		J04076 // H	g9845523	full length
GenBank	Exemplar s	Homo sapie	C1K3N3 ///	gb:NM_000596.1 /DB_		BC035263	g4504614	full length
GenBank	Exemplar s	Homo sapie	C9J2K0 ///	gb:NM_005025.1 /DB_		AK290082	g4826903	full length
GenBank	Exemplar s	Homo sapie	B4DDD0 //	gb:NM_001274.1 /DB_		AF016582	g4502802	full length
GenBank	Exemplar s	Homo sapie	A6NIT2 ///	gb:NM_002637.1 /DB_		AK123357	g4505778	full length
GenBank	Exemplar s	Homo sapie	P05161	gb:NM_005101.1 /DB_		AY168648	g4826773	full length
GenBank	Exemplar s	Homo sapie	D3DTE9 ///	gb:NM_00	GENSCAN	AF100928	g4757731	full length
GenBank	Exemplar s	Homo sapie	A8K7Z2 ///	gb:NM_00	ENSP0000	ENST0000	g13435403	full length
GenBank	Exemplar s	Homo sapie	B2R7N9 ///	gb:NM_005014.1 /DB_		AB000114	g4826875	full length
GenBank	Exemplar s	Homo sapie	B4E332 ///	gb:NM_003240.1 /DB_		AF081513	g4503440	full length
GenBank	Exemplar s	Homo sapie	A0FJ57 ///	gb:NM_024426.1 /DB_		BC032861	g13386509	full length
GenBank	Exemplar s	Homo sapie	B4DGH0 //	gb:NM_021067.1 /DB_		ENST0000	g10800147	full length
GenBank	Exemplar s	Homo sapie	B4DH80 ///	gb:NM_004430.1 /DB_		ENST0000	g4758251	full length
GenBank	Exemplar s	Homo sapie	B3KPW1 //	gb:NM_017523.1 /DB_		AK292710	g8923794	full length
GenBank	Exemplar s	Homo sapie	B2R7X4 ///	gb:NM_004490.1 /DB_		AK301961	g4758477	full length
GenBank	Exemplar s	Homo sapie	B2RAJ1 ///	gb:NM_00	ENSP0000	BC142677	g4506870	
GenBank	Exemplar s	Homo sapie	A8MPV7 //	gb:NM_001	ENSP0000	AB001025	g4506758	full length
GenBank	Consensus	Homo sapie	O14543 ///	gb:BG035761 /DB_XR		AB004904	Hs.296176.	full length
GenBank	Exemplar s	Homo sapie	B4DHQ7 //	gb:NM_00	ENSP0000	AB208934	g5032222	full length
GenBank	Exemplar s	Homo sapie	B4DLU2 //	gb:NM_00	ENSP0000	BC117443	g6006009	full length
GenBank	Exemplar s	Homo sapie	B7Z442 ///	gb:NM_000896.1 /DB_		AB002454	g4503240	full length
GenBank	Consensus	Homo sapie	B1ALF6 ///	gb:AV725365 /DB_XR		AK094076	Hs.198296.	full length
GenBank	Exemplar s	Homo sapie	B1ALF6 ///	gb:NM_003070.1 /DB_		AK094076	g4507068	full length
GenBank	Exemplar s	Homo sapie	A6NNU8 //	gb:NM_000475.2 /DB_		BC011564	g5016089	full length
GenBank	Exemplar s	Homo sapie	O95141	gb:NM_018985.1 /DB_		NR_00213	g9506770	
GenBank	Exemplar s	Homo sapie	O75346	gb:NM_021047.1 /DB_		AK074757	g10567821	full length
GenBank	Exemplar s	Homo sapie	B7ZBC5 ///	gb:NM_015855.1 /DB_		M60614 // I	g7706770	
GenBank	Exemplar s	Homo sapie	B4DHY0 //	gb:NM_00	ENSP0000	AB018282	g4759133	full length

GenBank	Exemplar s	Homo sapie	P43088 ///	gb:NM_00	ENSP0000	AF004021	g4506260	full length
GenBank	Exemplar s	Homo sapie	Q14004 ///	gb:NM_003718.1 /DB_		AB058694	g4502710	full length
GenBank	Exemplar s	Homo sapie	O75293 ///	gb:NM_015675.1 /DB_		AF087853	g9945331	full length
GenBank	Exemplar s	Homo sapie	B4DVR4 //	gb:NM_005775.1 /DB_		AF037261	g5032072	full length
GenBank	Exemplar s	Homo sapie	B3KQ12 ///	gb:NM_007274.1 /DB_		AB074415	g6857796	full length
GenBank	Exemplar s	Homo sapie	P37275 ///	gb:NM_030751.1 /DB_		AB047786	g13540478	full length
GenBank	Exemplar s	Homo sapie	B4DJ46 ///	gb:NM_031218.1 /DB_		AK295921	g13654291	full length
GenBank	Exemplar s	Homo sapie	A0FIZ3 ///	gb:D83043.1 /DB_XRE		AF026218	g1871135	full length
GenBank	Consensus	Homo sapie	A8MVA3 /	gb:AW301641 /DB_XR		ENST0000	Hs.78305.0	full length
GenBank	Exemplar s	Homo sapie	P41134	gb:D13889.	GENSCAN	AK291152	g464181	full length
GenBank	Exemplar s	Homo sapie	Q12796 ///	gb:AF279899.1 /DB_X		AF279899	g12751123	full length
GenBank	Exemplar s	Homo sapie	A0FIZ3 ///	gb:L42024.	ENSP0000	AK026595	g804748	full length
GenBank	Exemplar s	Homo sapie	B4DVN6 //	gb:M24779.1 /DB_XR		M24779 //	g1066790	full length
GenBank	Consensus	Homo sapie	A4ZVU7 //	gb:AL574096 /DB_XR		AK129833	Hs.295944.	full length
GenBank	Exemplar s	Homo sapie	A4ZVU7 //	gb:L27624.1 /DB_XRE		AK129833	g441149	full length
GenBank	Consensus	Homo sapie	P47928	gb:AW157094 /DB_XR		AJ420553 /	Hs.34853.0	full length
GenBank	Consensus	Homo sapie	P47928	gb:AL022726 /DB_XR		AJ420553 /	Hs.34853.0	full length
GenBank	Exemplar s	Homo sapie	O75293 ///	gb:AF087853.1 /DB_X		AF087853	g12061050	full length
GenBank	Exemplar s	Homo sapie	O75293 ///	gb:AF078077.1 /DB_X		AF078077	g3978391	full length
GenBank	Exemplar s	Homo sapie	Q12982	gb:BC002461.1 /DB_X		BC002461	g12803290	full length
GenBank	Exemplar s	Homo sapie	B2RAH1 //	gb:D87328.1 /DB_XRE		D87328 //	g1813423	full length
GenBank	Exemplar s	Homo sapie	B7Z642 ///	gb:D49958.	ENSP0000	BC022508	g1663516	full length
GenBank	Consensus	Homo sapie	Q01850	gb:AL582414 /DB_XR		BC017503	Hs.75124.0	full length
GenBank	Exemplar s	Homo sapie	O43688 ///	gb:AF0477	GENSCAN	AB209696	g2911497	full length
GenBank	Exemplar s	Homo sapie	Q9BQJ4	gb:AL1365	ENSP0000	BC039242	g13276606	full length
GenBank	Exemplar s	Homo sapie	B3KT74 ///	gb:BC002857.1 /DB_X		AK000710	g12804008	full length
GenBank	Consensus	Homo sapie	B6EC88 ///	gb:AA761181 /DB_XR		AK000168	Hs.286124.	full length
GenBank	Exemplar s	Homo sapie	P19875 ///	gb:M57731.1 /DB_XR		BC015753	g183626	full length
GenBank	Exemplar s	Homo sapie	Q9Y2B0	gb:BC001027.1 /DB_X		BC001027	g12654402	full length
GenBank	Consensus	Homo sapie	B4DNX8 //	gb:AW193656 /DB_XR		AB024401	Hs.46700.4	full length
GenBank	Exemplar s	Homo sapie	B3KT71 ///	gb:AF288389.1 /DB_X		AF288389	g12620187	full length
GenBank	Exemplar s	Homo sapie	A2RRQ4 //	gb:U50748.	NP_001185	ENST0000	g3236285	full length
GenBank	Exemplar s	Homo sapie	B4DYY5 //	gb:BC003170.1 /DB_X		AJ243669 /	g13111994	full length
GenBank	Exemplar s	Homo sapie	A5D905 ///	gb:BC002704.1 /DB_X		AK096686	g12803734	full length
GenBank	Exemplar s	Homo sapie	B4DFL2 ///	gb:U52144.1 /DB_XRE		AK299987	g1277202	full length
GenBank	Exemplar s	Homo sapie	B7Z5P4 ///	gb:BC004349.1 /DB_X		BC004349	g13279301	full length
GenBank	Exemplar s	Homo sapie	O60245	gb:AB0067	NP_115833	AB006757	g2979421	full length
GenBank	Exemplar s	Homo sapie	A6NEC7 //	gb:AB003476.1 /DB_X		AB003476	g2081606	full length
GenBank	Exemplar s	Homo sapie	A8K370 ///	gb:AF153430.1 /DB_X		AB209829	g6580936	full length
GenBank	Exemplar s	Homo sapie	A8K5I5 ///	gb:U13395.1 /DB_XRE		AF211943	g538131	full length
GenBank	Exemplar s	Homo sapie	C9IYI2 ///	gb:AF119889.1 /DB_X		ENST0000	g7770214	
GenBank	Exemplar s	Homo sapie	B4DML7 //	gb:D49728.1 /DB_XRE		D49728 //	g1813881	full length
GenBank	Exemplar s	Homo sapie	P12319 ///	gb:BC0059	GENSCAN	BC005912	g13543505	full length
GenBank	Exemplar s	Homo sapie	P12272 ///	gb:BC005961.1 /DB_X		BC005961	g13543620	full length
GenBank	Consensus	Homo sapie	A6XNC9 //	gb:BF340228 /DB_XR		BC000013	Hs.77326.1	full length

GenBank	Consensus s	Homo sapie	P41222 /// (	gb:NM_000954.1 /DB_	AY026356	Hs.8272.0	full length
GenBank	Consensus s	Homo sapie	A2VCL3 ///	gb:AK022874.1 /DB_X	AB088369 /	Hs.108779.	full length
GenBank	Consensus s	Homo sapie	B3KWA1 /	gb:AI926544 /DB_XRE	ENST0000	Hs.303154.	full length
GenBank	Consensus s	Homo sapie	B4DEE3 ///	gb:AC004382 /DB_XR	AL136884 /	Hs.4288.1	full length
GenBank	Consensus s	Homo sapie	A8K619 ///	gb:D83782.	ENSP0000	AK091005	Hs.78442.0	full length
GenBank	Consensus s	Homo sapie	Q6NUJ9 ///	gb:AW043713 /DB_XR	AF545571 /	Hs.70823.0	full length
GenBank	Consensus s	Homo sapie	Q6NUJ9 ///	gb:BE500977 /DB_XRE	AF545571 /	Hs.70823.0	full length
GenBank	Consensus s	Homo sapie	Q6ICB0	gb:BF057059 /DB_XRE	AF038183 /	Hs.12421.0	full length
GenBank	Consensus s	Homo sapie	O14524	gb:AW2052	ENSP0000	ENST0000	Hs.14912.0	full length
GenBank	Consensus s	Homo sapie	B4DKE9 ///	gb:AL023584 /DB_XR	ENST0000	Hs.75063.0	full length
GenBank	Consensus s	Homo sapie	B2R838 ///	gb:BG054844 /DB_XR	BC012513 /	Hs.6838.0	full length
GenBank	Consensus s	Homo sapie	Q6ZTF7 ///	gb:AI950273 /DB_XRE	AF052114 /	Hs.112844.	full length
GenBank	Consensus s	Homo sapie	Q15018	gb:D63877.1 /DB_XRE	BC008999 /	Hs.82324.0	full length
GenBank	Consensus s	Homo sapie	B4DSQ7 ///	gb:AA1265	ENSP0000	AL832563 /	Hs.167988.	full length
GenBank	Consensus s	Homo sapie	B4E265 ///	gb:AB011166.1 /DB_X	BC034441 /	Hs.103283.	full length
GenBank	Consensus s	Homo sapie	P49716 /// (	gb:AV655640 /DB_XR	BC094715 /	Hs.76722.1	full length
GenBank	Consensus s	Homo sapie	B3KNW8 /	gb:BG403615 /DB_XR	AB058697 /	Hs.80961.1	full length
GenBank	Consensus s	Homo sapie	C9J338 /// (	gb:R59093 /DB_XREF=	ENST0000	Hs.170204.	full length
GenBank	Consensus s	Homo sapie	A2RU67 ///	gb:AB0409	ENSP0000	BC039267 /	Hs.6189.0	full length
GenBank	Consensus s	Homo sapie	B2RTS3 ///	gb:AA917899 /DB_XR	AB210041 /	Hs.169378.	full length
GenBank	Consensus s	Homo sapie	A4FVC0 ///	gb:AI613483 /DB_XRE	BC054491 /	Hs.324504.	full length
GenBank	Consensus s	Homo sapie	A8K0D3 ///	gb:AU1503	ENSP0000	BC023286 /	Hs.20021.1	full length
GenBank	Consensus s	Homo sapie	A2A283 ///	gb:BF5115	ENSP0000	ENST0000	Hs.6139.2	full length
GenBank	Consensus s	Homo sapie	B4E3M8 ///	gb:BF515597 /DB_XRE	AK093307	Hs.12328.0	full length
GenBank	Consensus s	Homo sapie	A2A418 ///	gb:BE675337 /DB_XRE	AK096280	Hs.290070.	full length
GenBank	Consensus s	Homo sapie	B1ANK7 //	gb:AA669797 /DB_XR	BC003108 /	Hs.75653.1	full length
GenBank	Consensus s	Homo sapie	Q96M98	gb:BF224076 /DB_XRE	AF546872 /	Hs.307438.	full length
GenBank	Consensus s	Homo sapie	P05413 /// (	gb:AI041520 /DB_XRE	NM_00410	Hs.49881.1	full length
GenBank	Consensus s	Homo sapie	B3FHX2 ///	gb:BF440025 /DB_XRE	NM_00251	Hs.235935.	full length
GenBank	Consensus s	Homo sapie	B1AKS5 ///	gb:AW085556 /DB_XR	ENST0000	Hs.152663.	full length
GenBank	Consensus s	Homo sapie	Q0VDD5	gb:AF070569.1 /DB_X	BX648321 /	Hs.29206.0	full length
GenBank	Consensus s	Homo sapie	B3KQ42 ///	gb:AW968301 /DB_XR	AK299315	Hs.78743.1	full length
GenBank	Consensus s	Homo sapie	A8K088 ///	gb:U79273.1 /DB_XRE	U79273 // F	Hs.239483.	full length
GenBank	Consensus s	Homo sapie	A4QPB2	gb:AL137651.1 /DB_X	ENST0000	Hs.272317.	full length
GenBank	Consensus s	Homo sapie	B3KTP1 ///	gb:AL359052.1 /DB_X	AL359052 /	Hs.311054.	full length
GenBank	Consensus s	Homo sapie	B4DEP8 ///	gb:H84390 /DB_XREF=	ENST0000	Hs.25300.1	full length
GenBank	Consensus s	Homo sapie	C9J9W8 ///	gb:R59977 /DB_XREF=	ENST0000	Hs.158196.	full length
GenBank	Consensus s	Homo sapiens		gb:AF035278.1 /DB_X	AK092850	Hs.100841.0	
GenBank	Consensus s	Homo sapie	A8MYS5 //	gb:AL0492	ENSP0000	AF159615 /	Hs.133968.	full length
GenBank	Consensus s	Homo sapiens		gb:AL049991.1 /DB_X	AA515614	Hs.226103.0	
GenBank	Consensus s	Homo sapiens		gb:AU148255 /DB_XR	AK024213	Hs.287627.0	
GenBank	Consensus s	Homo sapie	C9JLA2 ///	gb:AL049332.1 /DB_X	AL049332 /	Hs.77311.2	full length
GenBank	Consensus s	Homo sapie	O95661	gb:AK021882.1 /DB_X	AK021882	Hs.194695.	full length
GenBank	Consensus s	Homo sapie	Q6NSF1 ///	gb:AW139369 /DB_XR	AB040887 /	Hs.285848.	full length
GenBank	Consensus s	Homo sapie	A4D0S7 ///	gb:AK027128.1 /DB_X	AK027128	Hs.288982.	full length

GenBank	Consensus s	Homo sapiens		gb:AU157200 /DB_XR		AK023600	Hs.301390.0	
GenBank	Consensus s	Homo sapiens		gb:AL080106.1 /DB_X		AL080106 /	Hs.306323.0	
GenBank	Consensus s	Homo sapiens		gb:AL1374	GENSCAN	GENSCAN	Hs.306457.0	
GenBank	Consensus s	Homo sapie	B7Z5U7 ///	gb:S77154.1 /DB_XRE		ENST0000	Hs.82120.1	full length
GenBank	Consensus s	Homo sapie	B7Z377 ///	gb:AJ224143.1 /DB_X		BC000409 /	Hs.79402.3	full length
GenBank	Consensus s	Homo sapiens		gb:AL110206.1 /DB_X		AL110206 /	Hs.306339.0	
GenBank	Consensus s	Homo sapiens		gb:AL121994 /DB_XR		ENST0000	Hs.302117.0	
GenBank	Consensus s	Homo sapie	P13500 ///	gb:S69738.1 /DB_XRE		BC009716 /	Hs.303649.	full length
GenBank	Consensus s	Homo sapiens		gb:AK025152.1 /DB_X		AK025152	Hs.306773.0	
GenBank	Consensus s	Homo sapie	Q6AW80 //	gb:X89894.1 /DB_XRE		ENST0000	Hs.80561.2	full length
GenBank	Consensus s	Homo sapie	P69849 ///	gb:AL512687.1 /DB_X		AK027144	Hs.227823.	full length
GenBank	Consensus s	Homo sapie	A2AAS2 ///	gb:M80469 GENSCAN		ENST0000	Hs.85242.0	full length
GenBank	Consensus s	Homo sapiens		gb:AW874308 /DB_XR		ENST0000	Hs.332964.0	
GenBank	Consensus s	Homo sapie	C9K0A9 ///	gb:AA721025 /DB_XR		ENST0000	Hs.293253.	full length
GenBank	Consensus s	Homo sapiens		gb:BF725121 /DB_XR		AI354513 /	Hs.272108.	est
GenBank	Exemplar s	Homo sapie	B2R577 ///	gb:NM_014624.2 /DB_		BC001431 /	g9845517	full length
GenBank	Exemplar s	Homo sapie	A2A2F4 ///	gb:NM_02	ENSP0000	AF224278 /	g9910497	full length
GenBank	Consensus s	Homo sapie	A2BDE7 ///	gb:NM_007350.1 /DB_		AK304224	Hs.82101.0	full length
GenBank	Consensus s	Homo sapie	A2BDE7 ///	gb:NM_007350.1 /DB_		ENST0000	Hs.82101.0	full length
GenBank	Consensus s	Homo sapie	B4DSK2 ///	gb:BE5425	ENSP0000	AF247703 /	Hs.14896.0	full length
GenBank	Exemplar s	Homo sapie	Q9BYD3	gb:NM_015956.1 /DB_		AB049635	g7705721	full length
GenBank	Exemplar s	Homo sapie	C9JCH9 ///	gb:NM_01	ENSP0000	AF257182 /	g8923700	full length
GenBank	Exemplar s	Homo sapie	B4DW16 //	gb:NM_01	ENSP0000	BC015591 /	g8922751	full length
GenBank	Exemplar s	Homo sapie	D3DUA6 //	gb:NM_01	ENSP0000	AB035480	g7706185	full length
GenBank	Exemplar s	Homo sapie	Q96AM0 //	gb:NM_021730.1 /DB_		AK057464	g11119423	full length
GenBank	Exemplar s	Homo sapie	D3DTB2 ///	gb:NM_024709.1 /DB_		AK125403	g13376004	full length
GenBank	Consensus s	Homo sapie	B4E0X4 ///	gb:BG223334 /DB_XR		BC010579 /	Hs.224137.	full length
GenBank	Exemplar s	Homo sapie	B2RA37 ///	gb:NM_016173.1 /DB_		AF172244 /	g7705408	full length
GenBank	Exemplar s	Homo sapie	Q86U90	gb:NM_024640.1 /DB_		AK129676	g13375875	full length
GenBank	Exemplar s	Homo sapie	A0FK00 ///	gb:NM_00	ENSP0000	AF075575 /	g4503430	full length
GenBank	Exemplar s	Homo sapie	Q9H6D3 ///	gb:NM_018053.1 /DB_		AK054909	g8922341	full length
GenBank	Exemplar s	Homo sapie	Q24JP5	gb:NM_01	ENSP0000	BC114569 /	g8923509	full length
GenBank	Exemplar s	Homo sapie	B4DFQ6 ///	gb:NM_025149.1 /DB_		AK294205	g13376740	full length
GenBank	Exemplar s	Homo sapie	D3YTC1 ///	gb:NM_016622.1 /DB_		BC020651 /	g7706161	full length
GenBank	Exemplar s	Homo sapie	B7ZLA4 ///	gb:NM_024558.1 /DB_		AK129564	g13375724	full length
GenBank	Exemplar s	Homo sapie	Q9HC36	gb:NM_018146.1 /DB_		BC011550 /	g8922533	full length
GenBank	Exemplar s	Homo sapie	Q8WVD5	gb:NM_016422.1 /DB_		AF214680 /	g7706776	full length
GenBank	Exemplar s	Homo sapie	B3KT87 ///	gb:NM_01	ENSP0000	ENST0000	g8922795	full length
GenBank	Exemplar s	Homo sapie	B4DWA5 /	gb:NM_018326.1 /DB_		ENST0000	g8922872	full length
GenBank	Exemplar s	Homo sapie	B4DSE9 ///	gb:NM_019045.1 /DB_		BC028697 /	g9506636	full length
GenBank	Exemplar s	Homo sapie	B3KUG6 //	gb:NM_017912.1 /DB_		AF336798 /	g8923589	full length
GenBank	Exemplar s	Homo sapie	Q8IUN4 ///	gb:NM_016270.1 /DB_		AF134053 /	g7706468	full length
GenBank	Exemplar s	Homo sapie	B4DT06 ///	gb:NM_02	ENSP0000	AJ277442 /	g11545913	full length
GenBank	Exemplar s	Homo sapie	Q86VZ2	gb:NM_019069.1 /DB_		BC043494 /	g9506644	full length
GenBank	Exemplar s	Homo sapie	B3KWI1 ///	gb:NM_017654.1 /DB_		AF445355 /	g8923080	full length

GenBank	Exemplar s	Homo sapie	Q6PHY4 ///	gb:NM_004923.1 /DB_		BC064579	g4758741	full length
GenBank	Exemplar s	Homo sapie	B9A055 ///	gb:NM_014181.1 /DB_		BC036082	g7661817	full length
GenBank	Exemplar s	Homo sapie	B7Z790 ///	gb:NM_022098.1 /DB_		AL834310	g11559924	full length
GenBank	Exemplar s	Homo sapie	B3KVR5 //	gb:NM_017805.1 /DB_		AK123179	g8923375	full length
GenBank	Exemplar s	Homo sapie	C9JPL0 ///	gb:NM_020307.1 /DB_		AF180920	g9945319	full length
GenBank	Exemplar s	Homo sapie	D3DRE7 ///	gb:NM_022466.1 /DB_		AF230808	g11968012	full length
GenBank	Exemplar s	Homo sapie	B4DJI7 ///	gb:NM_013323.1 /DB_		AF121861	g7019538	full length
GenBank	Exemplar s	Homo sapie	A8K364 ///	gb:NM_018846.1 /DB_		AF111113	g9055325	full length
GenBank	Exemplar s	Homo sapie	B4DDS9 ///	gb:NM_024935.1 /DB_		AK293321	g13376407	full length
GenBank	Exemplar s	Homo sapie	A8K322 ///	gb:NM_006550.1 /DB_		AF007866	g5729829	full length
GenBank	Exemplar s	Homo sapie	B4DF77 ///	gb:NM_018026.1 /DB_		BC010096	g8922284	full length
GenBank	Exemplar s	Homo sapie	A8K572 ///	gb:NM_025184.1 /DB_		AK026254	g13376775	full length
GenBank	Exemplar s	Homo sapie	Q96PQ7	gb:NM_015990.1 /DB_		AF123320	g10242378	
GenBank	Exemplar s	Homo sapie	B4DSE1 ///	gb:AF105421.1 /DB_X		AF105421	g4838128	full length
GenBank	Exemplar s	Homo sapie	B7ZMF5 //	gb:U11058.2 /DB_XRE		ENST0000	g7914977	full length
GenBank	Consensus	Homo sapie	A0PJE4 ///	gb:AI694023 /DB_XRE		AK123507	Hs.6685.0	full length
GenBank	Consensus	Homo sapie	P69849 ///	gb:N39536 /DB_XREF		AK027144	Hs.322466.	full length
GenBank	Consensus	Homo sapie	A2AAS2 //	gb:BE138825 /DB_XR		ENST0000	Hs.110309.	full length
GenBank	Consensus	Homo sapie	A6NEG5 //	gb:BF062886 /DB_XR		AB031052	Hs.98289.1	full length
GenBank	Consensus	Homo sapie	A7U7M2 //	gb:AL1333	ENSP0000	AF086354	Hs.121281.	full length
GenBank	Consensus	Homo sapie	B4DLZ6 ///	gb:AK001363.1 /DB_X		AK297225	Hs.48604.1	full length
GenBank	Consensus	Homo sapiens		gb:AV700891 /DB_XR		AY216265	Hs.292477.0	
GenBank	Consensus	Homo sapiens		gb:AW972292 /DB_XR		XR_108684	Hs.292998.0	
GenBank	Exemplar s	Homo sapie	B8ZZT7 ///	gb:AF060925.1 /DB_X		AF060925	g12001987	full length
GenBank	Consensus	Homo sapie	C9JQ48 ///	gb:AW303359 /DB_XR		BC031481	Hs.6120.0	full length
GenBank	Consensus	Homo sapie	A6NEC1 //	gb:AU137607 /DB_XR		AB063115	Hs.23467.0	full length
GenBank	Consensus	Homo sapie	C9IYT4 ///	gb:AA044921 /DB_XR		AK125062	Hs.44423.0	full length
GenBank	Consensus	Homo sapie	Q9H816	gb:AI703304 /DB_XRE		BC029687	Hs.115660.	full length
GenBank	Exemplar s	Homo sapie	Q5HYL6 //	gb:AF177171.1 /DB_X		AF177171	g6934243	full length
GenBank	Consensus	Homo sapie	B3KMG4 /	gb:AA8549	ENSP0000	AY358503	Hs.168640.	full length
GenBank	Consensus	Homo sapie	B1AKK6 //	gb:AI159874 /DB_XRE		AF312864	Hs.12532.0	full length
GenBank	Exemplar s	Homo sapie	C9J5G8 ///	gb:AB037925.1 /DB_X		AB037925	g13516830	full length
GenBank	Exemplar s	Homo sapie	A8MSZ2 //	gb:AB014737.1 /DB_X		AB014730	g12248772	full length
GenBank	Exemplar s	Homo sapie	A8K5F3 ///	gb:BC004270.1 /DB_X		AB209145	g13279079	full length
GenBank	Exemplar s	Homo sapie	A1L0U7 ///	gb:AL136805.1 /DB_X		ENST0000	g12053120	full length
GenBank	Consensus	Homo sapie	Q9H1B7	gb:AI932310 /DB_XRE		BC108292	Hs.179260.	full length
GenBank	Exemplar s	Homo sapie	A1A564 ///	gb:AF317391.1 /DB_X		AF317391	g11907997	full length
GenBank	Exemplar s	Homo sapie	C9JI11 ///	gb:AF151831.1 /DB_X		AB040922	g4929614	full length
GenBank	Exemplar s	Homo sapie	A0JP06 ///	gb:AL136867.1 /DB_X		AB051470	g12053238	full length
GenBank	Exemplar s	Homo sapie	B8ZZE5 ///	gb:AF3255	ENSP0000	AF325503	g11991655	full length
GenBank	Exemplar s	Homo sapie	D3DV12 ///	gb:AF286592.1 /DB_X		AF187845	g10444116	full length
GenBank	Exemplar s	Homo sapie	A5PKX9 ///	gb:AB044807.1 /DB_X		AB044807	g11933154	full length
GenBank	Exemplar s	Homo sapie	Q9H397	gb:AF130079.1 /DB_X		AF130079	g11493462	
GenBank	Exemplar s	Homo sapie	B8ZZ69 ///	gb:AF128846.1 /DB_X		AF128846	g6580814	full length
GenBank	Exemplar s	Homo sapie	B2RDT5 ///	gb:BC0062	ENSP0000	ENST0000	g13623391	full length

GenBank	Exemplar s	Homo sapie	B7Z3T4 ///	gb:AF0812	GENSCAN	AF081249 /	g4587966	full length
GenBank	Consensus s	Homo sapie	B5MEC5 //	gb:BF2475	ENSP0000	ENST0000	Hs.193063.	full length
GenBank	Consensus s	Homo sapie	Q6AHX3 //	gb:AL1185	ENSP0000	AK074041	Hs.165563.	full length
GenBank	Consensus s	Homo sapie	B4E0U9 ///	gb:BF796046 /DB_XRI		BC065280 /	Hs.17448.0	full length
GenBank	Consensus s	Homo sapie	Q14258 ///	gb:BE563152 /DB_XRI		ENST0000	Hs.10362.0	full length
GenBank	Consensus s	Homo sapie	D3DW06 //	gb:AK001947.1 /DB_X		AL833069 /	Hs.171917.	full length
GenBank	Consensus s	Homo sapie	Q49A97 ///	gb:BE964325 /DB_XRI		AK023161	Hs.17283.1	full length
GenBank	Consensus s	Homo sapie	B3KXL2 //	gb:AL035661 /DB_XRI		AK125058	Hs.7218.0	full length
GenBank	Consensus s	Homo sapie	B4DTA7 //	gb:BF107618 /DB_XRI		AY189937	Hs.250655.	full length
GenBank	Consensus s	Homo sapie	Q96MK8	gb:AL575306 /DB_XRI		BC063626 /	Hs.279525.0	
GenBank	Consensus s	Homo sapie	B4DWX0 /	gb:BF512188 /DB_XRI		AB032961	Hs.16758.0	full length
GenBank	Consensus s	Homo sapie	B4DK20 ///	gb:AI818048 /DB_XRE		AJ420510 /	Hs.7759.0	full length
GenBank	Consensus s	Homo sapie	B8ZZ37 ///	gb:AI963008 /DB_XRE		BX537494	Hs.232400.	full length
GenBank	Consensus s	Homo sapie	A7E2A6 ///	gb:AF131774.1 /DB_X		ENST0000	Hs.62119.0	full length
GenBank	Consensus s	Homo sapie	Q8NI37	gb:AW300598 /DB_XR		AK098051	Hs.13854.0	full length
GenBank	Consensus s	Homo sapiens		gb:BF340290 /DB_XRI		BC017993 /	Hs.296141.0	
GenBank	Consensus s	Homo sapie	P22681	gb:AV710415 /DB_XR		ENST0000	Hs.90960.0	full length
GenBank	Consensus s	Homo sapiens		gb:AU155376 /DB_XR		AK125888	Hs.6630.0	
GenBank	Consensus s	Homo sapie	B3KNY6 //	gb:AI954700 /DB_XRE		AF419331 /	Hs.288038.	full length
GenBank	Consensus s	Homo sapie	D3DRM5 //	gb:AL528391 /DB_XRI		BC032136 /	Hs.278242.	full length
GenBank	Consensus s	Homo sapie	Q8TDB6	gb:AA577672 /DB_XR		BX648267	Hs.16331.0	full length
GenBank	Consensus s	Homo sapie	A5PLN2 ///	gb:AI638279 /DB_XRE		AL109785 /	Hs.119155.	full length
GenBank	Consensus s	Homo sapie	Q8N6U0 ///	gb:AI091372 /DB_XRE		AB053121	Hs.6607.0	full length
GenBank	Consensus s	Homo sapie	C9J9V2 ///	gb:AI921788 /DB_XRE		BC001622 /	Hs.30488.1	full length
GenBank	Consensus s	Homo sapiens		gb:AI825833 /DB_XRE		BC036544 /	Hs.155364.0	
GenBank	Consensus s	Homo sapie	B2R6J3 ///	gb:AV702487 /DB_XR		AK295211	Hs.12106.0	full length
GenBank	Consensus s	Homo sapie	A8MRR6 //	gb:BE502436 /DB_XRI		BC012198 /	Hs.7962.0	full length
GenBank	Consensus s	Homo sapie	B2RCC7 ///	gb:BF6805	ENSP0000	AF455138 /	Hs.118258.	full length
GenBank	Consensus s	Homo sapie	C9JCP4 ///	gb:AI954660 /DB_XRE		AL161961 /	Hs.17767.0	full length
GenBank	Consensus s	Homo sapie	B3KW24 //	gb:AA524005 /DB_XR		ENST0000	Hs.88594.0	full length
GenBank	Consensus s	Homo sapie	A4D214 ///	gb:BG231691 /DB_XR		BC012777 /	Hs.11607.0	full length
GenBank	Consensus s	Homo sapie	Q96GX3 ///	gb:AI309554 /DB_XRE		AB075482	Hs.154697.	full length
GenBank	Consensus s	Homo sapie	A7MD47 //	gb:AI741051 /DB_XRE		ENST0000	Hs.296317.	full length
GenBank	Consensus s	Homo sapie	B0YIW9 ///	gb:AW270158 /DB_XR		AL133611 /	Hs.25362.0	full length
GenBank	Consensus s	Homo sapie	A8MUS2 //	gb:AI672662 /DB_XRE		ENST0000	Hs.6567.1	full length
GenBank	Consensus s	Homo sapie	B4E3D2 ///	gb:BE218238 /DB_XRI		AB051491	Hs.283709.	full length
GenBank	Consensus s	Homo sapie	Q96E14	gb:AW138157 /DB_XR		BC013040 /	Hs.77448.2	full length
GenBank	Consensus s	Homo sapiens		gb:AI672159 /DB_XRE		BC090942 /	Hs.91389.0	
GenBank	Consensus s	Homo sapie	B3KUL1 //	gb:BE551849 /DB_XRI		NM_00113	Hs.108082.	full length
GenBank	Consensus s	Homo sapie	A8K2A5 ///	gb:AI984061 /DB_XRE		AK290170	Hs.116567.	full length
GenBank	Consensus s	Homo sapie	Q8N6N6	gb:H27948 /DB_XREF=		ENST0000	Hs.14478.0	full length
GenBank	Consensus s	Homo sapie	B1AK40 ///	gb:AI341467 /DB_XRE		ENST0000	Hs.322482.	full length
GenBank	Consensus s	Homo sapie	Q9NPA8	gb:BF433516 /DB_XRI		ENST0000	Hs.44243.0	full length
GenBank	Consensus s	Homo sapie	A8K6G4 ///	gb:AA1479	ENSP0000	AK055628	Hs.8895.0	full length
GenBank	Consensus s	Homo sapie	B0QY31 ///	gb:T51255 /DB_XREF=		AK057067	Hs.5722.1	full length

GenBank	Consensus	Homo sapie	B4DYQ4 //	gb:AI674565 /DB_XRE	AL137761	Hs.8379.0	full length
GenBank	Consensus	Homo sapie	Q06210 ///	gb:AF131846.1 /DB_X	NM_00205	Hs.13396.0	full length
GenBank	Consensus	Homo sapie	P47928	gb:AV646610 /DB_XR	AA001053	Hs.34853.1	full length
GenBank	Consensus	Homo sapie	B3KSF5 ///	gb:AK002203.1 /DB_X	AK123698	Hs.10260.0	full length
GenBank	Consensus	Homo sapiens		gb:BF438330 /DB_XR	BC067285	Hs.182469.0	
GenBank	Consensus	Homo sapie	C9J520 ///	gb:N50665 /DB_XREF	ENST0000	Hs.300511.	full length
GenBank	Consensus	Homo sapie	Q6P5X5	gb:AA194312 /DB_XR	AK095271	Hs.119960.	full length
GenBank	Consensus	Homo sapie	Q7Z7L8	gb:AW276078 /DB_XR	NM_00114	Hs.127824.	full length
GenBank	Consensus	Homo sapie	C9J1Q8 ///	gb:N93191 ENSP0000	AK026464	Hs.26216.0	full length
GenBank	Consensus	Homo sapie	A8K2P6 ///	gb:AA603467 /DB_XR	BC011625	Hs.182740.	full length
GenBank	Consensus	Homo sapie	A6NMA2 /	gb:AW593303 /DB_XR	AB033099	Hs.23413.1	
GenBank	Consensus	Homo sapie	Q25QX8 ///	gb:AI474448 /DB_XRE	AL834299	Hs.8184.0	full length
GenBank	Consensus	Homo sapie	B7WNX9 /	gb:AA811509 /DB_XR	AK096952	Hs.103441.	full length
GenBank	Consensus	Homo sapie	Q6NW40	gb:BE206621 /DB_XR	BC067736	Hs.108972.	full length
GenBank	Consensus	Homo sapie	Q5H9R4 ///	gb:AW519141 /DB_XR	AY726601	Hs.69705.0	full length
GenBank	Consensus	Homo sapie	Q7RTY1	gb:BG4015 ENSP0000	ENST0000	Hs.238927.	full length
GenBank	Consensus	Homo sapie	A6NEC7 ///	gb:BF511276 /DB_XR	ENST0000	Hs.38022.0	full length
GenBank	Consensus	Homo sapie	A6NEC7 ///	gb:BF511276 /DB_XR	ENST0000	Hs.38022.0	full length
GenBank	Consensus	Homo sapie	Q6ICF3 ///	gb:BE501980 /DB_XR	AK127072	Hs.108358.	full length
GenBank	Consensus	Homo sapie	O14543 ///	gb:AI244908 /DB_XRE	BC060858	Hs.311405.	full length
GenBank	Consensus	Homo sapie	Q5VVE5 //	gb:AA5573 ENSP0000	AK091806	Hs.26040.0	full length
GenBank	Consensus	Homo sapie	B2RBM1 //	gb:AL589605 /DB_XR	AL832322	Hs.85428.0	full length
GenBank	Consensus	Homo sapie	Q49A68 ///	gb:AI67117 ENSP0000	AF147306	Hs.280858.	full length
GenBank	Consensus	Homo sapie	Q96HQ8	gb:N90774 /DB_XREF	BC008254	Hs.252433.	full length
GenBank	Consensus	Homo sapiens		gb:AI798680 /DB_XRE	AA436252	Hs.25933.0	est
GenBank	Consensus	Homo sapie	B7Z1J9 ///	gb:AI139988 /DB_XRE	AK128653	Hs.298262.	full length
GenBank	Consensus	Homo sapie	B7Z1I7 ///	gb:AI653107 /DB_XRE	BX538345	Hs.30643.0	full length
GenBank	Consensus	Homo sapie	A8K014 ///	gb:AL552470 /DB_XR	BC017117	Hs.155924.	full length
GenBank	Consensus	Homo sapie	B2RBG2 ///	gb:AW292746 /DB_XR	AF006003	Hs.20072.2	full length
GenBank	Consensus	Homo sapie	Q5SGD2	gb:AW274846 /DB_XR	BC035116	Hs.19339.0	full length
GenBank	Consensus	Homo sapiens		gb:AL137310.1 /DB_X	AK124576	Hs.4749.0	
GenBank	Consensus	Homo sapiens		gb:BE048571 /DB_XR	ENST0000	Hs.108785.0	
GenBank	Consensus	Homo sapie	Q86WA0 //	gb:AI989706 /DB_XRE	BC042804	Hs.21454.0	full length
GenBank	Consensus	Homo sapie	B3KP42 ///	gb:AI363213 /DB_XRE	U00948 //	Hs.278634.	full length
GenBank	Consensus	Homo sapiens		gb:BF197118 /DB_XR	BC056670	Hs.184156.0	
GenBank	Consensus	Homo sapie	Q5SGD2	gb:AI590190 /DB_XRE	BC035116	Hs.12731.0	full length
GenBank	Consensus	Homo sapiens		gb:T87628 /DB_XREF	ENST0000	Hs.184993.0	
GenBank	Consensus	Homo sapiens		gb:AI491983 /DB_XRE	ENST0000	Hs.322704.0	
GenBank	Consensus	Homo sapie	Q8N512	gb:AA894611 /DB_XR	BC037415	Hs.85279.1	
GenBank	Consensus	Homo sapie	B3KPW1 //	gb:AA142842 /DB_XR	BX649188	Hs.154993.	full length
GenBank	Consensus	Homo sapie	A4D0V7 ///	gb:BF7241 ENSP0000	AL832619	Hs.24144.0	full length
GenBank	Consensus	Homo sapiens		gb:AW236803 /DB_XR	AK001875	Hs.24321.0	
GenBank	Consensus	Homo sapiens		gb:AI693516 /DB_XRE	AA298713	Hs.28625.0	est
GenBank	Consensus	Homo sapie	A5D6Y4 ///	gb:AI279868 /DB_XRE	BC042363	Hs.55888.1	full length
GenBank	Consensus	Homo sapie	B0V0L0 ///	gb:AA775731 /DB_XR	ENST0000	Hs.117406.	full length

GenBank	Consensus	Homo sapie	B3KUA4 //	gb:AI379517 /DB_XR	AK096811	Hs.127826.	full length
GenBank	Consensus	Homo sapie	B4DHY0 //	gb:AI570494 /DB_XR	AK093005	Hs.215937.	full length
GenBank	Consensus	Homo sapie	A1YZ20 ///	gb:AI692659 /DB_XR	AY198414	Hs.289088.	full length
GenBank	Consensus	Homo sapie	B4E3D2 ///	gb:AI073486 /DB_XR	AB051491	Hs.283709.	full length
GenBank	Consensus	Homo sapie	B9EG57 ///	gb:BF055127 /DB_XR	AK095570	Hs.110041.	full length
GenBank	Consensus	Homo sapie	Q5T0N1	gb:AW024437 /DB_XR	AF435959	Hs.110667.	full length
GenBank	Consensus	Homo sapie	O15131 ///	gb:BG231980 /DB_XR	ENST0000	Hs.32615.0	full length
GenBank	Consensus	Homo sapie	B4DZU5 //	gb:AA641254 /DB_XR	BC033728	Hs.306088.	full length
GenBank	Consensus	Homo sapie	C9JFR7 ///	gb:BF593856 /DB_XR	NM_01894	Hs.157301.	full length
GenBank	Consensus	Homo sapiens		gb:AI609256 /DB_XR	ENST0000	Hs.270956.1	
GenBank	Consensus	Homo sapiens		gb:AA868461 /DB_XR	AA868461	Hs.7753.2	est
GenBank	Consensus	Homo sapie	B4E223 ///	gb:AI890299 /DB_XR	AF086471	Hs.44425.0	full length
GenBank	Consensus	Homo sapie	B7WNX9 /	gb:AI380156 /DB_XR	AK096952	Hs.103441.	full length
GenBank	Consensus	Homo sapie	C9IYC1 ///	gb:AW629527 /DB_XR	AK123232	Hs.127780.	full length
GenBank	Consensus	Homo sapie	A6NIT2 ///	gb:BE503584 /DB_XR	ENST0000	Hs.296095.	full length
GenBank	Consensus	Homo sapie	A2A2Y4 ///	gb:BF589413 /DB_XR	BX647549	Hs.55501.0	full length
GenBank	Consensus	Homo sapie	Q5QHF1	gb:AI625235 /DB_XR	AK124175	Hs.284158.	full length
GenBank	Consensus	Homo sapie	Q96BM0	gb:AL039706 /DB_XR	CR625015	Hs.19414.0	full length
GenBank	Consensus	Homo sapie	B7Z3T4 ///	gb:AL044056 /DB_XR	ENST0000	Hs.158047.	full length
GenBank	Consensus	Homo sapie	B4DS74 ///	gb:T90642 /DB_XREF	AA045814	Hs.326416.	full length
GenBank	Consensus	Homo sapie	B4DNN8 //	gb:AF272898.1 /DB_X	ENST0000	Hs.135118.	full length
GenBank	Consensus	Homo sapie	A6NC05	gb:AI418538 /DB_XR	NM_00116	Hs.49573.0	full length
GenBank	Consensus	Homo sapiens		gb:BF111884 /DB_XR	BX649153	Hs.79953.0	
GenBank	Consensus	Homo sapie	D3DQ62 ///	gb:AI566130 /DB_XR	ENST0000	Hs.292805.	full length
GenBank	Consensus	Homo sapiens		gb:AA195276 /DB_XR	AK126749	Hs.263858.0	
GenBank	Consensus	Homo sapiens		gb:AI360054 /DB_XR	AA659718	Hs.17910.0	est
GenBank	Consensus	Homo sapiens		gb:BE674309 /DB_XR	AF086547	Hs.59525.0	
GenBank	Consensus	Homo sapie	C9JX76 ///	gb:AL034550 /DB_XR	AK097804	Hs.126373.	full length
GenBank	Consensus	Homo sapie	B7Z2T7 ///	gb:BE672499 /DB_XR	ENST0000	Hs.129997.	full length
GenBank	Consensus	Homo sapiens		gb:AW953794 /DB_XR	CR622072	Hs.12549.0	
GenBank	Consensus	Homo sapie	A8MXG8	gb:AI479923 /DB_XR	ENST0000	Hs.148425.0	
GenBank	Consensus	Homo sapie	A6NEC7 //	gb:BF114967 /DB_XR	AA987332	Hs.38022.1	full length
GenBank	Consensus	Homo sapie	B4DT97 ///	gb:BE674103 /DB_XR	BC051874	Hs.130909.	full length
GenBank	Consensus	Homo sapie	B4DRE2 ///	gb:AA683602 /DB_XR	ENST0000	Hs.50745.0	full length
GenBank	Consensus	Homo sapiens		gb:BE676062 /DB_XR	ENST0000	Hs.321669.2	
GenBank	Consensus	Homo sapiens		gb:AI371550 /DB_XR	AA129958	Hs.154173.	est
GenBank	Consensus	Homo sapie	Q6IQ55 ///	gb:BF433088 /DB_XR	AI689827 /	Hs.125836.	full length
GenBank	Consensus	Homo sapie	A8K793 ///	gb:AL359575.1 /DB_X	AF425266	Hs.23765.0	full length
GenBank	Consensus	Homo sapie	B4DDN3 //	gb:AB0329 ENSP0000	ENST0000	Hs.173560.	full length
GenBank	Consensus	Homo sapie	Q9ULE6	gb:AB033100.1 /DB_X	ENST0000	Hs.300646.	full length
GenBank	Consensus	Homo sapie	A6PVX2 //	gb:AU152102 /DB_XR	AK023055	Hs.199647.	full length
GenBank	Consensus	Homo sapie	A6NLQ3 //	gb:AK027184.1 /DB_X	AK027184	Hs.99872.2	full length
GenBank	Consensus	Homo sapie	A8K4M9 //	gb:AF130076.1 /DB_X	AY373756	Hs.22116.4	full length
GenBank	Consensus	Homo sapie	A2A3H9 ///	gb:AK025185.1 /DB_X	AF489824	Hs.289005.	full length
GenBank	Consensus	Homo sapie	B4DZQ0 //	gb:AI657019 /DB_XR	AK023612	Hs.145629.	full length

GenBank	Consensus s	Homo sapie	A5PKZ1 ///	gb:AK0221	ENSP0000(	AK022198	Hs.168830.	full length
GenBank	Consensus s	Homo sapie	A8K4H5 ///	gb:AK021494.1 /DB_X		ENST0000(	Hs.166486.	full length
GenBank	Consensus s	Homo sapie	A3KMR5 //	gb:AK022257.1 /DB_X		AK022257	Hs.179647.	full length
GenBank	Consensus s	Homo sapiens		gb:BE815259 /DB_XRI		AK024522	Hs.194101.0	
GenBank	Consensus s	Homo sapie	Q75NE6	gb:AA256157 /DB_XR		AB176707	Hs.24115.0	full length
GenBank	Consensus s	Homo sapie	Q4FD35 ///	gb:AI962891 /DB_XRE		BX648311	Hs.273294.	full length
GenBank	Consensus s	Homo sapiens		gb:AK022461.1 /DB_X		AK022461	Hs.287528.0	
GenBank	Consensus s	Homo sapiens		gb:AK027139.1 /DB_X		AK027139	Hs.33130.0	
GenBank	Consensus s	Homo sapiens		gb:AU144570 /DB_XR		AK021581	Hs.170264.0	
GenBank	Consensus s	Homo sapie	B7ZKR8 ///	gb:AK000110.1 /DB_X		AK000110	Hs.178518.	full length
GenBank	Consensus s	Homo sapie	B2RAT6 ///	gb:AA453223 /DB_XR		AK096137	Hs.75641.1	full length
GenBank	Consensus s	Homo sapie	C9JP51 /// (	gb:AU158601 /DB_XR		AK024378	Hs.141660.	full length
GenBank	Consensus s	Homo sapie	B3KVG3 //	gb:AU145382 /DB_XR		AK096233	Hs.229084.0	
GenBank	Consensus s	Homo sapie	C9JCE0 ///	gb:N59653 /DB_XREF		AB209547	Hs.231967.	full length
GenBank	Consensus s	Homo sapie	A8K6R4 ///	gb:BF514791 /DB_XRI		AA731778	Hs.293914.	full length
GenBank	Consensus s	Homo sapie	Q6UWR5 /	gb:AB0330	ENSP0000(	AK309308	Hs.100747.	full length
GenBank	Consensus s	Homo sapie	A8K4A1 ///	gb:AK000455.1 /DB_X		AK000455	Hs.14632.1	full length
GenBank	Consensus s	Homo sapiens		gb:AK000850.1 /DB_X		GQ497714	Hs.272203.0	
GenBank	Consensus s	Homo sapie	Q9NYI4	gb:BE540060 /DB_XRI		AA303392	Hs.272415.0	
GenBank	Consensus s	Homo sapie	C9J998 /// (	gb:AK001834.1 /DB_X		AK001834	Hs.3542.1	full length
GenBank	Consensus s	Homo sapiens		gb:AL049975.1 /DB_X		AL049975	Hs.274510.0	
GenBank	Consensus s	Homo sapiens		gb:AL109791.1 /DB_X		AL109791	Hs.241559.0	
GenBank	Consensus s	Homo sapie	A6NKL4 //	gb:AK021547.1 /DB_X		AK021547	Hs.22983.1	full length
GenBank	Consensus s	Homo sapie	B4DUV6 //	gb:AB032979.1 /DB_X		AB032979	Hs.128791.	full length
GenBank	Consensus s	Homo sapiens		gb:AU147174 /DB_XR		AK022155	Hs.296697.0	
GenBank	Consensus s	Homo sapiens		gb:AL137541.1 /DB_X		AL137541	Hs.306471.0	
GenBank	Consensus s	Homo sapiens		gb:AK000019.1 /DB_X		AK000019	Hs.306375.0	
GenBank	Consensus s	Homo sapiens		gb:AK021431.1 /DB_X		AK021431	Hs.235543.0	
GenBank	Consensus s	Homo sapie	Q96HQ2	gb:AL571598 /DB_XRI		BC008293	Hs.293659.	full length
GenBank	Consensus s	Homo sapie	Q8IWZ6	gb:AI683802 /DB_XRE		ENST0000(	Hs.136182.	full length
GenBank	Consensus s	Homo sapie	Q6ZTF7 ///	gb:BF956762 /DB_XRI		AK098378	Hs.53112.0	full length
GenBank	Consensus s	Homo sapiens		gb:AI684439 /DB_XRE		AA987505	Hs.331099.	est
GenBank	Consensus s	Homo sapie	Q96D59	gb:BE7961	ENSP0000(	BC013036	Hs.211374.	full length
GenBank	Consensus s	Homo sapie	B4E2F1 ///	gb:BG260886 /DB_XR		ENST0000(	Hs.138360.	full length
GenBank	Consensus s	Homo sapie	B3KXT2 ///	gb:BE780502 /DB_XRI		AF502591	Hs.145704.	full length
GenBank	Consensus s	Homo sapiens		gb:AA398756 /DB_XR		AK098016	Hs.21108.0	
GenBank	Consensus s	Homo sapie	O60939 /// (	gb:AA447729 /DB_XR		NM_00458	Hs.12714.0	full length
GenBank	Consensus s	Homo sapie	B3KVC8 //	gb:AI88825	ENSP0000(	AK093417	Hs.307526.	full length
GenBank	Consensus s	Homo sapie	B5MEA6 //	gb:AI539542 /DB_XRE		AK090826	Hs.143810.	full length
GenBank	Consensus s	Homo sapiens		gb:AW960145 /DB_XR		AK093529	Hs.100636.0	
GenBank	Consensus s	Homo sapiens		gb:AI742077 /DB_XRE		AI434798 /	Hs.164303.	est
GenBank	Consensus s	Homo sapiens		gb:AI914925 /DB_XRE		AI914925 /	Hs.222240.	est
GenBank	Consensus s	Homo sapie	B4DUU9 //	gb:AI992283 /DB_XRE		ENST0000(	Hs.35437.0	full length
GenBank	Consensus s	Homo sapiens		gb:BF000047 /DB_XRI		BC050400	Hs.178144.0	
GenBank	Consensus s	Homo sapiens		gb:AA523939 /DB_XR		AA235472	Hs.165258.	est

GenBank	Consensus s	Homo sapie	B4DIF3 ///	gb:BE672408 /DB_XR		ENST0000	Hs.107708.	full length
GenBank	Consensus s	Homo sapie	A8K5E1 ///	gb:AI672373 /DB_XRE		ENST0000	Hs.183950.	full length
GenBank	Consensus s	Homo sapie	Q3BBU4 //	gb:AW269499 /DB_XR		AK123260	Hs.247677.	full length
GenBank	Consensus s	Homo sapiens		gb:AA767373 /DB_XR		AA767373	Hs.35669.0	
GenBank	Consensus s	Homo sapie	B3KT16 ///	gb:BF4323	ENSP0000	AK094780	Hs.63163.0	full length
GenBank	Consensus s	Homo sapiens		gb:AI860775 /DB_XRE		AA425940	Hs.98506.0	est
GenBank	Consensus s	Homo sapie	C9JT49 ///	gb:BF056459 /DB_XR		ENST0000	Hs.126389.	full length
GenBank	Consensus s	Homo sapiens		gb:H15073 /DB_XREF		AI283763 /	Hs.151124.	est
GenBank	Consensus s	Homo sapiens		gb:AI760366 /DB_XRE		AK098572	Hs.144923.0	
GenBank	Consensus s	Homo sapie	B3KT77 ///	gb:AW975772 /DB_XR		AK130856	Hs.120277.	full length
GenBank	Consensus s	Homo sapiens		gb:BF515552 /DB_XR		AA827702	Hs.244583.	est
GenBank	Consensus s	Homo sapiens		gb:AA890487 /DB_XR		N90564 // z	Hs.24598.0	est
GenBank	Consensus s	Homo sapiens		gb:BE348304 /DB_XR		AI681904 /	Hs.202259.	est
GenBank	Consensus s	Homo sapiens		gb:AV736334 /DB_XR		AV737724	Hs.293379.	est
GenBank	Consensus s	Homo sapiens		gb:BE669493 /DB_XR		ENST0000	Hs.170427.0	
GenBank	Consensus s	Homo sapiens		gb:BE501281 /DB_XR		BE501281 /	Hs.232311.0	
GenBank	Consensus s	Homo sapiens		gb:N62721 /DB_XREF		BC071723 /	Hs.47142.0	
GenBank	Consensus s	Homo sapiens		gb:AA033987 /DB_XR		AA033987	Hs.59300.0	
GenBank	Consensus s	Homo sapie	Q6X854	gb:AI694300 /DB_XRE		AY250185	Hs.46730.0	
GenBank	Consensus s	Homo sapiens		gb:BF110268 /DB_XR		AI694640 /	Hs.264433.	est
GenBank	Consensus s	Homo sapie	Q5VU92	gb:AW572906 /DB_XR		BC035674 /	Hs.120403.	full length
GenBank	Consensus s	Homo sapiens		gb:AW015521 /DB_XR		AI306503 /	Hs.141604.	est
GenBank	Consensus s	Homo sapie	B4E0B1 ///	gb:AI923675 /DB_XRE		AL832814 /	Hs.133526.	full length
GenBank	Consensus s	Homo sapie	B4DQF0 ///	gb:AW392551 /DB_XR		ENST0000	Hs.180559.	full length
GenBank	Consensus s	Homo sapie	B4DLB8 ///	gb:AL574435 /DB_XR		CR605922 /	Hs.176725.	full length
GenBank	Consensus s	Homo sapiens		gb:AW675572 /DB_XR		AI248270 /	Hs.193620.0	
GenBank	Consensus s	Homo sapiens		gb:AA322245 /DB_XR		AA322245	Hs.290165.	est
GenBank	Consensus s	Homo sapiens		gb:AI538454 /DB_XRE		BC060883 /	Hs.87636.0	
GenBank	Consensus s	Homo sapie	Q05D32	gb:AW169159 /DB_XR		ENST0000	Hs.125882.	full length
GenBank	Consensus s	Homo sapie	D3DQA2 //	gb:AW364833 /DB_XR		BC005979 /	Hs.165681.	full length
GenBank	Consensus s	Homo sapie	Q6AI35 ///	gb:AI28418	GENSCAN	AF423307 /	Hs.154009.	full length
GenBank	Consensus s	Homo sapiens		gb:AI972146 /DB_XRE		AA731334	Hs.192756.0	
GenBank	Consensus s	Homo sapiens		gb:AI308862 /DB_XRE		XR_114661	Hs.167028.0	
GenBank	Consensus s	Homo sapie	D3DQZ2 //	gb:AI12753	ENSP0000	AY054392	Hs.146442.	full length
GenBank	Consensus s	Homo sapiens		gb:BE674693 /DB_XR		AA629007	Hs.190447.	est
GenBank	Consensus s	Homo sapie	A8K972 ///	gb:AA993400 /DB_XR		BC075857 /	Hs.161274.	full length
GenBank	Consensus s	Homo sapie	A8KA89 ///	gb:BF435923 /DB_XR		ENST0000	Hs.121682.	full length
GenBank	Consensus s	Homo sapiens		gb:AI243098 /DB_XRE		AA290627	Hs.178398.	est
GenBank	Consensus s	Homo sapiens		gb:BE349858 /DB_XR		AI277134 /	Hs.148078.	est
GenBank	Consensus s	Homo sapie	B4DKF6 ///	gb:N50117 /DB_XREF		ENST0000	Hs.25131.0	full length
GenBank	Consensus s	Homo sapiens		gb:BF002339 /DB_XR		BF002339 /	Hs.158528.0	
GenBank	Consensus s	Homo sapie	A4D1T5 ///	gb:AA699958 /DB_XR		ENST0000	Hs.188521.	full length
GenBank	Consensus s	Homo sapiens		gb:AI253622 /DB_XRE		AK095426	Hs.145411.0	
GenBank	Consensus s	Homo sapiens		gb:AA947873 /DB_XR		AA947873	Hs.134501.0	
GenBank	Consensus s	Homo sapiens		gb:AI652000 /DB_XRE		AI652000 /	Hs.195048.	est

GenBank	Consensus s	Homo sapie	B2RB37 ///	gb:H18004 /DB_XREF=		AK095773	Hs.260282.	full length
GenBank	Consensus s	Homo sapie	B4DEN1 ///	gb:AI939308 /DB_XRE		AK055501	Hs.134772.	full length
GenBank	Consensus s	Homo sapiens		gb:AI435335 /DB_XRE		AI276722 /	Hs.270036.	est
GenBank	Consensus s	Homo sapiens		gb:AA702111 /DB_XR		AA702111	Hs.270047.0	
GenBank	Consensus s	Homo sapiens		gb:AI654048 /DB_XRE		AI654048 /	Hs.196556.	est
GenBank	Consensus s	Homo sapie	C9JCP4 ///	gb:AA936632 /DB_XR		ENST0000	Hs.189284.	full length
GenBank	Consensus s	Homo sapie	A6NC62 ///	gb:BE618393 /DB_XR		ENST0000	Hs.54811.0	full length
GenBank	Consensus s	Homo sapie	B7Z295 ///	gb:W35132 /DB_XREF		ENST0000	Hs.267442.	full length
GenBank	Consensus s	Homo sapiens		gb:W80457 /DB_XREF		AA504359	Hs.110067.	est
GenBank	Consensus s	Homo sapiens		gb:BF109952 /DB_XR		BC037791 /	Hs.283396.0	
GenBank	Consensus s	Homo sapiens		gb:AW469777 /DB_XR		BC024230 /	Hs.145225.0	
GenBank	Consensus s	Homo sapiens		gb:BF724558 /DB_XR		AA382174	Hs.160999.	est
GenBank	Consensus s	Homo sapiens		gb:AI679812 /DB_XRE		AI679236 /	Hs.43057.0	est
GenBank	Consensus s	Homo sapiens		gb:AI040305 /DB_XRE		AI040305 /	Hs.56071.0	est
GenBank	Consensus s	Homo sapie	B3KTW4 //	gb:AI864271 /DB_XRE		AK096187	Hs.211648.	full length
GenBank	Consensus s	Homo sapie	B4DWX9 /	gb:AW975	ENSP0000	BC030693 /	Hs.170504.	full length
GenBank	Consensus s	Homo sapie	B3KM80 //	gb:BF056472 /DB_XR		ENST0000	Hs.253767.	full length
GenBank	Consensus s	Homo sapiens		gb:BE897518 /DB_XR		ENST0000	Hs.125494.0	
GenBank	Consensus s	Homo sapie	B2RBJ8 ///	gb:AA769438 /DB_XR		ENST0000	Hs.152346.	full length
GenBank	Consensus s	Homo sapiens		gb:AI678258 /DB_XRE		AB073353	Hs.174257.0	
GenBank	Consensus s	Homo sapiens		gb:BE857296 /DB_XR		AA706527	Hs.270293.	est
GenBank	Consensus s	Homo sapiens		gb:AW976631 /DB_XR		AA744532	Hs.152940.	est
GenBank	Consensus s	Homo sapie	B2RC57 ///	gb:N50406 /DB_XREF=		AA513171	Hs.191349.	full length
GenBank	Consensus s	Homo sapiens		gb:AW024656 /DB_XR		AK090817	Hs.233382.0	
GenBank	Consensus s	Homo sapiens		gb:AA424811 /DB_XR		AA424811	Hs.152155.	est
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Hs.687894	Hs.687894
Hs.674515	Hs.674515
Hs.676870	Hs.676870
Hs.720920	Hs.720920
Hs.559668	Hs.559668
Hs.722246	Hs.722246
Hs.687369	Hs.687369
Hs.709347	Hs.709347
Hs.436061	Hs.436061
Hs.272011	Hs.272011
Hs.406990	Hs.406990
Hs.631902	Hs.631902
Hs.661470	Hs.661470
Hs.497967	Hs.497967
Hs.612096	Hs.612096
Hs.131686	Hs.131686
Hs.444541	Hs.444541
Hs.502182	Hs.502182
Hs.687690	Hs.687690
Hs.533913	Hs.533913
Hs.47712	Hs.47712
Hs.662809	Hs.662809
Hs.687462	Hs.687462
Hs.477315	Hs.477315
Hs.655788	Hs.655788
Hs.667765	Hs.667765
Hs.669851	Hs.669851

Hs.104613	Hs.104613
Hs.381219	Hs.381219
Hs.667872	Hs.667872
Hs.669878	Hs.669878
Hs.195642	Hs.195642
Hs.396178	Hs.396178
Hs.98321	Hs.98321
Hs.663284	Hs.663284
Hs.724197	Hs.724197
Hs.636976	Hs.636976
Hs.659096	Hs.659096
Hs.660113	Hs.660113
Hs.468140	Hs.468140
Hs.439643	Hs.439643
Hs.79110	Hs.79110
Hs.406917	Hs.406917
Hs.561499	Hs.561499
Hs.619246	Hs.619246
Hs.697578	Hs.697578
Hs.526754	Hs.526754
Hs.560092	Hs.560092
Hs.662515	Hs.662515
Hs.658202	Hs.658202
Hs.17518	Hs.17518
Hs.672490	Hs.672490
Hs.452864	Hs.452864
Hs.271955	Hs.271955
Hs.660667	Hs.660667
Hs.691259	Hs.691259
Hs.716764	Hs.716764
Hs.661554	Hs.661554
Hs.664632	Hs.664632
Hs.667717	Hs.667717
Hs.87856	Hs.87856
Hs.21631	Hs.21631
Hs.657629	Hs.657629
Hs.596813	Hs.596813

Hs.673919	Hs.673919
Hs.410830	Hs.410830
Hs.201378	Hs.201378
Hs.710901	Hs.710901
Hs.652450	Hs.652450
Hs.162889	Hs.162889
Hs.124128	Hs.124128
Hs.666767	Hs.666767
Hs.653288	Hs.653288
Hs.555274	Hs.555274
Hs.437060	Hs.437060
Hs.369368	Hs.369368
Hs.120323	Hs.120323
Hs.37617	Hs.37617
Hs.458312	Hs.458312
Hs.707026	Hs.707026
Hs.130607	Hs.130607
Hs.631593	Hs.631593
Hs.719460	Hs.719460
Hs.102336	Hs.102336

Supplementary Table 3. GO analysis of the differentially methylated and expressed genes

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits
Gene expression profiling							
Cellular Component							
GOTERM_C	GO:0070013	62	12.653061	4.30E-04	6595, 38840	289	1779
GOTERM_C	GO:0031974	64	13.061224	4.45E-04	6595, 38840	289	1856
GOTERM_C	GO:0043233	63	12.857143	4.54E-04	6595, 38840	289	1820
GOTERM_C	GO:0031901	4	0.8163265	0.0012079	9765, 55361	289	10
GOTERM_C	GO:0045121	11	2.244898	0.001478	3778, 23426	289	143
GOTERM_C	GO:0005794	34	6.9387755	0.0023353	117248, 112	289	872
GOTERM_C	GO:0005901	6	1.2244898	0.0061394	3778, 5743,	289	52
GOTERM_C	GO:0031981	48	9.7959184	0.0064283	6595, 55215	289	1450
Biological Process							
GOTERM_B	GO:0010033	38	7.755102	7.41E-06	1959, 27161	321	721
GOTERM_B	GO:0009719	26	5.3061224	0.0000121	1959, 6772,	321	405
GOTERM_B	GO:0009725	24	4.8979592	0.0000212	1959, 6772,	321	367
GOTERM_B	GO:0033554	30	6.122449	0.0000781	55215, 9319	321	566
GOTERM_B	GO:0045449	90	18.367347	0.000104	6595, 8531,	321	2601
GOTERM_B	GO:0042127	36	7.3469388	0.000238	6595, 3087,	321	787
GOTERM_B	GO:0043434	13	2.6530612	0.000298	1959, 7832,	321	154
GOTERM_B	GO:0042981	36	7.3469388	0.000355	8531, 4853,	321	804
GOTERM_B	GO:0043067	36	7.3469388	0.000426	8531, 4853,	321	812
GOTERM_B	GO:0010941	36	7.3469388	0.000454	8531, 4853,	321	815
Molecular Function							
GOTERM_M	GO:0030528	63	12.857143	0.0000276	6595, 8531,	319	1512
GOTERM_M	GO:0016564	19	3.877551	0.000799	8531, 54880	319	316
GOTERM_M	GO:0003700	40	8.1632653	0.0016139	8531, 1959,	319	975
GOTERM_M	GO:0005111	3	0.6122449	0.0017652	654466, 387	319	3
GOTERM_M	GO:0008134	23	4.6938776	0.0077304	6595, 9319,	319	513
GOTERM_M	GO:0043566	10	2.0408163	0.0093879	8531, 23013	319	145
DNA methylation profiling							
Cellular Component							
GOTERM_C	GO:0031012	102	3.3618985	1.96E-09	NM_001166	2123	345
GOTERM_C	GO:0005578	95	3.13118	5.93E-09	NM_001166	2123	320
GOTERM_C	GO:0005886	728	23.994726	1.51E-07	NM_001711	2123	3777
GOTERM_C	GO:0044459	450	14.831905	1.67E-07	NM_078476	2123	2203
GOTERM_C	GO:0015629	77	2.5379038	9.23E-07	NM_001077	2123	269
GOTERM_C	GO:0045202	91	2.9993408	1.37E-05	NM_014954	2123	355
GOTERM_C	GO:0005856	284	9.3605801	3.33E-05	NM_144705	2123	1381
GOTERM_C	GO:0044420	38	1.252472	4.30E-05	NM_002291	2123	117
GOTERM_C	GO:0030054	121	3.9881345	5.25E-05	NM_176877	2123	518

GOTERM_(	GO:0005604	26	0.8569545	5.71E-04	NM_002291	2123	78

Biological Process

GOTERM_I	GO:0007155	200	6.5919578	3.64E-17	NM_002291	2203	700
GOTERM_I	GO:0022610	200	6.5919578	4.30E-17	NM_002291	2203	701
GOTERM_I	GO:0007156	59	1.9446276	3.20E-14	NM_020630	2203	131
GOTERM_I	GO:0016337	92	3.0323006	4.33E-12	NM_014005	2203	276
GOTERM_I	GO:0043062	52	1.713909	1.33E-06	NM_001142	2203	163
GOTERM_I	GO:0050808	25	0.8239947	1.31E-05	NM_001142	2203	61
GOTERM_I	GO:0051056	68	2.2412657	1.87E-05	NM_000267	2203	252
GOTERM_I	GO:0001501	80	2.6367831	5.43E-05	NM_001007	2203	319
GOTERM_I	GO:0030182	103	3.3948583	7.13E-05	NM_001077	2203	438
GOTERM_I	GO:0016339	13	0.4284773	7.75E-05	NM_015669	2203	23

Molecular Function

GOTERM_I	GO:0005509	241	7.9433092	3.68E-15	NM_018100	2125	919
GOTERM_I	GO:0003779	98	3.2300593	7.31E-10	NM_001077	2125	326
GOTERM_I	GO:0060589	115	3.7903757	3.30E-09	NM_000267	2125	413
GOTERM_I	GO:0008092	134	4.4166117	3.74E-09	NM_001077	2125	504
GOTERM_I	GO:0030695	112	3.6914964	7.06E-09	NM_000267	2125	404
GOTERM_I	GO:0005083	81	2.6697429	5.64E-08	NM_000267	2125	274
GOTERM_I	GO:0005089	29	0.9558339	6.89E-06	NM_001042	2125	74
GOTERM_I	GO:0005085	47	1.5491101	1.31E-05	NM_001042	2125	152
GOTERM_I	GO:0005088	30	0.9887937	9.54E-05	NM_001042	2125	88
GOTERM_I	GO:0046872	752	24.785761	1.06E-04	NM_001083	2125	4140

Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
12782	1.5414048	0.1229674	0.1229674	0.5746692
12782	1.5251163	0.1269209	0.065613	0.5943979
12782	1.5309822	0.1294016	0.0451409	0.6068207
12782	17.691349	0.3083105	0.0880358	1.6060669
12782	3.4021826	0.3630842	0.0862731	1.96197
12782	1.7245008	0.509873	0.1120576	3.0836079
12782	5.1032739	0.8471498	0.2353432	7.9190009
12782	1.4641117	0.8601202	0.2179773	8.2769529
13528	2.2211449	0.0155041	0.0155041	0.0128165
13528	2.7054959	0.0251644	0.0126624	0.0209039
13528	2.7559653	0.0436542	0.0147684	0.0366072
13528	2.2337439	0.1518179	0.0403292	0.1349763
13528	1.4582458	0.1961518	0.0427292	0.178944
13528	1.9277749	0.3948605	0.0803076	0.4111767
13528	3.5575515	0.4663068	0.085799	0.5137584
13528	1.8870135	0.5269942	0.0893357	0.61222
13528	1.8684223	0.5929214	0.0950368	0.7345163
13528	1.8615446	0.6165994	0.0914156	0.7832994
12983	1.6957941	0.0147247	0.0147247	0.0401067
12983	2.4470954	0.3496123	0.1935338	1.1565768
12983	1.669705	0.5806311	0.2514881	2.3225776
12983	40.69906	0.6134513	0.2115012	2.5375967
12983	1.8247142	0.9846262	0.5661332	10.676302
12983	2.8068317	0.9937462	0.5707692	12.822776
12782	1.7800406	1.34E-06	1.34E-06	2.95E-06
12782	1.7874029	4.04E-06	2.02E-06	8.91E-06
12782	1.1604681	1.03E-04	3.43E-05	2.27E-04
12782	1.229835	1.14E-04	2.85E-05	2.51E-04
12782	1.7234047	6.28E-04	1.26E-04	0.0013861
12782	1.5433409	0.0093144	0.0015585	0.0206448
12782	1.2381506	0.0224021	0.0032315	0.0499758
12782	1.9554493	0.0288817	0.0036567	0.0646398
12782	1.4063857	0.0351374	0.0039665	0.0788882

12782	2.0069085	0.3220977	0.0381293	0.8540449

13528	1.7544906	1.59E-13	1.59E-13	6.84E-14
13528	1.7519878	1.87E-13	9.36E-14	8.06E-14
13528	2.7656665	1.39E-10	4.65E-11	6.00E-11
13528	2.0469057	1.89E-08	4.72E-09	8.12E-09
13528	1.9590018	0.0057837	0.0011594	0.0024953
13528	2.5166874	0.0555825	0.0094859	0.0245981
13528	1.6570189	0.0781764	0.0115614	0.0350117
13528	1.5399918	0.2107852	0.0291561	0.1017806
13528	1.4440499	0.2671569	0.0339464	0.1336229
13528	3.4708402	0.2868755	0.0332448	0.1453402

12983	1.6022034	5.61E-12	5.61E-12	6.11E-12
12983	1.8366424	1.12E-06	5.60E-07	1.22E-06
12983	1.7012334	5.05E-06	1.68E-06	5.49E-06
12983	1.6243903	5.73E-06	1.43E-06	6.23E-06
12983	1.6937635	1.08E-05	2.16E-06	1.18E-05
12983	1.8061365	8.65E-05	1.44E-05	9.40E-05
12983	2.3943211	0.0105055	0.0015076	0.0114826
12983	1.8891672	0.0199048	0.00251	0.0218589
12983	2.0828342	0.1360143	0.0161131	0.1588393
12983	1.1097716	0.1504967	0.0161781	0.177189

Supplementary Table 4. KEGG analysis of the differentially methylated and expressed genes

Category	**Term**	**Count**	**%**	**PValue**	**Genes**	**List Total**	**Pop Hits**	**Pop Total**	**Fold Enrichm**
Gene expression profiling									
KEGG_PATH	hsa04621:NO	5	1.020408163	0.053516706	22861, 257397	118	62	5085	3.475259705
KEGG_PATH	hsa04115:p53	5	1.020408163	0.070474132	4616, 54205, 3	118	68	5085	3.168619143
KEGG_PATH	hsa04940:Typ	4	0.816326531	0.071294595	3481, 3106, 72	118	42	5085	4.104116223
DNA methylation profiling									
KEGG_PATH	hsa04940:Typ	21	0.69215557	2.33E-06	NM_0010071	838	42	5085	3.034009547
KEGG_PATH	hsa05332:Graf	19	0.626235992	1.30E-05	NM_00101507	838	39	5085	2.95621443
KEGG_PATH	hsa05416:Vira	26	0.856954515	8.74E-05	NM_002209,	838	71	5085	2.222091499
KEGG_PATH	hsa04810:Reg	57	1.878707976	1.74E-04	NM_0010071	838	215	5085	1.608730643
KEGG_PATH	hsa04320:Dors	13	0.428477258	2.35E-04	NM_152431,	838	25	5085	3.155369928
KEGG_PATH	hsa05330:Allo	16	0.527356625	2.84E-04	NM_005516,	838	36	5085	2.696897375
KEGG_PATH	hsa04510:Foca	52	1.713909031	6.57E-04	NM_002291,	838	201	5085	1.569835785
KEGG_PATH	hsa05320:Aut	19	0.626235992	8.13E-04	NM_000547,	838	51	5085	2.260634564
KEGG_PATH	hsa04514:Cell	37	1.219512195	0.001014299	NM_002209,	838	132	5085	1.70088414
KEGG_PATH	hsa04612:Anti	24	0.791034937	0.006370738	NM_000544,	838	83	5085	1.754607931
KEGG_PATH	hsa04512:EC	24	0.791034937	0.007447833	NM_000089,	838	84	5085	1.733719741
KEGG_PATH	hsa00061:Fatt	5	0.164798945	0.008270093	NM_198839,	838	6	5085	5.056682578
KEGG_PATH	hsa05412:Arrh	22	0.725115359	0.009233787	NM_018398,	838	76	5085	1.756531843
KEGG_PATH	hsa04672:Intes	16	0.527356625	0.009863862	NM_0011355	838	49	5085	1.98139399
KEGG_PATH	hsa05310:Asth	11	0.36255768	0.013891037	NM_002122,	838	29	5085	2.301662415
KEGG_PATH	hsa04020:Calc	41	1.351351351	0.017411163	NM_173201,	838	176	5085	1.41357263
KEGG_PATH	hsa04666:Fc g	25	0.823994726	0.017671993	NM_012296,	838	95	5085	1.59684713
KEGG_PATH	hsa04520:Adh	21	0.69215557	0.021567903	NM_005433,	838	77	5085	1.654914298
KEGG_PATH	hsa04350:TGF	23	0.758075148	0.02226972	NM_0011662	838	87	5085	1.604188956
KEGG_PATH	hsa05414:Dila	24	0.791034937	0.022473783	NM_016592,	838	92	5085	1.582961503
KEGG_PATH	hsa04910:Insu	32	1.05471325	0.029420156	NM_0010071	838	135	5085	1.438345267

KEGG_PATH	hsa00650:Buta	11	0.36255768	0.042076638	NM_202000,	838	34	5085	1.963182648
KEGG_PATH	hsa04530:Tigh	31	1.021753461	0.043321594	NM_012301,	838	134	5085	1.403795462
KEGG_PATH	hsa04360:Axo	30	0.988793672	0.044229559	NM_005761,	838	129	5085	1.411167231
KEGG_PATH	hsa00072:Synt	5	0.164798945	0.045957705	NM_004051,	838	9	5085	3.371121718
KEGG_PATH	hsa04144:End	40	1.318391562	0.051430995	NM_014914,	838	184	5085	1.319134585
KEGG_PATH	hsa00561:Glyc	13	0.428477258	0.055380837	NM_00112812	838	45	5085	1.752983294
KEGG_PATH	hsa00360:Phe	8	0.263678312	0.056734772	NM_00103001	838	22	5085	2.206552397
KEGG_PATH	hsa04650:Natu	30	0.988793672	0.062391905	NM_002209,	838	133	5085	1.368726111
KEGG_PATH	hsa04960:Ald	12	0.395517469	0.062549803	NM_0010071	838	41	5085	1.776005588
KEGG_PATH	hsa00140:Ster	13	0.428477258	0.064188055	NM_001077,	838	46	5085	1.714874961
KEGG_PATH	hsa00150:And	11	0.36255768	0.070733173	NM_001077,	838	37	5085	1.804005676
KEGG_PATH	hsa04930:Typ	13	0.428477258	0.07386813	NM_0010071	838	47	5085	1.67838826
KEGG_PATH	hsa04330:Not	13	0.428477258	0.07386813	NM_004416,	838	47	5085	1.67838826
KEGG_PATH	hsa04010:MA	54	1.779828609	0.075890176	NM_018398,	838	267	5085	1.227239817
KEGG_PATH	hsa05410:Hyp	20	0.659195781	0.095028312	NM_018398,	838	85	5085	1.427769198
KEGG_PATH	hsa00280:Vali	12	0.395517469	0.095983605	NM_152740,	838	44	5085	1.654914298
KEGG_PATH	hsa05220:Chr	18	0.593276203	0.099431835	NM_001259,	838	75	5085	1.456324582

Bonferroni	**Benjamini**	**FDR**
0.999124093	0.999124093	47.20512051
0.99991341	0.990694606	57.20332245
0.999922664	0.957395038	57.63997017
4.41E-04	4.41E-04	0.002896075
0.002455763	0.001228636	0.01615354
0.016391141	0.005493841	0.108527501
0.032320246	0.008179881	0.215627032
0.043530871	0.008861853	0.291993887
0.052207024	0.008896718	0.351672133
0.116871044	0.017598175	0.813253554
0.142487089	0.019031451	1.004890974
0.17452783	0.021085604	1.252267143
0.701182179	0.113781831	7.629596086
0.756565788	0.120539152	8.865319265
0.791860488	0.122602867	9.798425089
0.826797372	0.126169363	10.88084721
0.846418706	0.125255322	11.5820763
0.928910203	0.16159508	15.94554194
0.963836112	0.187371228	19.59650512
0.965605941	0.179816949	19.86114069
0.983770669	0.204624413	23.71975184
0.985828906	0.200708045	24.39641382
0.986377081	0.193297302	24.59212544
0.996460763	0.235669107	30.98285453

0.999703848	0.308783179	41.36332545
0.999768384	0.305061363	42.30265351
0.999806434	0.299699301	42.97897243
0.999862507	0.299301364	44.24612287
0.999953652	0.318746481	48.09051112
0.999978937	0.328884514	50.7117385
0.999983938	0.325816187	51.58185642
0.999994847	0.342862316	55.0668425
0.999995009	0.334307463	55.16071759
0.999996414	0.332665921	56.12411927
0.999999048	0.351620257	59.7862519
0.999999497	0.355643514	61.43883504
0.999999497	0.355643514	61.43883504
0.999999668	0.355142923	62.47137475
0.999999994	0.416784631	71.05974306
0.999999995	0.411257198	71.4368226
0.999999997	0.414312673	72.7606646

Supplementary Table 5. Correlation coefficient between DNA methylation and gene expression

Gene_Symbol	**Correlation**	**PValue**
AFAP1	-0.8157	0.0478
AIFM1	-0.4463	0.3750
ALS2CR11	-0.9727	0.0011
ANKRD11	-0.1326	0.8023
CCL2	-0.7982	0.0570
CREM	-0.5314	0.2779
CXorf36	-0.4024	0.4290
CYP4X1	-0.8657	0.0258
DCAF12L1	-0.7923	0.0602
DDB2	-0.8432	0.0349
DIP2C	-0.9099	0.0118
DNAJC5	0.7179	0.1082
FAHD1	0.7905	0.0613
FAM188B	-0.3107	0.5490
FBN1	0.9877	0.0002
FLJ44606	-0.8789	0.0211
GALNTL2	-0.7676	0.0747
GEMIN8	-0.8161	0.0476
GNG4	-0.7021	0.1199
HCG4	-0.2242	0.6693
HLA-B	-0.6937	0.1263
HLA-F	0.3826	0.4541
HRH1	0.8904	0.0174
HSD17B1	-0.7144	0.1107
INADL	0.4581	0.3609
ITGBL1	-0.9121	0.0113
KCNMA1	0.9327	0.0066
KIAA1683	-0.9292	0.0073
MAD1L1	0.8704	0.0241
MAFK	-0.5973	0.2106
MGC16121	-0.2832	0.5865
MRVI1	0.5219	0.2883
NAV2	0.9307	0.0070
NBAS	0.7831	0.0655
NOV	-0.6855	0.1328
NR0B1	-0.9329	0.0066
NRK	0.5257	0.2841
ODZ2	0.5779	0.2296
PLXNC1	0.8238	0.0438
PPAP2C	0.9049	0.0131

PRDM1	-0.9685	0.0015
PSRC1	0.8949	0.0160
RAB21	0.5101	0.3013
RASSF5	-0.6767	0.1399
RGMB	-0.8395	0.0366
RLIM	0.8612	0.0276
RNF213	0.9727	0.0011
SSBP2	-0.9556	0.0029
TMEM132A	-0.8893	0.0177
TNIK	0.9714	0.0012
TPRG1	-0.0872	0.8696
TRIM14	0.5752	0.2323
WDR44	-0.2468	0.6373
ZFAND3	0.9352	0.0062
ZNF503	-0.9249	0.0082

Supplementary Table 6. Transcription factors prediction for differentially methylated CpG site

Sequence	Gene_Sym	Factor na	Start positi	End positi	Dissimilari	String	RE equall	RE query
cg2591200	AFAP1	Elk-1 [T00	941	949	9.979803	CTTCCG	0.10681	0.11027
cg0261454	AFAP1	Elk-1 [T00	1005	1013	9.979803	CTTCCG	0.10681	0.11027
cg2639478	AFAP1	Elk-1 [T00	971	979	9.979803	CTTCCG	0.10681	0.11027
cg2591200	AFAP1	c-Ets-1 [T	13	19	9.969337	ATTCCC	0.24414	0.23698
cg2591200	AFAP1	c-Ets-1 [T	449	455	9.969337	TGGGAA	0.24414	0.23698
cg2591200	AFAP1	c-Ets-1 [T	632	638	9.969337	TGGGAA	0.24414	0.23698
cg0261454	AFAP1	c-Ets-1 [T	77	83	9.969337	ATTCCC	0.24414	0.23698
cg0261454	AFAP1	c-Ets-1 [T	513	519	9.969337	TGGGAA	0.24414	0.23698
cg0261454	AFAP1	c-Ets-1 [T	696	702	9.969337	TGGGAA	0.24414	0.23698
cg2639478	AFAP1	c-Ets-1 [T	43	49	9.969337	ATTCCC	0.24414	0.23698
cg2639478	AFAP1	c-Ets-1 [T	479	485	9.969337	TGGGAA	0.24414	0.23698
cg2639478	AFAP1	c-Ets-1 [T	662	668	9.969337	TGGGAA	0.24414	0.23698
cg0161265	AFAP1	LEF-1 [T0	748	755	9.937995	CTTTGG	0.12207	0.1238
cg2591200	AFAP1	PEA3 [T0	1768	1776	9.937959	GTCCAT	0.18311	0.18382
cg0261454	AFAP1	PEA3 [T0	1832	1840	9.937959	GTCCAT	0.18311	0.18382
cg2639478	AFAP1	PEA3 [T0	1798	1806	9.937959	GTCCAT	0.18311	0.18382
cg0675819	AFAP1	MAZ [T00	1774	1786	9.826821	GCCCCT	0.00435	0.00501
cg0675819	AFAP1	MAZ [T00	1873	1885	9.826821	GCCCCT	0.00435	0.00501
cg0161265	AFAP1	c-Myb [T0	1165	1172	9.815171	TCAAGT	0.36621	0.34605
cg0161265	AFAP1	c-Myb [T0	1815	1822	9.815171	TAACTT	0.36621	0.34605
cg2591200	AFAP1	XBP-1 [T	824	829	9.789909	CGCCAT	1.95312	1.94901
cg2591200	AFAP1	XBP-1 [T	828	833	9.789909	ATGGCT	1.95312	1.94901
cg2591200	AFAP1	XBP-1 [T	875	880	9.789909	ATGTCT	1.95312	1.94901
cg2591200	AFAP1	XBP-1 [T	1410	1415	9.789909	CGCCAT	1.95312	1.94901
cg2591200	AFAP1	XBP-1 [T	1436	1441	9.789909	CGCCAT	1.95312	1.94901
cg0261454	AFAP1	XBP-1 [T	888	893	9.789909	CGCCAT	1.95312	1.94901
cg0261454	AFAP1	XBP-1 [T	892	897	9.789909	ATGGCT	1.95312	1.94901
cg0261454	AFAP1	XBP-1 [T	939	944	9.789909	ATGTCT	1.95312	1.94901
cg0261454	AFAP1	XBP-1 [T	1474	1479	9.789909	CGCCAT	1.95312	1.94901
cg0261454	AFAP1	XBP-1 [T	1500	1505	9.789909	CGCCAT	1.95312	1.94901
cg2639478	AFAP1	XBP-1 [T	854	859	9.789909	CGCCAT	1.95312	1.94901
cg2639478	AFAP1	XBP-1 [T	858	863	9.789909	ATGGCT	1.95312	1.94901
cg2639478	AFAP1	XBP-1 [T	905	910	9.789909	ATGTCT	1.95312	1.94901
cg2639478	AFAP1	XBP-1 [T	1440	1445	9.789909	CGCCAT	1.95312	1.94901
cg2639478	AFAP1	XBP-1 [T	1466	1471	9.789909	CGCCAT	1.95312	1.94901
cg0675819	AFAP1	XBP-1 [T	98	103	9.789909	AGCCAT	1.95312	1.94901
cg0675819	AFAP1	XBP-1 [T	620	625	9.789909	ATGTCT	1.95312	1.94901
cg0161265	AFAP1	XBP-1 [T	223	228	9.789909	ATGGCT	1.95312	1.94901
cg0161265	AFAP1	XBP-1 [T	354	359	9.789909	CGCCAT	1.95312	1.94901
cg0161265	AFAP1	XBP-1 [T	1116	1121	9.789909	ATGGCT	1.95312	1.94901
cg0161265	AFAP1	XBP-1 [T	1148	1153	9.789909	ATGGCT	1.95312	1.94901
cg0161265	AFAP1	XBP-1 [T	1345	1350	9.789909	ATGTCT	1.95312	1.94901
cg0161265	AFAP1	XBP-1 [T	1384	1389	9.789909	CGCCAT	1.95312	1.94901
cg2591200	AFAP1	NF-kappa	490	500	9.780609	GGCTGC	0.02289	0.02536
cg0261454	AFAP1	NF-kappa	554	564	9.780609	GGCTGC	0.02289	0.02536
cg2639478	AFAP1	NF-kappa	520	530	9.780609	GGCTGC	0.02289	0.02536

cg2591200	AFAP1	NF-1 [T00	660	667	9.761671	TTGGAG	0.24414	0.24488
cg0261454	AFAP1	NF-1 [T00	724	731	9.761671	TTGGAG	0.24414	0.24488
cg2639478	AFAP1	NF-1 [T00	690	697	9.761671	TTGGAG	0.24414	0.24488
cg0161265	AFAP1	NF-1 [T00	522	529	9.761671	AGCACC	0.24414	0.24488
cg0161265	AFAP1	NF-AT2 [	1098	1107	9.755755	GGAAAG	0.08774	0.08205
cg0675819	AFAP1	Elk-1 [T00	451	459	9.754368	AGATGG	0.10681	0.11027
cg2591200	AFAP1	PR B [T00	686	692	9.743489	AACACA	1.09863	1.0981
cg2591200	AFAP1	PR B [T00	693	699	9.743489	AACACG	1.09863	1.0981
cg2591200	AFAP1	PR B [T00	1316	1322	9.743489	CTGTGT	1.09863	1.0981
cg2591200	AFAP1	PR A [T01	686	692	9.743489	AACACA	1.09863	1.0981
cg2591200	AFAP1	PR A [T01	693	699	9.743489	AACACG	1.09863	1.0981
cg2591200	AFAP1	PR A [T01	1316	1322	9.743489	CTGTGT	1.09863	1.0981
cg0261454	AFAP1	PR B [T00	750	756	9.743489	AACACA	1.09863	1.0981
cg0261454	AFAP1	PR B [T00	757	763	9.743489	AACACG	1.09863	1.0981
cg0261454	AFAP1	PR B [T00	1380	1386	9.743489	CTGTGT	1.09863	1.0981
cg0261454	AFAP1	PR A [T01	750	756	9.743489	AACACA	1.09863	1.0981
cg0261454	AFAP1	PR A [T01	757	763	9.743489	AACACG	1.09863	1.0981
cg0261454	AFAP1	PR A [T01	1380	1386	9.743489	CTGTGT	1.09863	1.0981
cg2639478	AFAP1	PR B [T00	716	722	9.743489	AACACA	1.09863	1.0981
cg2639478	AFAP1	PR B [T00	723	729	9.743489	AACACG	1.09863	1.0981
cg2639478	AFAP1	PR B [T00	1346	1352	9.743489	CTGTGT	1.09863	1.0981
cg2639478	AFAP1	PR A [T01	716	722	9.743489	AACACA	1.09863	1.0981
cg2639478	AFAP1	PR A [T01	723	729	9.743489	AACACG	1.09863	1.0981
cg2639478	AFAP1	PR A [T01	1346	1352	9.743489	CTGTGT	1.09863	1.0981
cg0675819	AFAP1	PR B [T00	545	551	9.743489	AACACG	1.09863	1.0981
cg0675819	AFAP1	PR B [T00	1280	1286	9.743489	AACACG	1.09863	1.0981
cg0675819	AFAP1	PR B [T00	1593	1599	9.743489	AACACA	1.09863	1.0981
cg0675819	AFAP1	PR A [T01	545	551	9.743489	AACACG	1.09863	1.0981
cg0675819	AFAP1	PR A [T01	1280	1286	9.743489	AACACG	1.09863	1.0981
cg0675819	AFAP1	PR A [T01	1593	1599	9.743489	AACACA	1.09863	1.0981
cg0161265	AFAP1	PR B [T00	14	20	9.743489	AACACG	1.09863	1.0981
cg0161265	AFAP1	PR B [T00	1197	1203	9.743489	TCGTGT	1.09863	1.0981
cg0161265	AFAP1	PR A [T01	14	20	9.743489	AACACG	1.09863	1.0981
cg0161265	AFAP1	PR A [T01	1197	1203	9.743489	TCGTGT	1.09863	1.0981
cg2591200	AFAP1	c-Myb [T0	1192	1199	9.729271	TAACTG	0.36621	0.34746
cg0261454	AFAP1	c-Myb [T0	1256	1263	9.729271	TAACTG	0.36621	0.34746
cg2639478	AFAP1	c-Myb [T0	1222	1229	9.729271	TAACTG	0.36621	0.34746
cg0161265	AFAP1	c-Myb [T0	1301	1308	9.729271	TAACTG	0.36621	0.34746
cg2591200	AFAP1	LEF-1 [T0	1790	1797	9.72404	CTTTGC	0.21362	0.21229
cg0261454	AFAP1	LEF-1 [T0	1854	1861	9.72404	CTTTGC	0.21362	0.21229
cg2639478	AFAP1	LEF-1 [T0	1820	1827	9.72404	CTTTGC	0.21362	0.21229
cg0161265	AFAP1	LEF-1 [T0	751	758	9.72404	TGGCAA	0.21362	0.21229
cg0675819	AFAP1	Elk-1 [T00	1086	1094	9.719998	CCACGG	0.07629	0.0786
cg2591200	AFAP1	c-Ets-1 [T	156	162	9.713162	ATTCCC	0.36621	0.37402
cg0261454	AFAP1	c-Ets-1 [T	220	226	9.713162	ATTCCC	0.36621	0.37402
cg2639478	AFAP1	c-Ets-1 [T	186	192	9.713162	ATTCCC	0.36621	0.37402
cg0675819	AFAP1	c-Ets-1 [T	251	257	9.713162	GGGGAA	0.36621	0.37402
cg0161265	AFAP1	c-Ets-1 [T	185	191	9.713162	GGGGAA	0.36621	0.37402

cg0675819	AFAP1	RAR-beta	983	992	9.641259	CCTCAA	0.21362	0.22369
cg2591200	AFAP1	HNF-1C [	802	810	9.639597	GTTAAT	0.19836	0.18179
cg0261454	AFAP1	HNF-1C [	866	874	9.639597	GTTAAT	0.19836	0.18179
cg2639478	AFAP1	HNF-1C [	832	840	9.639597	GTTAAT	0.19836	0.18179
cg0161265	AFAP1	EBF [T05	5	15	9.62688	GCCCCT	0.06866	0.07687
cg0161265	AFAP1	RAR-beta	486	495	9.622793	TGGGTT	0.21362	0.22369
cg0161265	AFAP1	RAR-beta	1122	1131	9.622793	CAGGAA	0.21362	0.22369
cg2591200	AFAP1	c-Ets-1 [T	626	632	9.585075	CGGGAA	0.36621	0.37402
cg0261454	AFAP1	c-Ets-1 [T	690	696	9.585075	CGGGAA	0.36621	0.37402
cg2639478	AFAP1	c-Ets-1 [T	656	662	9.585075	CGGGAA	0.36621	0.37402
cg0675819	AFAP1	c-Ets-1 [T	1926	1932	9.585075	ATTCCC	0.36621	0.37402
cg2591200	AFAP1	MAZ [T00	1469	1481	9.576901	TGCCCT	0.01425	0.01587
cg0261454	AFAP1	MAZ [T00	1533	1545	9.576901	TGCCCT	0.01425	0.01587
cg2639478	AFAP1	MAZ [T00	1499	1511	9.576901	TGCCCT	0.01425	0.01587
cg0675819	AFAP1	EBF [T05	1303	1313	9.574945	ACCCCT	0.06866	0.07687
cg2591200	AFAP1	TFIID [T0	550	556	9.552105	TGAGAA	1.46484	1.37777
cg2591200	AFAP1	TFIID [T0	667	673	9.552105	TGGGAA	1.46484	1.37777
cg2591200	AFAP1	TFIID [T0	869	875	9.552105	TTCCAA	1.46484	1.37777
cg2591200	AFAP1	TFIID [T0	1200	1206	9.552105	TGAGAA	1.46484	1.37777
cg2591200	AFAP1	TFIID [T0	1493	1499	9.552105	TGTCAA	1.46484	1.37777
cg2591200	AFAP1	TFIID [T0	1614	1620	9.552105	TTTGAC	1.46484	1.37777
cg2591200	AFAP1	TFIID [T0	1698	1704	9.552105	TTTCCC	1.46484	1.37777
cg2591200	AFAP1	TFIID [T0	1700	1706	9.552105	TCCCAA	1.46484	1.37777
cg2591200	AFAP1	Pax-5 [T0	455	461	9.552105	TTGGCC	1.46484	1.61918
cg2591200	AFAP1	Pax-5 [T0	1004	1010	9.552105	GGGCCA	1.46484	1.61918
cg2591200	AFAP1	Pax-5 [T0	1580	1586	9.552105	GGGCCA	1.46484	1.61918
cg0261454	AFAP1	TFIID [T0	614	620	9.552105	TGAGAA	1.46484	1.37777
cg0261454	AFAP1	TFIID [T0	731	737	9.552105	TGGGAA	1.46484	1.37777
cg0261454	AFAP1	TFIID [T0	933	939	9.552105	TTCCAA	1.46484	1.37777
cg0261454	AFAP1	TFIID [T0	1264	1270	9.552105	TGAGAA	1.46484	1.37777
cg0261454	AFAP1	TFIID [T0	1557	1563	9.552105	TGTCAA	1.46484	1.37777
cg0261454	AFAP1	TFIID [T0	1678	1684	9.552105	TTTGAC	1.46484	1.37777
cg0261454	AFAP1	TFIID [T0	1762	1768	9.552105	TTTCCC	1.46484	1.37777
cg0261454	AFAP1	TFIID [T0	1764	1770	9.552105	TCCCAA	1.46484	1.37777
cg0261454	AFAP1	Pax-5 [T0	519	525	9.552105	TTGGCC	1.46484	1.61918
cg0261454	AFAP1	Pax-5 [T0	1068	1074	9.552105	GGGCCA	1.46484	1.61918
cg0261454	AFAP1	Pax-5 [T0	1644	1650	9.552105	GGGCCA	1.46484	1.61918
cg2639478	AFAP1	TFIID [T0	580	586	9.552105	TGAGAA	1.46484	1.37777
cg2639478	AFAP1	TFIID [T0	697	703	9.552105	TGGGAA	1.46484	1.37777
cg2639478	AFAP1	TFIID [T0	899	905	9.552105	TTCCAA	1.46484	1.37777
cg2639478	AFAP1	TFIID [T0	1230	1236	9.552105	TGAGAA	1.46484	1.37777
cg2639478	AFAP1	TFIID [T0	1523	1529	9.552105	TGTCAA	1.46484	1.37777
cg2639478	AFAP1	TFIID [T0	1644	1650	9.552105	TTTGAC	1.46484	1.37777
cg2639478	AFAP1	TFIID [T0	1728	1734	9.552105	TTTCCC	1.46484	1.37777
cg2639478	AFAP1	TFIID [T0	1730	1736	9.552105	TCCCAA	1.46484	1.37777
cg2639478	AFAP1	Pax-5 [T0	485	491	9.552105	TTGGCC	1.46484	1.61918
cg2639478	AFAP1	Pax-5 [T0	1034	1040	9.552105	GGGCCA	1.46484	1.61918
cg2639478	AFAP1	Pax-5 [T0	1610	1616	9.552105	GGGCCA	1.46484	1.61918

cg0675819	AFAP1	Pax-5 [T0	934	940	9.552105	GGGCAA	1.46484	1.61918
cg0675819	AFAP1	Pax-5 [T0	1289	1295	9.552105	GGGCGG	1.46484	1.61918
cg0161265	AFAP1	TFIID [T0	178	184	9.552105	TTTGGG	1.46484	1.37777
cg0161265	AFAP1	TFIID [T0	332	338	9.552105	TGTGAA	1.46484	1.37777
cg0161265	AFAP1	TFIID [T0	751	757	9.552105	TGGCAA	1.46484	1.37777
cg0161265	AFAP1	TFIID [T0	1401	1407	9.552105	TGTGAA	1.46484	1.37777
cg0161265	AFAP1	TFIID [T0	1739	1745	9.552105	TGGGAA	1.46484	1.37777
cg0161265	AFAP1	Pax-5 [T0	775	781	9.552105	GTGGCC	1.46484	1.61918
cg0161265	AFAP1	Pax-5 [T0	1256	1262	9.552105	GTGGCC	1.46484	1.61918
cg2591200	AFAP1	NF-AT1 [T	592	600	9.521781	TGCATT	0.16785	0.16528
cg2591200	AFAP1	NF-AT1 [T	1900	1908	9.521781	GGAAAT	0.16785	0.16528
cg0261454	AFAP1	NF-AT1 [T	656	664	9.521781	TGCATT	0.16785	0.16528
cg0261454	AFAP1	NF-AT1 [T	1964	1972	9.521781	GGAAAT	0.16785	0.16528
cg2639478	AFAP1	NF-AT1 [T	622	630	9.521781	TGCATT	0.16785	0.16528
cg2639478	AFAP1	NF-AT1 [T	1930	1938	9.521781	GGAAAT	0.16785	0.16528
cg2591200	AFAP1	FOXP3 [T	180	185	9.512894	AAGAAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	221	226	9.512894	AATAAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	225	230	9.512894	ACCAAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	372	377	9.512894	GTTCTC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	676	681	9.512894	GGCAAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	819	824	9.512894	ATAAAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	912	917	9.512894	AGCAAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	1105	1110	9.512894	ATAAAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	1144	1149	9.512894	GTTTAC	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	1320	1325	9.512894	GTTTAT	7.32422	7.22156
cg2591200	AFAP1	FOXP3 [T	1443	1448	9.512894	CAGAAC	7.32422	7.22156
cg2591200	AFAP1	TFII-I [T0	39	44	9.512894	GGATTT	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	256	261	9.512894	GGAAAA	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	265	270	9.512894	GGAAGG	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	291	296	9.512894	GGAAGG	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	306	311	9.512894	CCGTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	325	330	9.512894	CCTTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	379	384	9.512894	CCTTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	451	456	9.512894	GGAATT	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	499	504	9.512894	CCGTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	555	560	9.512894	AAATCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	669	674	9.512894	GGAAAC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	784	789	9.512894	CCTTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	952	957	9.512894	GGAAGG	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1030	1035	9.512894	CCTTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1035	1040	9.512894	CCATCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1126	1131	9.512894	GGACTT	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1226	1231	9.512894	GGAAAA	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1281	1286	9.512894	GGAAAC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1353	1358	9.512894	GGACGG	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1412	1417	9.512894	CCATCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1697	1702	9.512894	GTTTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1770	1775	9.512894	CCATCC	7.32422	7.44385

cg2591200	AFAP1	TFII-I [T0	1889	1894	9.512894	GTGTCC	7.32422	7.44385
cg2591200	AFAP1	TFII-I [T0	1948	1953	9.512894	GGACTT	7.32422	7.44385
cg0261454	AFAP1	FOXP3 [T	244	249	9.512894	AAGAAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	285	290	9.512894	AATAAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	289	294	9.512894	ACCAAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	436	441	9.512894	GTTCTC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	740	745	9.512894	GGCAAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	883	888	9.512894	ATAAAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	976	981	9.512894	AGCAAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	1169	1174	9.512894	ATAAAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	1208	1213	9.512894	GTTTAC	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	1384	1389	9.512894	GTTTAT	7.32422	7.22156
cg0261454	AFAP1	FOXP3 [T	1507	1512	9.512894	CAGAAC	7.32422	7.22156
cg0261454	AFAP1	TFII-I [T0	103	108	9.512894	GGATTT	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	320	325	9.512894	GGAAAA	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	329	334	9.512894	GGAAGG	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	355	360	9.512894	GGAAGG	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	370	375	9.512894	CCGTCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	389	394	9.512894	CCTTCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	443	448	9.512894	CCTTCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	515	520	9.512894	GGAATT	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	563	568	9.512894	CCGTCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	619	624	9.512894	AAATCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	733	738	9.512894	GGAAAC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	848	853	9.512894	CCTTCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1016	1021	9.512894	GGAAGG	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1094	1099	9.512894	CCTTCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1099	1104	9.512894	CCATCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1190	1195	9.512894	GGACTT	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1290	1295	9.512894	GGAAAA	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1345	1350	9.512894	GGAAAC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1417	1422	9.512894	GGACGG	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1476	1481	9.512894	CCATCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1761	1766	9.512894	GTTTCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1834	1839	9.512894	CCATCC	7.32422	7.44385
cg0261454	AFAP1	TFII-I [T0	1953	1958	9.512894	GTGTCC	7.32422	7.44385
cg2639478	AFAP1	FOXP3 [T	210	215	9.512894	AAGAAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	251	256	9.512894	AATAAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	255	260	9.512894	ACCAAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	402	407	9.512894	GTTCTC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	706	711	9.512894	GGCAAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	849	854	9.512894	ATAAAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	942	947	9.512894	AGCAAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	1135	1140	9.512894	ATAAAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	1174	1179	9.512894	GTTTAC	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	1350	1355	9.512894	GTTTAT	7.32422	7.22156
cg2639478	AFAP1	FOXP3 [T	1473	1478	9.512894	CAGAAC	7.32422	7.22156
cg2639478	AFAP1	TFII-I [T0	69	74	9.512894	GGATTT	7.32422	7.44385

cg2639478	AFAP1	TFII-I [T0	286	291	9.512894	GGAAAA	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	295	300	9.512894	GGAAGG	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	321	326	9.512894	GGAAGG	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	336	341	9.512894	CCGTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	355	360	9.512894	CCTTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	409	414	9.512894	CCTTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	481	486	9.512894	GGAATT	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	529	534	9.512894	CCGTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	585	590	9.512894	AAATCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	699	704	9.512894	GGAAAC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	814	819	9.512894	CCTTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	982	987	9.512894	GGAAGG	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1060	1065	9.512894	CCTTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1065	1070	9.512894	CCATCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1156	1161	9.512894	GGACTT	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1256	1261	9.512894	GGAAAA	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1311	1316	9.512894	GGAAAC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1383	1388	9.512894	GGACGG	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1442	1447	9.512894	CCATCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1727	1732	9.512894	GTTTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1800	1805	9.512894	CCATCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1919	1924	9.512894	GTGTCC	7.32422	7.44385
cg2639478	AFAP1	TFII-I [T0	1978	1983	9.512894	GGACTT	7.32422	7.44385
cg0675819	AFAP1	FOXP3 [T	32	37	9.512894	GTTATG	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	359	364	9.512894	GTTTAG	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	463	468	9.512894	AGCAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	489	494	9.512894	AGCAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	556	561	9.512894	GTTCTC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	718	723	9.512894	CAGAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	742	747	9.512894	CAGAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	826	831	9.512894	GTTATG	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1092	1097	9.512894	AAGAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1149	1154	9.512894	CTAAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1295	1300	9.512894	CAGAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1476	1481	9.512894	ACCAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1566	1571	9.512894	GTTATG	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1590	1595	9.512894	CGCAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1662	1667	9.512894	AAGAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1702	1707	9.512894	CCCAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1859	1864	9.512894	AGCAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1947	1952	9.512894	AATAAC	7.32422	7.22156
cg0675819	AFAP1	FOXP3 [T	1955	1960	9.512894	GTTGGC	7.32422	7.22156
cg0675819	AFAP1	TFII-I [T0	123	128	9.512894	CCGTCC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	247	252	9.512894	GGAAGG	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	253	258	9.512894	GGAATT	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	338	343	9.512894	CCTTCC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	541	546	9.512894	GGACAA	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	629	634	9.512894	CCATCC	7.32422	7.44385

cg0675819	AFAP1	TFII-I [T0	686	691	9.512894	GGAATT	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	873	878	9.512894	GGACAC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1118	1123	9.512894	GGACAC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1155	1160	9.512894	CCTTCC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1193	1198	9.512894	TTATCC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1197	1202	9.512894	CCTTCC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1502	1507	9.512894	GGACTT	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1691	1696	9.512894	CCTTCC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1751	1756	9.512894	CGATCC	7.32422	7.44385
cg0675819	AFAP1	TFII-I [T0	1868	1873	9.512894	GGACGG	7.32422	7.44385
cg0161265	AFAP1	FOXP3 [T	114	119	9.512894	GTTATG	7.32422	7.22156
cg0161265	AFAP1	FOXP3 [T	291	296	9.512894	AATAAC	7.32422	7.22156
cg0161265	AFAP1	FOXP3 [T	541	546	9.512894	GTTGGG	7.32422	7.22156
cg0161265	AFAP1	FOXP3 [T	743	748	9.512894	GTTCTC	7.32422	7.22156
cg0161265	AFAP1	FOXP3 [T	1488	1493	9.512894	GTTGCT	7.32422	7.22156
cg0161265	AFAP1	FOXP3 [T	1797	1802	9.512894	ACCAAC	7.32422	7.22156
cg0161265	AFAP1	FOXP3 [T	1955	1960	9.512894	GTAAAC	7.32422	7.22156
cg0161265	AFAP1	TFII-I [T0	52	57	9.512894	AAATCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	349	354	9.512894	GTATCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	360	365	9.512894	GGAAGG	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	548	553	9.512894	AAGTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	682	687	9.512894	GGACCG	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	797	802	9.512894	GGAAAC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	846	851	9.512894	TTTTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	973	978	9.512894	GGACGG	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1081	1086	9.512894	GGAACG	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1136	1141	9.512894	CGTTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1309	1314	9.512894	AAGTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1354	1359	9.512894	GGAAAC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1378	1383	9.512894	TTTTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1434	1439	9.512894	GGAAGG	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1478	1483	9.512894	GGAAGG	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1582	1587	9.512894	AATTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1673	1678	9.512894	TTTTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1832	1837	9.512894	GGAAGG	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1856	1861	9.512894	GGAATT	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1858	1863	9.512894	AATTCC	7.32422	7.44385
cg0161265	AFAP1	TFII-I [T0	1904	1909	9.512894	AATTCC	7.32422	7.44385
cg0161265	AFAP1	c-Jun [T00	935	941	9.511322	TGACCA	0.73242	0.7366
cg0675819	AFAP1	Ik-1 [T027	1878	1890	9.497194	TCCCAG	0.02941	0.03137
cg2591200	AFAP1	TCF-4E [T	521	527	9.453578	CTTTGA	0.48828	0.46934
cg2591200	AFAP1	TCF-4E [T	1494	1500	9.453578	GTCAAA	0.48828	0.46934
cg2591200	AFAP1	TCF-4E [T	1613	1619	9.453578	CTTTGA	0.48828	0.46934
cg0261454	AFAP1	TCF-4E [T	585	591	9.453578	CTTTGA	0.48828	0.46934
cg0261454	AFAP1	TCF-4E [T	1558	1564	9.453578	GTCAAA	0.48828	0.46934
cg0261454	AFAP1	TCF-4E [T	1677	1683	9.453578	CTTTGA	0.48828	0.46934
cg2639478	AFAP1	TCF-4E [T	551	557	9.453578	CTTTGA	0.48828	0.46934
cg2639478	AFAP1	TCF-4E [T	1524	1530	9.453578	GTCAAA	0.48828	0.46934

cg2639478	AFAP1	TCF-4E [T	1643	1649	9.453578	CTTTGAC	0.48828	0.46934
cg0675819	AFAP1	TCF-4E [T	1940	1946	9.453578	TACAAA(	0.48828	0.46934
cg0161265	AFAP1	c-Jun [T00	600	606	9.442241	TGACGG(	0.73242	0.7366
cg0161265	AFAP1	c-Jun [T00	1588	1594	9.442241	TGACAG(	0.73242	0.7366
cg2591200	AFAP1	NFI/CTF [	162	169	9.352332	CCAAGG'	0.54932	0.55369
cg2591200	AFAP1	NFI/CTF [	1506	1513	9.352332	CCAAGG(	0.54932	0.55369
cg2591200	AFAP1	NFI/CTF [	1603	1610	9.352332	ATCCTTC	0.54932	0.55369
cg2591200	AFAP1	NFI/CTF [	1862	1869	9.352332	CCAAAG(	0.54932	0.55369
cg0261454	AFAP1	NFI/CTF [	226	233	9.352332	CCAAGG'	0.54932	0.55369
cg0261454	AFAP1	NFI/CTF [	1570	1577	9.352332	CCAAGG(	0.54932	0.55369
cg0261454	AFAP1	NFI/CTF [	1667	1674	9.352332	ATCCTTC	0.54932	0.55369
cg0261454	AFAP1	NFI/CTF [	1926	1933	9.352332	CCAAAG(	0.54932	0.55369
cg2639478	AFAP1	NFI/CTF [	192	199	9.352332	CCAAGG'	0.54932	0.55369
cg2639478	AFAP1	NFI/CTF [	1536	1543	9.352332	CCAAGG(	0.54932	0.55369
cg2639478	AFAP1	NFI/CTF [	1633	1640	9.352332	ATCCTTC	0.54932	0.55369
cg2639478	AFAP1	NFI/CTF [	1892	1899	9.352332	CCAAAG(	0.54932	0.55369
cg2591200	AFAP1	AP-1 [T00	1688	1696	9.3434	TGACTG/	0.09155	0.08441
cg0261454	AFAP1	AP-1 [T00	1752	1760	9.3434	TGACTG/	0.09155	0.08441
cg2639478	AFAP1	AP-1 [T00	1718	1726	9.3434	TGACTG/	0.09155	0.08441
cg0161265	AFAP1	CTF [T001	763	774	9.306712	CTGCCA/	0.01717	0.01814
cg0161265	AFAP1	c-Ets-1 [T(	1137	1143	9.276861	GTTCCC/	0.36621	0.37402
cg2591200	AFAP1	SRY [T00!	1492	1500	9.264664	ATGTCA/	0.12207	0.11857
cg0261454	AFAP1	SRY [T00!	1556	1564	9.264664	ATGTCA/	0.12207	0.11857
cg2639478	AFAP1	SRY [T00!	1522	1530	9.264664	ATGTCA/	0.12207	0.11857
cg0161265	AFAP1	SRY [T00!	1152	1160	9.264664	CTTTGCA	0.12207	0.11857
cg0161265	AFAP1	RBP-Jkapp	903	914	9.256527	ATGGTG(	0.01884	0.01884
cg0161265	AFAP1	RBP-Jkapp	924	935	9.256527	ATGGTG(	0.01884	0.01884
cg0161265	AFAP1	AP-1 [T00	1366	1374	9.256161	AGTCAG'	0.09155	0.08441
cg2591200	AFAP1	c-Ets-1 [T(	868	874	9.19359	ATTCCA/	0.85449	0.84987
cg0261454	AFAP1	c-Ets-1 [T(	932	938	9.19359	ATTCCA/	0.85449	0.84987
cg2639478	AFAP1	c-Ets-1 [T(	898	904	9.19359	ATTCCA/	0.85449	0.84987
cg0161265	AFAP1	NF-AT1 [T	1231	1239	9.18189	CCGCTTT	0.22888	0.22581
cg0675819	AFAP1	AP-1 [T00	1583	1591	9.168921	TGACTA/	0.24414	0.23028
cg0161265	AFAP1	PXR-1:RX	1527	1534	9.122407	GGCGTT(	0.24414	0.24356
cg0675819	AFAP1	COUP-TF.	672	684	9.093379	CCGTGA(	0.01878	0.01921
cg0161265	AFAP1	Egr-3 [T0C	1757	1769	9.093379	TGCACC(	0.01878	0.01978
cg2591200	AFAP1	LEF-1 [T0	1493	1500	9.082175	TGTCAA/	0.54932	0.53171
cg2591200	AFAP1	LEF-1 [T0	1613	1620	9.082175	CTTTGAC	0.54932	0.53171
cg0261454	AFAP1	LEF-1 [T0	1557	1564	9.082175	TGTCAA/	0.54932	0.53171
cg0261454	AFAP1	LEF-1 [T0	1677	1684	9.082175	CTTTGAC	0.54932	0.53171
cg2639478	AFAP1	LEF-1 [T0	1523	1530	9.082175	TGTCAA/	0.54932	0.53171
cg2639478	AFAP1	LEF-1 [T0	1643	1650	9.082175	CTTTGAC	0.54932	0.53171
cg0161265	AFAP1	c-Ets-1 [T(	326	332	9.065503	ATGGAA'	0.85449	0.84987
cg0161265	AFAP1	E2F-1 [T0	995	1002	9.028527	GTCCCC(	0.27466	0.30178
cg2591200	AFAP1	GR [T050'	519	525	8.971049	GGCTTTC	0.61035	0.5928
cg2591200	AFAP1	GR [T050'	639	645	8.971049	GATTTTC	0.61035	0.5928
cg2591200	AFAP1	GR [T050'	656	662	8.971049	GCTTTTC	0.61035	0.5928
cg2591200	AFAP1	GR [T050'	962	968	8.971049	GATTTTC	0.61035	0.5928

cg2591200	AFAP1	GR [T0507	1703	1709	8.971049	CAAACA	0.61035	0.5928
cg0261454	AFAP1	GR [T0507	583	589	8.971049	GGCTTT	0.61035	0.5928
cg0261454	AFAP1	GR [T0507	703	709	8.971049	GATTTT	0.61035	0.5928
cg0261454	AFAP1	GR [T0507	720	726	8.971049	GCTTTT	0.61035	0.5928
cg0261454	AFAP1	GR [T0507	1026	1032	8.971049	GATTTT	0.61035	0.5928
cg0261454	AFAP1	GR [T0507	1767	1773	8.971049	CAAACA	0.61035	0.5928
cg2639478	AFAP1	GR [T0507	549	555	8.971049	GGCTTT	0.61035	0.5928
cg2639478	AFAP1	GR [T0507	669	675	8.971049	GATTTT	0.61035	0.5928
cg2639478	AFAP1	GR [T0507	686	692	8.971049	GCTTTT	0.61035	0.5928
cg2639478	AFAP1	GR [T0507	992	998	8.971049	GATTTT	0.61035	0.5928
cg2639478	AFAP1	GR [T0507	1733	1739	8.971049	CAAACA	0.61035	0.5928
cg0675819	AFAP1	GR [T0507	152	158	8.971049	CAAAAG	0.61035	0.5928
cg0675819	AFAP1	GR [T0507	1278	1284	8.971049	CAAACA	0.61035	0.5928
cg0161265	AFAP1	GR [T0507	1150	1156	8.971049	GGCTTT	0.61035	0.5928
cg0161265	AFAP1	c-Myb [T0	1611	1618	8.947824	AGAAGT	0.39673	0.37851
cg0675819	AFAP1	Elk-1 [T00	1228	1236	8.931691	AGCGGG	0.24414	0.26271
cg2591200	AFAP1	c-Ets-2 [T	485	493	8.912323	TTCCTG	0.27466	0.27171
cg0261454	AFAP1	c-Ets-2 [T	549	557	8.912323	TTCCTG	0.27466	0.27171
cg2639478	AFAP1	c-Ets-2 [T	515	523	8.912323	TTCCTG	0.27466	0.27171
cg0675819	AFAP1	c-Ets-2 [T	237	245	8.912323	GCCCAG	0.27466	0.27171
cg0675819	AFAP1	c-Ets-2 [T	1666	1674	8.912323	ACCCAG	0.27466	0.27171
cg0161265	AFAP1	c-Ets-2 [T	164	172	8.912323	TTCCTG	0.27466	0.27171
cg0161265	AFAP1	c-Ets-2 [T	1119	1127	8.912323	GCTCAG	0.27466	0.27171
cg2591200	AFAP1	HNF-4alph	1605	1617	8.87767	CCTTGG	0.01502	0.01406
cg0261454	AFAP1	HNF-4alph	1669	1681	8.87767	CCTTGG	0.01502	0.01406
cg2639478	AFAP1	HNF-4alph	1635	1647	8.87767	CCTTGG	0.01502	0.01406
cg0161265	AFAP1	AP-1 [T00	1539	1547	8.862731	TGACTT	0.24414	0.23028
cg0675819	AFAP1	AP-1 [T00	80	88	8.82837	TGACTT	0.24414	0.23028
cg0675819	AFAP1	PR B [T00	1882	1888	8.827054	AGCTGT	0.36621	0.35051
cg0675819	AFAP1	PR B [T00	1951	1957	8.827054	ACCTGT	0.36621	0.35051
cg0675819	AFAP1	PR A [T01	1882	1888	8.827054	AGCTGT	0.36621	0.35051
cg0675819	AFAP1	PR A [T01	1951	1957	8.827054	ACCTGT	0.36621	0.35051
cg2591200	AFAP1	NFI/CTF [	1812	1819	8.814757	TCTTTTG	0.48828	0.48845
cg0261454	AFAP1	NFI/CTF [	1876	1883	8.814757	TCTTTTG	0.48828	0.48845
cg2639478	AFAP1	NFI/CTF [	1842	1849	8.814757	TCTTTTG	0.48828	0.48845
cg0675819	AFAP1	NFI/CTF [	1848	1855	8.814757	CCAAGA	0.48828	0.48845
cg2591200	AFAP1	c-Ets-1 [T	345	351	8.809329	CTGGAA	0.85449	0.84987
cg0261454	AFAP1	c-Ets-1 [T	409	415	8.809329	CTGGAA	0.85449	0.84987
cg2639478	AFAP1	c-Ets-1 [T	375	381	8.809329	CTGGAA	0.85449	0.84987
cg0161265	AFAP1	c-Ets-1 [T	1854	1860	8.809329	CTGGAA	0.85449	0.84987
cg0675819	AFAP1	Elk-1 [T00	339	347	8.797343	CTTCCA	0.24414	0.26271
cg0675819	AFAP1	Elk-1 [T00	1505	1513	8.797343	CTTCCA	0.24414	0.26271
cg0675819	AFAP1	NF-AT2 [	952	961	8.794303	GACCCT	0.05341	0.05145
cg2591200	AFAP1	NF-1 [T00	1502	1509	8.790071	CCTCCC	0.24414	0.24339
cg2591200	AFAP1	NF-1 [T00	1698	1705	8.790071	TTTCCC	0.24414	0.24339
cg0261454	AFAP1	NF-1 [T00	1566	1573	8.790071	CCTCCC	0.24414	0.24339
cg0261454	AFAP1	NF-1 [T00	1762	1769	8.790071	TTTCCC	0.24414	0.24339
cg2639478	AFAP1	NF-1 [T00	1532	1539	8.790071	CCTCCC	0.24414	0.24339

cg2639478	AFAP1	NF-1 [T00	1728	1735	8.790071	TTTCCC	0.24414	0.24339
cg0675819	AFAP1	NF-1 [T00	1198	1205	8.790071	CTTCCC	0.24414	0.24339
cg0675819	AFAP1	NF-1 [T00	1699	1706	8.790071	TCTCCC	0.24414	0.24339
cg0161265	AFAP1	NF-1 [T00	179	186	8.790071	TTGGGA	0.24414	0.24339
cg0161265	AFAP1	NF-1 [T00	750	757	8.790071	TTGGCA	0.24414	0.24339
cg0675819	AFAP1	MAZ [T00	1330	1342	8.779528	TGCCCT	0.01413	0.01595
cg0675819	AFAP1	MAZ [T00	1431	1443	8.779528	GCGCGG	0.01413	0.01595
cg0675819	AFAP1	LEF-1 [T0	1939	1946	8.759086	TTACAA	0.54932	0.53171
cg0161265	AFAP1	LEF-1 [T0	623	630	8.759086	CTTTGC	0.54932	0.53171
cg0161265	AFAP1	LEF-1 [T0	1152	1159	8.759086	CTTTGC	0.54932	0.53171
cg2591200	AFAP1	XBP-1 [T	30	35	8.75604	ATGAAA	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	135	140	8.75604	ATGATA	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	209	214	8.75604	GTTCAT	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	512	517	8.75604	ATGAGC	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	549	554	8.75604	ATGAGA	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	1073	1078	8.75604	GCTCAT	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	1199	1204	8.75604	ATGAGA	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	1345	1350	8.75604	TTTCAT	2.92969	2.75329
cg2591200	AFAP1	XBP-1 [T	1807	1812	8.75604	TCTCAT	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	94	99	8.75604	ATGAAA	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	199	204	8.75604	ATGATA	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	273	278	8.75604	GTTCAT	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	576	581	8.75604	ATGAGC	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	613	618	8.75604	ATGAGA	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	1137	1142	8.75604	GCTCAT	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	1263	1268	8.75604	ATGAGA	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	1409	1414	8.75604	TTTCAT	2.92969	2.75329
cg0261454	AFAP1	XBP-1 [T	1871	1876	8.75604	TCTCAT	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	60	65	8.75604	ATGAAA	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	165	170	8.75604	ATGATA	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	239	244	8.75604	GTTCAT	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	542	547	8.75604	ATGAGC	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	579	584	8.75604	ATGAGA	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	1103	1108	8.75604	GCTCAT	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	1229	1234	8.75604	ATGAGA	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	1375	1380	8.75604	TTTCAT	2.92969	2.75329
cg2639478	AFAP1	XBP-1 [T	1837	1842	8.75604	TCTCAT	2.92969	2.75329
cg0675819	AFAP1	XBP-1 [T	558	563	8.75604	TCTCAT	2.92969	2.75329
cg0675819	AFAP1	XBP-1 [T	808	813	8.75604	TCTCAT	2.92969	2.75329
cg0675819	AFAP1	XBP-1 [T	1027	1032	8.75604	ATGAGA	2.92969	2.75329
cg0675819	AFAP1	XBP-1 [T	1069	1074	8.75604	ATGAAC	2.92969	2.75329
cg0161265	AFAP1	XBP-1 [T	117	122	8.75604	ATGAAA	2.92969	2.75329
cg0161265	AFAP1	XBP-1 [T	1660	1665	8.75604	ATGAAC	2.92969	2.75329
cg0161265	AFAP1	XBP-1 [T	1893	1898	8.75604	ATGAGC	2.92969	2.75329
cg2591200	AFAP1	STAT1bet	466	475	8.695301	CTTTCC	0.22316	0.2175
cg2591200	AFAP1	STAT1bet	483	492	8.695301	CTTTCC	0.22316	0.2175
cg0261454	AFAP1	STAT1bet	530	539	8.695301	CTTTCC	0.22316	0.2175
cg0261454	AFAP1	STAT1bet	547	556	8.695301	CTTTCC	0.22316	0.2175

cg2639478	AFAP1	STAT1bet	496	505	8.695301	CTTTCCA	0.22316	0.2175
cg2639478	AFAP1	STAT1bet	513	522	8.695301	CTTTCCT	0.22316	0.2175
cg0675819	AFAP1	STAT1bet	238	247	8.695301	CCCAGG	0.22316	0.2175
cg0161265	AFAP1	STAT1bet	1350	1359	8.695301	TGGGGG	0.22316	0.2175
cg0161265	AFAP1	STAT1bet	1737	1746	8.695301	GCTGGG	0.22316	0.2175
cg0675819	AFAP1	HNF-1B [	1583	1591	8.688037	TGACTA	0.11444	0.10456
cg2591200	AFAP1	c-Jun [T00	810	816	8.571705	TGACTG	0.12207	0.1249
cg0261454	AFAP1	c-Jun [T00	874	880	8.571705	TGACTG	0.12207	0.1249
cg2639478	AFAP1	c-Jun [T00	840	846	8.571705	TGACTG	0.12207	0.1249
cg2591200	AFAP1	IRF-1 [T0	596	604	8.570857	TTTCCA	0.20599	0.20245
cg0261454	AFAP1	IRF-1 [T0	660	668	8.570857	TTTCCA	0.20599	0.20245
cg2639478	AFAP1	IRF-1 [T0	626	634	8.570857	TTTCCA	0.20599	0.20245
cg2591200	AFAP1	RAR-beta	1017	1026	8.55975	CGGGTT	0.26703	0.27434
cg0261454	AFAP1	RAR-beta	1081	1090	8.55975	CGGGTT	0.26703	0.27434
cg2639478	AFAP1	RAR-beta	1047	1056	8.55975	CGGGTT	0.26703	0.27434
cg0675819	AFAP1	RAR-beta	1475	1484	8.541284	CACCAA	0.26703	0.27434
cg0675819	AFAP1	RAR-beta	1661	1670	8.541284	AAAGAA	0.26703	0.27434
cg0161265	AFAP1	RAR-beta	362	371	8.541284	AAGGAA	0.26703	0.27434
cg0675819	AFAP1	p53 [T006	663	669	8.537081	GGGCTC	0.12207	0.13169
cg2591200	AFAP1	USF2 [T0	1625	1634	8.532138	TGTACA	0.103	0.10815
cg0261454	AFAP1	USF2 [T0	1689	1698	8.532138	TGTACA	0.103	0.10815
cg2639478	AFAP1	USF2 [T0	1655	1664	8.532138	TGTACA	0.103	0.10815
cg0161265	AFAP1	USF2 [T0	662	671	8.532138	TGCCCA	0.103	0.10815
cg2591200	AFAP1	c-Ets-1 [T	1607	1613	8.501115	TTGGAA	0.24414	0.23702
cg0261454	AFAP1	c-Ets-1 [T	1671	1677	8.501115	TTGGAA	0.24414	0.23702
cg2639478	AFAP1	c-Ets-1 [T	1637	1643	8.501115	TTGGAA	0.24414	0.23702
cg2591200	AFAP1	MAZ [T00	1846	1858	8.483703	AACCCT	0.00525	0.00581
cg0261454	AFAP1	MAZ [T00	1910	1922	8.483703	AACCCT	0.00525	0.00581
cg2639478	AFAP1	MAZ [T00	1876	1888	8.483703	AACCCT	0.00525	0.00581
cg2591200	AFAP1	LEF-1 [T0	521	528	8.457856	CTTTGA	0.15259	0.154
cg0261454	AFAP1	LEF-1 [T0	585	592	8.457856	CTTTGA	0.15259	0.154
cg2639478	AFAP1	LEF-1 [T0	551	558	8.457856	CTTTGA	0.15259	0.154
cg2591200	AFAP1	AhR:Arnt	1745	1754	8.431005	CCACGC	0.07439	0.08553
cg0261454	AFAP1	AhR:Arnt	1809	1818	8.431005	CCACGC	0.07439	0.08553
cg2639478	AFAP1	AhR:Arnt	1775	1784	8.431005	CCACGC	0.07439	0.08553
cg0161265	AFAP1	AhR:Arnt	226	235	8.431005	GCTCGC	0.07439	0.08553
cg0675819	AFAP1	PPAR-alp	234	244	8.384593	GAGGCC	0.02003	0.02186
cg0161265	AFAP1	c-Ets-1 [T	1888	1894	8.373028	GTTCCA	0.24414	0.23702
cg2591200	AFAP1	HNF-3alp	427	434	8.343064	AATTTA	0.27466	0.23078
cg2591200	AFAP1	HNF-3alp	581	588	8.343064	TTAAAA	0.27466	0.23078
cg0261454	AFAP1	HNF-3alp	491	498	8.343064	AATTTA	0.27466	0.23078
cg0261454	AFAP1	HNF-3alp	645	652	8.343064	TTAAAA	0.27466	0.23078
cg2639478	AFAP1	HNF-3alp	457	464	8.343064	AATTTA	0.27466	0.23078
cg2639478	AFAP1	HNF-3alp	611	618	8.343064	TTAAAA	0.27466	0.23078
cg2591200	AFAP1	c-Ets-2 [T	786	794	8.339336	TTCCTG	0.13733	0.13927
cg0261454	AFAP1	c-Ets-2 [T	850	858	8.339336	TTCCTG	0.13733	0.13927
cg2639478	AFAP1	c-Ets-2 [T	816	824	8.339336	TTCCTG	0.13733	0.13927
cg0675819	AFAP1	c-Ets-2 [T	1057	1065	8.339336	CCGCAG	0.13733	0.13927

cg0161265	AFAP1	c-Ets-2 [T(	1860	1868	8.339336	TTCCTGC	0.13733	0.13927
cg2591200	AFAP1	PR B [T00	391	397	8.338824	CTCTGTT	1.09863	1.09384
cg2591200	AFAP1	PR A [T01	391	397	8.338824	CTCTGTT	1.09863	1.09384
cg0261454	AFAP1	PR B [T00	4	10	8.338824	CTCTGTT	1.09863	1.09384
cg0261454	AFAP1	PR B [T00	455	461	8.338824	CTCTGTT	1.09863	1.09384
cg0261454	AFAP1	PR A [T01	4	10	8.338824	CTCTGTT	1.09863	1.09384
cg0261454	AFAP1	PR A [T01	455	461	8.338824	CTCTGTT	1.09863	1.09384
cg2639478	AFAP1	PR B [T00	421	427	8.338824	CTCTGTT	1.09863	1.09384
cg2639478	AFAP1	PR A [T01	421	427	8.338824	CTCTGTT	1.09863	1.09384
cg0675819	AFAP1	PR B [T00	192	198	8.338824	AACAGA	1.09863	1.09384
cg0675819	AFAP1	PR B [T00	492	498	8.338824	AACAGC	1.09863	1.09384
cg0675819	AFAP1	PR B [T00	1562	1568	8.338824	TTCTGTT	1.09863	1.09384
cg0675819	AFAP1	PR B [T00	1862	1868	8.338824	AACAGC	1.09863	1.09384
cg0675819	AFAP1	PR A [T01	192	198	8.338824	AACAGA	1.09863	1.09384
cg0675819	AFAP1	PR A [T01	492	498	8.338824	AACAGC	1.09863	1.09384
cg0675819	AFAP1	PR A [T01	1562	1568	8.338824	TTCTGTT	1.09863	1.09384
cg0675819	AFAP1	PR A [T01	1862	1868	8.338824	AACAGC	1.09863	1.09384
cg0161265	AFAP1	PR B [T00	1665	1671	8.338824	CTCTGTT	1.09863	1.09384
cg0161265	AFAP1	PR A [T01	1665	1671	8.338824	CTCTGTT	1.09863	1.09384
cg2591200	AFAP1	ATF3 [T01	904	911	8.313799	TGACGC	0.27466	0.27379
cg0261454	AFAP1	ATF3 [T01	968	975	8.313799	TGACGC	0.27466	0.27379
cg2639478	AFAP1	ATF3 [T01	934	941	8.313799	TGACGC	0.27466	0.27379
cg2591200	AFAP1	GR-alpha [	163	167	8.281568	CAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	175	179	8.281568	GAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	253	257	8.281568	GGAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	262	266	8.281568	GAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	266	270	8.281568	GAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	274	278	8.281568	GGAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	285	289	8.281568	GGAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	288	292	8.281568	GGAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	292	296	8.281568	GAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	310	314	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	325	329	8.281568	CCTTC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	362	366	8.281568	CAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	379	383	8.281568	CCTTC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	681	685	8.281568	CCTTG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	784	788	8.281568	CCTTC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	953	957	8.281568	GAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	973	977	8.281568	CCTTG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	989	993	8.281568	GGAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	994	998	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	997	1001	8.281568	CCTCG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1001	1005	8.281568	GGAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1030	1034	8.281568	CCTTC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1039	1043	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1042	1046	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1137	1141	8.281568	CCTTG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1294	1298	8.281568	CAAGG	7.8125	8.20394

cg2591200	AFAP1	GR-alpha [	1459	1463	8.281568	GGAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1466	1470	8.281568	CCTTG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1472	1476	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1502	1506	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1507	1511	8.281568	CAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1577	1581	8.281568	CAAGG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1592	1596	8.281568	CCTTC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1605	1609	8.281568	CCTTG	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1636	1640	8.281568	CCTTC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1782	1786	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1837	1841	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1849	1853	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1894	1898	8.281568	CCTCC	7.8125	8.20394
cg2591200	AFAP1	GR-alpha [	1957	1961	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	227	231	8.281568	CAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	239	243	8.281568	GAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	317	321	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	326	330	8.281568	GAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	330	334	8.281568	GAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	338	342	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	349	353	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	352	356	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	356	360	8.281568	GAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	374	378	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	389	393	8.281568	CCTTC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	426	430	8.281568	CAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	443	447	8.281568	CCTTC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	745	749	8.281568	CCTTG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	848	852	8.281568	CCTTC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1017	1021	8.281568	GAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1037	1041	8.281568	CCTTG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1053	1057	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1058	1062	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1061	1065	8.281568	CCTCG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1065	1069	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1094	1098	8.281568	CCTTC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1103	1107	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1106	1110	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1201	1205	8.281568	CCTTG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1358	1362	8.281568	CAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1523	1527	8.281568	GGAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1530	1534	8.281568	CCTTG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1536	1540	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1566	1570	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1571	1575	8.281568	CAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1641	1645	8.281568	CAAGG	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1656	1660	8.281568	CCTTC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1669	1673	8.281568	CCTTG	7.8125	8.20394

cg0261454	AFAP1	GR-alpha [	1700	1704	8.281568	CCTTC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1846	1850	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1901	1905	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1913	1917	8.281568	CCTCC	7.8125	8.20394
cg0261454	AFAP1	GR-alpha [	1958	1962	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	193	197	8.281568	CAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	205	209	8.281568	GAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	283	287	8.281568	GGAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	292	296	8.281568	GAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	296	300	8.281568	GAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	304	308	8.281568	GGAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	315	319	8.281568	GGAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	318	322	8.281568	GGAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	322	326	8.281568	GAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	340	344	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	355	359	8.281568	CCTTC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	392	396	8.281568	CAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	409	413	8.281568	CCTTC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	711	715	8.281568	CCTTG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	814	818	8.281568	CCTTC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	983	987	8.281568	GAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1003	1007	8.281568	CCTTG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1019	1023	8.281568	GGAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1024	1028	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1027	1031	8.281568	CCTCG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1031	1035	8.281568	GGAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1060	1064	8.281568	CCTTC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1069	1073	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1072	1076	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1167	1171	8.281568	CCTTG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1324	1328	8.281568	CAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1489	1493	8.281568	GGAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1496	1500	8.281568	CCTTG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1502	1506	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1532	1536	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1537	1541	8.281568	CAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1607	1611	8.281568	CAAGG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1622	1626	8.281568	CCTTC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1635	1639	8.281568	CCTTG	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1666	1670	8.281568	CCTTC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1812	1816	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1867	1871	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1879	1883	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1924	1928	8.281568	CCTCC	7.8125	8.20394
cg2639478	AFAP1	GR-alpha [	1987	1991	8.281568	GGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha [	4	8	8.281568	CAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha [	196	200	8.281568	GAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha [	228	232	8.281568	CAAGG	7.8125	8.20394

cg0675819	AFAP1	GR-alpha |	233	237	8.281568	GGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	248	252	8.281568	GAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	277	281	8.281568	CCTCG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	338	342	8.281568	CCTTC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	587	591	8.281568	GGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	660	664	8.281568	CGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	678	682	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	781	785	8.281568	CCTCG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	788	792	8.281568	GAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	853	857	8.281568	GGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	862	866	8.281568	CGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	962	966	8.281568	CCTTC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1020	1024	8.281568	GAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1035	1039	8.281568	CAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1044	1048	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1155	1159	8.281568	CCTTC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1197	1201	8.281568	CCTTC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1251	1255	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1320	1324	8.281568	CCTCG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1327	1331	8.281568	CCTTG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1333	1337	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1348	1352	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1384	1388	8.281568	CCTTC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1427	1431	8.281568	GAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1436	1440	8.281568	GGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1448	1452	8.281568	CCTTG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1452	1456	8.281568	GGAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1465	1469	8.281568	CCTCG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1512	1516	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1641	1645	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1688	1692	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1691	1695	8.281568	CCTTC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1765	1769	8.281568	GAAGG	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1777	1781	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1876	1880	8.281568	CCTCC	7.8125	8.20394
cg0675819	AFAP1	GR-alpha |	1903	1907	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	151	155	8.281568	CAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	182	186	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	342	346	8.281568	CAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	361	365	8.281568	GAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	382	386	8.281568	CCTCC	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	441	445	8.281568	CCTCC	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	571	575	8.281568	CCTCC	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	574	578	8.281568	CCTTG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	711	715	8.281568	CCTTC	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	813	817	8.281568	GAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	832	836	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha |	943	947	8.281568	GGAGG	7.8125	8.20394

cg0161265	AFAP1	GR-alpha [	947	951	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1060	1064	8.281568	CCTCC	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1078	1082	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1261	1265	8.281568	CCTTG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1361	1365	8.281568	CAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1431	1435	8.281568	GAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1435	1439	8.281568	GAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1479	1483	8.281568	GAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1524	1528	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1597	1601	8.281568	CCTCC	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1721	1725	8.281568	GAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1829	1833	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1833	1837	8.281568	GAAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1838	1842	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1847	1851	8.281568	GGAGG	7.8125	8.20394
cg0161265	AFAP1	GR-alpha [	1975	1979	8.281568	CGAGG	7.8125	8.20394
cg2591200	AFAP1	GCF [T00	957	965	8.256755	GCGCAG	0.09155	0.09762
cg0261454	AFAP1	GCF [T00	1021	1029	8.256755	GCGCAG	0.09155	0.09762
cg2639478	AFAP1	GCF [T00	987	995	8.256755	GCGCAG	0.09155	0.09762
cg0675819	AFAP1	c-Jun [T00	675	681	8.242207	TGACCT	0.48828	0.47447
cg0675819	AFAP1	HNF-1B [	385	393	8.241969	AGTTAA	0.06866	0.0616
cg2591200	AFAP1	HNF-1C [	1961	1969	8.214954	GTTACT	0.19836	0.18126
cg2639478	AFAP1	HNF-1C [	1991	1999	8.214954	GTTACT	0.19836	0.18126
cg0161265	AFAP1	NF-AT2 [	1669	1678	8.21356	GTTTTTT	0.08965	0.08482
cg2591200	AFAP1	p53 [T006	724	730	8.208781	GGGGCC	0.48828	0.55336
cg2591200	AFAP1	p53 [T006	725	731	8.208781	GGGCCC	0.48828	0.55336
cg0261454	AFAP1	p53 [T006	788	794	8.208781	GGGGCC	0.48828	0.55336
cg0261454	AFAP1	p53 [T006	789	795	8.208781	GGGCCC	0.48828	0.55336
cg2639478	AFAP1	p53 [T006	754	760	8.208781	GGGGCC	0.48828	0.55336
cg2639478	AFAP1	p53 [T006	755	761	8.208781	GGGCCC	0.48828	0.55336
cg0675819	AFAP1	ENKTF-1	225	232	8.19852	TGGCAA	0.73242	0.80254
cg0675819	AFAP1	ENKTF-1	994	1001	8.19852	TGGCTG	0.73242	0.80254
cg0675819	AFAP1	ENKTF-1	1484	1491	8.19852	TGGCGG	0.73242	0.80254
cg0675819	AFAP1	ENKTF-1	1957	1964	8.19852	TGGCCA	0.73242	0.80254
cg0161265	AFAP1	ENKTF-1	1381	1388	8.19852	TCCCGC	0.73242	0.80254
cg2591200	AFAP1	SRY [T00	1859	1867	8.174786	TCACCA	0.15259	0.14791
cg0261454	AFAP1	SRY [T00	1923	1931	8.174786	TCACCA	0.15259	0.14791
cg2639478	AFAP1	SRY [T00	1889	1897	8.174786	TCACCA	0.15259	0.14791
cg0675819	AFAP1	p53 [T006	945	951	8.162057	AGCGCC	0.48828	0.55336
cg0161265	AFAP1	c-Jun [T00	39	45	8.128539	TGACAT	0.48828	0.47447
cg0161265	AFAP1	NF-AT1 [	1375	1383	8.12076	GTGTTTT	0.1297	0.12846
cg2591200	AFAP1	LEF-1 [T0	22	29	8.117221	ATTCAA	0.12207	0.11275
cg0261454	AFAP1	LEF-1 [T0	86	93	8.117221	ATTCAA	0.12207	0.11275
cg2639478	AFAP1	LEF-1 [T0	52	59	8.117221	ATTCAA	0.12207	0.11275
cg0675819	AFAP1	LEF-1 [T0	444	451	8.117221	CTTTGA	0.12207	0.11275
cg0161265	AFAP1	LEF-1 [T0	1924	1931	8.117221	TTTCAA	0.12207	0.11275
cg2591200	AFAP1	AR [T000	1629	1637	8.11332	CACCTG	0.19836	0.20641
cg0261454	AFAP1	AR [T000	1693	1701	8.11332	CACCTG	0.19836	0.20641

cg2639478	AFAP1	AR [T000	1659	1667	8.11332	CACCTG	0.19836	0.20641
cg2591200	AFAP1	VDR [T00	209	217	8.079962	GTTCAT	0.24414	0.22992
cg0261454	AFAP1	VDR [T00	273	281	8.079962	GTTCAT	0.24414	0.22992
cg2639478	AFAP1	VDR [T00	239	247	8.079962	GTTCAT	0.24414	0.22992
cg2591200	AFAP1	IRF-1 [T0	467	475	8.078284	TTTCCA	0.25177	0.2462
cg2591200	AFAP1	IRF-1 [T0	1896	1904	8.078284	TCCCGG	0.25177	0.2462
cg0261454	AFAP1	IRF-1 [T0	531	539	8.078284	TTTCCA	0.25177	0.2462
cg0261454	AFAP1	IRF-1 [T0	1960	1968	8.078284	TCCCGG	0.25177	0.2462
cg2639478	AFAP1	IRF-1 [T0	497	505	8.078284	TTTCCA	0.25177	0.2462
cg2639478	AFAP1	IRF-1 [T0	1926	1934	8.078284	TCCCGG	0.25177	0.2462
cg2591200	AFAP1	GR-alpha [	36	40	8.073878	CCTGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	250	254	8.073878	GCAGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	329	333	8.073878	CCTGC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	368	372	8.073878	CCAGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	384	388	8.073878	CCTGC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	411	415	8.073878	CCTGC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	487	491	8.073878	CCTGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	572	576	8.073878	CCTGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	620	624	8.073878	CCTGC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	730	734	8.073878	CCTGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	761	765	8.073878	CCTGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	788	792	8.073878	CCTGC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	949	953	8.073878	GCAGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	979	983	8.073878	CCAGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	1306	1310	8.073878	CCTAC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	1400	1404	8.073878	GCAGG	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	1528	1532	8.073878	CCTGC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	1785	1789	8.073878	CCTGC	7.8125	8.20289
cg2591200	AFAP1	GR-alpha [	1795	1799	8.073878	CCTGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	50	54	8.073878	CCTAG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	51	55	8.073878	CTAGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	100	104	8.073878	CCTGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	314	318	8.073878	GCAGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	393	397	8.073878	CCTGC	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	432	436	8.073878	CCAGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	448	452	8.073878	CCTGC	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	475	479	8.073878	CCTGC	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	551	555	8.073878	CCTGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	636	640	8.073878	CCTGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	684	688	8.073878	CCTGC	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	794	798	8.073878	CCTGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	825	829	8.073878	CCTGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	852	856	8.073878	CCTGC	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	1013	1017	8.073878	GCAGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	1043	1047	8.073878	CCAGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	1370	1374	8.073878	CCTAC	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	1464	1468	8.073878	GCAGG	7.8125	8.20289
cg0261454	AFAP1	GR-alpha [	1592	1596	8.073878	CCTGC	7.8125	8.20289

cg0261454	AFAP1	GR-alpha |	1849	1853	8.073878	CCTGC	7.8125	8.20289
cg0261454	AFAP1	GR-alpha |	1859	1863	8.073878	CCTGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	16	20	8.073878	CCTAG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	17	21	8.073878	CTAGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	66	70	8.073878	CCTGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	280	284	8.073878	GCAGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	359	363	8.073878	CCTGC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	398	402	8.073878	CCAGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	414	418	8.073878	CCTGC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	441	445	8.073878	CCTGC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	517	521	8.073878	CCTGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	602	606	8.073878	CCTGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	650	654	8.073878	CCTGC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	760	764	8.073878	CCTGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	791	795	8.073878	CCTGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	818	822	8.073878	CCTGC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	979	983	8.073878	GCAGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	1009	1013	8.073878	CCAGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	1336	1340	8.073878	CCTAC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	1430	1434	8.073878	GCAGG	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	1558	1562	8.073878	CCTGC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	1815	1819	8.073878	CCTGC	7.8125	8.20289
cg2639478	AFAP1	GR-alpha |	1825	1829	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	72	76	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	127	131	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	219	223	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	239	243	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	327	331	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	334	338	8.073878	CCTGC	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	365	369	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	435	439	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	499	503	8.073878	GCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	692	696	8.073878	GCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	698	702	8.073878	GCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	888	892	8.073878	GCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1059	1063	8.073878	GCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1114	1118	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1136	1140	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1258	1262	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1286	1290	8.073878	CTAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1306	1310	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1316	1320	8.073878	CCTGC	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1362	1366	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1482	1486	8.073878	CCTGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1515	1519	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1668	1672	8.073878	CCAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1809	1813	8.073878	CTAGG	7.8125	8.20289
cg0675819	AFAP1	GR-alpha |	1960	1964	8.073878	CCAGG	7.8125	8.20289

cg0161265	AFAP1	GR-alpha [	73	77	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	78	82	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	105	109	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	166	170	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	385	389	8.073878	CCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	484	488	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	553	557	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	579	583	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	646	650	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	679	683	8.073878	CCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	758	762	8.073878	GCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	793	797	8.073878	CCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	897	901	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	918	922	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1007	1011	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1011	1015	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1020	1024	8.073878	CCTAG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1070	1074	8.073878	CTAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1265	1269	8.073878	GCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1519	1523	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1634	1638	8.073878	CCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1751	1755	8.073878	CCTAC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1766	1770	8.073878	CCTAC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1789	1793	8.073878	CCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1844	1848	8.073878	GCAGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1853	1857	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1862	1866	8.073878	CCTGC	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1938	1942	8.073878	CCTGG	7.8125	8.20289
cg0161265	AFAP1	GR-alpha [	1988	1992	8.073878	CCTGC	7.8125	8.20289
cg0675819	AFAP1	AR [T000	1118	1126	8.055836	GGACAC	0.19836	0.20641
cg2591200	AFAP1	TFIID [T0	43	49	8.014558	TTACAA	2.19727	1.99811
cg2591200	AFAP1	TFIID [T0	125	131	8.014558	TTTCTAA	2.19727	1.99811
cg2591200	AFAP1	TFIID [T0	236	242	8.014558	TTTCTAA	2.19727	1.99811
cg2591200	AFAP1	TFIID [T0	422	428	8.014558	TCTCAA	2.19727	1.99811
cg2591200	AFAP1	TFIID [T0	850	856	8.014558	TTACAA	2.19727	1.99811
cg2591200	AFAP1	TFIID [T0	1345	1351	8.014558	TTTCATA	2.19727	1.99811
cg2591200	AFAP1	Pax-5 [T0	724	730	8.014558	GGGGCC	2.19727	2.42766
cg2591200	AFAP1	Pax-5 [T0	725	731	8.014558	GGGCCC	2.19727	2.42766
cg2591200	AFAP1	Pax-5 [T0	756	762	8.014558	GGGCAC	2.19727	2.42766
cg2591200	AFAP1	Pax-5 [T0	779	785	8.014558	GCTGCC	2.19727	2.42766
cg2591200	AFAP1	Pax-5 [T0	1154	1160	8.014558	GGGCTC	2.19727	2.42766
cg2591200	AFAP1	Pax-5 [T0	1599	1605	8.014558	GGGCAT	2.19727	2.42766
cg2591200	AFAP1	Pax-5 [T0	1645	1651	8.014558	GGTGCC	2.19727	2.42766
cg0261454	AFAP1	TFIID [T0	107	113	8.014558	TTACAA	2.19727	1.99811
cg0261454	AFAP1	TFIID [T0	189	195	8.014558	TTTCTAA	2.19727	1.99811
cg0261454	AFAP1	TFIID [T0	300	306	8.014558	TTTCTAA	2.19727	1.99811
cg0261454	AFAP1	TFIID [T0	486	492	8.014558	TCTCAA	2.19727	1.99811
cg0261454	AFAP1	TFIID [T0	914	920	8.014558	TTACAA	2.19727	1.99811

cg0261454	AFAP1	TFIID [T0	1409	1415	8.014558	TTTCATA	2.19727	1.99811
cg0261454	AFAP1	Pax-5 [T0	788	794	8.014558	GGGGCC	2.19727	2.42766
cg0261454	AFAP1	Pax-5 [T0	789	795	8.014558	GGGCCC	2.19727	2.42766
cg0261454	AFAP1	Pax-5 [T0	820	826	8.014558	GGGCAC	2.19727	2.42766
cg0261454	AFAP1	Pax-5 [T0	843	849	8.014558	GCTGCC	2.19727	2.42766
cg0261454	AFAP1	Pax-5 [T0	1218	1224	8.014558	GGGCTC	2.19727	2.42766
cg0261454	AFAP1	Pax-5 [T0	1663	1669	8.014558	GGGCAT	2.19727	2.42766
cg0261454	AFAP1	Pax-5 [T0	1709	1715	8.014558	GGTGCC	2.19727	2.42766
cg2639478	AFAP1	TFIID [T0	73	79	8.014558	TTACAA	2.19727	1.99811
cg2639478	AFAP1	TFIID [T0	155	161	8.014558	TTTCTAA	2.19727	1.99811
cg2639478	AFAP1	TFIID [T0	266	272	8.014558	TTTCTAA	2.19727	1.99811
cg2639478	AFAP1	TFIID [T0	452	458	8.014558	TCTCAA	2.19727	1.99811
cg2639478	AFAP1	TFIID [T0	880	886	8.014558	TTACAA	2.19727	1.99811
cg2639478	AFAP1	TFIID [T0	1375	1381	8.014558	TTTCATA	2.19727	1.99811
cg2639478	AFAP1	Pax-5 [T0	754	760	8.014558	GGGGCC	2.19727	2.42766
cg2639478	AFAP1	Pax-5 [T0	755	761	8.014558	GGGCCC	2.19727	2.42766
cg2639478	AFAP1	Pax-5 [T0	786	792	8.014558	GGGCAC	2.19727	2.42766
cg2639478	AFAP1	Pax-5 [T0	809	815	8.014558	GCTGCC	2.19727	2.42766
cg2639478	AFAP1	Pax-5 [T0	1184	1190	8.014558	GGGCTC	2.19727	2.42766
cg2639478	AFAP1	Pax-5 [T0	1629	1635	8.014558	GGGCAT	2.19727	2.42766
cg2639478	AFAP1	Pax-5 [T0	1675	1681	8.014558	GGTGCC	2.19727	2.42766
cg0675819	AFAP1	TFIID [T0	132	138	8.014558	TAAGAA	2.19727	1.99811
cg0675819	AFAP1	TFIID [T0	393	399	8.014558	TTTGAA	2.19727	1.99811
cg0675819	AFAP1	TFIID [T0	445	451	8.014558	TTTGAA	2.19727	1.99811
cg0675819	AFAP1	TFIID [T0	1653	1659	8.014558	TTAGAA	2.19727	1.99811
cg0675819	AFAP1	TFIID [T0	1887	1893	8.014558	TTTCTGA	2.19727	1.99811
cg0675819	AFAP1	TFIID [T0	1939	1945	8.014558	TTACAA	2.19727	1.99811
cg0675819	AFAP1	TFIID [T0	1989	1995	8.014558	TCAGAA	2.19727	1.99811
cg0675819	AFAP1	Pax-5 [T0	172	178	8.014558	GCAGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	234	240	8.014558	GAGGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	271	277	8.014558	GGAGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	303	309	8.014558	TCGGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	588	594	8.014558	GAGGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	623	629	8.014558	TCTGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	800	806	8.014558	TCTGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	830	836	8.014558	TGTGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	891	897	8.014558	GGGCTC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	1261	1267	8.014558	GGTGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	1572	1578	8.014558	GCAGCC	2.19727	2.42766
cg0675819	AFAP1	Pax-5 [T0	1981	1987	8.014558	GGGCAC	2.19727	2.42766
cg0161265	AFAP1	TFIID [T0	116	122	8.014558	TATGAA	2.19727	1.99811
cg0161265	AFAP1	TFIID [T0	398	404	8.014558	TTTGAA	2.19727	1.99811
cg0161265	AFAP1	TFIID [T0	427	433	8.014558	TTTGTTA	2.19727	1.99811
cg0161265	AFAP1	TFIID [T0	477	483	8.014558	TTACAA	2.19727	1.99811
cg0161265	AFAP1	TFIID [T0	1153	1159	8.014558	TTTGCA	2.19727	1.99811
cg0161265	AFAP1	TFIID [T0	1213	1219	8.014558	TTTCTTA	2.19727	1.99811
cg0161265	AFAP1	TFIID [T0	1336	1342	8.014558	TCTGAA	2.19727	1.99811
cg0161265	AFAP1	TFIID [T0	1924	1930	8.014558	TTTCAA	2.19727	1.99811

cg0161265	AFAP1	Pax-5 [T0(	88	94	8.014558	GGGCCT(	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	388	394	8.014558	GGGCAC	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	568	574	8.014558	GGGCCT(	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	660	666	8.014558	GCTGCC(	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	885	891	8.014558	TGGGCC(	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	886	892	8.014558	GGGCCC.	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	950	956	8.014558	GGGCTC(	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	1057	1063	8.014558	GGGCCT(	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	1746	1752	8.014558	GAGGCC	2.19727	2.42766
cg0161265	AFAP1	Pax-5 [T0(	1848	1854	8.014558	GAGGCC	2.19727	2.42766
cg0161265	AFAP1	USF2 [T0(	1172	1181	8.007902	CAGGTG	0.01717	0.01801
cg2591200	AFAP1	MEF-2A ['	1243	1253	7.982343	AAACAA	0.04005	0.03447
cg0261454	AFAP1	MEF-2A ['	1307	1317	7.982343	AAACAA	0.04005	0.03447
cg2639478	AFAP1	MEF-2A ['	1273	1283	7.982343	AAACAA	0.04005	0.03447
cg0161265	AFAP1	MEF-2A ['	284	294	7.982343	ACACAT.	0.04005	0.03447
cg0675819	AFAP1	ETF [T002	1264	1274	7.870358	GCCCCC.	0.07153	0.08737
cg0161265	AFAP1	ETF [T002	943	953	7.870358	GGAGGG	0.07153	0.08737
cg2591200	AFAP1	c-Ets-2 [T(	1828	1836	7.84116	TTCCTGA	0.32043	0.30792
cg0261454	AFAP1	c-Ets-2 [T(	49	57	7.84116	TCCTAG(	0.32043	0.30792
cg0261454	AFAP1	c-Ets-2 [T(	1892	1900	7.84116	TTCCTGA	0.32043	0.30792
cg2639478	AFAP1	c-Ets-2 [T(	15	23	7.84116	TCCTAG(	0.32043	0.30792
cg2639478	AFAP1	c-Ets-2 [T(	1858	1866	7.84116	TTCCTGA	0.32043	0.30792
cg0161265	AFAP1	c-Ets-2 [T(	1584	1592	7.84116	TTCCTGA	0.32043	0.30792
cg0675819	AFAP1	p53 [T006'	271	277	7.833758	GGAGCC	0.48828	0.55336
cg0161265	AFAP1	p53 [T006'	950	956	7.833758	GGGCTC(	0.48828	0.55336
cg2591200	AFAP1	IRF-1 [T0(	484	492	7.82345	TTTCCTC	0.25177	0.2462
cg0261454	AFAP1	IRF-1 [T0(	548	556	7.82345	TTTCCTC	0.25177	0.2462
cg2639478	AFAP1	IRF-1 [T0(	514	522	7.82345	TTTCCTC	0.25177	0.2462
cg0675819	AFAP1	RXR-alpha	1676	1682	7.815913	GCCACC(	0.24414	0.26389
cg2591200	AFAP1	T3R-beta1	1711	1719	7.813363	TCACCC(	0.27466	0.28753
cg0261454	AFAP1	T3R-beta1	1775	1783	7.813363	TCACCC(	0.27466	0.28753
cg2639478	AFAP1	T3R-beta1	1741	1749	7.813363	TCACCC(	0.27466	0.28753
cg0675819	AFAP1	T3R-beta1	531	539	7.813363	GGCCGG'	0.27466	0.28753
cg0161265	AFAP1	T3R-beta1	594	602	7.813363	GGTGGG'	0.27466	0.28753
cg2591200	AFAP1	EBF [T054	750	760	7.780217	AGCTCA(	0.04196	0.04563
cg0261454	AFAP1	EBF [T054	814	824	7.780217	AGCTCA(	0.04196	0.04563
cg2639478	AFAP1	EBF [T054	780	790	7.780217	AGCTCA(	0.04196	0.04563
cg2591200	AFAP1	c-Ets-2 [T(	1763	1771	7.76635	TTCCTGT	0.32043	0.30792
cg0261454	AFAP1	c-Ets-2 [T(	1827	1835	7.76635	TTCCTGT	0.32043	0.30792
cg2639478	AFAP1	c-Ets-2 [T(	1793	1801	7.76635	TTCCTGT	0.32043	0.30792
cg2591200	AFAP1	NF-AT1 [T	480	488	7.744746	TTCCTTT	0.19836	0.19379
cg0261454	AFAP1	NF-AT1 [T	544	552	7.744746	TTCCTTT	0.19836	0.19379
cg2639478	AFAP1	NF-AT1 [T	510	518	7.744746	TTCCTTT	0.19836	0.19379
cg0675819	AFAP1	NF-AT1 [T	242	250	7.744746	GGAAAG	0.19836	0.19379
cg2591200	AFAP1	c-Myb [T0	1884	1891	7.739476	GAACTG'	0.42725	0.40917
cg0261454	AFAP1	c-Myb [T0	1948	1955	7.739476	GAACTG'	0.42725	0.40917
cg2639478	AFAP1	c-Myb [T0	1914	1921	7.739476	GAACTG'	0.42725	0.40917
cg0161265	AFAP1	c-Myb [T0	739	746	7.739476	CACAGT'	0.42725	0.40917

cg2591200	AFAP1	NF-1 [T00	1607	1614	7.693985	TTGGAA	0.24414	0.23756
cg0261454	AFAP1	NF-1 [T00	1671	1678	7.693985	TTGGAA	0.24414	0.23756
cg2639478	AFAP1	NF-1 [T00	1637	1644	7.693985	TTGGAA	0.24414	0.23756
cg2591200	AFAP1	STAT5A [	1615	1627	7.681787	TTGACA	0.00894	0.00812
cg0261454	AFAP1	STAT5A [	1679	1691	7.681787	TTGACA	0.00894	0.00812
cg2639478	AFAP1	STAT5A [	1645	1657	7.681787	TTGACA	0.00894	0.00812
cg2591200	AFAP1	EBF [T05	1724	1734	7.659914	ACCTCA	0.01144	0.0122
cg0261454	AFAP1	EBF [T05	1788	1798	7.659914	ACCTCA	0.01144	0.0122
cg2639478	AFAP1	EBF [T05	1754	1764	7.659914	ACCTCA	0.01144	0.0122
cg2591200	AFAP1	c-Ets-1 [T	1083	1089	7.642098	TCGGAA	0.48828	0.48642
cg0261454	AFAP1	c-Ets-1 [T	1147	1153	7.642098	TCGGAA	0.48828	0.48642
cg2639478	AFAP1	c-Ets-1 [T	1113	1119	7.642098	TCGGAA	0.48828	0.48642
cg0675819	AFAP1	p53 [T006	821	827	7.641867	GGGCCG	0.73242	0.79826
cg0675819	AFAP1	p53 [T006	1324	1330	7.641867	GGGCCT	0.73242	0.79826
cg0675819	AFAP1	p53 [T006	1518	1524	7.641867	GGGCCG	0.73242	0.79826
cg0675819	AFAP1	p53 [T006	1870	1876	7.641867	ACGGCC	0.73242	0.79826
cg0161265	AFAP1	p53 [T006	608	614	7.641867	AAGGCC	0.73242	0.79826
cg0161265	AFAP1	p53 [T006	975	981	7.641867	ACGGCC	0.73242	0.79826
cg0675819	AFAP1	LEF-1 [T0	762	769	7.6105	CTTTGG	0.21362	0.21504
cg2591200	AFAP1	RBP-Jkap	12	23	7.593528	GATTCC	0.02337	0.02319
cg0261454	AFAP1	RBP-Jkap	76	87	7.593528	GATTCC	0.02337	0.02319
cg2639478	AFAP1	RBP-Jkap	42	53	7.593528	GATTCC	0.02337	0.02319
cg2591200	AFAP1	NFI/CTF [	656	663	7.587343	GCTTTTC	0.36621	0.36269
cg2591200	AFAP1	NFI/CTF [	871	878	7.587343	CCAAAT	0.36621	0.36269
cg0261454	AFAP1	NFI/CTF [	720	727	7.587343	GCTTTTC	0.36621	0.36269
cg0261454	AFAP1	NFI/CTF [	935	942	7.587343	CCAAAT	0.36621	0.36269
cg2639478	AFAP1	NFI/CTF [	686	693	7.587343	GCTTTTC	0.36621	0.36269
cg2639478	AFAP1	NFI/CTF [	901	908	7.587343	CCAAAT	0.36621	0.36269
cg0675819	AFAP1	NFI/CTF [	178	185	7.587343	CCAAGT	0.36621	0.36269
cg0161265	AFAP1	NFI/CTF [	780	787	7.587343	CCAAGA	0.36621	0.36269
cg2591200	AFAP1	c-Myb [T0	885	892	7.545286	AGCAGT	0.42725	0.40917
cg0261454	AFAP1	c-Myb [T0	949	956	7.545286	AGCAGT	0.42725	0.40917
cg2639478	AFAP1	c-Myb [T0	915	922	7.545286	AGCAGT	0.42725	0.40917
cg0161265	AFAP1	c-Jun [T00	196	202	7.538568	TGACAT	0.48828	0.48672
cg0675819	AFAP1	PPAR-alph	588	598	7.529496	GAGGCC	0.04482	0.04884
cg0675819	AFAP1	PPAR-alph	1893	1903	7.529496	AAGACC	0.04482	0.04884
cg2591200	AFAP1	GR [T050	142	148	7.527031	AATTTTC	1.83105	1.71535
cg2591200	AFAP1	GR [T050	185	191	7.527031	CAAAAG	1.83105	1.71535
cg2591200	AFAP1	GR [T050	1812	1818	7.527031	TCTTTTG	1.83105	1.71535
cg2591200	AFAP1	GR [T050	1863	1869	7.527031	CAAAGC	1.83105	1.71535
cg0261454	AFAP1	GR [T050	206	212	7.527031	AATTTTC	1.83105	1.71535
cg0261454	AFAP1	GR [T050	249	255	7.527031	CAAAAG	1.83105	1.71535
cg0261454	AFAP1	GR [T050	1876	1882	7.527031	TCTTTTG	1.83105	1.71535
cg0261454	AFAP1	GR [T050	1927	1933	7.527031	CAAAGC	1.83105	1.71535
cg2639478	AFAP1	GR [T050	172	178	7.527031	AATTTTC	1.83105	1.71535
cg2639478	AFAP1	GR [T050	215	221	7.527031	CAAAAG	1.83105	1.71535
cg2639478	AFAP1	GR [T050	1842	1848	7.527031	TCTTTTG	1.83105	1.71535
cg2639478	AFAP1	GR [T050	1893	1899	7.527031	CAAAGC	1.83105	1.71535

cg0161265	AFAP1	GR [T050	395	401	7.527031	CATTTC	1.83105	1.71535
cg0161265	AFAP1	GR [T050	499	505	7.527031	CAAAAT	1.83105	1.71535
cg0161265	AFAP1	GR [T050	754	760	7.527031	CAAAGC	1.83105	1.71535
cg0161265	AFAP1	GR [T050	802	808	7.527031	CTATTC	1.83105	1.71535
cg0161265	AFAP1	GR [T050	866	872	7.527031	CATTTC	1.83105	1.71535
cg0161265	AFAP1	PXR-1:RX	12	19	7.486257	TGAACA	0.24414	0.24326
cg0675819	AFAP1	IRF-1 [T0	238	246	7.477948	CCCAGG	0.14496	0.14723
cg0675819	AFAP1	C/EBPalph	1827	1833	7.465744	TTCAAT	0.48828	0.45033
cg0161265	AFAP1	C/EBPalph	899	905	7.465744	TGCAAT	0.48828	0.45033
cg0161265	AFAP1	C/EBPalph	920	926	7.465744	TGCAAT	0.48828	0.45033
cg0675819	AFAP1	AR [T000	65	73	7.429939	AGCCTG	0.25177	0.2544
cg2591200	AFAP1	PEA3 [T0	1410	1418	7.421728	CGCCAT	0.34332	0.35389
cg2591200	AFAP1	PEA3 [T0	1599	1607	7.421728	GGGCAT	0.34332	0.35389
cg0261454	AFAP1	PEA3 [T0	1474	1482	7.421728	CGCCAT	0.34332	0.35389
cg0261454	AFAP1	PEA3 [T0	1663	1671	7.421728	GGGCAT	0.34332	0.35389
cg2639478	AFAP1	PEA3 [T0	1440	1448	7.421728	CGCCAT	0.34332	0.35389
cg2639478	AFAP1	PEA3 [T0	1629	1637	7.421728	GGGCAT	0.34332	0.35389
cg0675819	AFAP1	PEA3 [T0	1079	1087	7.421728	ACACAT	0.34332	0.35389
cg0675819	AFAP1	AR [T000	1812	1820	7.406474	GGACAG	0.25177	0.2544
cg0161265	AFAP1	AR [T000	1426	1434	7.406474	GGACAG	0.25177	0.2544
cg0675819	AFAP1	C/EBPalph	379	385	7.396431	AATTGG	0.48828	0.45033
cg0161265	AFAP1	C/EBPalph	1191	1197	7.396431	TCCAAT	0.48828	0.45033
cg0161265	AFAP1	IRF-1 [T0	1350	1358	7.387351	TGGGGG	0.14496	0.14723
cg0675819	AFAP1	c-Ets-1 [T	684	690	7.385924	GCGGAA	0.48828	0.48642
cg0675819	AFAP1	PPAR-alph	1597	1607	7.370536	CAGTCC	0.04482	0.04884
cg0675819	AFAP1	E2F-1 [T0	496	503	7.336545	GCGGCA	0.45776	0.49661
cg0675819	AFAP1	E2F-1 [T0	684	691	7.336545	GCGGAA	0.45776	0.49661
cg0161265	AFAP1	RBP-Jkap	1021	1032	7.279684	CTAGTG	0.02337	0.02319
cg2591200	AFAP1	c-Ets-2 [T	327	335	7.268173	TTCCTG	0.09155	0.08977
cg2591200	AFAP1	c-Ets-2 [T	409	417	7.268173	TTCCTG	0.09155	0.08977
cg2591200	AFAP1	c-Ets-2 [T	947	955	7.268173	CAGCAG	0.09155	0.08977
cg0261454	AFAP1	c-Ets-2 [T	391	399	7.268173	TTCCTG	0.09155	0.08977
cg0261454	AFAP1	c-Ets-2 [T	473	481	7.268173	TTCCTG	0.09155	0.08977
cg0261454	AFAP1	c-Ets-2 [T	1011	1019	7.268173	CAGCAG	0.09155	0.08977
cg2639478	AFAP1	c-Ets-2 [T	357	365	7.268173	TTCCTG	0.09155	0.08977
cg2639478	AFAP1	c-Ets-2 [T	439	447	7.268173	TTCCTG	0.09155	0.08977
cg2639478	AFAP1	c-Ets-2 [T	977	985	7.268173	CAGCAG	0.09155	0.08977
cg0675819	AFAP1	p53 [T006	1460	1466	7.266844	ACAGCC	0.73242	0.79826
cg0675819	AFAP1	p53 [T006	1771	1777	7.266844	ACAGCC	0.73242	0.79826
cg0675819	AFAP1	p53 [T006	1965	1971	7.266844	ACAGCC	0.73242	0.79826
cg2591200	AFAP1	c-Ets-1 [T	314	320	7.257837	CCGGAA	0.48828	0.48642
cg0261454	AFAP1	c-Ets-1 [T	378	384	7.257837	CCGGAA	0.48828	0.48642
cg2639478	AFAP1	c-Ets-1 [T	344	350	7.257837	CCGGAA	0.48828	0.48642
cg0161265	AFAP1	c-Ets-1 [T	1905	1911	7.257837	ATTCCG	0.48828	0.48642
cg0675819	AFAP1	HNF-1C [	386	394	7.229698	GTTAAT	0.08392	0.07499
cg0161265	AFAP1	NF-AT1 [	1741	1749	7.211175	GGAAAG	0.15259	0.14325
cg2591200	AFAP1	c-Ets-1 [T	667	673	7.199436	TGGGAA	0.73242	0.73732
cg2591200	AFAP1	c-Ets-1 [T	1698	1704	7.199436	TTTCCC	0.73242	0.73732

cg0261454	AFAP1	c-Ets-1 [T0	731	737	7.199436	TGGGAA	0.73242	0.73732
cg0261454	AFAP1	c-Ets-1 [T0	1762	1768	7.199436	TTTCCCA	0.73242	0.73732
cg2639478	AFAP1	c-Ets-1 [T0	697	703	7.199436	TGGGAA	0.73242	0.73732
cg2639478	AFAP1	c-Ets-1 [T0	1728	1734	7.199436	TTTCCCA	0.73242	0.73732
cg0161265	AFAP1	c-Ets-1 [T0	1739	1745	7.199436	TGGGAA	0.73242	0.73732
cg0675819	AFAP1	MAZ [T00	1345	1357	7.18478	CACCCTC	0.00918	0.01018
cg2591200	AFAP1	c-Jun [T00	1369	1375	7.178905	TGACCCC	0.73242	0.73062
cg0261454	AFAP1	c-Jun [T00	1433	1439	7.178905	TGACCCC	0.73242	0.73062
cg2639478	AFAP1	c-Jun [T00	1399	1405	7.178905	TGACCCC	0.73242	0.73062
cg0161265	AFAP1	c-Jun [T00	807	813	7.178905	TGACCCC	0.73242	0.73062
cg2591200	AFAP1	SRY [T009	21	29	7.175614	AATTCAA	0.30518	0.29547
cg0261454	AFAP1	SRY [T009	85	93	7.175614	AATTCAA	0.30518	0.29547
cg2639478	AFAP1	SRY [T009	51	59	7.175614	AATTCAA	0.30518	0.29547
cg0675819	AFAP1	SRY [T009	444	452	7.175614	CTTTGAA	0.30518	0.29547
cg0161265	AFAP1	SRY [T009	1923	1931	7.175614	CTTTCAA	0.30518	0.29547
cg2591200	AFAP1	XBP-1 [T0	153	158	7.172312	ATGATT	2.92969	2.7512
cg2591200	AFAP1	XBP-1 [T0	637	642	7.172312	ATGATT	2.92969	2.7512
cg2591200	AFAP1	XBP-1 [T0	1048	1053	7.172312	CTTCAT	2.92969	2.7512
cg2591200	AFAP1	XBP-1 [T0	1051	1056	7.172312	CATCAT	2.92969	2.7512
cg2591200	AFAP1	XBP-1 [T0	1060	1065	7.172312	ACTCAT	2.92969	2.7512
cg2591200	AFAP1	XBP-1 [T0	1087	1092	7.172312	AATCAT	2.92969	2.7512
cg2591200	AFAP1	XBP-1 [T0	1416	1421	7.172312	CCTCAT	2.92969	2.7512
cg2591200	AFAP1	XBP-1 [T0	1975	1980	7.172312	ATGAGG	2.92969	2.7512
cg0261454	AFAP1	XBP-1 [T0	217	222	7.172312	ATGATT	2.92969	2.7512
cg0261454	AFAP1	XBP-1 [T0	701	706	7.172312	ATGATT	2.92969	2.7512
cg0261454	AFAP1	XBP-1 [T0	1112	1117	7.172312	CTTCAT	2.92969	2.7512
cg0261454	AFAP1	XBP-1 [T0	1115	1120	7.172312	CATCAT	2.92969	2.7512
cg0261454	AFAP1	XBP-1 [T0	1124	1129	7.172312	ACTCAT	2.92969	2.7512
cg0261454	AFAP1	XBP-1 [T0	1151	1156	7.172312	AATCAT	2.92969	2.7512
cg0261454	AFAP1	XBP-1 [T0	1480	1485	7.172312	CCTCAT	2.92969	2.7512
cg2639478	AFAP1	XBP-1 [T0	183	188	7.172312	ATGATT	2.92969	2.7512
cg2639478	AFAP1	XBP-1 [T0	667	672	7.172312	ATGATT	2.92969	2.7512
cg2639478	AFAP1	XBP-1 [T0	1078	1083	7.172312	CTTCAT	2.92969	2.7512
cg2639478	AFAP1	XBP-1 [T0	1081	1086	7.172312	CATCAT	2.92969	2.7512
cg2639478	AFAP1	XBP-1 [T0	1090	1095	7.172312	ACTCAT	2.92969	2.7512
cg2639478	AFAP1	XBP-1 [T0	1117	1122	7.172312	AATCAT	2.92969	2.7512
cg2639478	AFAP1	XBP-1 [T0	1446	1451	7.172312	CCTCAT	2.92969	2.7512
cg0675819	AFAP1	XBP-1 [T0	348	353	7.172312	CCTCAT	2.92969	2.7512
cg0675819	AFAP1	XBP-1 [T0	406	411	7.172312	ACTCAT	2.92969	2.7512
cg0675819	AFAP1	XBP-1 [T0	429	434	7.172312	ATGATG	2.92969	2.7512
cg0675819	AFAP1	XBP-1 [T0	571	576	7.172312	CATCAT	2.92969	2.7512
cg0675819	AFAP1	XBP-1 [T0	963	968	7.172312	CTTCAT	2.92969	2.7512
cg0675819	AFAP1	XBP-1 [T0	976	981	7.172312	ATGAAT	2.92969	2.7512
cg0161265	AFAP1	XBP-1 [T0	863	868	7.172312	ATTCAT	2.92969	2.7512
cg0161265	AFAP1	XBP-1 [T0	879	884	7.172312	ATGAAG	2.92969	2.7512
cg0161265	AFAP1	XBP-1 [T0	1293	1298	7.172312	ATGAAT	2.92969	2.7512
cg0161265	AFAP1	XBP-1 [T0	1510	1515	7.172312	ATGAAT	2.92969	2.7512
cg0161265	AFAP1	p53 [T006	885	891	7.153797	TGGGCCC	1.09863	1.22478

cg0161265	AFAP1	p53 [T006	886	892	7.153797	GGGCCC	1.09863	1.22478
cg2591200	AFAP1	p53 [T006	1004	1010	7.150251	GGGCCA	1.09863	1.22478
cg2591200	AFAP1	p53 [T006	1580	1586	7.150251	GGGCCA	1.09863	1.22478
cg0261454	AFAP1	p53 [T006	1068	1074	7.150251	GGGCCA	1.09863	1.22478
cg0261454	AFAP1	p53 [T006	1644	1650	7.150251	GGGCCA	1.09863	1.22478
cg2639478	AFAP1	p53 [T006	1034	1040	7.150251	GGGCCA	1.09863	1.22478
cg2639478	AFAP1	p53 [T006	1610	1616	7.150251	GGGCCA	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	775	781	7.150251	GTGGCC	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	1256	1262	7.150251	GTGGCC	1.09863	1.22478
cg2591200	AFAP1	HNF-1B [	1960	1968	7.148274	GGTTAC	0.07629	0.07044
cg2639478	AFAP1	HNF-1B [	1990	1998	7.148274	GGTTAC	0.07629	0.07044
cg0161265	AFAP1	c-Jun [T00	1558	1564	7.096776	TGACTG	0.73242	0.73062
cg2591200	AFAP1	NF-AT1 [	256	264	7.095752	GGAAAA	0.15259	0.14325
cg0261454	AFAP1	NF-AT1 [	320	328	7.095752	GGAAAA	0.15259	0.14325
cg2639478	AFAP1	NF-AT1 [	286	294	7.095752	GGAAAA	0.15259	0.14325
cg2591200	AFAP1	c-Ets-1 [T	1224	1230	7.071349	AGGGAA	0.73242	0.73732
cg0261454	AFAP1	c-Ets-1 [T	1288	1294	7.071349	AGGGAA	0.73242	0.73732
cg2639478	AFAP1	c-Ets-1 [T	1254	1260	7.071349	AGGGAA	0.73242	0.73732
cg0161265	AFAP1	c-Ets-1 [T	795	801	7.071349	AGGGAA	0.73242	0.73732
cg0161265	AFAP1	c-Ets-1 [T	847	853	7.071349	TTTCCCT	0.73242	0.73732
cg2591200	AFAP1	c-Jun [T00	1930	1936	7.052189	TGACTA	0.73242	0.73062
cg2639478	AFAP1	c-Jun [T00	1960	1966	7.052189	TGACTA	0.73242	0.73062
cg2591200	AFAP1	NFI/CTF [	226	233	7.014249	CCAACC	0.73242	0.74795
cg0261454	AFAP1	NFI/CTF [	290	297	7.014249	CCAACC	0.73242	0.74795
cg2639478	AFAP1	NFI/CTF [	256	263	7.014249	CCAACC	0.73242	0.74795
cg0675819	AFAP1	NFI/CTF [	1477	1484	7.014249	CCAACC	0.73242	0.74795
cg2591200	AFAP1	HNF-3alp	1246	1253	7.000129	CAAAAA	0.82397	0.71909
cg0261454	AFAP1	HNF-3alp	1310	1317	7.000129	CAAAAA	0.82397	0.71909
cg2639478	AFAP1	HNF-3alp	1276	1283	7.000129	CAAAAA	0.82397	0.71909
cg0675819	AFAP1	HNF-3alp	424	431	7.000129	TAAAAA	0.82397	0.71909
cg0161265	AFAP1	HNF-3alp	252	259	7.000129	TATAAA	0.82397	0.71909
cg0161265	AFAP1	HNF-3alp	268	275	7.000129	TATTTAT	0.82397	0.71909
cg0161265	AFAP1	HNF-3alp	395	402	7.000129	CATTTC	0.82397	0.71909
cg0161265	AFAP1	HNF-3alp	858	865	7.000129	AGAAAA	0.82397	0.71909
cg0161265	AFAP1	HNF-3alp	1623	1630	7.000129	GATTTTT	0.82397	0.71909
cg0675819	AFAP1	EBF [T05	1512	1522	6.976098	CCTCCA	0.03052	0.03432
cg2591200	AFAP1	IRF-1 [T0	665	673	6.968314	GCTGGG	0.1297	0.12685
cg2591200	AFAP1	IRF-1 [T0	1698	1706	6.968314	TTTCCCA	0.1297	0.12685
cg0261454	AFAP1	IRF-1 [T0	729	737	6.968314	GCTGGG	0.1297	0.12685
cg0261454	AFAP1	IRF-1 [T0	1762	1770	6.968314	TTTCCCA	0.1297	0.12685
cg2639478	AFAP1	IRF-1 [T0	695	703	6.968314	GCTGGG	0.1297	0.12685
cg2639478	AFAP1	IRF-1 [T0	1728	1736	6.968314	TTTCCCA	0.1297	0.12685
cg0161265	AFAP1	IRF-1 [T0	1737	1745	6.968314	GCTGGG	0.1297	0.12685
cg2591200	AFAP1	IRF-1 [T0	1277	1285	6.954318	CAGTGG	0.1297	0.12685
cg0261454	AFAP1	IRF-1 [T0	1341	1349	6.954318	CAGTGG	0.1297	0.12685
cg2639478	AFAP1	IRF-1 [T0	1307	1315	6.954318	CAGTGG	0.1297	0.12685
cg2591200	AFAP1	NF-1 [T00	457	464	6.948522	GGCCCC	0.48828	0.50205
cg0261454	AFAP1	NF-1 [T00	521	528	6.948522	GGCCCC	0.48828	0.50205

cg2639478	AFAP1	NF-1 [T00	487	494	6.948522	GGCCCC	0.48828	0.50205
cg0675819	AFAP1	NF-1 [T00	174	181	6.948522	AGCCCC	0.48828	0.50205
cg0161265	AFAP1	NF-1 [T00	1941	1948	6.948522	GGCCCC	0.48828	0.50205
cg0675819	AFAP1	c-Ets-1 [T	957	963	6.943262	TTTCCC	0.73242	0.73732
cg0161265	AFAP1	c-Ets-1 [T	1096	1102	6.943262	GGGGAA	0.73242	0.73732
cg0161265	AFAP1	c-Ets-1 [T	1352	1358	6.943262	GGGGAA	0.73242	0.73732
cg2591200	AFAP1	ENKTF-1	296	303	6.942764	GGACGC	1.46484	1.56616
cg2591200	AFAP1	ENKTF-1	732	739	6.942764	TGGCAT	1.46484	1.56616
cg2591200	AFAP1	ENKTF-1	967	974	6.942764	TGGCGT	1.46484	1.56616
cg2591200	AFAP1	ENKTF-1	1433	1440	6.942764	TTCCGC	1.46484	1.56616
cg2591200	AFAP1	ENKTF-1	1717	1724	6.942764	CTCTGC	1.46484	1.56616
cg0261454	AFAP1	ENKTF-1	360	367	6.942764	GGACGC	1.46484	1.56616
cg0261454	AFAP1	ENKTF-1	796	803	6.942764	TGGCAT	1.46484	1.56616
cg0261454	AFAP1	ENKTF-1	1031	1038	6.942764	TGGCGT	1.46484	1.56616
cg0261454	AFAP1	ENKTF-1	1497	1504	6.942764	TTCCGC	1.46484	1.56616
cg0261454	AFAP1	ENKTF-1	1781	1788	6.942764	CTCTGC	1.46484	1.56616
cg2639478	AFAP1	ENKTF-1	326	333	6.942764	GGACGC	1.46484	1.56616
cg2639478	AFAP1	ENKTF-1	762	769	6.942764	TGGCAT	1.46484	1.56616
cg2639478	AFAP1	ENKTF-1	997	1004	6.942764	TGGCGT	1.46484	1.56616
cg2639478	AFAP1	ENKTF-1	1463	1470	6.942764	TTCCGC	1.46484	1.56616
cg2639478	AFAP1	ENKTF-1	1747	1754	6.942764	CTCTGC	1.46484	1.56616
cg0675819	AFAP1	ENKTF-1	216	223	6.942764	TGGCCT	1.46484	1.56616
cg0675819	AFAP1	ENKTF-1	278	285	6.942764	CTCGGC	1.46484	1.56616
cg0675819	AFAP1	ENKTF-1	1272	1279	6.942764	CACAGC	1.46484	1.56616
cg0161265	AFAP1	ENKTF-1	107	114	6.942764	TGGCTT	1.46484	1.56616
cg0161265	AFAP1	ENKTF-1	351	358	6.942764	ATCCGC	1.46484	1.56616
cg0161265	AFAP1	ENKTF-1	751	758	6.942764	TGGCAA	1.46484	1.56616
cg0161265	AFAP1	ENKTF-1	961	968	6.942764	TGGCAA	1.46484	1.56616
cg0161265	AFAP1	ENKTF-1	991	998	6.942764	TGGCGT	1.46484	1.56616
cg0161265	AFAP1	ENKTF-1	1033	1040	6.942764	TGGCGT	1.46484	1.56616
cg0161265	AFAP1	ENKTF-1	1784	1791	6.942764	CACGGC	1.46484	1.56616
cg0675819	AFAP1	p53 [T006	234	240	6.938545	GAGGCC	1.09863	1.22478
cg0675819	AFAP1	p53 [T006	588	594	6.938545	GAGGCC	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	88	94	6.938545	GGGCCT	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	568	574	6.938545	GGGCCT	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	1057	1063	6.938545	GGGCCT	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	1746	1752	6.938545	GAGGCC	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	1848	1854	6.938545	GAGGCC	1.09863	1.22478
cg0261454	AFAP1	VDR [T00	16	24	6.925682	AAACTG	0.42725	0.41
cg0161265	AFAP1	VDR [T00	271	279	6.925682	TTATTG	0.42725	0.41
cg0161265	AFAP1	VDR [T00	1169	1177	6.925682	GTTCAG	0.42725	0.41
cg0161265	AFAP1	VDR [T00	1657	1665	6.925682	ACTATG	0.42725	0.41
cg0161265	AFAP1	MAZ [T00	942	954	6.916183	TGGAGG	0.00918	0.01018
cg0675819	AFAP1	p53 [T006	51	57	6.891821	GGGCGG	1.09863	1.22478
cg0675819	AFAP1	p53 [T006	551	557	6.891821	GGGCGG	1.09863	1.22478
cg0161265	AFAP1	p53 [T006	1483	1489	6.891821	GGGCGG	1.09863	1.22478
cg0161265	AFAP1	EBF [T05	382	392	6.872118	CCTCCA	0.03052	0.03432
cg0675819	AFAP1	C/EBPalp	688	694	6.85549	AATTGC	0.73242	0.68282

cg0675819	AFAP1	E2F-1 [T0	1486	1493	6.839754	GCGGCA	0.30518	0.33862
cg2591200	AFAP1	PEA3 [T0	1033	1041	6.824411	TCCCAT	0.22888	0.22744
cg0261454	AFAP1	PEA3 [T0	1097	1105	6.824411	TCCCAT	0.22888	0.22744
cg2639478	AFAP1	PEA3 [T0	1063	1071	6.824411	TCCCAT	0.22888	0.22744
cg0675819	AFAP1	PEA3 [T0	611	619	6.824411	TGGCAT	0.22888	0.22744
cg2591200	AFAP1	AR [T0004	1763	1771	6.817719	TTCCTGT	0.23651	0.23986
cg0261454	AFAP1	AR [T0004	1827	1835	6.817719	TTCCTGT	0.23651	0.23986
cg2639478	AFAP1	AR [T0004	1793	1801	6.817719	TTCCTGT	0.23651	0.23986
cg0161265	AFAP1	c-Ets-1 [T	1379	1385	6.815175	TTTCCC	0.73242	0.73732
cg2591200	AFAP1	c-Jun [T00	1616	1622	6.787369	TGACAG	0.73242	0.73062
cg0261454	AFAP1	c-Jun [T00	1680	1686	6.787369	TGACAG	0.73242	0.73062
cg2639478	AFAP1	c-Jun [T00	1646	1652	6.787369	TGACAG	0.73242	0.73062
cg2591200	AFAP1	NFI/CTF [	887	894	6.786076	CAGTTT	0.73242	0.74795
cg0261454	AFAP1	NFI/CTF [	951	958	6.786076	CAGTTT	0.73242	0.74795
cg2639478	AFAP1	NFI/CTF [	917	924	6.786076	CAGTTT	0.73242	0.74795
cg0675819	AFAP1	NFI/CTF [	1577	1584	6.786076	CCAAGC	0.73242	0.74795
cg0675819	AFAP1	NFI/CTF [	1843	1850	6.786076	CCAAAC	0.73242	0.74795
cg0161265	AFAP1	NFI/CTF [	526	533	6.786076	CCAATC	0.73242	0.74795
cg0161265	AFAP1	NFI/CTF [	766	773	6.786076	CCAATC	0.73242	0.74795
cg0161265	AFAP1	NFI/CTF [	1945	1952	6.786076	CCAAGC	0.73242	0.74795
cg2591200	AFAP1	p53 [T006	1154	1160	6.778774	GGGCTC	1.09863	1.22478
cg0261454	AFAP1	p53 [T006	1218	1224	6.778774	GGGCTC	1.09863	1.22478
cg2639478	AFAP1	p53 [T006	1184	1190	6.778774	GGGCTC	1.09863	1.22478
cg0675819	AFAP1	p53 [T006	891	897	6.778774	GGGCTC	1.09863	1.22478
cg0675819	AFAP1	ATF3 [T0	80	87	6.744803	TGACTT	0.27466	0.26471
cg0161265	AFAP1	ATF3 [T0	196	203	6.744803	TGACAT	0.27466	0.26471
cg0161265	AFAP1	ATF3 [T0	1033	1040	6.744803	TGGCGT	0.27466	0.26471
cg0161265	AFAP1	ATF3 [T0	1546	1553	6.744803	TTTCGTC	0.27466	0.26471
cg0161265	AFAP1	AR [T0004	1013	1021	6.725174	TGGATG	0.19836	0.20813
cg2591200	AFAP1	NF-1 [T00	1272	1279	6.722386	TTGGGC	0.24414	0.2565
cg0261454	AFAP1	NF-1 [T00	1336	1343	6.722386	TTGGGC	0.24414	0.2565
cg2639478	AFAP1	NF-1 [T00	1302	1309	6.722386	TTGGGC	0.24414	0.2565
cg0675819	AFAP1	NF-1 [T00	1956	1963	6.722386	TTGGCC	0.24414	0.2565
cg0161265	AFAP1	NF-1 [T00	542	549	6.722386	TTGGGC	0.24414	0.2565
cg2591200	AFAP1	T3R-beta1	1293	1301	6.702681	ACAAGG	0.21362	0.2251
cg0261454	AFAP1	T3R-beta1	1357	1365	6.702681	ACAAGG	0.21362	0.2251
cg2639478	AFAP1	T3R-beta1	1323	1331	6.702681	ACAAGG	0.21362	0.2251
cg2591200	AFAP1	c-Ets-1 [T	1432	1438	6.693449	GTTCCG	0.48828	0.48842
cg0261454	AFAP1	c-Ets-1 [T	1496	1502	6.693449	GTTCCG	0.48828	0.48842
cg2639478	AFAP1	c-Ets-1 [T	1462	1468	6.693449	GTTCCG	0.48828	0.48842
cg0675819	AFAP1	NF-kappa	1439	1449	6.69019	GGGGAG	0.03052	0.03409
cg0675819	AFAP1	HNF-1C	1582	1590	6.678556	CTGACT	0.05341	0.04756
cg2591200	AFAP1	PXR-1:RX	684	691	6.668182	TGAACA	0.24414	0.23169
cg0261454	AFAP1	PXR-1:RX	748	755	6.668182	TGAACA	0.24414	0.23169
cg2639478	AFAP1	PXR-1:RX	714	721	6.668182	TGAACA	0.24414	0.23169
cg0675819	AFAP1	GATA-2	1817	1825	6.666667	GCTGTA	0.24414	0.2357
cg0675819	AFAP1	c-Fos [T00	254	263	6.660217	GAATTG	0.04578	0.04485
cg2591200	AFAP1	AR [T0004	1886	1894	6.617912	ACTGTG	0.19836	0.20813

cg0261454	AFAP1	AR [T0004	1950	1958	6.617912	ACTGTG	0.19836	0.20813
cg2639478	AFAP1	AR [T0004	1916	1924	6.617912	ACTGTG	0.19836	0.20813
cg2591200	AFAP1	FOXP3 [T	1912	1917	6.581441	GTTGAA	0.97656	0.904
cg2591200	AFAP1	TFII-I [T0	278	283	6.581441	GGAGTG	0.97656	0.9991
cg0261454	AFAP1	FOXP3 [T	8	13	6.581441	GTTTTA	0.97656	0.904
cg0261454	AFAP1	FOXP3 [T	63	68	6.581441	TAAAAC	0.97656	0.904
cg0261454	AFAP1	FOXP3 [T	1976	1981	6.581441	GTTGAA	0.97656	0.904
cg0261454	AFAP1	TFII-I [T0	342	347	6.581441	GGAGTG	0.97656	0.9991
cg2639478	AFAP1	FOXP3 [T	29	34	6.581441	TAAAAC	0.97656	0.904
cg2639478	AFAP1	FOXP3 [T	1942	1947	6.581441	GTTGAA	0.97656	0.904
cg2639478	AFAP1	TFII-I [T0	308	313	6.581441	GGAGTG	0.97656	0.9991
cg0675819	AFAP1	FOXP3 [T	1838	1843	6.581441	TTCAAC	0.97656	0.904
cg0675819	AFAP1	TFII-I [T0	16	21	6.581441	GGAGAT	0.97656	0.9991
cg0675819	AFAP1	TFII-I [T0	564	569	6.581441	CACTCC	0.97656	0.9991
cg0675819	AFAP1	TFII-I [T0	575	580	6.581441	ATCTCC	0.97656	0.9991
cg0675819	AFAP1	TFII-I [T0	812	817	6.581441	ATCTCC	0.97656	0.9991
cg0675819	AFAP1	TFII-I [T0	967	972	6.581441	ATCTCC	0.97656	0.9991
cg0675819	AFAP1	TFII-I [T0	1001	1006	6.581441	GGAGAT	0.97656	0.9991
cg0675819	AFAP1	TFII-I [T0	1205	1210	6.581441	ATCTCC	0.97656	0.9991
cg0675819	AFAP1	TFII-I [T0	1340	1345	6.581441	CACTCC	0.97656	0.9991
cg0161265	AFAP1	FOXP3 [T	1205	1210	6.581441	TAAAAC	0.97656	0.904
cg0161265	AFAP1	TFII-I [T0	704	709	6.581441	ATCTCC	0.97656	0.9991
cg0161265	AFAP1	c-Ets-1 [T	1908	1914	6.565361	CCGGAA	0.48828	0.48842
cg0675819	AFAP1	p53 [T006	172	178	6.563521	GCAGCC	0.48828	0.54643
cg0675819	AFAP1	p53 [T006	1572	1578	6.563521	GCAGCC	0.48828	0.54643
cg0161265	AFAP1	IRF-1 [T0	1379	1387	6.549276	TTTCCCC	0.19073	0.1875
cg0261454	AFAP1	PXR-1:RX	20	27	6.5446	TGAACA	0.24414	0.23169
cg0161265	AFAP1	PXR-1:RX	275	282	6.5446	TGAACA	0.24414	0.23169
cg2591200	AFAP1	c-Myb [T0	914	921	6.539977	CAACTT	0.30518	0.30272
cg0261454	AFAP1	c-Myb [T0	978	985	6.539977	CAACTT	0.30518	0.30272
cg2639478	AFAP1	c-Myb [T0	944	951	6.539977	CAACTT	0.30518	0.30272
cg2591200	AFAP1	NF-AT2 [	462	471	6.521557	CAAGCT	0.01907	0.01803
cg0261454	AFAP1	NF-AT2 [	526	535	6.521557	CAAGCT	0.01907	0.01803
cg2639478	AFAP1	NF-AT2 [	492	501	6.521557	CAAGCT	0.01907	0.01803
cg2591200	AFAP1	TCF-4 [T0	1492	1501	6.509564	ATGTCA	0.04959	0.04686
cg0261454	AFAP1	TCF-4 [T0	1556	1565	6.509564	ATGTCA	0.04959	0.04686
cg2639478	AFAP1	TCF-4 [T0	1522	1531	6.509564	ATGTCA	0.04959	0.04686
cg2591200	AFAP1	XBP-1 [T	715	720	6.478682	TGGCAT	0.97656	0.99906
cg2591200	AFAP1	XBP-1 [T	732	737	6.478682	TGGCAT	0.97656	0.99906
cg2591200	AFAP1	XBP-1 [T	1533	1538	6.478682	TGGCAT	0.97656	0.99906
cg2591200	AFAP1	XBP-1 [T	1599	1604	6.478682	GGGCAT	0.97656	0.99906
cg2591200	AFAP1	XBP-1 [T	1671	1676	6.478682	TGGCAT	0.97656	0.99906
cg0261454	AFAP1	XBP-1 [T	779	784	6.478682	TGGCAT	0.97656	0.99906
cg0261454	AFAP1	XBP-1 [T	796	801	6.478682	TGGCAT	0.97656	0.99906
cg0261454	AFAP1	XBP-1 [T	1597	1602	6.478682	TGGCAT	0.97656	0.99906
cg0261454	AFAP1	XBP-1 [T	1663	1668	6.478682	GGGCAT	0.97656	0.99906
cg0261454	AFAP1	XBP-1 [T	1735	1740	6.478682	TGGCAT	0.97656	0.99906
cg2639478	AFAP1	XBP-1 [T	745	750	6.478682	TGGCAT	0.97656	0.99906

cg2639478	AFAP1	XBP-1 [T	762	767	6.478682	TGGCAT	0.97656	0.99906
cg2639478	AFAP1	XBP-1 [T	1563	1568	6.478682	TGGCAT	0.97656	0.99906
cg2639478	AFAP1	XBP-1 [T	1629	1634	6.478682	GGGCAT	0.97656	0.99906
cg2639478	AFAP1	XBP-1 [T	1701	1706	6.478682	TGGCAT	0.97656	0.99906
cg0675819	AFAP1	XBP-1 [T	611	616	6.478682	TGGCAT	0.97656	0.99906
cg0675819	AFAP1	XBP-1 [T	1674	1679	6.478682	ATGCCA	0.97656	0.99906
cg0161265	AFAP1	XBP-1 [T	170	175	6.478682	GGGCAT	0.97656	0.99906
cg0161265	AFAP1	C/EBPalp	962	968	6.460799	GGCAAT	0.48828	0.47407
cg0161265	AFAP1	RAR-beta	1353	1362	6.39673	GGGAAA	0.18311	0.1857
cg2591200	AFAP1	C/EBPalp	453	459	6.391486	AATTGG	0.48828	0.47407
cg0261454	AFAP1	C/EBPalp	517	523	6.391486	AATTGG	0.48828	0.47407
cg2639478	AFAP1	C/EBPalp	483	489	6.391486	AATTGG	0.48828	0.47407
cg0675819	AFAP1	MAZ [T0	1041	1053	6.387406	CTCCCT	0.00316	0.00367
cg2591200	AFAP1	TCF-4E [T	23	29	6.302385	TTCAAA	0.61035	0.59686
cg2591200	AFAP1	TCF-4E [T	1790	1796	6.302385	CTTTGC	0.61035	0.59686
cg2591200	AFAP1	TCF-4E [T	1861	1867	6.302385	ACCAAA	0.61035	0.59686
cg0261454	AFAP1	TCF-4E [T	87	93	6.302385	TTCAAA	0.61035	0.59686
cg0261454	AFAP1	TCF-4E [T	1854	1860	6.302385	CTTTGC	0.61035	0.59686
cg0261454	AFAP1	TCF-4E [T	1925	1931	6.302385	ACCAAA	0.61035	0.59686
cg2639478	AFAP1	TCF-4E [T	53	59	6.302385	TTCAAA	0.61035	0.59686
cg2639478	AFAP1	TCF-4E [T	1820	1826	6.302385	CTTTGC	0.61035	0.59686
cg2639478	AFAP1	TCF-4E [T	1891	1897	6.302385	ACCAAA	0.61035	0.59686
cg0675819	AFAP1	TCF-4E [T	444	450	6.302385	CTTTGA	0.61035	0.59686
cg0675819	AFAP1	TCF-4E [T	1658	1664	6.302385	AACAAA	0.61035	0.59686
cg0161265	AFAP1	TCF-4E [T	623	629	6.302385	CTTTGC	0.61035	0.59686
cg0161265	AFAP1	TCF-4E [T	752	758	6.302385	GGCAAA	0.61035	0.59686
cg0161265	AFAP1	TCF-4E [T	1925	1931	6.302385	TTCAAA	0.61035	0.59686
cg2591200	AFAP1	GR-alpha [	398	402	6.263098	CCTTA	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	524	528	6.263098	TGAGG	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1219	1223	6.263098	CCTTA	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1222	1226	6.263098	TAAGG	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1385	1389	6.263098	CCTCA	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1416	1420	6.263098	CCTCA	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1653	1657	6.263098	CCTCA	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1725	1729	6.263098	CCTCA	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1976	1980	6.263098	TGAGG	3.90625	3.89624
cg2591200	AFAP1	GR-alpha [	1984	1988	6.263098	TAAGG	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	462	466	6.263098	CCTTA	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	588	592	6.263098	TGAGG	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	1283	1287	6.263098	CCTTA	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	1286	1290	6.263098	TAAGG	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	1449	1453	6.263098	CCTCA	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	1480	1484	6.263098	CCTCA	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	1717	1721	6.263098	CCTCA	3.90625	3.89624
cg0261454	AFAP1	GR-alpha [	1789	1793	6.263098	CCTCA	3.90625	3.89624
cg2639478	AFAP1	GR-alpha [	428	432	6.263098	CCTTA	3.90625	3.89624
cg2639478	AFAP1	GR-alpha [	554	558	6.263098	TGAGG	3.90625	3.89624
cg2639478	AFAP1	GR-alpha [	1249	1253	6.263098	CCTTA	3.90625	3.89624

cg2639478	AFAP1	GR-alpha [	1252	1256	6.263098	TAAGG	3.90625	3.89624
cg2639478	AFAP1	GR-alpha [	1415	1419	6.263098	CCTCA	3.90625	3.89624
cg2639478	AFAP1	GR-alpha [	1446	1450	6.263098	CCTCA	3.90625	3.89624
cg2639478	AFAP1	GR-alpha [	1683	1687	6.263098	CCTCA	3.90625	3.89624
cg2639478	AFAP1	GR-alpha [	1755	1759	6.263098	CCTCA	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	161	165	6.263098	TGAGG	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	187	191	6.263098	TGAGG	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	266	270	6.263098	CCTCA	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	348	352	6.263098	CCTCA	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	537	541	6.263098	TGAGG	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	818	822	6.263098	TGAGG	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	848	852	6.263098	TGAGG	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	905	909	6.263098	TGAGG	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	983	987	6.263098	CCTCA	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	1191	1195	6.263098	CCTTA	3.90625	3.89624
cg0675819	AFAP1	GR-alpha [	1987	1991	6.263098	CCTCA	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	99	103	6.263098	CCTCA	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	558	562	6.263098	TAAGG	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	584	588	6.263098	TGAGG	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	607	611	6.263098	TAAGG	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	734	738	6.263098	CCTCA	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	982	986	6.263098	TGAGG	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	1270	1274	6.263098	CCTCA	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	1285	1289	6.263098	CCTTA	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	1685	1689	6.263098	CCTTA	3.90625	3.89624
cg0161265	AFAP1	GR-alpha [	1876	1880	6.263098	TAAGG	3.90625	3.89624
cg0675819	AFAP1	c-Myb [T0	1094	1101	6.259888	GAACTG	0.30518	0.30272
cg2591200	AFAP1	NF-AT2 [	1693	1702	6.245826	GACAGT	0.04196	0.03934
cg0261454	AFAP1	NF-AT2 [	1757	1766	6.245826	GACAGT	0.04196	0.03934
cg2639478	AFAP1	NF-AT2 [	1723	1732	6.245826	GACAGT	0.04196	0.03934
cg0161265	AFAP1	C/EBPalph	272	278	6.245236	TATTGA	0.97656	0.91422
cg0161265	AFAP1	C/EBPalph	1712	1718	6.245236	TATTGC	0.97656	0.91422
cg2591200	AFAP1	IRF-1 [T0	252	260	6.24301	AGGAGG	0.16785	0.16217
cg0261454	AFAP1	IRF-1 [T0	316	324	6.24301	AGGAGG	0.16785	0.16217
cg2639478	AFAP1	IRF-1 [T0	282	290	6.24301	AGGAGG	0.16785	0.16217
cg0675819	AFAP1	c-Fos [T00	1031	1040	6.236188	GAGTCA	0.09155	0.09198
cg0161265	AFAP1	POU2F2 (	312	322	6.233489	TGCTTT	0.01431	0.01219
cg2591200	AFAP1	NF-AT1 [	592	601	6.201624	TGCATT	0.03815	0.03661
cg0261454	AFAP1	NF-AT1 [	656	665	6.201624	TGCATT	0.03815	0.03661
cg2639478	AFAP1	NF-AT1 [	622	631	6.201624	TGCATT	0.03815	0.03661
cg0675819	AFAP1	p53 [T006	1289	1295	6.188498	GGGCGG	0.61035	0.68483
cg0161265	AFAP1	HNF-4alph	313	325	6.184269	GCTTTA	0.00501	0.00461
cg2591200	AFAP1	c-Ets-1 [T	596	602	6.167515	TTTCCAC	0.36621	0.36174
cg2591200	AFAP1	c-Ets-1 [T	1279	1285	6.167515	GTGGAA	0.36621	0.36174
cg0261454	AFAP1	c-Ets-1 [T	660	666	6.167515	TTTCCAC	0.36621	0.36174
cg0261454	AFAP1	c-Ets-1 [T	1343	1349	6.167515	GTGGAA	0.36621	0.36174
cg2639478	AFAP1	c-Ets-1 [T	626	632	6.167515	TTTCCAC	0.36621	0.36174
cg2639478	AFAP1	c-Ets-1 [T	1309	1315	6.167515	GTGGAA	0.36621	0.36174

cg0161265	AFAP1	c-Jun [T00	1547	1553	6.152811	TTCGTCA	0.36621	0.34478
cg2591200	AFAP1	NF-AT1 [T	1226	1234	6.150044	GGAAAA	0.06866	0.06621
cg0261454	AFAP1	NF-AT1 [T	1290	1298	6.150044	GGAAAA	0.06866	0.06621
cg2639478	AFAP1	NF-AT1 [T	1256	1264	6.150044	GGAAAA	0.06866	0.06621
cg0675819	AFAP1	RXR-alpha	776	782	6.119461	GCGACC	0.73242	0.78318
cg0675819	AFAP1	AR [T000	1855	1863	6.110872	GGACAG	0.24414	0.25115
cg2591200	AFAP1	p53 [T006	455	461	6.095267	TTGGCC	0.61035	0.68483
cg0261454	AFAP1	p53 [T006	519	525	6.095267	TTGGCC	0.61035	0.68483
cg2639478	AFAP1	p53 [T006	485	491	6.095267	TTGGCC	0.61035	0.68483
cg2591200	AFAP1	GR-alpha [	710	714	6.055408	CCTGA	3.90625	3.89835
cg2591200	AFAP1	GR-alpha [	753	757	6.055408	TCAGG	3.90625	3.89835
cg2591200	AFAP1	GR-alpha [	772	776	6.055408	CCTGA	3.90625	3.89835
cg2591200	AFAP1	GR-alpha [	1727	1731	6.055408	TCAGG	3.90625	3.89835
cg2591200	AFAP1	GR-alpha [	1830	1834	6.055408	CCTGA	3.90625	3.89835
cg2591200	AFAP1	GR-alpha [	1853	1857	6.055408	CCTGA	3.90625	3.89835
cg2591200	AFAP1	GR-alpha [	1954	1958	6.055408	TTAGG	3.90625	3.89835
cg2591200	AFAP1	GR-alpha [	1982	1986	6.055408	CCTAA	3.90625	3.89835
cg0261454	AFAP1	GR-alpha [	774	778	6.055408	CCTGA	3.90625	3.89835
cg0261454	AFAP1	GR-alpha [	817	821	6.055408	TCAGG	3.90625	3.89835
cg0261454	AFAP1	GR-alpha [	836	840	6.055408	CCTGA	3.90625	3.89835
cg0261454	AFAP1	GR-alpha [	1791	1795	6.055408	TCAGG	3.90625	3.89835
cg0261454	AFAP1	GR-alpha [	1894	1898	6.055408	CCTGA	3.90625	3.89835
cg0261454	AFAP1	GR-alpha [	1917	1921	6.055408	CCTGA	3.90625	3.89835
cg2639478	AFAP1	GR-alpha [	740	744	6.055408	CCTGA	3.90625	3.89835
cg2639478	AFAP1	GR-alpha [	783	787	6.055408	TCAGG	3.90625	3.89835
cg2639478	AFAP1	GR-alpha [	802	806	6.055408	CCTGA	3.90625	3.89835
cg2639478	AFAP1	GR-alpha [	1757	1761	6.055408	TCAGG	3.90625	3.89835
cg2639478	AFAP1	GR-alpha [	1860	1864	6.055408	CCTGA	3.90625	3.89835
cg2639478	AFAP1	GR-alpha [	1883	1887	6.055408	CCTGA	3.90625	3.89835
cg2639478	AFAP1	GR-alpha [	1984	1988	6.055408	TTAGG	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	111	115	6.055408	TCAGG	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	268	272	6.055408	TCAGG	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	297	301	6.055408	CCTGA	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	705	709	6.055408	TCAGG	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	816	820	6.055408	CCTGA	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	1141	1145	6.055408	CCTAA	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	1148	1152	6.055408	CCTAA	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	1356	1360	6.055408	TTAGG	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	1636	1640	6.055408	TTAGG	3.90625	3.89835
cg0675819	AFAP1	GR-alpha [	1756	1760	6.055408	CCTAA	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	375	379	6.055408	TCAGG	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	458	462	6.055408	TTAGG	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	693	697	6.055408	TCAGG	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	980	984	6.055408	CCTGA	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	1121	1125	6.055408	TCAGG	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	1171	1175	6.055408	TCAGG	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	1299	1303	6.055408	CCTAA	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	1532	1536	6.055408	TCAGG	3.90625	3.89835

cg0161265	AFAP1	GR-alpha [	1586	1590	6.055408	CCTGA	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	1687	1691	6.055408	TTAGG	3.90625	3.89835
cg0161265	AFAP1	GR-alpha [	1771	1775	6.055408	TCAGG	3.90625	3.89835
cg2591200	AFAP1	c-Myb [T0	1693	1700	6.04018	GACAGT	0.21362	0.2053
cg0261454	AFAP1	c-Myb [T0	1757	1764	6.04018	GACAGT	0.21362	0.2053
cg2639478	AFAP1	c-Myb [T0	1723	1730	6.04018	GACAGT	0.21362	0.2053
cg2591200	AFAP1	c-Ets-1 [T	467	473	6.039428	TTTCCAC	0.36621	0.36174
cg0261454	AFAP1	c-Ets-1 [T	531	537	6.039428	TTTCCAC	0.36621	0.36174
cg2639478	AFAP1	c-Ets-1 [T	497	503	6.039428	TTTCCAC	0.36621	0.36174
cg0161265	AFAP1	HNF-1B [	718	726	6.006024	TTACTA	0.09918	0.08736
cg2591200	AFAP1	NF-AT1 [	1694	1702	6.003834	ACAGTT	0.06866	0.06621
cg0261454	AFAP1	NF-AT1 [	1758	1766	6.003834	ACAGTT	0.06866	0.06621
cg2639478	AFAP1	NF-AT1 [	1724	1732	6.003834	ACAGTT	0.06866	0.06621
cg2591200	AFAP1	C/EBPalph	1258	1264	5.996794	AACAAT	0.97656	0.91422
cg0261454	AFAP1	C/EBPalph	1322	1328	5.996794	AACAAT	0.97656	0.91422
cg2639478	AFAP1	C/EBPalph	1288	1294	5.996794	AACAAT	0.97656	0.91422
cg0675819	AFAP1	RXR-alpha	1488	1494	5.937582	GGCACC	0.73242	0.78318
cg0675819	AFAP1	RXR-alpha	1982	1988	5.937582	GGCACC	0.73242	0.78318
cg0161265	AFAP1	RXR-alpha	389	395	5.937582	GGCACC	0.73242	0.78318
cg0161265	AFAP1	RXR-alpha	597	603	5.937582	GGGTGA	0.73242	0.78318
cg0161265	AFAP1	RXR-alpha	1536	1542	5.937582	GGGTGA	0.73242	0.78318
cg0675819	AFAP1	AR [T000	541	549	5.8965	GGACAA	0.24414	0.25115
cg0675819	AFAP1	p53 [T006	303	309	5.883561	TCGGCC	0.61035	0.68483
cg2591200	AFAP1	STAT4 [T	265	270	5.882353	GGAAGG	0.48828	0.51201
cg2591200	AFAP1	STAT4 [T	291	296	5.882353	GGAAGG	0.48828	0.51201
cg2591200	AFAP1	STAT4 [T	325	330	5.882353	CCTTCC	0.48828	0.51201
cg2591200	AFAP1	STAT4 [T	379	384	5.882353	CCTTCC	0.48828	0.51201
cg2591200	AFAP1	STAT4 [T	784	789	5.882353	CCTTCC	0.48828	0.51201
cg2591200	AFAP1	STAT4 [T	952	957	5.882353	GGAAGG	0.48828	0.51201
cg2591200	AFAP1	STAT4 [T	1030	1035	5.882353	CCTTCC	0.48828	0.51201
cg0261454	AFAP1	STAT4 [T	329	334	5.882353	GGAAGG	0.48828	0.51201
cg0261454	AFAP1	STAT4 [T	355	360	5.882353	GGAAGG	0.48828	0.51201
cg0261454	AFAP1	STAT4 [T	389	394	5.882353	CCTTCC	0.48828	0.51201
cg0261454	AFAP1	STAT4 [T	443	448	5.882353	CCTTCC	0.48828	0.51201
cg0261454	AFAP1	STAT4 [T	848	853	5.882353	CCTTCC	0.48828	0.51201
cg0261454	AFAP1	STAT4 [T	1016	1021	5.882353	GGAAGG	0.48828	0.51201
cg0261454	AFAP1	STAT4 [T	1094	1099	5.882353	CCTTCC	0.48828	0.51201
cg2639478	AFAP1	STAT4 [T	295	300	5.882353	GGAAGG	0.48828	0.51201
cg2639478	AFAP1	STAT4 [T	321	326	5.882353	GGAAGG	0.48828	0.51201
cg2639478	AFAP1	STAT4 [T	355	360	5.882353	CCTTCC	0.48828	0.51201
cg2639478	AFAP1	STAT4 [T	409	414	5.882353	CCTTCC	0.48828	0.51201
cg2639478	AFAP1	STAT4 [T	814	819	5.882353	CCTTCC	0.48828	0.51201
cg2639478	AFAP1	STAT4 [T	982	987	5.882353	GGAAGG	0.48828	0.51201
cg2639478	AFAP1	STAT4 [T	1060	1065	5.882353	CCTTCC	0.48828	0.51201
cg0675819	AFAP1	STAT4 [T	247	252	5.882353	GGAAGG	0.48828	0.51201
cg0675819	AFAP1	STAT4 [T	338	343	5.882353	CCTTCC	0.48828	0.51201
cg0675819	AFAP1	STAT4 [T	1155	1160	5.882353	CCTTCC	0.48828	0.51201
cg0675819	AFAP1	STAT4 [T	1197	1202	5.882353	CCTTCC	0.48828	0.51201

cg0675819	AFAP1	STAT4 [T	1691	1696	5.882353	CCTTCC	0.48828	0.51201
cg0161265	AFAP1	STAT4 [T	360	365	5.882353	GGAAGG	0.48828	0.51201
cg0161265	AFAP1	STAT4 [T	1434	1439	5.882353	GGAAGG	0.48828	0.51201
cg0161265	AFAP1	STAT4 [T	1478	1483	5.882353	GGAAGG	0.48828	0.51201
cg0161265	AFAP1	STAT4 [T	1832	1837	5.882353	GGAAGG	0.48828	0.51201
cg0675819	AFAP1	C/EBPalph	255	261	5.850545	AATTGA	0.97656	0.91422
cg0161265	AFAP1	E2F-1 [T0	1234	1241	5.846171	CTTTCCC	0.18311	0.19383
cg0675819	AFAP1	AP-1 [T00	299	307	5.818984	TGACTC	0.09155	0.09438
cg2591200	AFAP1	c-Ets-1 [T	1031	1037	5.814485	CTTCCC	0.36621	0.36174
cg0261454	AFAP1	c-Ets-1 [T	1095	1101	5.814485	CTTCCC	0.36621	0.36174
cg2639478	AFAP1	c-Ets-1 [T	1061	1067	5.814485	CTTCCC	0.36621	0.36174
cg0675819	AFAP1	c-Ets-1 [T	1198	1204	5.814485	CTTCCC	0.36621	0.36174
cg0161265	AFAP1	c-Ets-1 [T	907	913	5.814485	TGGGAA	0.36621	0.36174
cg0161265	AFAP1	c-Ets-1 [T	928	934	5.814485	TGGGAA	0.36621	0.36174
cg0161265	AFAP1	c-Ets-1 [T	1025	1031	5.814485	TGGGAA	0.36621	0.36174
cg0675819	AFAP1	c-Jun [T00	1616	1622	5.783074	TGACTTT	0.36621	0.34478
cg0161265	AFAP1	HNF-1C [	717	725	5.777116	CTTACT	0.14496	0.13124
cg0161265	AFAP1	NF-AT1 [	1098	1106	5.77403	GGAAAG	0.06866	0.06621
cg2591200	AFAP1	VDR [T00	680	688	5.771401	ACCTTG	0.42725	0.41266
cg2591200	AFAP1	VDR [T00	1879	1887	5.771401	GGACTG	0.42725	0.41266
cg0261454	AFAP1	VDR [T00	744	752	5.771401	ACCTTG	0.42725	0.41266
cg0261454	AFAP1	VDR [T00	1943	1951	5.771401	GGACTG	0.42725	0.41266
cg2639478	AFAP1	VDR [T00	710	718	5.771401	ACCTTG	0.42725	0.41266
cg2639478	AFAP1	VDR [T00	1909	1917	5.771401	GGACTG	0.42725	0.41266
cg0675819	AFAP1	VDR [T00	1066	1074	5.771401	CAAATG	0.42725	0.41266
cg0161265	AFAP1	VDR [T00	1530	1538	5.771401	GTTCAG	0.42725	0.41266
cg0161265	AFAP1	IRF-1 [T0	1094	1102	5.770812	GAGGGG	0.16785	0.16217
cg2591200	AFAP1	PPAR-alph	1594	1604	5.741676	TTCTGG	0.03529	0.03856
cg0261454	AFAP1	PPAR-alph	1658	1668	5.741676	TTCTGG	0.03529	0.03856
cg2639478	AFAP1	PPAR-alph	1624	1634	5.741676	TTCTGG	0.03529	0.03856
cg0161265	AFAP1	PPAR-alph	165	175	5.741676	TCCTGG	0.03529	0.03856
cg0161265	AFAP1	PPAR-alph	672	682	5.741676	TGCTGG	0.03529	0.03856
cg2591200	AFAP1	ENKTF-1	518	525	5.687009	TGGCTTT	0.73242	0.76357
cg2591200	AFAP1	ENKTF-1	821	828	5.687009	AAACGC	0.73242	0.76357
cg2591200	AFAP1	ENKTF-1	1407	1414	5.687009	GAGCGC	0.73242	0.76357
cg0261454	AFAP1	ENKTF-1	582	589	5.687009	TGGCTTT	0.73242	0.76357
cg0261454	AFAP1	ENKTF-1	885	892	5.687009	AAACGC	0.73242	0.76357
cg0261454	AFAP1	ENKTF-1	1471	1478	5.687009	GAGCGC	0.73242	0.76357
cg2639478	AFAP1	ENKTF-1	548	555	5.687009	TGGCTTT	0.73242	0.76357
cg2639478	AFAP1	ENKTF-1	851	858	5.687009	AAACGC	0.73242	0.76357
cg2639478	AFAP1	ENKTF-1	1437	1444	5.687009	GAGCGC	0.73242	0.76357
cg0161265	AFAP1	ENKTF-1	674	681	5.687009	CTGGGC	0.73242	0.76357
cg0161265	AFAP1	ENKTF-1	1117	1124	5.687009	TGGCTC	0.73242	0.76357
cg0161265	AFAP1	ENKTF-1	1149	1156	5.687009	TGGCTTT	0.73242	0.76357
cg0161265	AFAP1	ENKTF-1	1274	1281	5.687009	AAGCGC	0.73242	0.76357
cg2591200	AFAP1	c-Ets-1 [T	380	386	5.686398	CTTCCCT	0.36621	0.38732
cg0261454	AFAP1	c-Ets-1 [T	444	450	5.686398	CTTCCCT	0.36621	0.38732
cg2639478	AFAP1	c-Ets-1 [T	410	416	5.686398	CTTCCCT	0.36621	0.38732

cg0161265	AFAP1	c-Ets-1 [T	1918	1924	5.686398	CTTCCCT	0.36621	0.38732
cg2591200	AFAP1	T3R-beta1	1184	1192	5.591999	TCACCA	0.21362	0.21789
cg0261454	AFAP1	T3R-beta1	1248	1256	5.591999	TCACCA	0.21362	0.21789
cg2639478	AFAP1	T3R-beta1	1214	1222	5.591999	TCACCA	0.21362	0.21789
cg0161265	AFAP1	T3R-beta1	578	586	5.591999	GCCTGG	0.21362	0.21789
cg2591200	AFAP1	c-Jun [T00	1559	1565	5.590308	TGACAC	0.48828	0.49294
cg0261454	AFAP1	c-Jun [T00	1623	1629	5.590308	TGACAC	0.48828	0.49294
cg2639478	AFAP1	c-Jun [T00	1589	1595	5.590308	TGACAC	0.48828	0.49294
cg0161265	AFAP1	c-Jun [T00	618	624	5.590308	TGACAC	0.48828	0.49294
cg0161265	AFAP1	c-Jun [T00	785	791	5.590308	AGTGTC	0.48828	0.49294
cg0161265	AFAP1	RelA [T00	1351	1361	5.573947	GGGGGA	0.0124	0.01273
cg2591200	AFAP1	TCF-4 [T0	520	529	5.564029	GCTTTG	0.04959	0.04908
cg0261454	AFAP1	TCF-4 [T0	584	593	5.564029	GCTTTG	0.04959	0.04908
cg2639478	AFAP1	TCF-4 [T0	550	559	5.564029	GCTTTG	0.04959	0.04908
cg2591200	AFAP1	NFI/CTF [	461	468	5.558661	CCAAGC	0.54932	0.55504
cg2591200	AFAP1	NFI/CTF [	1702	1709	5.558661	CCAAAC	0.54932	0.55504
cg0261454	AFAP1	NFI/CTF [	525	532	5.558661	CCAAGC	0.54932	0.55504
cg0261454	AFAP1	NFI/CTF [	1766	1773	5.558661	CCAAAC	0.54932	0.55504
cg2639478	AFAP1	NFI/CTF [	491	498	5.558661	CCAAGC	0.54932	0.55504
cg2639478	AFAP1	NFI/CTF [	1732	1739	5.558661	CCAAAC	0.54932	0.55504
cg0675819	AFAP1	NFI/CTF [	1202	1209	5.558661	CCAATC	0.54932	0.55504
cg0675819	AFAP1	NFI/CTF [	1277	1284	5.558661	CCAAAC	0.54932	0.55504
cg0161265	AFAP1	NFI/CTF [	1470	1477	5.558661	ATGCTTC	0.54932	0.55504
cg2591200	AFAP1	c-Ets-1 [T	1025	1031	5.558311	CTTCCCC	0.36621	0.38732
cg0261454	AFAP1	c-Ets-1 [T	1089	1095	5.558311	CTTCCCC	0.36621	0.38732
cg2639478	AFAP1	c-Ets-1 [T	1055	1061	5.558311	CTTCCCC	0.36621	0.38732
cg0161265	AFAP1	c-Ets-1 [T	1476	1482	5.558311	GGGGAA	0.36621	0.38732
cg0161265	AFAP1	T3R-beta1	1533	1541	5.553412	CAGGGG	0.21362	0.21789
cg0675819	AFAP1	AP-1 [T00	1028	1036	5.54906	TGAGAG	0.09155	0.08822
cg2591200	AFAP1	TFIID [T0	237	243	5.544826	TTCTAA	0.73242	0.65314
cg2591200	AFAP1	TFIID [T0	1117	1123	5.544826	TGGTAA	0.73242	0.65314
cg2591200	AFAP1	TFIID [T0	1797	1803	5.544826	TGGTAA	0.73242	0.65314
cg2591200	AFAP1	TFIID [T0	1953	1959	5.544826	TTTAGG	0.73242	0.65314
cg2591200	AFAP1	TFIID [T0	1963	1969	5.544826	TACTAA	0.73242	0.65314
cg0261454	AFAP1	TFIID [T0	301	307	5.544826	TTCTAA	0.73242	0.65314
cg0261454	AFAP1	TFIID [T0	1181	1187	5.544826	TGGTAA	0.73242	0.65314
cg0261454	AFAP1	TFIID [T0	1861	1867	5.544826	TGGTAA	0.73242	0.65314
cg2639478	AFAP1	TFIID [T0	267	273	5.544826	TTCTAA	0.73242	0.65314
cg2639478	AFAP1	TFIID [T0	1147	1153	5.544826	TGGTAA	0.73242	0.65314
cg2639478	AFAP1	TFIID [T0	1827	1833	5.544826	TGGTAA	0.73242	0.65314
cg2639478	AFAP1	TFIID [T0	1983	1989	5.544826	TTTAGG	0.73242	0.65314
cg2639478	AFAP1	TFIID [T0	1993	1999	5.544826	TACTAA	0.73242	0.65314
cg0675819	AFAP1	TFIID [T0	374	380	5.544826	TGTTAA	0.73242	0.65314
cg0675819	AFAP1	TFIID [T0	1147	1153	5.544826	TCCTAA	0.73242	0.65314
cg0675819	AFAP1	Pax-5 [T0	51	57	5.544826	GGGCGG	0.73242	0.79
cg0675819	AFAP1	Pax-5 [T0	551	557	5.544826	GGGCGG	0.73242	0.79
cg0675819	AFAP1	Pax-5 [T0	945	951	5.544826	AGCGCC	0.73242	0.79
cg0161265	AFAP1	Pax-5 [T0	1483	1489	5.544826	GGGCGG	0.73242	0.79

cg2591200	AFAP1	NF-AT1 [	1280	1289	5.512555	TGGAAA	0.05913	0.05666
cg0261454	AFAP1	NF-AT1 [	1344	1353	5.512555	TGGAAA	0.05913	0.05666
cg2639478	AFAP1	NF-AT1 [	1310	1319	5.512555	TGGAAA	0.05913	0.05666
cg2591200	AFAP1	C/EBPalph	149	155	5.455853	AGCAAT	0.73242	0.68229
cg0261454	AFAP1	C/EBPalph	213	219	5.455853	AGCAAT	0.73242	0.68229
cg2639478	AFAP1	C/EBPalph	179	185	5.455853	AGCAAT	0.73242	0.68229
cg0675819	AFAP1	c-Ets-1 [T	1230	1236	5.430224	CGGGAA	0.36621	0.38732
cg0161265	AFAP1	c-Ets-1 [T	1567	1573	5.430224	CTTCCC	0.36621	0.38732
cg0161265	AFAP1	USF1 [T0	614	623	5.418177	CACGTG	0.04578	0.04717
cg0675819	AFAP1	NF-1 [T00	1573	1580	5.377909	CAGCCC	0.24414	0.25051
cg0161265	AFAP1	RAR-beta	423	432	5.370617	GGGGTT	0.15259	0.15813
cg0675819	AFAP1	AP-1 [T00	593	601	5.321703	CCAGAG	0.09155	0.08822
cg2591200	AFAP1	TCF-4 [T0	1612	1621	5.274366	ACTTTG	0.04959	0.04908
cg0261454	AFAP1	TCF-4 [T0	1676	1685	5.274366	ACTTTG	0.04959	0.04908
cg2639478	AFAP1	TCF-4 [T0	1642	1651	5.274366	ACTTTG	0.04959	0.04908
cg2591200	AFAP1	RXR-alpha	1987	1993	5.271235	GGGTGG	0.61035	0.65415
cg0675819	AFAP1	RXR-alpha	1047	1053	5.271235	CCCACC	0.61035	0.65415
cg0675819	AFAP1	RXR-alpha	1682	1688	5.271235	CCCACC	0.61035	0.65415
cg0161265	AFAP1	RXR-alpha	1761	1767	5.271235	CCCACC	0.61035	0.65415
cg0161265	AFAP1	NFI/CTF [	538	545	5.249259	GCCGTT	0.24414	0.25666
cg0675819	AFAP1	ETF [T002	1974	1984	5.246906	GTGCCC	0.02861	0.03569
cg0161265	AFAP1	NF-AT2 [	797	806	5.231211	GGAAAC	0.03815	0.03519
cg2591200	AFAP1	GR [T050	896	902	5.207533	GTCTTTC	0.24414	0.24013
cg2591200	AFAP1	GR [T050	1496	1502	5.207533	CAAAGA	0.24414	0.24013
cg0261454	AFAP1	GR [T050	960	966	5.207533	GTCTTTC	0.24414	0.24013
cg0261454	AFAP1	GR [T050	1560	1566	5.207533	CAAAGA	0.24414	0.24013
cg2639478	AFAP1	GR [T050	926	932	5.207533	GTCTTTC	0.24414	0.24013
cg2639478	AFAP1	GR [T050	1526	1532	5.207533	CAAAGA	0.24414	0.24013
cg0161265	AFAP1	GR [T050	729	735	5.207533	CAAAAC	0.24414	0.24013
cg0161265	AFAP1	GR [T050	1130	1136	5.207533	CAAAAC	0.24414	0.24013
cg0161265	AFAP1	c-Jun [T00	688	694	5.193102	TGACTT	0.61035	0.60573
cg2591200	AFAP1	c-Ets-2 [T	396	404	5.162974	TTCCTTA	0.13733	0.13279
cg0261454	AFAP1	c-Ets-2 [T	460	468	5.162974	TTCCTTA	0.13733	0.13279
cg2639478	AFAP1	c-Ets-2 [T	426	434	5.162974	TTCCTTA	0.13733	0.13279
cg0161265	AFAP1	EBF [T05	1631	1641	5.130966	AACCCA	0.02289	0.02569
cg0161265	AFAP1	NF-AT1 [	843	851	5.125037	CTTTTTT	0.05341	0.05073
cg0161265	AFAP1	NF-AT1 [	1670	1678	5.125037	TTTTTTT	0.05341	0.05073
cg0261454	AFAP1	POU2F2 (	7	17	5.123481	TGTTTTA	0.02432	0.02134
cg0675819	AFAP1	AR [T000	910	918	5.104816	GGACAG	0.11444	0.12256
cg2591200	AFAP1	AP-2alpha	187	192	5.100982	AAAGGC	0.97656	0.97517
cg2591200	AFAP1	AP-2alpha	246	251	5.100982	AAAGGC	0.97656	0.97517
cg2591200	AFAP1	AP-2alpha	1788	1793	5.100982	GCCTTT	0.97656	0.97517
cg0261454	AFAP1	AP-2alpha	251	256	5.100982	AAAGGC	0.97656	0.97517
cg0261454	AFAP1	AP-2alpha	310	315	5.100982	AAAGGC	0.97656	0.97517
cg0261454	AFAP1	AP-2alpha	1852	1857	5.100982	GCCTTT	0.97656	0.97517
cg2639478	AFAP1	AP-2alpha	217	222	5.100982	AAAGGC	0.97656	0.97517
cg2639478	AFAP1	AP-2alpha	276	281	5.100982	AAAGGC	0.97656	0.97517
cg2639478	AFAP1	AP-2alpha	1818	1823	5.100982	GCCTTT	0.97656	0.97517

cg0675819	AFAP1	AP-2alpha	1416	1421	5.100982	AAAGGC	0.97656	0.97517
cg0675819	AFAP1	AP-2alpha	1993	1998	5.100982	AAAGGC	0.97656	0.97517
cg0161265	AFAP1	AP-2alpha	402	407	5.100982	AAAGGC	0.97656	0.97517
cg0161265	AFAP1	AP-2alpha	452	457	5.100982	AAAGGC	0.97656	0.97517
cg0161265	AFAP1	AP-2alpha	1104	1109	5.100982	AAAGGC	0.97656	0.97517
cg0161265	AFAP1	NF-Y [T0(	1189	1196	5.094053	CTTCCA/	0.36621	0.35921
cg2591200	AFAP1	RXR-alpha	1710	1716	5.089356	ATCACC(	0.48828	0.51407
cg2591200	AFAP1	RXR-alpha	1870	1876	5.089356	GGGTGC'	0.48828	0.51407
cg0261454	AFAP1	RXR-alpha	1774	1780	5.089356	ATCACC(	0.48828	0.51407
cg0261454	AFAP1	RXR-alpha	1934	1940	5.089356	GGGTGC'	0.48828	0.51407
cg2639478	AFAP1	RXR-alpha	1740	1746	5.089356	ATCACC(	0.48828	0.51407
cg2639478	AFAP1	RXR-alpha	1900	1906	5.089356	GGGTGC'	0.48828	0.51407
cg0161265	AFAP1	RXR-alpha	155	161	5.089356	GGGTGC'	0.48828	0.51407
cg2591200	AFAP1	SRY [T00!	898	906	5.086565	CTTTGAT	0.06104	0.05662
cg0261454	AFAP1	SRY [T00!	962	970	5.086565	CTTTGAT	0.06104	0.05662
cg2639478	AFAP1	SRY [T00!	928	936	5.086565	CTTTGAT	0.06104	0.05662
cg0161265	AFAP1	SRY [T00!	321	329	5.086565	CTTTGAT	0.06104	0.05662
cg0675819	AFAP1	AP-1 [T00	258	266	5.059986	TGACTCT	0.12207	0.12309
cg2591200	AFAP1	USF2 [T0(	766	775	5.052423	CTGACA(	0.103	0.10797
cg0261454	AFAP1	USF2 [T0(	830	839	5.052423	CTGACA(	0.103	0.10797
cg2639478	AFAP1	USF2 [T0(	796	805	5.052423	CTGACA(	0.103	0.10797
cg0675819	AFAP1	USF2 [T0(	291	300	5.052423	GAGACA	0.103	0.10797
cg2591200	AFAP1	GR-beta [T	39	43	5.042296	GGATT	3.90625	3.7093
cg2591200	AFAP1	GR-beta [T	78	82	5.042296	GGATT	3.90625	3.7093
cg2591200	AFAP1	GR-beta [T	352	356	5.042296	AATCC	3.90625	3.7093
cg2591200	AFAP1	GR-beta [T	529	533	5.042296	AATCC	3.90625	3.7093
cg2591200	AFAP1	GR-beta [T	556	560	5.042296	AATCC	3.90625	3.7093
cg0261454	AFAP1	GR-beta [T	103	107	5.042296	GGATT	3.90625	3.7093
cg0261454	AFAP1	GR-beta [T	142	146	5.042296	GGATT	3.90625	3.7093
cg0261454	AFAP1	GR-beta [T	416	420	5.042296	AATCC	3.90625	3.7093
cg0261454	AFAP1	GR-beta [T	593	597	5.042296	AATCC	3.90625	3.7093
cg0261454	AFAP1	GR-beta [T	620	624	5.042296	AATCC	3.90625	3.7093
cg2639478	AFAP1	GR-beta [T	69	73	5.042296	GGATT	3.90625	3.7093
cg2639478	AFAP1	GR-beta [T	108	112	5.042296	GGATT	3.90625	3.7093
cg2639478	AFAP1	GR-beta [T	382	386	5.042296	AATCC	3.90625	3.7093
cg2639478	AFAP1	GR-beta [T	559	563	5.042296	AATCC	3.90625	3.7093
cg2639478	AFAP1	GR-beta [T	586	590	5.042296	AATCC	3.90625	3.7093
cg0675819	AFAP1	GR-beta [T	979	983	5.042296	AATCC	3.90625	3.7093
cg0675819	AFAP1	GR-beta [T	1559	1563	5.042296	GTATT	3.90625	3.7093
cg0161265	AFAP1	GR-beta [T	53	57	5.042296	AATCC	3.90625	3.7093
cg0161265	AFAP1	GR-beta [T	1248	1252	5.042296	AATCC	3.90625	3.7093
cg0161265	AFAP1	GR-beta [T	1296	1300	5.042296	AATCC	3.90625	3.7093
cg0161265	AFAP1	GR-beta [T	1463	1467	5.042296	GTATT	3.90625	3.7093
cg0161265	AFAP1	GR-beta [T	1644	1648	5.042296	AATAC	3.90625	3.7093
cg0675819	AFAP1	E2F-1 [T0	1348	1355	5.042045	CCTCCC(	0.18311	0.20394
cg0675819	AFAP1	E2F-1 [T0	1433	1440	5.042045	GCGGGA	0.18311	0.20394
cg0161265	AFAP1	c-Ets-1 [T(	1189	1195	5.038739	CTTCCA/	0.48828	0.48026
cg2591200	AFAP1	C/EBPalph	1513	1519	5.024728	TGCAAT(	0.97656	0.90302

cg0261454	AFAP1	C/EBPalph	1577	1583	5.024728	TGCAAT	0.97656	0.90302
cg2639478	AFAP1	C/EBPalph	1543	1549	5.024728	TGCAAT	0.97656	0.90302
cg0161265	AFAP1	C/EBPalph	1155	1161	5.024728	TGCAAT	0.97656	0.90302
cg0675819	AFAP1	NFI/CTF [	760	767	5.021086	TCCTTTC	0.24414	0.25666
cg2591200	AFAP1	c-Jun [T00	767	773	5.000337	TGACAC	0.61035	0.60573
cg2591200	AFAP1	c-Jun [T00	1832	1838	5.000337	TGACAC	0.61035	0.60573
cg0261454	AFAP1	c-Jun [T00	831	837	5.000337	TGACAC	0.61035	0.60573
cg0261454	AFAP1	c-Jun [T00	1896	1902	5.000337	TGACAC	0.61035	0.60573
cg2639478	AFAP1	c-Jun [T00	797	803	5.000337	TGACAC	0.61035	0.60573
cg2639478	AFAP1	c-Jun [T00	1862	1868	5.000337	TGACAC	0.61035	0.60573
cg0161265	AFAP1	c-Jun [T00	1034	1040	5.000337	GGCGTC	0.61035	0.60573
cg0675819	AFAP1	AR [T000	1963	1971	4.995624	GGACAG	0.11444	0.12256
cg0161265	AFAP1	HNF-1A [	430	437	4.972635	GTTAAC	0.36621	0.34064
cg0675819	AFAP1	c-Ets-1 [T	453	459	4.910652	ATGGAA	0.48828	0.48026
cg0161265	AFAP1	c-Ets-1 [T	358	364	4.910652	ATGGAA	0.48828	0.48026
cg0161265	AFAP1	AP-1 [T00	1362	1370	4.902944	AAGGAG	0.12207	0.12309
cg0675819	AFAP1	XBP-1 [T	432	437	4.894955	ATGCCT	0.97656	0.99839
cg0161265	AFAP1	XBP-1 [T	1682	1687	4.894955	ATGCCT	0.97656	0.99839
cg0161265	AFAP1	XBP-1 [T	1689	1694	4.894955	AGGCAT	0.97656	0.99839
cg0675819	AFAP1	AR [T000	873	881	4.890444	GGACAC	0.11444	0.12256
cg0675819	AFAP1	AP-2alpha	1140	1145	4.890408	GCCTAA	0.97656	0.97517
cg0675819	AFAP1	AP-2alpha	1636	1641	4.890408	TTAGGC	0.97656	0.97517
cg0161265	AFAP1	AP-2alpha	1687	1692	4.890408	TTAGGC	0.97656	0.97517
cg2591200	AFAP1	c-Jun [T00	1491	1497	4.883696	TATGTC	0.61035	0.60573
cg0261454	AFAP1	c-Jun [T00	1555	1561	4.883696	TATGTC	0.61035	0.60573
cg2639478	AFAP1	c-Jun [T00	1521	1527	4.883696	TATGTC	0.61035	0.60573
cg0161265	AFAP1	IRF-1 [T0	1235	1243	4.881305	TTTCCG	0.1297	0.12724
cg2591200	AFAP1	RXR-alph	336	342	4.86724	GGGTCT	0.48828	0.51407
cg2591200	AFAP1	RXR-alph	1730	1736	4.86724	GGGTCT	0.48828	0.51407
cg0261454	AFAP1	RXR-alph	400	406	4.86724	GGGTCT	0.48828	0.51407
cg0261454	AFAP1	RXR-alph	1794	1800	4.86724	GGGTCT	0.48828	0.51407
cg2639478	AFAP1	RXR-alph	366	372	4.86724	GGGTCT	0.48828	0.51407
cg2639478	AFAP1	RXR-alph	1760	1766	4.86724	GGGTCT	0.48828	0.51407
cg0675819	AFAP1	RXR-alph	1300	1306	4.86724	CATACC	0.48828	0.51407
cg0675819	AFAP1	NF-Y [T0	380	387	4.867193	ATTGGA	0.36621	0.35921
cg0675819	AFAP1	GCF [T00	1734	1742	4.846987	GCGCCG	0.27466	0.31905
cg0161265	AFAP1	C/EBPalph	1159	1165	4.845599	ATCAAT	0.97656	0.90302
cg2591200	AFAP1	c-Myb [T0	576	583	4.840682	GCAAGT	0.30518	0.30087
cg0261454	AFAP1	c-Myb [T0	640	647	4.840682	GCAAGT	0.30518	0.30087
cg2639478	AFAP1	c-Myb [T0	606	613	4.840682	GCAAGT	0.30518	0.30087
cg0161265	AFAP1	c-Myb [T0	1911	1918	4.840682	GAACTT	0.30518	0.30087
cg0675819	AFAP1	p53 [T006	1379	1385	4.786849	AGTGCC	0.48828	0.53921
cg0675819	AFAP1	p53 [T006	1973	1979	4.786849	AGTGCC	0.48828	0.53921
cg0675819	AFAP1	c-Ets-1 [T	37	43	4.782565	GTGGAA	0.48828	0.48026
cg0675819	AFAP1	c-Ets-1 [T	1692	1698	4.782565	CTTCCAC	0.48828	0.48026
cg2591200	AFAP1	FOXP3 [T	123	128	4.756447	GTTTTC	2.92969	2.82
cg2591200	AFAP1	FOXP3 [T	193	198	4.756447	AAAAAC	2.92969	2.82
cg2591200	AFAP1	FOXP3 [T	1020	1025	4.756447	GTTTTC	2.92969	2.82

cg2591200	AFAP1	FOXP3 [T	1229	1234	4.756447	AAAAAC	2.92969	2.82
cg2591200	AFAP1	FOXP3 [T	1235	1240	4.756447	AAAAAC	2.92969	2.82
cg2591200	AFAP1	FOXP3 [T	1241	1246	4.756447	AAAAAC	2.92969	2.82
cg2591200	AFAP1	FOXP3 [T	1255	1260	4.756447	AAAAAC	2.92969	2.82
cg2591200	AFAP1	FOXP3 [T	1326	1331	4.756447	AAAAAC	2.92969	2.82
cg2591200	AFAP1	TFII-I [T0	316	321	4.756447	GGAATG	2.92969	2.89715
cg2591200	AFAP1	TFII-I [T0	478	483	4.756447	ATTTCC	2.92969	2.89715
cg2591200	AFAP1	TFII-I [T0	595	600	4.756447	ATTTCC	2.92969	2.89715
cg2591200	AFAP1	TFII-I [T0	628	633	4.756447	GGAATG	2.92969	2.89715
cg2591200	AFAP1	TFII-I [T0	634	639	4.756447	GGAATG	2.92969	2.89715
cg2591200	AFAP1	TFII-I [T0	815	820	4.756447	GGATAT	2.92969	2.89715
cg2591200	AFAP1	TFII-I [T0	1879	1884	4.756447	GGACTG	2.92969	2.89715
cg2591200	AFAP1	TFII-I [T0	1900	1905	4.756447	GGAAAT	2.92969	2.89715
cg0261454	AFAP1	FOXP3 [T	14	19	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	25	30	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	187	192	4.756447	GTTTTC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	257	262	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	1084	1089	4.756447	GTTTTC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	1293	1298	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	1299	1304	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	1305	1310	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	1319	1324	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	FOXP3 [T	1390	1395	4.756447	AAAAAC	2.92969	2.82
cg0261454	AFAP1	TFII-I [T0	46	51	4.756447	ATATCC	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	380	385	4.756447	GGAATG	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	542	547	4.756447	ATTTCC	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	659	664	4.756447	ATTTCC	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	692	697	4.756447	GGAATG	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	698	703	4.756447	GGAATG	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	879	884	4.756447	GGATAT	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	1943	1948	4.756447	GGACTG	2.92969	2.89715
cg0261454	AFAP1	TFII-I [T0	1964	1969	4.756447	GGAAAT	2.92969	2.89715
cg2639478	AFAP1	FOXP3 [T	153	158	4.756447	GTTTTC	2.92969	2.82
cg2639478	AFAP1	FOXP3 [T	223	228	4.756447	AAAAAC	2.92969	2.82
cg2639478	AFAP1	FOXP3 [T	1050	1055	4.756447	GTTTTC	2.92969	2.82
cg2639478	AFAP1	FOXP3 [T	1259	1264	4.756447	AAAAAC	2.92969	2.82
cg2639478	AFAP1	FOXP3 [T	1265	1270	4.756447	AAAAAC	2.92969	2.82
cg2639478	AFAP1	FOXP3 [T	1271	1276	4.756447	AAAAAC	2.92969	2.82
cg2639478	AFAP1	FOXP3 [T	1285	1290	4.756447	AAAAAC	2.92969	2.82
cg2639478	AFAP1	FOXP3 [T	1356	1361	4.756447	AAAAAC	2.92969	2.82
cg2639478	AFAP1	TFII-I [T0	12	17	4.756447	ATATCC	2.92969	2.89715
cg2639478	AFAP1	TFII-I [T0	346	351	4.756447	GGAATG	2.92969	2.89715
cg2639478	AFAP1	TFII-I [T0	508	513	4.756447	ATTTCC	2.92969	2.89715
cg2639478	AFAP1	TFII-I [T0	625	630	4.756447	ATTTCC	2.92969	2.89715
cg2639478	AFAP1	TFII-I [T0	658	663	4.756447	GGAATG	2.92969	2.89715
cg2639478	AFAP1	TFII-I [T0	664	669	4.756447	GGAATG	2.92969	2.89715
cg2639478	AFAP1	TFII-I [T0	845	850	4.756447	GGATAT	2.92969	2.89715
cg2639478	AFAP1	TFII-I [T0	1909	1914	4.756447	GGACTG	2.92969	2.89715

cg2639478	AFAP1	TFII-I [T0	1930	1935	4.756447	GGAAAT	2.92969	2.89715
cg0675819	AFAP1	FOXP3 [T	78	83	4.756447	GTTGAC	2.92969	2.82
cg0675819	AFAP1	FOXP3 [T	118	123	4.756447	GAAAAC	2.92969	2.82
cg0675819	AFAP1	FOXP3 [T	136	141	4.756447	AAAAAC	2.92969	2.82
cg0675819	AFAP1	FOXP3 [T	984	989	4.756447	CTCAAC	2.92969	2.82
cg0675819	AFAP1	TFII-I [T0	1185	1190	4.756447	CAGTCC	2.92969	2.89715
cg0675819	AFAP1	TFII-I [T0	1597	1602	4.756447	CAGTCC	2.92969	2.89715
cg0675819	AFAP1	TFII-I [T0	1671	1676	4.756447	GGAATG	2.92969	2.89715
cg0675819	AFAP1	TFII-I [T0	1925	1930	4.756447	CATTCC	2.92969	2.89715
cg0161265	AFAP1	FOXP3 [T	176	181	4.756447	GTTTTG	2.92969	2.82
cg0161265	AFAP1	FOXP3 [T	260	265	4.756447	AAAAAC	2.92969	2.82
cg0161265	AFAP1	FOXP3 [T	489	494	4.756447	GTTTTT	2.92969	2.82
cg0161265	AFAP1	FOXP3 [T	729	734	4.756447	CAAAAC	2.92969	2.82
cg0161265	AFAP1	FOXP3 [T	788	793	4.756447	GTCAAC	2.92969	2.82
cg0161265	AFAP1	FOXP3 [T	1130	1135	4.756447	CAAAAC	2.92969	2.82
cg0161265	AFAP1	FOXP3 [T	1377	1382	4.756447	GTTTTC	2.92969	2.82
cg0161265	AFAP1	FOXP3 [T	1669	1674	4.756447	GTTTTT	2.92969	2.82
cg0161265	AFAP1	TFII-I [T0	328	333	4.756447	GGAATG	2.92969	2.89715
cg0161265	AFAP1	TFII-I [T0	1016	1021	4.756447	ATGTCC	2.92969	2.89715
cg0161265	AFAP1	TFII-I [T0	1410	1415	4.756447	GGACAT	2.92969	2.89715
cg0161265	AFAP1	TFII-I [T0	1498	1503	4.756447	GGACTG	2.92969	2.89715
cg0161265	AFAP1	TFII-I [T0	1931	1936	4.756447	GGACTG	2.92969	2.89715
cg0675819	AFAP1	Sp1 [T007	50	59	4.708577	CGGGCG	0.08583	0.0979
cg0161265	AFAP1	HNF-1A [	428	435	4.684871	TTGTTA	0.12207	0.10966
cg0675819	AFAP1	c-Ets-1 [T	339	345	4.654478	CTTCCA	0.85449	0.8381
cg0675819	AFAP1	c-Ets-1 [T	1505	1511	4.654478	CTTCCA	0.85449	0.8381
cg0675819	AFAP1	p53 [T006	1131	1137	4.645444	CGCGCC	0.24414	0.28373
cg0161265	AFAP1	c-Ets-1 [T	1235	1241	4.616023	TTTCCG	0.85449	0.8381
cg2591200	AFAP1	c-Ets-2 [T	173	181	4.589988	CTGAAG	0.06866	0.06805
cg0261454	AFAP1	c-Ets-2 [T	237	245	4.589988	CTGAAG	0.06866	0.06805
cg2639478	AFAP1	c-Ets-2 [T	203	211	4.589988	CTGAAG	0.06866	0.06805
cg0161265	AFAP1	NF-AT1 [	797	805	4.566689	GGAAAC	0.06866	0.06549
cg0161265	AFAP1	C/EBPalph	765	771	4.560723	GCCAAT	0.24414	0.24373
cg2591200	AFAP1	AP-1 [T00	1380	1388	4.553988	TGACTC	0.03052	0.03196
cg0261454	AFAP1	AP-1 [T00	1444	1452	4.553988	TGACTC	0.03052	0.03196
cg2639478	AFAP1	AP-1 [T00	1410	1418	4.553988	TGACTC	0.03052	0.03196
cg0161265	AFAP1	USF2 [T0	640	649	4.528187	ACTTCA	0.06866	0.07203
cg2591200	AFAP1	c-Ets-1 [T	1898	1904	4.487936	CCGGAA	0.85449	0.8381
cg0261454	AFAP1	c-Ets-1 [T	1962	1968	4.487936	CCGGAA	0.85449	0.8381
cg2639478	AFAP1	c-Ets-1 [T	1928	1934	4.487936	CCGGAA	0.85449	0.8381
cg0675819	AFAP1	T3R-beta1	787	795	4.481316	AGAAGG	0.27466	0.27245
cg0675819	AFAP1	T3R-beta1	1019	1027	4.481316	AGAAGG	0.27466	0.27245
cg2591200	AFAP1	T3R-beta1	804	812	4.462023	TAATGG	0.27466	0.27245
cg0261454	AFAP1	T3R-beta1	868	876	4.462023	TAATGG	0.27466	0.27245
cg2639478	AFAP1	T3R-beta1	834	842	4.462023	TAATGG	0.27466	0.27245
cg0675819	AFAP1	GATA-2 [	1190	1198	4.444445	CCCTTA	0.24414	0.23857
cg2591200	AFAP1	c-Jun [T00	1688	1694	4.441904	TGACTG	0.12207	0.11843
cg0261454	AFAP1	c-Jun [T00	1752	1758	4.441904	TGACTG	0.12207	0.11843

cg2639478	AFAP1	c-Jun [T00	1718	1724	4.441904	TGACTG	0.12207	0.11843
cg0161265	AFAP1	c-Jun [T00	1368	1374	4.441904	TCAGTC	0.12207	0.11843
cg0161265	AFAP1	AP-2alpha	1070	1075	4.438035	CTAGGC	0.97656	0.99839
cg0675819	AFAP1	Sp1 [T007	1288	1297	4.43736	AGGGCG	0.08583	0.0979
cg0675819	AFAP1	RXR-alph	1253	1259	4.423008	TCCACC	0.24414	0.25781
cg0675819	AFAP1	RXR-alph	1343	1349	4.423008	TCCACC	0.24414	0.25781
cg0161265	AFAP1	RXR-alph	461	467	4.423008	GGGTTG	0.24414	0.25781
cg0161265	AFAP1	AP-2alpha	558	563	4.422424	TAAGGC	0.97656	0.99839
cg0161265	AFAP1	AP-2alpha	607	612	4.422424	TAAGGC	0.97656	0.99839
cg0161265	AFAP1	AP-2alpha	1684	1689	4.422424	GCCTTA	0.97656	0.99839
cg2591200	AFAP1	STAT4 [T	178	183	4.411765	GGAAGA	1.95312	1.99838
cg2591200	AFAP1	STAT4 [T	316	321	4.411765	GGAATG	1.95312	1.99838
cg2591200	AFAP1	STAT4 [T	407	412	4.411765	TCTTCC	1.95312	1.99838
cg2591200	AFAP1	STAT4 [T	628	633	4.411765	GGAATG	1.95312	1.99838
cg2591200	AFAP1	STAT4 [T	634	639	4.411765	GGAATG	1.95312	1.99838
cg2591200	AFAP1	STAT4 [T	940	945	4.411765	TCTTCC	1.95312	1.99838
cg2591200	AFAP1	STAT4 [T	1024	1029	4.411765	TCTTCC	1.95312	1.99838
cg2591200	AFAP1	STAT4 [T	1761	1766	4.411765	GCTTCC	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	242	247	4.411765	GGAAGA	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	380	385	4.411765	GGAATG	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	471	476	4.411765	TCTTCC	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	692	697	4.411765	GGAATG	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	698	703	4.411765	GGAATG	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	1004	1009	4.411765	TCTTCC	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	1088	1093	4.411765	TCTTCC	1.95312	1.99838
cg0261454	AFAP1	STAT4 [T	1825	1830	4.411765	GCTTCC	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	208	213	4.411765	GGAAGA	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	346	351	4.411765	GGAATG	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	437	442	4.411765	TCTTCC	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	658	663	4.411765	GGAATG	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	664	669	4.411765	GGAATG	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	970	975	4.411765	TCTTCC	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	1054	1059	4.411765	TCTTCC	1.95312	1.99838
cg2639478	AFAP1	STAT4 [T	1791	1796	4.411765	GCTTCC	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	39	44	4.411765	GGAAGA	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	262	267	4.411765	TCTTCC	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	439	444	4.411765	GCTTCC	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	1090	1095	4.411765	GGAAGA	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	1104	1109	4.411765	GGAAGA	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	1455	1460	4.411765	GGAAGA	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	1671	1676	4.411765	GGAATG	1.95312	1.99838
cg0675819	AFAP1	STAT4 [T	1925	1930	4.411765	CATTCC	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	328	333	4.411765	GGAATG	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	587	592	4.411765	GGAAGC	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	1027	1032	4.411765	GGAAGC	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	1081	1086	4.411765	GGAACG	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	1136	1141	4.411765	CGTTCC	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	1188	1193	4.411765	GCTTCC	1.95312	1.99838

cg0161265	AFAP1	STAT4 [T	1391	1396	4.411765	TCTTCC	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	1566	1571	4.411765	TCTTCC	1.95312	1.99838
cg0161265	AFAP1	STAT4 [T	1917	1922	4.411765	GCTTCC	1.95312	1.99838
cg2591200	AFAP1	NF-AT1 [	475	483	4.396744	AGAATT	0.06866	0.06549
cg0261454	AFAP1	NF-AT1 [	539	547	4.396744	AGAATT	0.06866	0.06549
cg2639478	AFAP1	NF-AT1 [	505	513	4.396744	AGAATT	0.06866	0.06549
cg0675819	AFAP1	p53 [T006	766	772	4.33696	GGGCCA	0.24414	0.28373
cg0161265	AFAP1	p53 [T006	676	682	4.33696	GGGCCA	0.24414	0.28373
cg0161265	AFAP1	p53 [T006	1939	1945	4.33696	CTGGCC	0.24414	0.28373
cg2591200	AFAP1	HOXD9 [	1250	1259	4.321431	AATAAA	0.03433	0.02831
cg2591200	AFAP1	HOXD10 [	1250	1259	4.321431	AATAAA	0.03433	0.02831
cg0261454	AFAP1	HOXD9 [	1314	1323	4.321431	AATAAA	0.03433	0.02831
cg0261454	AFAP1	HOXD10 [	1314	1323	4.321431	AATAAA	0.03433	0.02831
cg2639478	AFAP1	HOXD9 [	1280	1289	4.321431	AATAAA	0.03433	0.02831
cg2639478	AFAP1	HOXD10 [	1280	1289	4.321431	AATAAA	0.03433	0.02831
cg0161265	AFAP1	HOXD9 [	189	198	4.321431	AATAAA	0.03433	0.02831
cg0161265	AFAP1	HOXD10 [	189	198	4.321431	AATAAA	0.03433	0.02831
cg0161265	AFAP1	PEA3 [T0	1013	1021	4.30818	TGGATG	0.13733	0.13607
cg0675819	AFAP1	RAR-beta	1068	1077	4.289108	AATGAA	0.14496	0.14853
cg2591200	AFAP1	c-Ets-1 [T	525	531	4.282938	GAGGAA	0.85449	0.8381
cg0261454	AFAP1	c-Ets-1 [T	589	595	4.282938	GAGGAA	0.85449	0.8381
cg2639478	AFAP1	c-Ets-1 [T	555	561	4.282938	GAGGAA	0.85449	0.8381
cg2591200	AFAP1	RXR-alpha	1357	1363	4.24113	GGGACC	0.97656	1.02803
cg0261454	AFAP1	RXR-alpha	1421	1427	4.24113	GGGACC	0.97656	1.02803
cg2639478	AFAP1	RXR-alpha	1387	1393	4.24113	GGGACC	0.97656	1.02803
cg0161265	AFAP1	RXR-alpha	68	74	4.24113	GGGACC	0.97656	1.02803
cg0675819	AFAP1	AR [T000	665	673	4.241082	GCTCTG	0.06866	0.06981
cg2591200	AFAP1	AP-2alpha	1305	1310	4.211849	GCCTAC	0.97656	1.02535
cg0261454	AFAP1	AP-2alpha	1369	1374	4.211849	GCCTAC	0.97656	1.02535
cg2639478	AFAP1	AP-2alpha	1335	1340	4.211849	GCCTAC	0.97656	1.02535
cg2591200	AFAP1	GR-beta [	154	158	4.201913	TGATT	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	221	225	4.201913	AATAA	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	349	353	4.201913	AATAA	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	638	642	4.201913	TGATT	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	866	870	4.201913	CGATT	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	1087	1091	4.201913	AATCA	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	1104	1108	4.201913	AATAA	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	1174	1178	4.201913	TTATT	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	1182	1186	4.201913	AATCA	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	1250	1254	4.201913	AATAA	7.8125	7.23274
cg2591200	AFAP1	GR-beta [	1857	1861	4.201913	AATCA	7.8125	7.23274
cg0261454	AFAP1	GR-beta [	218	222	4.201913	TGATT	7.8125	7.23274
cg0261454	AFAP1	GR-beta [	285	289	4.201913	AATAA	7.8125	7.23274
cg0261454	AFAP1	GR-beta [	413	417	4.201913	AATAA	7.8125	7.23274
cg0261454	AFAP1	GR-beta [	702	706	4.201913	TGATT	7.8125	7.23274
cg0261454	AFAP1	GR-beta [	930	934	4.201913	CGATT	7.8125	7.23274
cg0261454	AFAP1	GR-beta [	1151	1155	4.201913	AATCA	7.8125	7.23274
cg0261454	AFAP1	GR-beta [	1168	1172	4.201913	AATAA	7.8125	7.23274

cg0261454	AFAP1	GR-beta [T	1238	1242	4.201913	TTATT	7.8125	7.23274
cg0261454	AFAP1	GR-beta [T	1246	1250	4.201913	AATCA	7.8125	7.23274
cg0261454	AFAP1	GR-beta [T	1314	1318	4.201913	AATAA	7.8125	7.23274
cg0261454	AFAP1	GR-beta [T	1921	1925	4.201913	AATCA	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	184	188	4.201913	TGATT	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	251	255	4.201913	AATAA	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	379	383	4.201913	AATAA	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	668	672	4.201913	TGATT	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	896	900	4.201913	CGATT	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	1117	1121	4.201913	AATCA	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	1134	1138	4.201913	AATAA	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	1204	1208	4.201913	TTATT	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	1212	1216	4.201913	AATCA	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	1280	1284	4.201913	AATAA	7.8125	7.23274
cg2639478	AFAP1	GR-beta [T	1887	1891	4.201913	AATCA	7.8125	7.23274
cg0675819	AFAP1	GR-beta [T	91	95	4.201913	AATAA	7.8125	7.23274
cg0675819	AFAP1	GR-beta [T	715	719	4.201913	AATCA	7.8125	7.23274
cg0675819	AFAP1	GR-beta [T	1628	1632	4.201913	AATCA	7.8125	7.23274
cg0675819	AFAP1	GR-beta [T	1728	1732	4.201913	AATAA	7.8125	7.23274
cg0675819	AFAP1	GR-beta [T	1947	1951	4.201913	AATAA	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	121	125	4.201913	AATCA	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	189	193	4.201913	AATAA	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	271	275	4.201913	TTATT	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	291	295	4.201913	AATAA	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	297	301	4.201913	TTATT	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	528	532	4.201913	AATCA	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	768	772	4.201913	AATCA	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	802	806	4.201913	CTATT	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	1158	1162	4.201913	AATCA	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	1543	1547	4.201913	TTATT	7.8125	7.23274
cg0161265	AFAP1	GR-beta [T	1622	1626	4.201913	TGATT	7.8125	7.23274
cg0675819	AFAP1	NF-Y [T0	1199	1206	4.186615	TTCCCA	0.18311	0.17499
cg0675819	AFAP1	c-Ets-1 [T	1669	1675	4.154851	CAGGAA	0.24414	0.23719
cg0161265	AFAP1	c-Ets-1 [T	1583	1589	4.154851	ATTCCTC	0.24414	0.23719
cg0161265	AFAP1	c-Ets-1 [T	1859	1865	4.154851	ATTCCTC	0.24414	0.23719
cg2591200	AFAP1	NF-AT1 [T	463	472	4.134416	AAGCTT	0.08392	0.07965
cg0261454	AFAP1	NF-AT1 [T	527	536	4.134416	AAGCTT	0.08392	0.07965
cg2639478	AFAP1	NF-AT1 [T	493	502	4.134416	AAGCTT	0.08392	0.07965
cg0675819	AFAP1	c-Jun [T00	299	305	4.1298	TGACTC	0.24414	0.23729
cg2591200	AFAP1	p53 [T006	615	621	4.125254	CAGGCC	0.73242	0.82434
cg0261454	AFAP1	p53 [T006	679	685	4.125254	CAGGCC	0.73242	0.82434
cg2639478	AFAP1	p53 [T006	645	651	4.125254	CAGGCC	0.73242	0.82434
cg0675819	AFAP1	p53 [T006	331	337	4.125254	GGGCCT	0.73242	0.82434
cg0675819	AFAP1	p53 [T006	530	536	4.125254	GGGCCG	0.73242	0.82434
cg0161265	AFAP1	p53 [T006	376	382	4.125254	CAGGCC	0.73242	0.82434
cg0161265	AFAP1	p53 [T006	1790	1796	4.125254	CAGGCC	0.73242	0.82434
cg0161265	AFAP1	POU2F2 (	473	483	4.120113	TGAATT	0.01717	0.01453
cg0675819	AFAP1	SRY [T00	1938	1946	4.087393	TTTACA	0.12207	0.11312

cg2591200	AFAP1	p53 [T006	756	762	4.083527	GGGCAC	0.73242	0.82434
cg2591200	AFAP1	p53 [T006	1645	1651	4.083527	GGTGCC	0.73242	0.82434
cg0261454	AFAP1	p53 [T006	820	826	4.083527	GGGCAC	0.73242	0.82434
cg0261454	AFAP1	p53 [T006	1709	1715	4.083527	GGTGCC	0.73242	0.82434
cg2639478	AFAP1	p53 [T006	786	792	4.083527	GGGCAC	0.73242	0.82434
cg2639478	AFAP1	p53 [T006	1675	1681	4.083527	GGTGCC	0.73242	0.82434
cg0675819	AFAP1	p53 [T006	1261	1267	4.083527	GGTGCC	0.73242	0.82434
cg0675819	AFAP1	p53 [T006	1981	1987	4.083527	GGGCAC	0.73242	0.82434
cg0161265	AFAP1	p53 [T006	388	394	4.083527	GGGCAC	0.73242	0.82434
cg0161265	AFAP1	Sp1 [T007	1482	1491	4.07139	GGGGCG	0.08965	0.10391
cg0675819	AFAP1	NF-AT1 [T	953	961	4.056854	ACCCTT	0.07629	0.07182
cg0675819	AFAP1	RXR-alpha	1495	1501	4.019014	GGGTCT	0.97656	1.02803
cg0675819	AFAP1	RXR-alpha	1713	1719	4.019014	CACACC	0.97656	1.02803
cg0675819	AFAP1	RXR-alpha	1893	1899	4.019014	AAGACC	0.97656	1.02803
cg0161265	AFAP1	RXR-alpha	1355	1361	4.019014	GAAACC	0.97656	1.02803
cg2591200	AFAP1	c-Ets-2 [T	480	488	4.017001	TTCCTTT	0.16022	0.15061
cg0261454	AFAP1	c-Ets-2 [T	544	552	4.017001	TTCCTTT	0.16022	0.15061
cg2639478	AFAP1	c-Ets-2 [T	510	518	4.017001	TTCCTTT	0.16022	0.15061
cg0675819	AFAP1	c-Ets-2 [T	242	250	4.017001	GGAAAG	0.16022	0.15061
cg0161265	AFAP1	c-Ets-2 [T	1675	1683	4.017001	TTCCTTT	0.16022	0.15061
cg2591200	AFAP1	TFIID [T0	42	48	4.007279	TTTACA	1.09863	0.94722
cg2591200	AFAP1	TFIID [T0	1321	1327	4.007279	TTTATA	1.09863	0.94722
cg2591200	AFAP1	TFIID [T0	1322	1328	4.007279	TTATAA	1.09863	0.94722
cg2591200	AFAP1	Pax-5 [T0	1274	1280	4.007279	GGGCAG	1.09863	1.18533
cg0261454	AFAP1	TFIID [T0	9	15	4.007279	TTTTAA	1.09863	0.94722
cg0261454	AFAP1	TFIID [T0	60	66	4.007279	TAGTAA	1.09863	0.94722
cg0261454	AFAP1	TFIID [T0	106	112	4.007279	TTTACA	1.09863	0.94722
cg0261454	AFAP1	TFIID [T0	1385	1391	4.007279	TTTATA	1.09863	0.94722
cg0261454	AFAP1	TFIID [T0	1386	1392	4.007279	TTATAA	1.09863	0.94722
cg0261454	AFAP1	Pax-5 [T0	1338	1344	4.007279	GGGCAG	1.09863	1.18533
cg2639478	AFAP1	TFIID [T0	26	32	4.007279	TAGTAA	1.09863	0.94722
cg2639478	AFAP1	TFIID [T0	72	78	4.007279	TTTACA	1.09863	0.94722
cg2639478	AFAP1	TFIID [T0	1351	1357	4.007279	TTTATA	1.09863	0.94722
cg2639478	AFAP1	TFIID [T0	1352	1358	4.007279	TTATAA	1.09863	0.94722
cg2639478	AFAP1	Pax-5 [T0	1304	1310	4.007279	GGGCAG	1.09863	1.18533
cg0675819	AFAP1	TFIID [T0	1722	1728	4.007279	TTTTAA	1.09863	0.94722
cg0675819	AFAP1	TFIID [T0	1938	1944	4.007279	TTTACA	1.09863	0.94722
cg0675819	AFAP1	Pax-5 [T0	663	669	4.007279	GGGCTC	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	821	827	4.007279	GGGCCG	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1324	1330	4.007279	GGGCCT	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1379	1385	4.007279	AGTGCC	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1460	1466	4.007279	ACAGCC	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1518	1524	4.007279	GGGCCG	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1771	1777	4.007279	ACAGCC	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1870	1876	4.007279	ACGGCC	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1965	1971	4.007279	ACAGCC	1.09863	1.18533
cg0675819	AFAP1	Pax-5 [T0	1973	1979	4.007279	AGTGCC	1.09863	1.18533
cg0161265	AFAP1	TFIID [T0	492	498	4.007279	TTTACA	1.09863	0.94722

cg0161265	AFAP1	TFIID [T0	1202	1208	4.007279	TTGTAA	1.09863	0.94722
cg0161265	AFAP1	TFIID [T0	1626	1632	4.007279	TTTTAA	1.09863	0.94722
cg0161265	AFAP1	Pax-5 [T0	608	614	4.007279	AAGGCC	1.09863	1.18533
cg0161265	AFAP1	Pax-5 [T0	975	981	4.007279	ACGGCC	1.09863	1.18533
cg0161265	AFAP1	Pax-5 [T0	1933	1939	4.007279	ACTGCC	1.09863	1.18533
cg2591200	AFAP1	USF2 [T0	755	764	4.003951	AGGGCA	0.01144	0.01199
cg0261454	AFAP1	USF2 [T0	819	828	4.003951	AGGGCA	0.01144	0.01199
cg2639478	AFAP1	USF2 [T0	785	794	4.003951	AGGGCA	0.01144	0.01199
cg2591200	AFAP1	c-Myb [T0	1824	1831	3.973336	TAACTT	0.09155	0.09116
cg0261454	AFAP1	c-Myb [T0	1888	1895	3.973336	TAACTT	0.09155	0.09116
cg2639478	AFAP1	c-Myb [T0	1854	1861	3.973336	TAACTT	0.09155	0.09116
cg2591200	AFAP1	AP-2alpha	1507	1512	3.970052	CAAGGC	0.97656	1.02535
cg0261454	AFAP1	AP-2alpha	1571	1576	3.970052	CAAGGC	0.97656	1.02535
cg2639478	AFAP1	AP-2alpha	1537	1542	3.970052	CAAGGC	0.97656	1.02535
cg0675819	AFAP1	AP-2alpha	1326	1331	3.970052	GCCTTG	0.97656	1.02535
cg0675819	AFAP1	AP-2alpha	1447	1452	3.970052	GCCTTG	0.97656	1.02535
cg0161265	AFAP1	p53 [T006	2	8	3.961937	CTAGCC	0.73242	0.82434
cg0261454	AFAP1	c-Ets-1 [T	52	58	3.846637	TAGGAA	0.24414	0.23719
cg2639478	AFAP1	c-Ets-1 [T	18	24	3.846637	TAGGAA	0.24414	0.23719
cg0161265	AFAP1	EBF [T05	977	987	3.842007	GGCCCT	0.0248	0.02839
cg0675819	AFAP1	c-Jun [T00	1583	1589	3.807346	TGACTA	0.24414	0.23729
cg2591200	AFAP1	NFI/CTF [	1576	1583	3.793671	CCAAGG	0.18311	0.19063
cg0261454	AFAP1	NFI/CTF [	1640	1647	3.793671	CCAAGG	0.18311	0.19063
cg2639478	AFAP1	NFI/CTF [	1606	1613	3.793671	CCAAGG	0.18311	0.19063
cg2591200	AFAP1	E2F-1 [T0	940	947	3.784875	TCTTCC	0.15259	0.15999
cg0261454	AFAP1	E2F-1 [T0	1004	1011	3.784875	TCTTCC	0.15259	0.15999
cg2639478	AFAP1	E2F-1 [T0	970	977	3.784875	TCTTCC	0.15259	0.15999
cg0675819	AFAP1	E2F-1 [T0	1291	1298	3.784875	GCGGCA	0.15259	0.15999
cg2591200	AFAP1	USF1 [T0	1542	1551	3.775819	CACGTG	0.08011	0.08435
cg0261454	AFAP1	USF1 [T0	1606	1615	3.775819	CACGTG	0.08011	0.08435
cg2639478	AFAP1	USF1 [T0	1572	1581	3.775819	CACGTG	0.08011	0.08435
cg2591200	AFAP1	GR [T050	25	31	3.763516	CAAAGA	0.73242	0.6946
cg0261454	AFAP1	GR [T050	89	95	3.763516	CAAAGA	0.73242	0.6946
cg2639478	AFAP1	GR [T050	55	61	3.763516	CAAAGA	0.73242	0.6946
cg0675819	AFAP1	GR [T050	1660	1666	3.763516	CAAAGA	0.73242	0.6946
cg0675819	AFAP1	GR [T050	1942	1948	3.763516	CAAAGA	0.73242	0.6946
cg0161265	AFAP1	GR [T050	175	181	3.763516	TGTTTT	0.73242	0.6946
cg0161265	AFAP1	GR [T050	746	752	3.763516	CTCTTT	0.73242	0.6946
cg2591200	AFAP1	E2F [T002	965	974	3.762198	TTTGGC	0.04578	0.04554
cg0261454	AFAP1	E2F [T002	1029	1038	3.762198	TTTGGC	0.04578	0.04554
cg2639478	AFAP1	E2F [T002	995	1004	3.762198	TTTGGC	0.04578	0.04554
cg0675819	AFAP1	p53 [T006	342	348	3.750231	CCAGCC	0.73242	0.82434
cg0161265	AFAP1	p53 [T006	1982	1988	3.750231	CCAGCC	0.73242	0.82434
cg2591200	AFAP1	AP-2alpha	324	329	3.743866	GCCTTC	0.48828	0.5124
cg2591200	AFAP1	AP-2alpha	378	383	3.743866	GCCTTC	0.48828	0.5124
cg2591200	AFAP1	AP-2alpha	953	958	3.743866	GAAGGC	0.48828	0.5124
cg0261454	AFAP1	AP-2alpha	388	393	3.743866	GCCTTC	0.48828	0.5124
cg0261454	AFAP1	AP-2alpha	442	447	3.743866	GCCTTC	0.48828	0.5124

cg0261454	AFAP1	AP-2alpha	1017	1022	3.743866	GAAGGC	0.48828	0.5124
cg2639478	AFAP1	AP-2alpha	354	359	3.743866	GCCTTC	0.48828	0.5124
cg2639478	AFAP1	AP-2alpha	408	413	3.743866	GCCTTC	0.48828	0.5124
cg2639478	AFAP1	AP-2alpha	983	988	3.743866	GAAGGC	0.48828	0.5124
cg0675819	AFAP1	AP-2alpha	196	201	3.743866	GAAGGC	0.48828	0.5124
cg0675819	AFAP1	AP-2alpha	337	342	3.743866	GCCTTC	0.48828	0.5124
cg0675819	AFAP1	AP-2alpha	1427	1432	3.743866	GAAGGC	0.48828	0.5124
cg0675819	AFAP1	AP-2alpha	1765	1770	3.743866	GAAGGC	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	813	818	3.743866	GAAGGC	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	1435	1440	3.743866	GAAGGC	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	1721	1726	3.743866	GAAGGC	0.48828	0.5124
cg0675819	AFAP1	Sp1 [T007	550	559	3.734601	GGGGCG	0.07439	0.08783
cg2591200	AFAP1	c-Ets-1 [T	395	401	3.71855	GTTCCT	0.61035	0.61936
cg0261454	AFAP1	c-Ets-1 [T	459	465	3.71855	GTTCCT	0.61035	0.61936
cg2639478	AFAP1	c-Ets-1 [T	425	431	3.71855	GTTCCT	0.61035	0.61936
cg0161265	AFAP1	c-Ets-1 [T	362	368	3.71855	AAGGAA	0.61035	0.61936
cg0161265	AFAP1	PEA3 [T0	467	475	3.710864	TGGATG	0.09155	0.08745
cg2591200	AFAP1	IRF-1 [T0	479	487	3.692688	TTTCCTT	0.06866	0.0661
cg0261454	AFAP1	IRF-1 [T0	543	551	3.692688	TTTCCTT	0.06866	0.0661
cg2639478	AFAP1	IRF-1 [T0	509	517	3.692688	TTTCCTT	0.06866	0.0661
cg0161265	AFAP1	IRF-1 [T0	1674	1682	3.692688	TTTCCTT	0.06866	0.0661
cg0161265	AFAP1	IRF-1 [T0	793	801	3.689552	CCAGGG	0.06866	0.0661
cg2591200	AFAP1	NF-AT2 [	474	483	3.689016	AAGAAT	0.03433	0.03138
cg0261454	AFAP1	NF-AT2 [	538	547	3.689016	AAGAAT	0.03433	0.03138
cg2639478	AFAP1	NF-AT2 [	504	513	3.689016	AAGAAT	0.03433	0.03138
cg0675819	AFAP1	c-Ets-1 [T	188	194	3.590463	GAGGAA	0.61035	0.61936
cg0161265	AFAP1	c-Ets-1 [T	1079	1085	3.590463	GAGGAA	0.61035	0.61936
cg2591200	AFAP1	p53 [T006	698	704	3.586914	GGGCGA	0.73242	0.80362
cg2591200	AFAP1	p53 [T006	1777	1783	3.586914	CTCGCC	0.73242	0.80362
cg0261454	AFAP1	p53 [T006	762	768	3.586914	GGGCGA	0.73242	0.80362
cg0261454	AFAP1	p53 [T006	1841	1847	3.586914	CTCGCC	0.73242	0.80362
cg2639478	AFAP1	p53 [T006	728	734	3.586914	GGGCGA	0.73242	0.80362
cg2639478	AFAP1	p53 [T006	1807	1813	3.586914	CTCGCC	0.73242	0.80362
cg0161265	AFAP1	c-Fos [T00	1365	1374	3.579011	GAGTCA	0.05341	0.05266
cg0675819	AFAP1	RXR-alpha	950	956	3.574782	CCGACC	1.09863	1.1653
cg0161265	AFAP1	C/EBPalph	525	531	3.555778	ACCAAT	0.24414	0.23261
cg0675819	AFAP1	E2F-1 [T0	1229	1236	3.55167	GCGGGA	0.15259	0.16507
cg2591200	AFAP1	c-Ets-2 [T	260	268	3.518824	AAGAAG	0.18311	0.18314
cg0261454	AFAP1	c-Ets-2 [T	324	332	3.518824	AAGAAG	0.18311	0.18314
cg2639478	AFAP1	c-Ets-2 [T	290	298	3.518824	AAGAAG	0.18311	0.18314
cg0161265	AFAP1	c-Ets-2 [T	359	367	3.518824	TGGAAG	0.18311	0.18314
cg0161265	AFAP1	c-Ets-2 [T	1429	1437	3.518824	CAGAAG	0.18311	0.18314
cg2591200	AFAP1	p53 [T006	1274	1280	3.516613	GGGCAG	0.73242	0.80362
cg0261454	AFAP1	p53 [T006	1338	1344	3.516613	GGGCAG	0.73242	0.80362
cg2639478	AFAP1	p53 [T006	1304	1310	3.516613	GGGCAG	0.73242	0.80362
cg0161265	AFAP1	p53 [T006	1933	1939	3.516613	ACTGCC	0.73242	0.80362
cg2591200	AFAP1	HNF-3alph	142	149	3.500065	AATTTC	0.27466	0.23175
cg2591200	AFAP1	HNF-3alph	1100	1107	3.500065	AAAAAA	0.27466	0.23175

cg0261454	AFAP1	HNF-3alp	34	41	3.500065	AAAAAA	0.27466	0.23175
cg0261454	AFAP1	HNF-3alp	206	213	3.500065	AATTTT	0.27466	0.23175
cg0261454	AFAP1	HNF-3alp	1164	1171	3.500065	AAAAAA	0.27466	0.23175
cg2639478	AFAP1	HNF-3alp	0	7	3.500065	AAAAAA	0.27466	0.23175
cg2639478	AFAP1	HNF-3alp	172	179	3.500065	AATTTT	0.27466	0.23175
cg2639478	AFAP1	HNF-3alp	1130	1137	3.500065	AAAAAA	0.27466	0.23175
cg0161265	AFAP1	HNF-3alp	498	505	3.500065	ACAAAA	0.27466	0.23175
cg0161265	AFAP1	PPAR-alp	1493	1503	3.498013	TACTGG	0.01431	0.015
cg0161265	AFAP1	NF-Y [T0	763	770	3.490142	CTGCCA	0.48828	0.48427
cg0161265	AFAP1	VDR [T00	8	16	3.462841	CCTGTG	0.21362	0.21283
cg0675819	AFAP1	c-Ets-1 [T	1060	1066	3.462376	CAGGAA	0.61035	0.61936
cg0161265	AFAP1	c-Ets-1 [T	163	169	3.462376	GTTCCT	0.61035	0.61936
cg0161265	AFAP1	c-Ets-1 [T	1122	1128	3.462376	CAGGAA	0.61035	0.61936
cg0161265	AFAP1	MAZ [T00	1833	1845	3.45303	GAAGGG	0.00167	0.00198
cg0161265	AFAP1	HNF-1B [	289	297	3.426751	TAAATA	0.04578	0.04011
cg0675819	AFAP1	PXR-1:RX	1070	1077	3.395883	TGAACC	0.12207	0.11883
cg2591200	AFAP1	RXR-alph	1145	1151	3.392904	TTTACC	1.09863	1.1653
cg2591200	AFAP1	RXR-alph	1992	1998	3.392904	GGGTCC	1.09863	1.1653
cg0261454	AFAP1	RXR-alph	1209	1215	3.392904	TTTACC	1.09863	1.1653
cg2639478	AFAP1	RXR-alph	1175	1181	3.392904	TTTACC	1.09863	1.1653
cg0161265	AFAP1	RXR-alph	364	370	3.392904	GGAACC	1.09863	1.1653
cg0161265	AFAP1	RXR-alph	1124	1130	3.392904	GGAACC	1.09863	1.1653
cg0161265	AFAP1	RXR-alph	1639	1645	3.392904	GGGTAA	1.09863	1.1653
cg0675819	AFAP1	Elk-1 [T00	263	271	3.381796	CTTCCT	0.04578	0.04517
cg2591200	AFAP1	p53 [T006	1746	1752	3.375208	CACGCC	0.73242	0.80362
cg0261454	AFAP1	p53 [T006	1810	1816	3.375208	CACGCC	0.73242	0.80362
cg2639478	AFAP1	p53 [T006	1776	1782	3.375208	CACGCC	0.73242	0.80362
cg0161265	AFAP1	p53 [T006	998	1004	3.375208	CCCGCC	0.73242	0.80362
cg2591200	AFAP1	ATF3 [T0	1490	1497	3.372402	TTATGT	0.09155	0.08824
cg0261454	AFAP1	ATF3 [T0	1554	1561	3.372402	TTATGT	0.09155	0.08824
cg2639478	AFAP1	ATF3 [T0	1520	1527	3.372402	TTATGT	0.09155	0.08824
cg0675819	AFAP1	ATF3 [T0	147	154	3.372402	TGACGC	0.09155	0.08824
cg2591200	AFAP1	T3R-beta1	1387	1395	3.370634	TCACCA	0.27466	0.27326
cg0261454	AFAP1	T3R-beta1	1451	1459	3.370634	TCACCA	0.27466	0.27326
cg2639478	AFAP1	T3R-beta1	1417	1425	3.370634	TCACCA	0.27466	0.27326
cg0161265	AFAP1	T3R-beta1	643	651	3.370634	TCACCT	0.27466	0.27326
cg2591200	AFAP1	GR-beta [	11	15	3.361531	AGATT	3.90625	3.51525
cg2591200	AFAP1	GR-beta [	170	174	3.361531	AATCT	3.90625	3.51525
cg2591200	AFAP1	GR-beta [	585	589	3.361531	AATCT	3.90625	3.51525
cg2591200	AFAP1	GR-beta [	846	850	3.361531	AATCT	3.90625	3.51525
cg2591200	AFAP1	GR-beta [	961	965	3.361531	AGATT	3.90625	3.51525
cg2591200	AFAP1	GR-beta [	1093	1097	3.361531	AATCT	3.90625	3.51525
cg2591200	AFAP1	GR-beta [	1516	1520	3.361531	AATCT	3.90625	3.51525
cg2591200	AFAP1	GR-beta [	1567	1571	3.361531	AATAT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	38	42	3.361531	AATAT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	45	49	3.361531	AATAT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	75	79	3.361531	AGATT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	234	238	3.361531	AATCT	3.90625	3.51525

cg0261454	AFAP1	GR-beta [T	649	653	3.361531	AATCT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [T	910	914	3.361531	AATCT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [T	1025	1029	3.361531	AGATT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [T	1157	1161	3.361531	AATCT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [T	1580	1584	3.361531	AATCT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [T	1631	1635	3.361531	AATAT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	4	8	3.361531	AATAT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	11	15	3.361531	AATAT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	41	45	3.361531	AGATT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	200	204	3.361531	AATCT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	615	619	3.361531	AATCT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	876	880	3.361531	AATCT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	991	995	3.361531	AGATT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	1123	1127	3.361531	AATCT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	1546	1550	3.361531	AATCT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [T	1597	1601	3.361531	AATAT	3.90625	3.51525
cg0675819	AFAP1	GR-beta [T	352	356	3.361531	ATATT	3.90625	3.51525
cg0675819	AFAP1	GR-beta [T	918	922	3.361531	AGATT	3.90625	3.51525
cg0675819	AFAP1	GR-beta [T	1204	1208	3.361531	AATCT	3.90625	3.51525
cg0675819	AFAP1	GR-beta [T	1650	1654	3.361531	ATATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	240	244	3.361531	AATAT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	267	271	3.361531	ATATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	502	506	3.361531	AATAT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	825	829	3.361531	AATCT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1513	1517	3.361531	AATCT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1618	1622	3.361531	AATCT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1710	1714	3.361531	AATAT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1711	1715	3.361531	ATATT	3.90625	3.51525
cg0675819	AFAP1	c-Ets-1 [T	1088	1094	3.359159	ACGGAA	0.61035	0.61936
cg0675819	AFAP1	IRF-1 [T0	957	965	3.352297	TTTCCCC	0.06866	0.0661
cg0161265	AFAP1	AR [T000	1410	1418	3.347826	GGACAT	0.06866	0.06629
cg0675819	AFAP1	c-Ets-2 [T	264	272	3.2883	TTCCTCA	0.18311	0.18314
cg0161265	AFAP1	c-Ets-2 [T	582	590	3.2883	GGTGAG	0.18311	0.18314
cg2591200	AFAP1	E2F-1 [T0	1431	1438	3.288084	TGTTCCC	0.15259	0.16507
cg0261454	AFAP1	E2F-1 [T0	1495	1502	3.288084	TGTTCCC	0.15259	0.16507
cg2639478	AFAP1	E2F-1 [T0	1461	1468	3.288084	TGTTCCC	0.15259	0.16507
cg2591200	AFAP1	Elk-1 [T00	1827	1835	3.247448	CTTCCTC	0.07629	0.07518
cg0261454	AFAP1	Elk-1 [T00	1891	1899	3.247448	CTTCCTC	0.07629	0.07518
cg2639478	AFAP1	Elk-1 [T00	1857	1865	3.247448	CTTCCTC	0.07629	0.07518
cg0161265	AFAP1	Elk-1 [T00	583	591	3.247448	GTGAGG	0.07629	0.07518
cg0675819	AFAP1	c-Jun [T00	258	264	3.244843	TGACTC	0.24414	0.2435
cg0675819	AFAP1	c-Jun [T00	595	601	3.244843	AGAGTC	0.24414	0.2435
cg0675819	AFAP1	c-Jun [T00	1030	1036	3.244843	AGAGTC	0.24414	0.2435
cg0161265	AFAP1	RAR-beta	1627	1636	3.244529	TTTAAA	0.12207	0.12558
cg2591200	AFAP1	c-Ets-1 [T	941	947	3.231072	CTTCCGC	0.24414	0.26272
cg0261454	AFAP1	c-Ets-1 [T	1005	1011	3.231072	CTTCCGC	0.24414	0.26272
cg2639478	AFAP1	c-Ets-1 [T	971	977	3.231072	CTTCCGC	0.24414	0.26272
cg2591200	AFAP1	AP-2alpha	419	424	3.229049	GCCTCT	0.48828	0.5124

cg0261454	AFAP1	AP-2alpha	483	488	3.229049	GCCTCT	0.48828	0.5124
cg2639478	AFAP1	AP-2alpha	449	454	3.229049	GCCTCT	0.48828	0.5124
cg0675819	AFAP1	AP-2alpha	1211	1216	3.229049	GCCTCT	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	90	95	3.229049	GCCTCT	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	146	151	3.229049	AGAGGC	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	1745	1750	3.229049	AGAGGC	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	1776	1781	3.229049	AGAGGC	0.48828	0.5124
cg0161265	AFAP1	AP-2alpha	1865	1870	3.229049	GCCTCT	0.48828	0.5124
cg0675819	AFAP1	RAR-beta	935	944	3.226064	GGCAAA	0.12207	0.12558
cg0675819	AFAP1	RAR-beta	1148	1157	3.226064	CCTAAA	0.12207	0.12558
cg2591200	AFAP1	RXR-alph	1018	1024	3.170788	GGGTTTT	0.24414	0.24551
cg0261454	AFAP1	RXR-alph	1082	1088	3.170788	GGGTTTT	0.24414	0.24551
cg2639478	AFAP1	RXR-alph	1048	1054	3.170788	GGGTTTT	0.24414	0.24551
cg0161265	AFAP1	RXR-alph	487	493	3.170788	GGGTTTT	0.24414	0.24551
cg2591200	AFAP1	TCF-4E [T	898	904	3.151193	CTTTGAT	0.24414	0.23169
cg0261454	AFAP1	TCF-4E [T	962	968	3.151193	CTTTGAT	0.24414	0.23169
cg2639478	AFAP1	TCF-4E [T	928	934	3.151193	CTTTGAT	0.24414	0.23169
cg0161265	AFAP1	TCF-4E [T	321	327	3.151193	CTTTGAT	0.24414	0.23169
cg0161265	AFAP1	TCF-4E [T	1152	1158	3.151193	CTTTGC	0.24414	0.23169
cg0675819	AFAP1	Elk-1 [T00	440	448	3.121991	CTTCCTT	0.07629	0.07518
cg2591200	AFAP1	TCF-4 [T0	897	906	3.085213	TCTTTG	0.03433	0.03101
cg0261454	AFAP1	TCF-4 [T0	961	970	3.085213	TCTTTG	0.03433	0.03101
cg2639478	AFAP1	TCF-4 [T0	927	936	3.085213	TCTTTG	0.03433	0.03101
cg2591200	AFAP1	Pax-5 [T0	698	704	3.075094	GGGCGA	0.12207	0.13819
cg2591200	AFAP1	Pax-5 [T0	1777	1783	3.075094	CTCGCC	0.12207	0.13819
cg0261454	AFAP1	Pax-5 [T0	762	768	3.075094	GGGCGA	0.12207	0.13819
cg0261454	AFAP1	Pax-5 [T0	1841	1847	3.075094	CTCGCC	0.12207	0.13819
cg2639478	AFAP1	Pax-5 [T0	728	734	3.075094	GGGCGA	0.12207	0.13819
cg2639478	AFAP1	Pax-5 [T0	1807	1813	3.075094	CTCGCC	0.12207	0.13819
cg0675819	AFAP1	p53 [T006	830	836	3.028543	TGTGCC	0.48828	0.53227
cg2591200	AFAP1	c-Fos [T00	532	541	3.022518	CCACTG	0.06104	0.06233
cg2591200	AFAP1	c-Fos [T00	1376	1385	3.022518	ACACTG	0.06104	0.06233
cg0261454	AFAP1	c-Fos [T00	596	605	3.022518	CCACTG	0.06104	0.06233
cg0261454	AFAP1	c-Fos [T00	1440	1449	3.022518	ACACTG	0.06104	0.06233
cg2639478	AFAP1	c-Fos [T00	562	571	3.022518	CCACTG	0.06104	0.06233
cg2639478	AFAP1	c-Fos [T00	1406	1415	3.022518	ACACTG	0.06104	0.06233
cg2591200	AFAP1	C/EBPalph	843	849	3.014837	AGCAAT	0.48828	0.47526
cg0261454	AFAP1	C/EBPalph	907	913	3.014837	AGCAAT	0.48828	0.47526
cg2639478	AFAP1	C/EBPalph	873	879	3.014837	AGCAAT	0.48828	0.47526
cg0675819	AFAP1	Elk-1 [T00	243	251	2.987643	GAAAGG	0.07629	0.07518
cg0675819	AFAP1	C/EBPalph	415	421	2.981957	CATTGT	0.48828	0.47526
cg0675819	AFAP1	c-Ets-2 [T	441	449	2.945838	TTCCTTT	0.06104	0.05567
cg2591200	AFAP1	STAT4 [T	12	17	2.941176	GATTCC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	155	160	2.941176	GATTCC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	347	352	2.941176	GGAATA	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	394	399	2.941176	TGTTCC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	466	471	2.941176	CTTTCC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	483	488	2.941176	CTTTCC	2.92969	2.92382

cg2591200	AFAP1	STAT4 [T	527	532	2.941176	GGAATC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	867	872	2.941176	GATTCC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	1085	1090	2.941176	GGAATC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	1431	1436	2.941176	TGTTCC	2.92969	2.92382
cg2591200	AFAP1	STAT4 [T	1826	1831	2.941176	ACTTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	76	81	2.941176	GATTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	219	224	2.941176	GATTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	411	416	2.941176	GGAATA	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	458	463	2.941176	TGTTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	530	535	2.941176	CTTTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	547	552	2.941176	CTTTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	591	596	2.941176	GGAATC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	931	936	2.941176	GATTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	1149	1154	2.941176	GGAATC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	1495	1500	2.941176	TGTTCC	2.92969	2.92382
cg0261454	AFAP1	STAT4 [T	1890	1895	2.941176	ACTTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	42	47	2.941176	GATTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	185	190	2.941176	GATTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	377	382	2.941176	GGAATA	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	424	429	2.941176	TGTTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	496	501	2.941176	CTTTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	513	518	2.941176	CTTTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	557	562	2.941176	GGAATC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	897	902	2.941176	GATTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	1115	1120	2.941176	GGAATC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	1461	1466	2.941176	TGTTCC	2.92969	2.92382
cg2639478	AFAP1	STAT4 [T	1856	1861	2.941176	ACTTCC	2.92969	2.92382
cg0675819	AFAP1	STAT4 [T	190	195	2.941176	GGAACA	2.92969	2.92382
cg0675819	AFAP1	STAT4 [T	242	247	2.941176	GGAAAG	2.92969	2.92382
cg0675819	AFAP1	STAT4 [T	455	460	2.941176	GGAAGT	2.92969	2.92382
cg0675819	AFAP1	STAT4 [T	956	961	2.941176	CTTTCC	2.92969	2.92382
cg0675819	AFAP1	STAT4 [T	1062	1067	2.941176	GGAACA	2.92969	2.92382
cg0675819	AFAP1	STAT4 [T	1232	1237	2.941176	GGAAGT	2.92969	2.92382
cg0675819	AFAP1	STAT4 [T	1504	1509	2.941176	ACTTCC	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	162	167	2.941176	TGTTCC	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	187	192	2.941176	GGAATA	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	364	369	2.941176	GGAACC	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	909	914	2.941176	GGAAGT	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	930	935	2.941176	GGAAGT	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	1098	1103	2.941176	GGAAAG	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	1124	1129	2.941176	GGAACC	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	1234	1239	2.941176	CTTTCC	2.92969	2.92382
cg0161265	AFAP1	STAT4 [T	1741	1746	2.941176	GGAAAG	2.92969	2.92382
cg0675819	AFAP1	NF-kappa	231	241	2.939121	GGGGAG	0.01669	0.01859
cg2591200	AFAP1	TCF-4 [T0	21	30	2.859093	AATTCA	0.03433	0.03101
cg0261454	AFAP1	TCF-4 [T0	85	94	2.859093	AATTCA	0.03433	0.03101
cg2639478	AFAP1	TCF-4 [T0	51	60	2.859093	AATTCA	0.03433	0.03101
cg2591200	AFAP1	p53 [T006	779	785	2.813291	GCTGCC	0.48828	0.53227

cg2591200	AFAP1	p53 [T006	1599	1605	2.813291	GGGCAT	0.48828	0.53227
cg0261454	AFAP1	p53 [T006	843	849	2.813291	GCTGCC	0.48828	0.53227
cg0261454	AFAP1	p53 [T006	1663	1669	2.813291	GGGCAT	0.48828	0.53227
cg2639478	AFAP1	p53 [T006	809	815	2.813291	GCTGCC	0.48828	0.53227
cg2639478	AFAP1	p53 [T006	1629	1635	2.813291	GGGCAT	0.48828	0.53227
cg0161265	AFAP1	p53 [T006	660	666	2.813291	GCTGCC	0.48828	0.53227
cg2591200	AFAP1	NF-1 [T00	455	462	2.813149	TTGGCC	0.24414	0.2566
cg2591200	AFAP1	NF-1 [T00	918	925	2.813149	TTGGTC	0.24414	0.2566
cg0261454	AFAP1	NF-1 [T00	519	526	2.813149	TTGGCC	0.24414	0.2566
cg0261454	AFAP1	NF-1 [T00	982	989	2.813149	TTGGTC	0.24414	0.2566
cg2639478	AFAP1	NF-1 [T00	485	492	2.813149	TTGGCC	0.24414	0.2566
cg2639478	AFAP1	NF-1 [T00	948	955	2.813149	TTGGTC	0.24414	0.2566
cg2591200	AFAP1	PR B [T00	1258	1264	2.80933	AACAAT	0.73242	0.66711
cg2591200	AFAP1	PR A [T01	1258	1264	2.80933	AACAAT	0.73242	0.66711
cg0261454	AFAP1	PR B [T00	28	34	2.80933	AACATT	0.73242	0.66711
cg0261454	AFAP1	PR B [T00	1322	1328	2.80933	AACAAT	0.73242	0.66711
cg0261454	AFAP1	PR A [T01	28	34	2.80933	AACATT	0.73242	0.66711
cg0261454	AFAP1	PR A [T01	1322	1328	2.80933	AACAAT	0.73242	0.66711
cg2639478	AFAP1	PR B [T00	1288	1294	2.80933	AACAAT	0.73242	0.66711
cg2639478	AFAP1	PR A [T01	1288	1294	2.80933	AACAAT	0.73242	0.66711
cg0675819	AFAP1	PR B [T00	1829	1835	2.80933	CAATGT	0.73242	0.66711
cg0675819	AFAP1	PR A [T01	1829	1835	2.80933	CAATGT	0.73242	0.66711
cg2591200	AFAP1	TBP [T007	1321	1330	2.807313	TTTATA	0.12207	0.10444
cg0261454	AFAP1	TBP [T007	1385	1394	2.807313	TTTATA	0.12207	0.10444
cg2639478	AFAP1	TBP [T007	1351	1360	2.807313	TTTATA	0.12207	0.10444
cg0161265	AFAP1	TBP [T007	853	862	2.807313	TTTATA	0.12207	0.10444
cg0675819	AFAP1	RXR-alph	1477	1483	2.726556	CCAACC	0.85449	0.89683
cg0161265	AFAP1	c-Ets-2 [T	1076	1084	2.715313	CGGGAG	0.07629	0.07844
cg0161265	AFAP1	c-Ets-2 [T	1827	1835	2.715313	CTGGAG	0.07629	0.07844
cg2591200	AFAP1	c-Jun [T00	1380	1386	2.654872	TGACTC	0.48828	0.48077
cg0261454	AFAP1	c-Jun [T00	1444	1450	2.654872	TGACTC	0.48828	0.48077
cg2639478	AFAP1	c-Jun [T00	1410	1416	2.654872	TGACTC	0.48828	0.48077
cg0161265	AFAP1	c-Jun [T00	1364	1370	2.654872	GGAGTC	0.48828	0.48077
cg2591200	AFAP1	NF-AT1 [	463	471	2.619709	AAGCTT	0.09155	0.08666
cg0261454	AFAP1	NF-AT1 [	527	535	2.619709	AAGCTT	0.09155	0.08666
cg2639478	AFAP1	NF-AT1 [	493	501	2.619709	AAGCTT	0.09155	0.08666
cg0675819	AFAP1	c-Fos [T00	295	304	2.598489	CACCTG	0.03052	0.0312
cg0675819	AFAP1	c-Fos [T00	596	605	2.598489	GAGTCA	0.03052	0.0312
cg2591200	AFAP1	LEF-1 [T0	1860	1867	2.558995	CACCAA	0.09155	0.09076
cg0261454	AFAP1	LEF-1 [T0	1924	1931	2.558995	CACCAA	0.09155	0.09076
cg2639478	AFAP1	LEF-1 [T0	1890	1897	2.558995	CACCAA	0.09155	0.09076
cg0675819	AFAP1	AP-2alpha	161	166	2.550491	TGAGGC	0.48828	0.51216
cg0161265	AFAP1	AP-2alpha	1269	1274	2.550491	GCCTCA	0.48828	0.51216
cg0675819	AFAP1	RXR-alph	30	36	2.544678	GGGTTA	0.85449	0.89683
cg0675819	AFAP1	RXR-alph	1663	1669	2.544678	AGAACC	0.85449	0.89683
cg0161265	AFAP1	RXR-alph	1757	1763	2.544678	TGCACC	0.85449	0.89683
cg0675819	AFAP1	c-Jun [T00	80	86	2.538231	TGACTT	0.48828	0.48077
cg0161265	AFAP1	c-Jun [T00	1539	1545	2.538231	TGACTT	0.48828	0.48077

cg0675819	AFAP1	RAR-beta:	891	902	2.492665	GGGCTC	0.00215	0.00241
cg2591200	AFAP1	C/EBPalph	1286	1292	2.441016	CTCAAT	0.48828	0.47439
cg0261454	AFAP1	C/EBPalph	1350	1356	2.441016	CTCAAT	0.48828	0.47439
cg2639478	AFAP1	C/EBPalph	1316	1322	2.441016	CTCAAT	0.48828	0.47439
cg0161265	AFAP1	C/EBPalph	42	48	2.441016	CATTGC	0.48828	0.47439
cg2591200	AFAP1	IRF-1 [T0	1222	1230	2.418514	TAAGGG	0.02289	0.02196
cg0261454	AFAP1	IRF-1 [T0	1286	1294	2.418514	TAAGGG	0.02289	0.02196
cg2639478	AFAP1	IRF-1 [T0	1252	1260	2.418514	TAAGGG	0.02289	0.02196
cg0161265	AFAP1	HNF-1C [	288	296	2.372238	ATAAAT	0.04578	0.04064
cg2591200	AFAP1	C/EBPalph	18	24	2.371703	CACAAT	0.48828	0.47439
cg0261454	AFAP1	C/EBPalph	82	88	2.371703	CACAAT	0.48828	0.47439
cg2639478	AFAP1	C/EBPalph	48	54	2.371703	CACAAT	0.48828	0.47439
cg2591200	AFAP1	c-Jun [T00	904	910	2.345465	TGACGC	0.48828	0.48077
cg2591200	AFAP1	c-Jun [T00	1663	1669	2.345465	TGACAC	0.48828	0.48077
cg0261454	AFAP1	c-Jun [T00	968	974	2.345465	TGACGC	0.48828	0.48077
cg0261454	AFAP1	c-Jun [T00	1727	1733	2.345465	TGACAC	0.48828	0.48077
cg2639478	AFAP1	c-Jun [T00	934	940	2.345465	TGACGC	0.48828	0.48077
cg2639478	AFAP1	c-Jun [T00	1693	1699	2.345465	TGACAC	0.48828	0.48077
cg0675819	AFAP1	c-Jun [T00	147	153	2.345465	TGACGC	0.48828	0.48077
cg0675819	AFAP1	Elk-1 [T00	1100	1108	2.299314	CAGAGG	0.09155	0.09306
cg0675819	AFAP1	Elk-1 [T00	1156	1164	2.299314	CTTCCTC	0.09155	0.09306
cg0161265	AFAP1	Elk-1 [T00	1392	1400	2.299314	CTTCCTC	0.09155	0.09306
cg2591200	AFAP1	T3R-beta1	1859	1867	2.221365	TCACCA	0.15259	0.15303
cg0261454	AFAP1	T3R-beta1	1923	1931	2.221365	TCACCA	0.15259	0.15303
cg2639478	AFAP1	T3R-beta1	1889	1897	2.221365	TCACCA	0.15259	0.15303
cg2591200	AFAP1	c-Ets-2 [T	522	530	2.217136	TTTGAG	0.16785	0.16456
cg0261454	AFAP1	c-Ets-2 [T	586	594	2.217136	TTTGAG	0.16785	0.16456
cg2639478	AFAP1	c-Ets-2 [T	552	560	2.217136	TTTGAG	0.16785	0.16456
cg0675819	AFAP1	c-Ets-2 [T	185	193	2.217136	TCTGAG	0.16785	0.16456
cg0161265	AFAP1	NF-Y [T0	523	530	2.194008	GCACCA	0.21362	0.20748
cg2591200	AFAP1	GATA-1 [	814	819	2.176375	TGGATA	3.90625	3.79558
cg0261454	AFAP1	GATA-1 [	47	52	2.176375	TATCCT	3.90625	3.79558
cg0261454	AFAP1	GATA-1 [	878	883	2.176375	TGGATA	3.90625	3.79558
cg2639478	AFAP1	GATA-1 [	13	18	2.176375	TATCCT	3.90625	3.79558
cg2639478	AFAP1	GATA-1 [	844	849	2.176375	TGGATA	3.90625	3.79558
cg0675819	AFAP1	GATA-1 [	1194	1199	2.176375	TATCCT	3.90625	3.79558
cg2591200	AFAP1	Elk-1 [T00	1762	1770	2.164966	CTTCCTC	0.05341	0.05461
cg0261454	AFAP1	Elk-1 [T00	1826	1834	2.164966	CTTCCTC	0.05341	0.05461
cg2639478	AFAP1	Elk-1 [T00	1792	1800	2.164966	CTTCCTC	0.05341	0.05461
cg2591200	AFAP1	RAR-beta	1818	1827	2.16302	GGGGTT	0.07629	0.07711
cg0261454	AFAP1	RAR-beta	1882	1891	2.16302	GGGGTT	0.07629	0.07711
cg2639478	AFAP1	RAR-beta	1848	1857	2.16302	GGGGTT	0.07629	0.07711
cg0161265	AFAP1	AR [T000	1419	1427	2.159336	GGACAG	0.03815	0.03779
cg2591200	AFAP1	RAR-beta	1842	1851	2.144554	AGCAAA	0.07629	0.07711
cg0261454	AFAP1	RAR-beta	1906	1915	2.144554	AGCAAA	0.07629	0.07711
cg2639478	AFAP1	RAR-beta	1872	1881	2.144554	AGCAAA	0.07629	0.07711
cg0675819	AFAP1	c-Ets-2 [T	1099	1107	2.142327	GCAGAG	0.16785	0.16456
cg0675819	AFAP1	c-Ets-2 [T	1157	1165	2.142327	TTCCTCT	0.16785	0.16456

cg0161265	AFAP1	c-Ets-2 [T0	1393	1401	2.142327	TTCCTCT	0.16785	0.16456
cg0675819	AFAP1	GCF [T003	1431	1439	2.140539	GCGCGG	0.09155	0.10473
cg0675819	AFAP1	AP-2alpha	862	867	2.098119	CGAGGC	0.97656	1.07805
cg0675819	AFAP1	AP-2alpha	1319	1324	2.098119	GCCTCG	0.97656	1.07805
cg2591200	AFAP1	HIF-1 [T01	1161	1169	2.008527	AGAGCA	0.1297	0.13373
cg0261454	AFAP1	HIF-1 [T01	1225	1233	2.008527	AGAGCA	0.1297	0.13373
cg2639478	AFAP1	HIF-1 [T01	1191	1199	2.008527	AGAGCA	0.1297	0.13373
cg0675819	AFAP1	LEF-1 [T0	1657	1664	2.004405	AAACAA	0.18311	0.17215
cg0675819	AFAP1	p53 [T006	934	940	1.970013	GGGCAA	0.36621	0.38097
cg0161265	AFAP1	GATA-1 [	350	355	1.896347	TATCCG	3.90625	3.79558
cg2591200	AFAP1	PR B [T00	1908	1914	1.892895	AAGTGT	0.12207	0.1127
cg2591200	AFAP1	PR A [T01	1908	1914	1.892895	AAGTGT	0.12207	0.1127
cg0261454	AFAP1	PR B [T00	1972	1978	1.892895	AAGTGT	0.12207	0.1127
cg0261454	AFAP1	PR A [T01	1972	1978	1.892895	AAGTGT	0.12207	0.1127
cg2639478	AFAP1	PR B [T00	1938	1944	1.892895	AAGTGT	0.12207	0.1127
cg2639478	AFAP1	PR A [T01	1938	1944	1.892895	AAGTGT	0.12207	0.1127
cg0675819	AFAP1	RXR-alpha	985	991	1.87833	TCAACC	0.12207	0.12517
cg2591200	AFAP1	AP-2alpha	989	994	1.871933	GGAGGC	0.97656	1.07805
cg2591200	AFAP1	AP-2alpha	993	998	1.871933	GCCTCC	0.97656	1.07805
cg0261454	AFAP1	AP-2alpha	1053	1058	1.871933	GGAGGC	0.97656	1.07805
cg0261454	AFAP1	AP-2alpha	1057	1062	1.871933	GCCTCC	0.97656	1.07805
cg2639478	AFAP1	AP-2alpha	1019	1024	1.871933	GGAGGC	0.97656	1.07805
cg2639478	AFAP1	AP-2alpha	1023	1028	1.871933	GCCTCC	0.97656	1.07805
cg0675819	AFAP1	AP-2alpha	233	238	1.871933	GGAGGC	0.97656	1.07805
cg0675819	AFAP1	AP-2alpha	587	592	1.871933	GGAGGC	0.97656	1.07805
cg0675819	AFAP1	AP-2alpha	853	858	1.871933	GGAGGC	0.97656	1.07805
cg0675819	AFAP1	AP-2alpha	1250	1255	1.871933	GCCTCC	0.97656	1.07805
cg0675819	AFAP1	AP-2alpha	1511	1516	1.871933	GCCTCC	0.97656	1.07805
cg0675819	AFAP1	AP-2alpha	1640	1645	1.871933	GCCTCC	0.97656	1.07805
cg0161265	AFAP1	AP-2alpha	440	445	1.871933	GCCTCC	0.97656	1.07805
cg0161265	AFAP1	AP-2alpha	570	575	1.871933	GCCTCC	0.97656	1.07805
cg0161265	AFAP1	AP-2alpha	1059	1064	1.871933	GCCTCC	0.97656	1.07805
cg0161265	AFAP1	AP-2alpha	1524	1529	1.871933	GGAGGC	0.97656	1.07805
cg0161265	AFAP1	AP-2alpha	1596	1601	1.871933	GCCTCC	0.97656	1.07805
cg0161265	AFAP1	AP-2alpha	1847	1852	1.871933	GGAGGC	0.97656	1.07805
cg2591200	AFAP1	TBP [T007	1319	1328	1.871542	TGTTTAT	0.18311	0.15671
cg0261454	AFAP1	TBP [T007	1383	1392	1.871542	TGTTTAT	0.18311	0.15671
cg2639478	AFAP1	TBP [T007	1349	1358	1.871542	TGTTTAT	0.18311	0.15671
cg2591200	AFAP1	USF1 [T0	1538	1547	1.858812	TCCCCA	0.03624	0.03891
cg0261454	AFAP1	USF1 [T0	1602	1611	1.858812	TCCCCA	0.03624	0.03891
cg2639478	AFAP1	USF1 [T0	1568	1577	1.858812	TCCCCA	0.03624	0.03891
cg0161265	AFAP1	TCF-4 [T0	320	329	1.850015	ACTTTG	0.04196	0.03736
cg2591200	AFAP1	HIF-1 [T01	1543	1551	1.839875	ACGTGC	0.1297	0.13373
cg0261454	AFAP1	HIF-1 [T01	1607	1615	1.839875	ACGTGC	0.1297	0.13373
cg2639478	AFAP1	HIF-1 [T01	1573	1581	1.839875	ACGTGC	0.1297	0.13373
cg2591200	AFAP1	TFII-I [T0	1587	1592	1.824994	CTCTCC	0.48828	0.51201
cg0261454	AFAP1	TFII-I [T0	1651	1656	1.824994	CTCTCC	0.48828	0.51201
cg2639478	AFAP1	TFII-I [T0	1617	1622	1.824994	CTCTCC	0.48828	0.51201

cg0675819	AFAP1	TFII-I [T0	649	654	1.824994	CTCTCC	0.48828	0.51201
cg0675819	AFAP1	TFII-I [T0	1698	1703	1.824994	CTCTCC	0.48828	0.51201
cg0161265	AFAP1	FOXP3 [T	494	499	1.824994	TACAAC	0.48828	0.46414
cg0161265	AFAP1	FOXP3 [T	1201	1206	1.824994	GTTGTA	0.48828	0.46414
cg0161265	AFAP1	TFII-I [T0	1774	1779	1.824994	GGAGAG	0.48828	0.51201
cg2591200	AFAP1	PXR-1:RX	1883	1890	1.759733	TGAACT	0.06104	0.05771
cg0261454	AFAP1	PXR-1:RX	1947	1954	1.759733	TGAACT	0.06104	0.05771
cg2639478	AFAP1	PXR-1:RX	1913	1920	1.759733	TGAACT	0.06104	0.05771
cg0161265	AFAP1	PXR-1:RX	1661	1668	1.759733	TGAACT	0.06104	0.05771
cg0675819	AFAP1	p53 [T006	623	629	1.758307	TCTGCC	0.36621	0.38097
cg0675819	AFAP1	p53 [T006	800	806	1.758307	TCTGCC	0.36621	0.38097
cg2591200	AFAP1	NF-Y [T0	454	461	1.749852	ATTGGC	0.18311	0.17671
cg0261454	AFAP1	NF-Y [T0	518	525	1.749852	ATTGGC	0.18311	0.17671
cg2639478	AFAP1	NF-Y [T0	484	491	1.749852	ATTGGC	0.18311	0.17671
cg0675819	AFAP1	AR [T000	368	376	1.727468	GGACAG	0.09155	0.09239
cg2591200	AFAP1	LEF-1 [T0	898	905	1.703176	CTTTGA	0.09155	0.08414
cg0261454	AFAP1	LEF-1 [T0	962	969	1.703176	CTTTGA	0.09155	0.08414
cg2639478	AFAP1	LEF-1 [T0	928	935	1.703176	CTTTGA	0.09155	0.08414
cg0161265	AFAP1	LEF-1 [T0	321	328	1.703176	CTTTGA	0.09155	0.08414
cg2591200	AFAP1	RXR-alph	1368	1374	1.696452	CTGACC	0.48828	0.52093
cg0261454	AFAP1	RXR-alph	1432	1438	1.696452	CTGACC	0.48828	0.52093
cg2639478	AFAP1	RXR-alph	1398	1404	1.696452	CTGACC	0.48828	0.52093
cg2591200	AFAP1	GR-beta [	21	25	1.680765	AATTC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	116	120	1.680765	AATTC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	215	219	1.680765	AATTC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	318	322	1.680765	AATGC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	452	456	1.680765	GAATT	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	476	480	1.680765	GAATT	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	593	597	1.680765	GCATT	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	858	862	1.680765	AATGC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	1261	1265	1.680765	AATGC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	1312	1316	1.680765	AATTC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	1802	1806	1.680765	AATGC	3.90625	3.70067
cg2591200	AFAP1	GR-beta [	1903	1907	1.680765	AATTC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	85	89	1.680765	AATTC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	180	184	1.680765	AATTC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	279	283	1.680765	AATTC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	382	386	1.680765	AATGC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	516	520	1.680765	GAATT	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	540	544	1.680765	GAATT	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	657	661	1.680765	GCATT	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	922	926	1.680765	AATGC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	1325	1329	1.680765	AATGC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	1376	1380	1.680765	AATTC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	1866	1870	1.680765	AATGC	3.90625	3.70067
cg0261454	AFAP1	GR-beta [	1967	1971	1.680765	AATTC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [	51	55	1.680765	AATTC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [	146	150	1.680765	AATTC	3.90625	3.70067

cg2639478	AFAP1	GR-beta [T	245	249	1.680765	AATTC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	348	352	1.680765	AATGC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	482	486	1.680765	GAATT	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	506	510	1.680765	GAATT	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	623	627	1.680765	GCATT	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	888	892	1.680765	AATGC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	1291	1295	1.680765	AATGC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	1342	1346	1.680765	AATTC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	1832	1836	1.680765	AATGC	3.90625	3.70067
cg2639478	AFAP1	GR-beta [T	1933	1937	1.680765	AATTC	3.90625	3.70067
cg0675819	AFAP1	GR-beta [T	254	258	1.680765	GAATT	3.90625	3.70067
cg0675819	AFAP1	GR-beta [T	687	691	1.680765	GAATT	3.90625	3.70067
cg0675819	AFAP1	GR-beta [T	1528	1532	1.680765	AATGC	3.90625	3.70067
cg0675819	AFAP1	GR-beta [T	1605	1609	1.680765	GCATT	3.90625	3.70067
cg0675819	AFAP1	GR-beta [T	1673	1677	1.680765	AATGC	3.90625	3.70067
cg0675819	AFAP1	GR-beta [T	1924	1928	1.680765	GCATT	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	210	214	1.680765	GAATT	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	211	215	1.680765	AATTC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	310	314	1.680765	AATGC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	474	478	1.680765	GAATT	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	862	866	1.680765	AATTC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	965	969	1.680765	AATGC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1162	1166	1.680765	AATTC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1194	1198	1.680765	AATTC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1581	1585	1.680765	GAATT	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1582	1586	1.680765	AATTC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1698	1702	1.680765	AATTC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1857	1861	1.680765	GAATT	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1858	1862	1.680765	AATTC	3.90625	3.70067
cg0161265	AFAP1	GR-beta [T	1904	1908	1.680765	AATTC	3.90625	3.70067
cg0675819	AFAP1	HNF-1B [	87	95	1.651022	AGTTAA	0.00763	0.00634
cg2591200	AFAP1	c-Ets-2 [T	251	259	1.64415	CAGGAG	0.04578	0.04602
cg2591200	AFAP1	c-Ets-2 [T	286	294	1.64415	GAGGAG	0.04578	0.04602
cg0261454	AFAP1	c-Ets-2 [T	315	323	1.64415	CAGGAG	0.04578	0.04602
cg0261454	AFAP1	c-Ets-2 [T	350	358	1.64415	GAGGAG	0.04578	0.04602
cg2639478	AFAP1	c-Ets-2 [T	281	289	1.64415	CAGGAG	0.04578	0.04602
cg2639478	AFAP1	c-Ets-2 [T	316	324	1.64415	GAGGAG	0.04578	0.04602
cg0675819	AFAP1	c-Ets-2 [T	1450	1458	1.64415	TTGGAG	0.04578	0.04602
cg2591200	AFAP1	c-Ets-1 [T	479	485	1.641124	TTTCCTT	0.36621	0.35197
cg0261454	AFAP1	c-Ets-1 [T	543	549	1.641124	TTTCCTT	0.36621	0.35197
cg2639478	AFAP1	c-Ets-1 [T	509	515	1.641124	TTTCCTT	0.36621	0.35197
cg0161265	AFAP1	c-Ets-1 [T	1674	1680	1.641124	TTTCCTT	0.36621	0.35197
cg2591200	AFAP1	C/EBPbeta	162	165	1.639871	CCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	226	229	1.639871	CCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	455	458	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	461	464	1.639871	CCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	660	663	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	871	874	1.639871	CCAA	15.625	15.23827

cg2591200	AFAP1	C/EBPbeta	891	894	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	918	921	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	966	969	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1187	1190	1.639871	CCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1272	1275	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1506	1509	1.639871	CCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1576	1579	1.639871	CCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1607	1610	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1702	1705	1.639871	CCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1816	1819	1.639871	TTGG	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1862	1865	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	226	229	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	290	293	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	519	522	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	525	528	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	724	727	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	935	938	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	955	958	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	982	985	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1030	1033	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1251	1254	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1336	1339	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1570	1573	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1640	1643	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1671	1674	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1766	1769	1.639871	CCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1880	1883	1.639871	TTGG	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1926	1929	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	192	195	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	256	259	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	485	488	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	491	494	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	690	693	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	901	904	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	921	924	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	948	951	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	996	999	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1217	1220	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1302	1305	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1536	1539	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1606	1609	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1637	1640	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1732	1735	1.639871	CCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1846	1849	1.639871	TTGG	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1892	1895	1.639871	CCAA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	178	181	1.639871	CCAA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	381	384	1.639871	TTGG	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	764	767	1.639871	TTGG	15.625	15.23827

cg0675819 AFAP1	C/EBPbeta	1202	1205	1.639871	CCAA	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1277	1280	1.639871	CCAA	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1450	1453	1.639871	TTGG	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1477	1480	1.639871	CCAA	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1500	1503	1.639871	TTGG	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1577	1580	1.639871	CCAA	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1703	1706	1.639871	CCAA	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1843	1846	1.639871	CCAA	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1848	1851	1.639871	CCAA	15.625	15.23827
cg0675819 AFAP1	C/EBPbeta	1956	1959	1.639871	TTGG	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	179	182	1.639871	TTGG	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	526	529	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	542	545	1.639871	TTGG	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	728	731	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	750	753	1.639871	TTGG	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	766	769	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	780	783	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1129	1132	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1192	1195	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1251	1254	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1360	1363	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1446	1449	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1474	1477	1.639871	TTGG	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1608	1611	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1695	1698	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1704	1707	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1798	1801	1.639871	CCAA	15.625	15.23827
cg0161265 AFAP1	C/EBPbeta	1945	1948	1.639871	CCAA	15.625	15.23827
cg2591200 AFAP1	PXR-1:RX	206	213	1.63615	AAAGTT	0.06104	0.05484
cg0261454 AFAP1	PXR-1:RX	270	277	1.63615	AAAGTT	0.06104	0.05484
cg2639478 AFAP1	PXR-1:RX	236	243	1.63615	AAAGTT	0.06104	0.05484
cg2591200 AFAP1	XBP-1 [T	1290	1295	1.583727	ATGACA	0.97656	0.94995
cg0261454 AFAP1	XBP-1 [T	1354	1359	1.583727	ATGACA	0.97656	0.94995
cg2639478 AFAP1	XBP-1 [T	1320	1325	1.583727	ATGACA	0.97656	0.94995
cg0161265 AFAP1	XBP-1 [T	195	200	1.583727	ATGACA	0.97656	0.94995
cg2591200 AFAP1	MAZ [T00	269	281	1.581133	GGTGGG	0.00143	0.00166
cg0261454 AFAP1	MAZ [T00	333	345	1.581133	GGTGGG	0.00143	0.00166
cg2639478 AFAP1	MAZ [T00	299	311	1.581133	GGTGGG	0.00143	0.00166
cg0161265 AFAP1	HIF-1 [T0	1084	1092	1.549104	ACGTGC	0.09155	0.09676
cg2591200 AFAP1	TFIID [T0	44	50	1.537547	TACAAA	0.73242	0.65627
cg2591200 AFAP1	TFIID [T0	658	664	1.537547	TTTTGG	0.73242	0.65627
cg2591200 AFAP1	TFIID [T0	851	857	1.537547	TACAAA	0.73242	0.65627
cg2591200 AFAP1	TFIID [T0	1097	1103	1.537547	TGTAAA	0.73242	0.65627
cg2591200 AFAP1	Pax-5 [T0	1450	1456	1.537547	CTTGCC	0.73242	0.83087
cg2591200 AFAP1	Pax-5 [T0	1467	1473	1.537547	CTTGCC	0.73242	0.83087
cg2591200 AFAP1	Pax-5 [T0	1746	1752	1.537547	CACGCC	0.73242	0.83087
cg0261454 AFAP1	TFIID [T0	108	114	1.537547	TACAAA	0.73242	0.65627
cg0261454 AFAP1	TFIID [T0	722	728	1.537547	TTTTGG	0.73242	0.65627

cg0261454	AFAP1	TFIID [T0	915	921	1.537547	TACAAA	0.73242	0.65627
cg0261454	AFAP1	TFIID [T0	1161	1167	1.537547	TGTAAA	0.73242	0.65627
cg0261454	AFAP1	Pax-5 [T0	1514	1520	1.537547	CTTGCC	0.73242	0.83087
cg0261454	AFAP1	Pax-5 [T0	1531	1537	1.537547	CTTGCC	0.73242	0.83087
cg0261454	AFAP1	Pax-5 [T0	1810	1816	1.537547	CACGCC	0.73242	0.83087
cg2639478	AFAP1	TFIID [T0	74	80	1.537547	TACAAA	0.73242	0.65627
cg2639478	AFAP1	TFIID [T0	688	694	1.537547	TTTTGG	0.73242	0.65627
cg2639478	AFAP1	TFIID [T0	881	887	1.537547	TACAAA	0.73242	0.65627
cg2639478	AFAP1	TFIID [T0	1127	1133	1.537547	TGTAAA	0.73242	0.65627
cg2639478	AFAP1	Pax-5 [T0	1480	1486	1.537547	CTTGCC	0.73242	0.83087
cg2639478	AFAP1	Pax-5 [T0	1497	1503	1.537547	CTTGCC	0.73242	0.83087
cg2639478	AFAP1	Pax-5 [T0	1776	1782	1.537547	CACGCC	0.73242	0.83087
cg0675819	AFAP1	TFIID [T0	392	398	1.537547	TTTTGA	0.73242	0.65627
cg0675819	AFAP1	Pax-5 [T0	484	490	1.537547	GGGCAA	0.73242	0.83087
cg0675819	AFAP1	Pax-5 [T0	766	772	1.537547	GGGCCA	0.73242	0.83087
cg0675819	AFAP1	Pax-5 [T0	1131	1137	1.537547	CGCGCC	0.73242	0.83087
cg0675819	AFAP1	Pax-5 [T0	1328	1334	1.537547	CTTGCC	0.73242	0.83087
cg0161265	AFAP1	TFIID [T0	397	403	1.537547	TTTTGA	0.73242	0.65627
cg0161265	AFAP1	TFIID [T0	491	497	1.537547	TTTTAC	0.73242	0.65627
cg0161265	AFAP1	TFIID [T0	1203	1209	1.537547	TGTAAA	0.73242	0.65627
cg0161265	AFAP1	TFIID [T0	1403	1409	1.537547	TGAAAA	0.73242	0.65627
cg0161265	AFAP1	Pax-5 [T0	2	8	1.537547	CTAGCC	0.73242	0.83087
cg0161265	AFAP1	Pax-5 [T0	94	100	1.537547	CTTGCC	0.73242	0.83087
cg0161265	AFAP1	Pax-5 [T0	544	550	1.537547	GGGCAA	0.73242	0.83087
cg0161265	AFAP1	Pax-5 [T0	676	682	1.537547	GGGCCA	0.73242	0.83087
cg0161265	AFAP1	Pax-5 [T0	998	1004	1.537547	CCCGCC	0.73242	0.83087
cg0161265	AFAP1	Pax-5 [T0	1939	1945	1.537547	CTGGCC	0.73242	0.83087
cg0161265	AFAP1	Sp1 [T007	996	1005	1.523913	TCCCCG	0.03242	0.03924
cg2591200	AFAP1	c-Ets-1 [T	254	260	1.513038	GAGGAA	0.36621	0.35197
cg0261454	AFAP1	c-Ets-1 [T	318	324	1.513038	GAGGAA	0.36621	0.35197
cg2639478	AFAP1	c-Ets-1 [T	284	290	1.513038	GAGGAA	0.36621	0.35197
cg2591200	AFAP1	RXR-alph	1844	1850	1.474336	CAAACC	0.48828	0.52093
cg0261454	AFAP1	RXR-alph	1908	1914	1.474336	CAAACC	0.48828	0.52093
cg2639478	AFAP1	RXR-alph	1874	1880	1.474336	CAAACC	0.48828	0.52093
cg0675819	AFAP1	RXR-alph	937	943	1.474336	CAAACC	0.48828	0.52093
cg0161265	AFAP1	RXR-alph	424	430	1.474336	GGGTTT	0.48828	0.52093
cg2591200	AFAP1	STAT4 [T	256	261	1.470588	GGAAAA	1.95312	1.90161
cg2591200	AFAP1	STAT4 [T	451	456	1.470588	GGAATT	1.95312	1.90161
cg2591200	AFAP1	STAT4 [T	669	674	1.470588	GGAAAC	1.95312	1.90161
cg2591200	AFAP1	STAT4 [T	1226	1231	1.470588	GGAAAA	1.95312	1.90161
cg2591200	AFAP1	STAT4 [T	1281	1286	1.470588	GGAAAC	1.95312	1.90161
cg2591200	AFAP1	STAT4 [T	1609	1614	1.470588	GGAACT	1.95312	1.90161
cg2591200	AFAP1	STAT4 [T	1697	1702	1.470588	GTTTCC	1.95312	1.90161
cg0261454	AFAP1	STAT4 [T	54	59	1.470588	GGAACT	1.95312	1.90161
cg0261454	AFAP1	STAT4 [T	320	325	1.470588	GGAAAA	1.95312	1.90161
cg0261454	AFAP1	STAT4 [T	515	520	1.470588	GGAATT	1.95312	1.90161
cg0261454	AFAP1	STAT4 [T	733	738	1.470588	GGAAAC	1.95312	1.90161
cg0261454	AFAP1	STAT4 [T	1290	1295	1.470588	GGAAAA	1.95312	1.90161

cg0261454	AFAP1	STAT4 [T	1345	1350	1.470588	GGAAAC	1.95312	1.90161
cg0261454	AFAP1	STAT4 [T	1673	1678	1.470588	GGAACT	1.95312	1.90161
cg0261454	AFAP1	STAT4 [T	1761	1766	1.470588	GTTTCC	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	20	25	1.470588	GGAACT	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	286	291	1.470588	GGAAAA	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	481	486	1.470588	GGAATT	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	699	704	1.470588	GGAAAC	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	1256	1261	1.470588	GGAAAA	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	1311	1316	1.470588	GGAAAC	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	1639	1644	1.470588	GGAACT	1.95312	1.90161
cg2639478	AFAP1	STAT4 [T	1727	1732	1.470588	GTTTCC	1.95312	1.90161
cg0675819	AFAP1	STAT4 [T	253	258	1.470588	GGAATT	1.95312	1.90161
cg0675819	AFAP1	STAT4 [T	686	691	1.470588	GGAATT	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	797	802	1.470588	GGAAAC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	846	851	1.470588	TTTTCC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1354	1359	1.470588	GGAAAC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1378	1383	1.470588	TTTTCC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1582	1587	1.470588	AATTCC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1673	1678	1.470588	TTTTCC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1856	1861	1.470588	GGAATT	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1858	1863	1.470588	AATTCC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1887	1892	1.470588	AGTTCC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1904	1909	1.470588	AATTCC	1.95312	1.90161
cg0161265	AFAP1	STAT4 [T	1910	1915	1.470588	GGAACT	1.95312	1.90161
cg2591200	AFAP1	GR [T050	192	198	1.444018	CAAAAA	0.12207	0.11476
cg2591200	AFAP1	GR [T050	1234	1240	1.444018	CAAAAA	0.12207	0.11476
cg2591200	AFAP1	GR [T050	1240	1246	1.444018	CAAAAA	0.12207	0.11476
cg0261454	AFAP1	GR [T050	24	30	1.444018	CAAAAA	0.12207	0.11476
cg0261454	AFAP1	GR [T050	256	262	1.444018	CAAAAA	0.12207	0.11476
cg0261454	AFAP1	GR [T050	1298	1304	1.444018	CAAAAA	0.12207	0.11476
cg0261454	AFAP1	GR [T050	1304	1310	1.444018	CAAAAA	0.12207	0.11476
cg2639478	AFAP1	GR [T050	222	228	1.444018	CAAAAA	0.12207	0.11476
cg2639478	AFAP1	GR [T050	1264	1270	1.444018	CAAAAA	0.12207	0.11476
cg2639478	AFAP1	GR [T050	1270	1276	1.444018	CAAAAA	0.12207	0.11476
cg2591200	AFAP1	PR B [T00	1428	1434	1.404665	GAGTGT	0.36621	0.35143
cg2591200	AFAP1	PR A [T01	1428	1434	1.404665	GAGTGT	0.36621	0.35143
cg0261454	AFAP1	PR B [T00	1492	1498	1.404665	GAGTGT	0.36621	0.35143
cg0261454	AFAP1	PR A [T01	1492	1498	1.404665	GAGTGT	0.36621	0.35143
cg2639478	AFAP1	PR B [T00	1458	1464	1.404665	GAGTGT	0.36621	0.35143
cg2639478	AFAP1	PR A [T01	1458	1464	1.404665	GAGTGT	0.36621	0.35143
cg0675819	AFAP1	PR B [T00	371	377	1.404665	CAGTGT	0.36621	0.35143
cg0675819	AFAP1	PR A [T01	371	377	1.404665	CAGTGT	0.36621	0.35143
cg0161265	AFAP1	PR B [T00	1373	1379	1.404665	CAGTGT	0.36621	0.35143
cg0161265	AFAP1	PR A [T01	1373	1379	1.404665	CAGTGT	0.36621	0.35143
cg2591200	AFAP1	c-Ets-1 [T	484	490	1.384951	TTTCCTC	0.36621	0.35197
cg0261454	AFAP1	c-Ets-1 [T	548	554	1.384951	TTTCCTC	0.36621	0.35197
cg2639478	AFAP1	c-Ets-1 [T	514	520	1.384951	TTTCCTC	0.36621	0.35197
cg0675819	AFAP1	c-Ets-1 [T	240	246	1.384951	CAGGAA	0.36621	0.35197

cg2591200	AFAP1	C/EBPbeta	24	27	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	146	149	1.366559	TTGA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	424	427	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	523	526	1.366559	TTGA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	683	686	1.366559	TTGA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	900	903	1.366559	TTGA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	975	978	1.366559	TTGA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1139	1142	1.366559	TTGA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1158	1161	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1287	1290	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1495	1498	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1565	1568	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1615	1618	1.366559	TTGA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1906	1909	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	C/EBPbeta	1913	1916	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	88	91	1.366559	TCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	210	213	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	488	491	1.366559	TCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	587	590	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	747	750	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	964	967	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1039	1042	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1203	1206	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1222	1225	1.366559	TCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1351	1354	1.366559	TCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1559	1562	1.366559	TCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1629	1632	1.366559	TCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1679	1682	1.366559	TTGA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1970	1973	1.366559	TCAA	15.625	15.23827
cg0261454	AFAP1	C/EBPbeta	1977	1980	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	54	57	1.366559	TCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	176	179	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	454	457	1.366559	TCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	553	556	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	713	716	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	930	933	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1005	1008	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1169	1172	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1188	1191	1.366559	TCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1317	1320	1.366559	TCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1525	1528	1.366559	TCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1595	1598	1.366559	TCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1645	1648	1.366559	TTGA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1936	1939	1.366559	TCAA	15.625	15.23827
cg2639478	AFAP1	C/EBPbeta	1943	1946	1.366559	TTGA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	79	82	1.366559	TTGA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	257	260	1.366559	TTGA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	394	397	1.366559	TTGA	15.625	15.23827

cg0675819	AFAP1	C/EBPbeta	446	449	1.366559	TTGA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	985	988	1.366559	TCAA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	1034	1037	1.366559	TCAA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	1828	1831	1.366559	TCAA	15.625	15.23827
cg0675819	AFAP1	C/EBPbeta	1839	1842	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	274	277	1.366559	TTGA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	323	326	1.366559	TTGA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	341	344	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	399	402	1.366559	TTGA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	789	792	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	806	809	1.366559	TTGA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	1160	1163	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	1165	1168	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	1181	1184	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	1272	1275	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	1653	1656	1.366559	TCAA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	1819	1822	1.366559	TTGA	15.625	15.23827
cg0161265	AFAP1	C/EBPbeta	1926	1929	1.366559	TCAA	15.625	15.23827
cg2591200	AFAP1	AP-2alpha	614	619	1.357116	ACAGGC	0.48828	0.51319
cg0261454	AFAP1	AP-2alpha	678	683	1.357116	ACAGGC	0.48828	0.51319
cg2639478	AFAP1	AP-2alpha	644	649	1.357116	ACAGGC	0.48828	0.51319
cg0675819	AFAP1	AP-2alpha	66	71	1.357116	GCCTGT	0.48828	0.51319
cg0675819	AFAP1	AP-2alpha	1403	1408	1.357116	ACAGGC	0.48828	0.51319
cg0161265	AFAP1	AP-2alpha	81	86	1.357116	GCCTGT	0.48828	0.51319
cg0675819	AFAP1	HNF-3alph	1724	1731	1.342935	TTAAAA	0.03052	0.02477
cg2591200	AFAP1	C/EBPalph	1564	1570	1.220508	CTCAAT	0.24414	0.23153
cg0261454	AFAP1	C/EBPalph	1628	1634	1.220508	CTCAAT	0.24414	0.23153
cg2639478	AFAP1	C/EBPalph	1594	1600	1.220508	CTCAAT	0.24414	0.23153
cg2591200	AFAP1	HNF-1A [	1820	1827	1.213286	GGTTTA	0.48828	0.45029
cg0261454	AFAP1	HNF-1A [	1884	1891	1.213286	GGTTTA	0.48828	0.45029
cg2639478	AFAP1	HNF-1A [	1850	1857	1.213286	GGTTTA	0.48828	0.45029
cg0161265	AFAP1	HNF-1A [	1811	1818	1.213286	GGTTTA	0.48828	0.45029
cg0675819	AFAP1	PEA3 [T0	1905	1913	1.194633	AGGATG	0.06866	0.06787
cg2591200	AFAP1	STAT1bet	1896	1905	1.112096	TCCCGG	0.01144	0.01082
cg0261454	AFAP1	STAT1bet	1960	1969	1.112096	TCCCGG	0.01144	0.01082
cg2639478	AFAP1	STAT1bet	1926	1935	1.112096	TCCCGG	0.01144	0.01082
cg0675819	AFAP1	GATA-2 [	25	33	1.111111	AGATAG	0.09155	0.08894
cg0675819	AFAP1	T3R-beta1	1913	1921	1.110682	TCACCA	0.07629	0.07886
cg0675819	AFAP1	GCF [T00	941	949	1.070269	CCCCAG	0.18311	0.21473
cg2591200	AFAP1	HNF-1A [	802	809	1.069403	GTTAAT	0.48828	0.45029
cg0261454	AFAP1	HNF-1A [	866	873	1.069403	GTTAAT	0.48828	0.45029
cg2639478	AFAP1	HNF-1A [	832	839	1.069403	GTTAAT	0.48828	0.45029
cg2591200	AFAP1	GATA-1 [	135	140	1.038567	ATGATA	1.95312	1.80234
cg0261454	AFAP1	GATA-1 [	199	204	1.038567	ATGATA	1.95312	1.80234
cg2639478	AFAP1	GATA-1 [	165	170	1.038567	ATGATA	1.95312	1.80234
cg0675819	AFAP1	HIF-1 [T0	722	730	1.005355	ACGTGC	0.09918	0.10583
cg0675819	AFAP1	SRY [T00	1656	1664	0.999172	GAAACA	0.06104	0.0571
cg0161265	AFAP1	NF-kappa	1352	1362	0.987329	GGGGAA	0.00238	0.00262

cg2591200	AFAP1	Elk-1 [T00	174	182	0.957025	TGAAGG	0.03052	0.03046
cg2591200	AFAP1	Elk-1 [T00	261	269	0.957025	AGAAGG	0.03052	0.03046
cg0261454	AFAP1	Elk-1 [T00	238	246	0.957025	TGAAGG	0.03052	0.03046
cg0261454	AFAP1	Elk-1 [T00	325	333	0.957025	AGAAGG	0.03052	0.03046
cg2639478	AFAP1	Elk-1 [T00	204	212	0.957025	TGAAGG	0.03052	0.03046
cg2639478	AFAP1	Elk-1 [T00	291	299	0.957025	AGAAGG	0.03052	0.03046
cg0161265	AFAP1	Elk-1 [T00	1430	1438	0.957025	AGAAGG	0.03052	0.03046
cg2591200	AFAP1	TBP [T00	814	823	0.935771	TGGATA	0.12207	0.10448
cg0261454	AFAP1	TBP [T00	878	887	0.935771	TGGATA	0.12207	0.10448
cg2639478	AFAP1	TBP [T00	844	853	0.935771	TGGATA	0.12207	0.10448
cg0161265	AFAP1	TBP [T00	248	257	0.935771	CAGATA	0.12207	0.10448
cg2591200	AFAP1	HNF-1A [	1970	1977	0.925521	GTTAAA	0.48828	0.45029
cg0675819	AFAP1	HNF-1C [	88	96	0.90144	GTTAAT	0.00763	0.00634
cg0675819	AFAP1	GATA-1 [	1647	1652	0.863549	GTGATA	1.95312	1.80234
cg0675819	AFAP1	GATA-1 [	1821	1826	0.863549	TATCAC	1.95312	1.80234
cg0161265	AFAP1	GATA-1 [	874	879	0.863549	GTGATA	1.95312	1.80234
cg0675819	AFAP1	RXR-alph	471	477	0.848226	TGGACC	0.48828	0.51313
cg0161265	AFAP1	RXR-alph	806	812	0.848226	TTGACC	0.48828	0.51313
cg2591200	AFAP1	GR-beta [	20	24	0.840383	CAATT	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	129	133	0.840383	TAATT	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	130	134	0.840383	AATTA	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	134	138	0.840383	AATGA	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	141	145	0.840383	TAATT	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	152	156	0.840383	AATGA	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	214	218	0.840383	TAATT	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	447	451	0.840383	AATGG	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	453	457	0.840383	AATTG	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	548	552	0.840383	AATGA	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	630	634	0.840383	AATGG	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	636	640	0.840383	AATGA	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	805	809	0.840383	AATGG	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	1198	1202	0.840383	AATGA	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	1289	1293	0.840383	AATGA	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	1418	1422	0.840383	TCATT	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	1642	1646	0.840383	AATGG	7.8125	7.2174
cg2591200	AFAP1	GR-beta [	1974	1978	0.840383	AATGA	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	84	88	0.840383	CAATT	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	193	197	0.840383	TAATT	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	194	198	0.840383	AATTA	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	198	202	0.840383	AATGA	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	205	209	0.840383	TAATT	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	216	220	0.840383	AATGA	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	278	282	0.840383	TAATT	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	511	515	0.840383	AATGG	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	517	521	0.840383	AATTG	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	612	616	0.840383	AATGA	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	694	698	0.840383	AATGG	7.8125	7.2174
cg0261454	AFAP1	GR-beta [	700	704	0.840383	AATGA	7.8125	7.2174

cg0261454	AFAP1	GR-beta [T	869	873	0.840383	AATGG	7.8125	7.2174
cg0261454	AFAP1	GR-beta [T	1262	1266	0.840383	AATGA	7.8125	7.2174
cg0261454	AFAP1	GR-beta [T	1353	1357	0.840383	AATGA	7.8125	7.2174
cg0261454	AFAP1	GR-beta [T	1482	1486	0.840383	TCATT	7.8125	7.2174
cg0261454	AFAP1	GR-beta [T	1706	1710	0.840383	AATGG	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	50	54	0.840383	CAATT	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	159	163	0.840383	TAATT	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	160	164	0.840383	AATTA	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	164	168	0.840383	AATGA	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	171	175	0.840383	TAATT	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	182	186	0.840383	AATGA	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	244	248	0.840383	TAATT	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	477	481	0.840383	AATGG	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	483	487	0.840383	AATTG	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	578	582	0.840383	AATGA	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	660	664	0.840383	AATGG	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	666	670	0.840383	AATGA	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	835	839	0.840383	AATGG	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	1228	1232	0.840383	AATGA	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	1319	1323	0.840383	AATGA	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	1448	1452	0.840383	TCATT	7.8125	7.2174
cg2639478	AFAP1	GR-beta [T	1672	1676	0.840383	AATGG	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	93	97	0.840383	TAATT	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	94	98	0.840383	AATTA	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	255	259	0.840383	AATTG	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	379	383	0.840383	AATTG	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	388	392	0.840383	TAATT	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	428	432	0.840383	AATGA	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	688	692	0.840383	AATTG	7.8125	7.2174
cg0675819	AFAP1	GR-beta [T	1068	1072	0.840383	AATGA	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	194	198	0.840383	AATGA	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	256	260	0.840383	AATTA	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	394	398	0.840383	CCATT	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	475	479	0.840383	AATTA	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	865	869	0.840383	TCATT	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	902	906	0.840383	AATGG	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	923	927	0.840383	AATGG	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	1161	1165	0.840383	CAATT	7.8125	7.2174
cg0161265	AFAP1	GR-beta [T	1193	1197	0.840383	CAATT	7.8125	7.2174
cg0161265	AFAP1	PXR-1:RX	1166	1173	0.818075	CAAGTT	0.12207	0.11843
cg0675819	AFAP1	AP-2alpha	705	710	0.678558	TCAGGC	0.48828	0.51196
cg0161265	AFAP1	AP-2alpha	375	380	0.678558	TCAGGC	0.48828	0.51196
cg0161265	AFAP1	AP-2alpha	693	698	0.678558	TCAGGC	0.48828	0.51196
cg2591200	AFAP1	RXR-alpha	1819	1825	0.62611	GGGTTT	0.12207	0.11915
cg0261454	AFAP1	RXR-alpha	1883	1889	0.62611	GGGTTT	0.12207	0.11915
cg2639478	AFAP1	RXR-alpha	1849	1855	0.62611	GGGTTT	0.12207	0.11915
cg0675819	AFAP1	RXR-alpha	1150	1156	0.62611	TAAACC	0.12207	0.11915
cg0161265	AFAP1	RXR-alpha	1629	1635	0.62611	TAAACC	0.12207	0.11915

cg0675819	AFAP1	C/EBPalph	1201	1207	0.540941	CCCAAT	0.24414	0.24432
cg2591200	AFAP1	PR B [T00	1329	1335	0.48823	AACTGT	0.12207	0.11255
cg2591200	AFAP1	PR A [T01	1329	1335	0.48823	AACTGT	0.12207	0.11255
cg0261454	AFAP1	PR B [T00	1393	1399	0.48823	AACTGT	0.12207	0.11255
cg0261454	AFAP1	PR A [T01	1393	1399	0.48823	AACTGT	0.12207	0.11255
cg2639478	AFAP1	PR B [T00	1359	1365	0.48823	AACTGT	0.12207	0.11255
cg2639478	AFAP1	PR A [T01	1359	1365	0.48823	AACTGT	0.12207	0.11255
cg2591200	AFAP1	HNF-1A [	167	174	0.431647	GTTAAT	0.24414	0.21942
cg0261454	AFAP1	HNF-1A [	231	238	0.431647	GTTAAT	0.24414	0.21942
cg2639478	AFAP1	HNF-1A [	197	204	0.431647	GTTAAT	0.24414	0.21942
cg0161265	AFAP1	HNF-1A [	1615	1622	0.431647	GTTAAT	0.24414	0.21942
cg2591200	AFAP1	AP-1 [T00	536	544	0.401835	TGACTC	0.09155	0.08806
cg0261454	AFAP1	AP-1 [T00	600	608	0.401835	TGACTC	0.09155	0.08806
cg2639478	AFAP1	AP-1 [T00	566	574	0.401835	TGACTC	0.09155	0.08806
cg2591200	AFAP1	GATA-1 [	66	71	0.280028	AAGATA	0.97656	0.8795
cg0261454	AFAP1	GATA-1 [	130	135	0.280028	AAGATA	0.97656	0.8795
cg2639478	AFAP1	GATA-1 [	96	101	0.280028	AAGATA	0.97656	0.8795
cg0675819	AFAP1	GATA-1 [	24	29	0.280028	AAGATA	0.97656	0.8795
cg2591200	AFAP1	c-Ets-1 [T	176	182	0.256174	AAGGAA	0.24414	0.23743
cg2591200	AFAP1	c-Ets-1 [T	263	269	0.256174	AAGGAA	0.24414	0.23743
cg0261454	AFAP1	c-Ets-1 [T	240	246	0.256174	AAGGAA	0.24414	0.23743
cg0261454	AFAP1	c-Ets-1 [T	327	333	0.256174	AAGGAA	0.24414	0.23743
cg2639478	AFAP1	c-Ets-1 [T	206	212	0.256174	AAGGAA	0.24414	0.23743
cg2639478	AFAP1	c-Ets-1 [T	293	299	0.256174	AAGGAA	0.24414	0.23743
cg0675819	AFAP1	c-Ets-1 [T	245	251	0.256174	AAGGAA	0.24414	0.23743
cg0675819	AFAP1	c-Ets-1 [T	440	446	0.256174	CTTCCTT	0.24414	0.23743
cg0161265	AFAP1	c-Ets-1 [T	1432	1438	0.256174	AAGGAA	0.24414	0.23743
cg2591200	AFAP1	AP-2alpha	1794	1799	0.226186	GCCTGG	0.97656	1.07867
cg0261454	AFAP1	AP-2alpha	1858	1863	0.226186	GCCTGG	0.97656	1.07867
cg2639478	AFAP1	AP-2alpha	1824	1829	0.226186	GCCTGG	0.97656	1.07867
cg0675819	AFAP1	AP-2alpha	218	223	0.226186	GCCTGG	0.97656	1.07867
cg0675819	AFAP1	AP-2alpha	434	439	0.226186	GCCTGG	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	104	109	0.226186	GCCTGG	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	578	583	0.226186	GCCTGG	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	1010	1015	0.226186	GCCTGG	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	1789	1794	0.226186	CCAGGC	0.97656	1.07867
cg2591200	AFAP1	p53 [T006	1450	1456	0.211706	CTTGCC	0.36621	0.40082
cg2591200	AFAP1	p53 [T006	1467	1473	0.211706	CTTGCC	0.36621	0.40082
cg0261454	AFAP1	p53 [T006	1514	1520	0.211706	CTTGCC	0.36621	0.40082
cg0261454	AFAP1	p53 [T006	1531	1537	0.211706	CTTGCC	0.36621	0.40082
cg2639478	AFAP1	p53 [T006	1480	1486	0.211706	CTTGCC	0.36621	0.40082
cg2639478	AFAP1	p53 [T006	1497	1503	0.211706	CTTGCC	0.36621	0.40082
cg0675819	AFAP1	p53 [T006	484	490	0.211706	GGGCAA	0.36621	0.40082
cg0675819	AFAP1	p53 [T006	1328	1334	0.211706	CTTGCC	0.36621	0.40082
cg0161265	AFAP1	p53 [T006	94	100	0.211706	CTTGCC	0.36621	0.40082
cg0161265	AFAP1	p53 [T006	544	550	0.211706	GGGCAA	0.36621	0.40082
cg2591200	AFAP1	GR-alpha [	75	79	0.207689	AAAGG	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	187	191	0.207689	AAAGG	7.8125	7.79817

cg2591200	AFAP1	GR-alpha [	246	250	0.207689	AAAGG	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	420	424	0.207689	CCTCT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	482	486	0.207689	CCTTT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1045	1049	0.207689	CCTCT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1123	1127	0.207689	AAAGG	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1170	1174	0.207689	CCTCT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1204	1208	0.207689	AAAGG	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1211	1215	0.207689	CCTCT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1487	1491	0.207689	CCTTT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1586	1590	0.207689	CCTCT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1716	1720	0.207689	CCTCT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1751	1755	0.207689	CCTCT	7.8125	7.79817
cg2591200	AFAP1	GR-alpha [	1789	1793	0.207689	CCTTT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	139	143	0.207689	AAAGG	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	251	255	0.207689	AAAGG	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	310	314	0.207689	AAAGG	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	484	488	0.207689	CCTCT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	546	550	0.207689	CCTTT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1109	1113	0.207689	CCTCT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1187	1191	0.207689	AAAGG	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1234	1238	0.207689	CCTCT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1268	1272	0.207689	AAAGG	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1275	1279	0.207689	CCTCT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1551	1555	0.207689	CCTTT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1650	1654	0.207689	CCTCT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1780	1784	0.207689	CCTCT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1815	1819	0.207689	CCTCT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1853	1857	0.207689	CCTTT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	105	109	0.207689	AAAGG	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	217	221	0.207689	AAAGG	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	276	280	0.207689	AAAGG	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	450	454	0.207689	CCTCT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	512	516	0.207689	CCTTT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1075	1079	0.207689	CCTCT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1153	1157	0.207689	AAAGG	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1200	1204	0.207689	CCTCT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1234	1238	0.207689	AAAGG	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1241	1245	0.207689	CCTCT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1517	1521	0.207689	CCTTT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1616	1620	0.207689	CCTCT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1746	1750	0.207689	CCTCT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1781	1785	0.207689	CCTCT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1819	1823	0.207689	CCTTT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	244	248	0.207689	AAAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	443	447	0.207689	CCTTT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	646	650	0.207689	CCTCT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	761	765	0.207689	CCTTT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	955	959	0.207689	CCTTT	7.8125	7.79817

cg0675819	AFAP1	GR-alpha [	1101	1105	0.207689	AGAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1159	1163	0.207689	CCTCT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1212	1216	0.207689	CCTCT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1241	1245	0.207689	CCTCT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1416	1420	0.207689	AAAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1718	1722	0.207689	CCTCT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1851	1855	0.207689	AGAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1900	1904	0.207689	AGAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1993	1997	0.207689	AAAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	91	95	0.207689	CCTCT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	146	150	0.207689	AGAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	402	406	0.207689	AAAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	452	456	0.207689	AAAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	851	855	0.207689	CCTTT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	955	959	0.207689	CCTCT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1093	1097	0.207689	AGAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1104	1108	0.207689	AAAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1395	1399	0.207689	CCTCT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1407	1411	0.207689	AAAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1458	1462	0.207689	CCTCT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1677	1681	0.207689	CCTTT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1745	1749	0.207689	AGAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1776	1780	0.207689	AGAGG	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1866	1870	0.207689	CCTCT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1922	1926	0.207689	CCTTT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1928	1932	0.207689	AAAGG	7.8125	7.79817
cg0675819	AFAP1	HNF-1A [	375	382	0.143882	GTTAAA	0.24414	0.20853
cg0675819	AFAP1	HNF-1A [	386	393	0.143882	GTTAATT	0.24414	0.20853
cg2591200	AFAP1	Elk-1 [T00	287	295	0.134348	AGGAGG	0.06104	0.06399
cg2591200	AFAP1	Elk-1 [T00	326	334	0.134348	CTTCCTC	0.06104	0.06399
cg2591200	AFAP1	Elk-1 [T00	408	416	0.134348	CTTCCTC	0.06104	0.06399
cg2591200	AFAP1	Elk-1 [T00	785	793	0.134348	CTTCCTC	0.06104	0.06399
cg2591200	AFAP1	Elk-1 [T00	948	956	0.134348	AGCAGG	0.06104	0.06399
cg0261454	AFAP1	Elk-1 [T00	351	359	0.134348	AGGAGG	0.06104	0.06399
cg0261454	AFAP1	Elk-1 [T00	390	398	0.134348	CTTCCTC	0.06104	0.06399
cg0261454	AFAP1	Elk-1 [T00	472	480	0.134348	CTTCCTC	0.06104	0.06399
cg0261454	AFAP1	Elk-1 [T00	849	857	0.134348	CTTCCTC	0.06104	0.06399
cg0261454	AFAP1	Elk-1 [T00	1012	1020	0.134348	AGCAGG	0.06104	0.06399
cg2639478	AFAP1	Elk-1 [T00	317	325	0.134348	AGGAGG	0.06104	0.06399
cg2639478	AFAP1	Elk-1 [T00	356	364	0.134348	CTTCCTC	0.06104	0.06399
cg2639478	AFAP1	Elk-1 [T00	438	446	0.134348	CTTCCTC	0.06104	0.06399
cg2639478	AFAP1	Elk-1 [T00	815	823	0.134348	CTTCCTC	0.06104	0.06399
cg2639478	AFAP1	Elk-1 [T00	978	986	0.134348	AGCAGG	0.06104	0.06399
cg0675819	AFAP1	Elk-1 [T00	1451	1459	0.134348	TGGAGG	0.06104	0.06399
cg0161265	AFAP1	Elk-1 [T00	1828	1836	0.134348	TGGAGG	0.06104	0.06399
cg2591200	AFAP1	c-Ets-1 [T	289	295	0.128087	GAGGAA	0.24414	0.24982
cg0261454	AFAP1	c-Ets-1 [T	353	359	0.128087	GAGGAA	0.24414	0.24982
cg2639478	AFAP1	c-Ets-1 [T	319	325	0.128087	GAGGAA	0.24414	0.24982

cg0675819 AFAP1	c-Ets-1 [T	263	269	0.128087	CTTCCTC	0.24414	0.24982
cg0675819 AFAP1	c-Ets-1 [T	1102	1108	0.128087	GAGGAA	0.24414	0.24982
cg0675819 AFAP1	c-Ets-1 [T	1156	1162	0.128087	CTTCCTC	0.24414	0.24982
cg0675819 AFAP1	c-Ets-1 [T	1453	1459	0.128087	GAGGAA	0.24414	0.24982
cg0161265 AFAP1	c-Ets-1 [T	585	591	0.128087	GAGGAA	0.24414	0.24982
cg0161265 AFAP1	c-Ets-1 [T	1392	1398	0.128087	CTTCCTC	0.24414	0.24982
cg0161265 AFAP1	c-Ets-1 [T	1830	1836	0.128087	GAGGAA	0.24414	0.24982
cg2591200 AFAP1	GATA-1 [	1942	1947	0.105011	GAGATA	0.97656	0.92541
cg2639478 AFAP1	GATA-1 [	1972	1977	0.105011	GAGATA	0.97656	0.92541
cg2591200 AFAP1	GR-beta [	115	119	0	AAATT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	142	146	0	AATTT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	426	430	0	AAATT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	427	431	0	AATTT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	477	481	0	AATTT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	874	878	0	AATGT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	1311	1315	0	AAATT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	1392	1396	0	ACATT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	1623	1627	0	AATGT	3.90625	3.51525
cg2591200 AFAP1	GR-beta [	1902	1906	0	AAATT	3.90625	3.51525
cg2591200 AFAP1	XBP-1 [T	903	908	0	ATGACG	0.97656	0.94838
cg2591200 AFAP1	XBP-1 [T	1929	1934	0	ATGACT	0.97656	0.94838
cg2591200 AFAP1	TFIID [T0	70	76	0	TAAAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	124	130	0	TTTTCTA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	238	244	0	TCTAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	240	246	0	TAAAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	429	435	0	TTTAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	430	436	0	TTAAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	431	437	0	TAAAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	1099	1105	0	TAAAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	1177	1183	0	TTTTTAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	1252	1258	0	TAAAAA	1.09863	0.95175
cg2591200 AFAP1	TFIID [T0	1323	1329	0	TATAAA	1.09863	0.95175
cg2591200 AFAP1	c-Jun [T00	536	542	0	TGACTC	0.12207	0.11843
cg2591200 AFAP1	GR-alpha [	614	618	0	ACAGG	7.8125	7.79817
cg2591200 AFAP1	GR-alpha [	1631	1635	0	CCTGT	7.8125	7.79817
cg2591200 AFAP1	GR-alpha [	1765	1769	0	CCTGT	7.8125	7.79817
cg2591200 AFAP1	GR-alpha [	1945	1949	0	ATAGG	7.8125	7.79817
cg2591200 AFAP1	FOXP3 [T	690	695	0	CACAAC	1.46484	1.44953
cg2591200 AFAP1	FOXP3 [T	1548	1553	0	CACAAC	1.46484	1.44953
cg2591200 AFAP1	PR B [T00	1340	1346	0	GACTGT	0.36621	0.35051
cg2591200 AFAP1	PR A [T01	1340	1346	0	GACTGT	0.36621	0.35051
cg2591200 AFAP1	HNF-3alph	1175	1182	0	TATTTTT	0.09155	0.07727
cg2591200 AFAP1	C/EBPbeta	3	6	0	ACAA	15.625	15.26275
cg2591200 AFAP1	C/EBPbeta	19	22	0	ACAA	15.625	15.26275
cg2591200 AFAP1	C/EBPbeta	45	48	0	ACAA	15.625	15.26275
cg2591200 AFAP1	C/EBPbeta	121	124	0	TTGT	15.625	15.26275
cg2591200 AFAP1	C/EBPbeta	150	153	0	GCAA	15.625	15.26275
cg2591200 AFAP1	C/EBPbeta	184	187	0	ACAA	15.625	15.26275

cg2591200	AFAP1	C/EBPbeta	191	194	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	361	364	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	404	407	0	TTGT	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	545	548	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	564	567	0	TTGC	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	566	569	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	576	579	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	589	592	0	TTGT	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	607	610	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	643	646	0	TTGT	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	677	680	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	691	694	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	844	847	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	852	855	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	861	864	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	913	916	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1233	1236	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1239	1242	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1245	1248	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1259	1262	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1293	1296	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1309	1312	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1398	1401	0	TTGC	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1451	1454	0	TTGC	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1468	1471	0	TTGC	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1514	1517	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1549	1552	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1572	1575	0	GCAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1757	1760	0	ACAA	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1792	1795	0	TTGC	15.625	15.26275
cg2591200	AFAP1	C/EBPbeta	1843	1846	0	GCAA	15.625	15.26275
cg2591200	AFAP1	YY1 [T00	230	233	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	232	235	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	448	451	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	559	562	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	631	634	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	714	717	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	736	739	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	806	809	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	826	829	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	828	831	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	985	988	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	987	990	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1035	1038	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1351	1354	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1412	1415	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1438	1441	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1455	1458	0	CCAT	7.8125	7.79459

cg2591200	AFAP1	YY1 [T00	1457	1460	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1643	1646	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1770	1773	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1877	1880	0	ATGG	7.8125	7.79459
cg2591200	AFAP1	YY1 [T00	1925	1928	0	CCAT	7.8125	7.79459
cg2591200	AFAP1	TFII-I [T0	466	471	0	CTTTCC	1.46484	1.48598
cg2591200	AFAP1	TFII-I [T0	483	488	0	CTTTCC	1.46484	1.48598
cg2591200	AFAP1	TFII-I [T0	1632	1637	0	CTGTCC	1.46484	1.48598
cg2591200	AFAP1	TFII-I [T0	1766	1771	0	CTGTCC	1.46484	1.48598
cg2591200	AFAP1	STAT4 [T	478	483	0	ATTTCC	0.48828	0.46235
cg2591200	AFAP1	STAT4 [T	595	600	0	ATTTCC	0.48828	0.46235
cg2591200	AFAP1	STAT4 [T	1900	1905	0	GGAAAT	0.48828	0.46235
cg2591200	AFAP1	c-Ets-1 [T	326	332	0	CTTCCTC	0.24414	0.24982
cg2591200	AFAP1	c-Ets-1 [T	408	414	0	CTTCCTC	0.24414	0.24982
cg2591200	AFAP1	c-Ets-1 [T	785	791	0	CTTCCTC	0.24414	0.24982
cg2591200	AFAP1	c-Ets-1 [T	950	956	0	CAGGAA	0.24414	0.24982
cg2591200	AFAP1	c-Ets-1 [T	1762	1768	0	CTTCCTC	0.24414	0.24982
cg2591200	AFAP1	c-Ets-1 [T	1827	1833	0	CTTCCTC	0.24414	0.24982
cg2591200	AFAP1	ER-alpha [	976	980	0	TGACC	1.95312	1.99744
cg2591200	AFAP1	ER-alpha [	1369	1373	0	TGACC	1.95312	1.99744
cg2591200	AFAP1	GR [T050	4	10	0	CAAAAA	0.36621	0.33174
cg2591200	AFAP1	GR [T050	46	52	0	CAAAAA	0.36621	0.33174
cg2591200	AFAP1	GR [T050	853	859	0	CAAAAA	0.36621	0.33174
cg2591200	AFAP1	GR [T050	1246	1252	0	CAAAAA	0.36621	0.33174
cg2591200	AFAP1	c-Myc [T0	1542	1547	0	CACGTG	0.48828	0.51196
cg2591200	AFAP1	GATA-1 [	82	87	0	TATCTG	0.97656	0.92541
cg2591200	AFAP1	Pax-5 [T0	615	621	0	CAGGCC	1.09863	1.24633
cg2591200	AFAP1	Pax-5 [T0	620	626	0	CCTGCC	1.09863	1.24633
cg2591200	AFAP1	p53 [T006	620	626	0	CCTGCC	0.36621	0.40082
cg2591200	AFAP1	HNF-1A [	580	587	0	GTTAAA	0.24414	0.20853
cg0261454	AFAP1	GR-beta [	29	33	0	ACATT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	179	183	0	AAATT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	206	210	0	AATTT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	490	494	0	AAATT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	491	495	0	AATTT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	541	545	0	AATTT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	938	942	0	AATGT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	1375	1379	0	AAATT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	1456	1460	0	ACATT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	1687	1691	0	AATGT	3.90625	3.51525
cg0261454	AFAP1	GR-beta [	1966	1970	0	AAATT	3.90625	3.51525
cg0261454	AFAP1	XBP-1 [T	967	972	0	ATGACG	0.97656	0.94838
cg0261454	AFAP1	XBP-1 [T	1993	1998	0	ATGACT	0.97656	0.94838
cg0261454	AFAP1	TFIID [T0	10	16	0	TTTAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	11	17	0	TTAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	12	18	0	TAAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	32	38	0	TTAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	33	39	0	TAAAAA	1.09863	0.95175

cg0261454	AFAP1	TFIID [T0	134	140	0	TAAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	188	194	0	TTTTCTA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	302	308	0	TCTAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	304	310	0	TAAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	493	499	0	TTTAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	494	500	0	TTAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	495	501	0	TAAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	1163	1169	0	TAAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	1241	1247	0	TTTTTAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	1316	1322	0	TAAAAA	1.09863	0.95175
cg0261454	AFAP1	TFIID [T0	1387	1393	0	TATAAA	1.09863	0.95175
cg0261454	AFAP1	c-Jun [T00	600	606	0	TGACTC	0.12207	0.11843
cg0261454	AFAP1	GR-alpha [	678	682	0	ACAGG	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1695	1699	0	CCTGT	7.8125	7.79817
cg0261454	AFAP1	GR-alpha [	1829	1833	0	CCTGT	7.8125	7.79817
cg0261454	AFAP1	FOXP3 [T	754	759	0	CACAAC	1.46484	1.44953
cg0261454	AFAP1	FOXP3 [T	1612	1617	0	CACAAC	1.46484	1.44953
cg0261454	AFAP1	PR B [T00	1404	1410	0	GACTGT	0.36621	0.35051
cg0261454	AFAP1	PR A [T01	1404	1410	0	GACTGT	0.36621	0.35051
cg0261454	AFAP1	HNF-3alp	1239	1246	0	TATTTTT	0.09155	0.07727
cg0261454	AFAP1	C/EBPbeta	23	26	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	67	70	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	83	86	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	109	112	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	185	188	0	TTGT	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	214	217	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	248	251	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	255	258	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	425	428	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	468	471	0	TTGT	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	609	612	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	628	631	0	TTGC	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	630	633	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	640	643	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	653	656	0	TTGT	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	671	674	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	707	710	0	TTGT	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	741	744	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	755	758	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	908	911	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	916	919	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	925	928	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	977	980	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1297	1300	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1303	1306	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1309	1312	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1323	1326	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1357	1360	0	ACAA	15.625	15.26275

cg0261454	AFAP1	C/EBPbeta	1373	1376	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1462	1465	0	TTGC	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1515	1518	0	TTGC	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1532	1535	0	TTGC	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1578	1581	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1613	1616	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1636	1639	0	GCAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1821	1824	0	ACAA	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1856	1859	0	TTGC	15.625	15.26275
cg0261454	AFAP1	C/EBPbeta	1907	1910	0	GCAA	15.625	15.26275
cg0261454	AFAP1	YY1 [T00	294	297	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	296	299	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	512	515	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	623	626	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	695	698	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	778	781	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	800	803	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	870	873	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	890	893	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	892	895	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1049	1052	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1051	1054	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1099	1102	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1415	1418	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1476	1479	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1502	1505	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1519	1522	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1521	1524	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1707	1710	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1834	1837	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1941	1944	0	ATGG	7.8125	7.79459
cg0261454	AFAP1	YY1 [T00	1989	1992	0	CCAT	7.8125	7.79459
cg0261454	AFAP1	TFII-I [T0	530	535	0	CTTTCC	1.46484	1.48598
cg0261454	AFAP1	TFII-I [T0	547	552	0	CTTTCC	1.46484	1.48598
cg0261454	AFAP1	TFII-I [T0	1696	1701	0	CTGTCC	1.46484	1.48598
cg0261454	AFAP1	TFII-I [T0	1830	1835	0	CTGTCC	1.46484	1.48598
cg0261454	AFAP1	STAT4 [T	542	547	0	ATTTCC	0.48828	0.46235
cg0261454	AFAP1	STAT4 [T	659	664	0	ATTTCC	0.48828	0.46235
cg0261454	AFAP1	STAT4 [T	1964	1969	0	GGAAAT	0.48828	0.46235
cg0261454	AFAP1	c-Ets-1 [T	390	396	0	CTTCCTC	0.24414	0.24982
cg0261454	AFAP1	c-Ets-1 [T	472	478	0	CTTCCTC	0.24414	0.24982
cg0261454	AFAP1	c-Ets-1 [T	849	855	0	CTTCCTC	0.24414	0.24982
cg0261454	AFAP1	c-Ets-1 [T	1014	1020	0	CAGGAA	0.24414	0.24982
cg0261454	AFAP1	c-Ets-1 [T	1826	1832	0	CTTCCTC	0.24414	0.24982
cg0261454	AFAP1	c-Ets-1 [T	1891	1897	0	CTTCCTC	0.24414	0.24982
cg0261454	AFAP1	ER-alpha [	1040	1044	0	TGACC	1.95312	1.99744
cg0261454	AFAP1	ER-alpha [	1433	1437	0	TGACC	1.95312	1.99744
cg0261454	AFAP1	GR [T050	68	74	0	CAAAAA	0.36621	0.33174

cg0261454	AFAP1	GR [T050	110	116	0	CAAAAA	0.36621	0.33174
cg0261454	AFAP1	GR [T050	917	923	0	CAAAAA	0.36621	0.33174
cg0261454	AFAP1	GR [T050	1310	1316	0	CAAAAA	0.36621	0.33174
cg0261454	AFAP1	c-Myc [T0	1606	1611	0	CACGTG	0.48828	0.51196
cg0261454	AFAP1	GATA-1 [	146	151	0	TATCTG	0.97656	0.92541
cg0261454	AFAP1	Pax-5 [T0	679	685	0	CAGGCC	1.09863	1.24633
cg0261454	AFAP1	Pax-5 [T0	684	690	0	CCTGCC	1.09863	1.24633
cg0261454	AFAP1	p53 [T006	684	690	0	CCTGCC	0.36621	0.40082
cg0261454	AFAP1	HNF-1A [	644	651	0	GTTAAA	0.24414	0.20853
cg2639478	AFAP1	GR-beta [	145	149	0	AAATT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	172	176	0	AATTT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	456	460	0	AAATT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	457	461	0	AATTT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	507	511	0	AATTT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	904	908	0	AATGT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	1341	1345	0	AAATT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	1422	1426	0	ACATT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	1653	1657	0	AATGT	3.90625	3.51525
cg2639478	AFAP1	GR-beta [	1932	1936	0	AAATT	3.90625	3.51525
cg2639478	AFAP1	XBP-1 [T	933	938	0	ATGACG	0.97656	0.94838
cg2639478	AFAP1	XBP-1 [T	1959	1964	0	ATGACT	0.97656	0.94838
cg2639478	AFAP1	TFIID [T0	100	106	0	TAAAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	154	160	0	TTTTCTA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	268	274	0	TCTAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	270	276	0	TAAAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	459	465	0	TTTAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	460	466	0	TTAAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	461	467	0	TAAAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	1129	1135	0	TAAAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	1207	1213	0	TTTTTAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	1282	1288	0	TAAAAA	1.09863	0.95175
cg2639478	AFAP1	TFIID [T0	1353	1359	0	TATAAA	1.09863	0.95175
cg2639478	AFAP1	c-Jun [T00	566	572	0	TGACTC	0.12207	0.11843
cg2639478	AFAP1	GR-alpha [	644	648	0	ACAGG	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1661	1665	0	CCTGT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1795	1799	0	CCTGT	7.8125	7.79817
cg2639478	AFAP1	GR-alpha [	1975	1979	0	ATAGG	7.8125	7.79817
cg2639478	AFAP1	FOXP3 [T	720	725	0	CACAAC	1.46484	1.44953
cg2639478	AFAP1	FOXP3 [T	1578	1583	0	CACAAC	1.46484	1.44953
cg2639478	AFAP1	PR B [T00	1370	1376	0	GACTGT	0.36621	0.35051
cg2639478	AFAP1	PR A [T01	1370	1376	0	GACTGT	0.36621	0.35051
cg2639478	AFAP1	HNF-3alph	1205	1212	0	TATTTTT	0.09155	0.07727
cg2639478	AFAP1	C/EBPbeta	33	36	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	49	52	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	75	78	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	151	154	0	TTGT	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	180	183	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	214	217	0	ACAA	15.625	15.26275

cg2639478	AFAP1	C/EBPbeta	221	224	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	391	394	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	434	437	0	TTGT	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	575	578	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	594	597	0	TTGC	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	596	599	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	606	609	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	619	622	0	TTGT	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	637	640	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	673	676	0	TTGT	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	707	710	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	721	724	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	874	877	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	882	885	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	891	894	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	943	946	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1263	1266	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1269	1272	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1275	1278	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1289	1292	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1323	1326	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1339	1342	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1428	1431	0	TTGC	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1481	1484	0	TTGC	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1498	1501	0	TTGC	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1544	1547	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1579	1582	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1602	1605	0	GCAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1787	1790	0	ACAA	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1822	1825	0	TTGC	15.625	15.26275
cg2639478	AFAP1	C/EBPbeta	1873	1876	0	GCAA	15.625	15.26275
cg2639478	AFAP1	YY1 [T00	260	263	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	262	265	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	478	481	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	589	592	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	661	664	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	744	747	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	766	769	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	836	839	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	856	859	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	858	861	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1015	1018	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1017	1020	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1065	1068	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1381	1384	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1442	1445	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1468	1471	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1485	1488	0	CCAT	7.8125	7.79459

cg2639478	AFAP1	YY1 [T00	1487	1490	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1673	1676	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1800	1803	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1907	1910	0	ATGG	7.8125	7.79459
cg2639478	AFAP1	YY1 [T00	1955	1958	0	CCAT	7.8125	7.79459
cg2639478	AFAP1	TFII-I [T0	496	501	0	CTTTCC	1.46484	1.48598
cg2639478	AFAP1	TFII-I [T0	513	518	0	CTTTCC	1.46484	1.48598
cg2639478	AFAP1	TFII-I [T0	1662	1667	0	CTGTCC	1.46484	1.48598
cg2639478	AFAP1	TFII-I [T0	1796	1801	0	CTGTCC	1.46484	1.48598
cg2639478	AFAP1	STAT4 [T	508	513	0	ATTTCC	0.48828	0.46235
cg2639478	AFAP1	STAT4 [T	625	630	0	ATTTCC	0.48828	0.46235
cg2639478	AFAP1	STAT4 [T	1930	1935	0	GGAAAT	0.48828	0.46235
cg2639478	AFAP1	c-Ets-1 [T	356	362	0	CTTCCTC	0.24414	0.24982
cg2639478	AFAP1	c-Ets-1 [T	438	444	0	CTTCCTC	0.24414	0.24982
cg2639478	AFAP1	c-Ets-1 [T	815	821	0	CTTCCTC	0.24414	0.24982
cg2639478	AFAP1	c-Ets-1 [T	980	986	0	CAGGAA	0.24414	0.24982
cg2639478	AFAP1	c-Ets-1 [T	1792	1798	0	CTTCCTC	0.24414	0.24982
cg2639478	AFAP1	c-Ets-1 [T	1857	1863	0	CTTCCTC	0.24414	0.24982
cg2639478	AFAP1	ER-alpha [	1006	1010	0	TGACC	1.95312	1.99744
cg2639478	AFAP1	ER-alpha [	1399	1403	0	TGACC	1.95312	1.99744
cg2639478	AFAP1	GR [T050	34	40	0	CAAAAA	0.36621	0.33174
cg2639478	AFAP1	GR [T050	76	82	0	CAAAAA	0.36621	0.33174
cg2639478	AFAP1	GR [T050	883	889	0	CAAAAA	0.36621	0.33174
cg2639478	AFAP1	GR [T050	1276	1282	0	CAAAAA	0.36621	0.33174
cg2639478	AFAP1	c-Myc [T0	1572	1577	0	CACGTG	0.48828	0.51196
cg2639478	AFAP1	GATA-1 [	112	117	0	TATCTG	0.97656	0.92541
cg2639478	AFAP1	Pax-5 [T0	645	651	0	CAGGCC	1.09863	1.24633
cg2639478	AFAP1	Pax-5 [T0	650	656	0	CCTGCC	1.09863	1.24633
cg2639478	AFAP1	p53 [T006	650	656	0	CCTGCC	0.36621	0.40082
cg2639478	AFAP1	HNF-1A [	610	617	0	GTTAAA	0.24414	0.20853
cg0675819	AFAP1	GR-beta [T	378	382	0	AAATT	3.90625	3.51525
cg0675819	AFAP1	GR-beta [T	389	393	0	AATTT	3.90625	3.51525
cg0675819	AFAP1	GR-beta [T	414	418	0	ACATT	3.90625	3.51525
cg0675819	AFAP1	GR-beta [T	1830	1834	0	AATGT	3.90625	3.51525
cg0675819	AFAP1	TFIID [T0	391	397	0	TTTTGA	1.09863	0.95175
cg0675819	AFAP1	TFIID [T0	1723	1729	0	TTTAAA	1.09863	0.95175
cg0675819	AFAP1	GR-alpha [	27	31	0	ATAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	67	71	0	CCTGT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	308	312	0	CCTAT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	617	621	0	CCTAT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1368	1372	0	CCTAT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1403	1407	0	ACAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1644	1648	0	CCTGT	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1795	1799	0	ACAGG	7.8125	7.79817
cg0675819	AFAP1	GR-alpha [	1952	1956	0	CCTGT	7.8125	7.79817
cg0675819	AFAP1	FOXP3 [T	542	547	0	GACAAC	1.46484	1.44953
cg0675819	AFAP1	FOXP3 [T	1535	1540	0	GTTGTT	1.46484	1.44953
cg0675819	AFAP1	C/EBPbeta	3	6	0	ACAA	15.625	15.26275

cg0675819	AFAP1	C/EBPbeta	151	154	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	227	230	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	417	420	0	TTGT	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	464	467	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	486	489	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	490	493	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	543	546	0	ACAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	690	693	0	TTGC	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	709	712	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	754	757	0	ACAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	936	939	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1065	1068	0	ACAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1122	1125	0	ACAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1329	1332	0	TTGC	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1536	1539	0	TTGT	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1591	1594	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1625	1628	0	ACAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1659	1662	0	ACAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1860	1863	0	GCAA	15.625	15.26275
cg0675819	AFAP1	C/EBPbeta	1941	1944	0	ACAA	15.625	15.26275
cg0675819	AFAP1	NF-1 [T00	764	771	0	TTGGGC	0.12207	0.13147
cg0675819	AFAP1	YY1 [T00	14	17	0	ATGG	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	100	103	0	CCAT	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	283	286	0	CCAT	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	453	456	0	ATGG	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	520	523	0	CCAT	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	570	573	0	CCAT	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	585	588	0	ATGG	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	629	632	0	CCAT	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	1569	1572	0	ATGG	7.8125	7.79459
cg0675819	AFAP1	YY1 [T00	1788	1791	0	CCAT	7.8125	7.79459
cg0675819	AFAP1	TFII-I [T0	68	73	0	CTGTCC	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	242	247	0	GGAAAG	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	368	373	0	GGACAG	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	668	673	0	CTGTCC	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	910	915	0	GGACAG	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	956	961	0	CTTTCC	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	1812	1817	0	GGACAG	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	1855	1860	0	GGACAG	1.46484	1.48598
cg0675819	AFAP1	TFII-I [T0	1963	1968	0	GGACAG	1.46484	1.48598
cg0675819	AFAP1	ER-alpha [	55	59	0	GGTCA	1.95312	1.99744
cg0675819	AFAP1	ER-alpha [	675	679	0	TGACC	1.95312	1.99744
cg0675819	AFAP1	RXR-alpha	1070	1076	0	TGAACC	0.24414	0.24342
cg0675819	AFAP1	GR [T050	390	396	0	ATTTTTC	0.36621	0.33174
cg0675819	AFAP1	Pax-5 [T0	331	337	0	GGGCCT	1.09863	1.24633
cg0675819	AFAP1	Pax-5 [T0	342	348	0	CCAGCC	1.09863	1.24633
cg0675819	AFAP1	Pax-5 [T0	530	536	0	GGGCCG	1.09863	1.24633
cg0675819	AFAP1	Pax-5 [T0	696	702	0	GGGCAG	1.09863	1.24633

cg0675819	AFAP1	p53 [T006	696	702	0	GGGCAG	0.36621	0.40082
cg0675819	AFAP1	AP-2alpha	333	338	0	GCCTGC	0.97656	1.07867
cg0675819	AFAP1	TCF-4 [T0	443	452	0	CCTTTG	0.01144	0.01102
cg0675819	AFAP1	IRF-2 [T01	1823	1828	0	TCACTT	0.48828	0.46235
cg0675819	AFAP1	HNF-1A [	88	95	0	GTTAAT	0.24414	0.20853
cg0161265	AFAP1	GR-beta [T	41	45	0	ACATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	255	259	0	AAATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	330	334	0	AATGT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	336	340	0	AAATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	337	341	0	AATTT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	861	865	0	AAATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1412	1416	0	ACATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1697	1701	0	AAATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1803	1807	0	ACATT	3.90625	3.51525
cg0161265	AFAP1	GR-beta [T	1903	1907	0	AAATT	3.90625	3.51525
cg0161265	AFAP1	XBP-1 [T	1549	1554	0	CGTCAT	0.97656	0.94838
cg0161265	AFAP1	TFIID [T0	258	264	0	TTAAAA	1.09863	0.95175
cg0161265	AFAP1	TFIID [T0	448	454	0	TTTAAA	1.09863	0.95175
cg0161265	AFAP1	TFIID [T0	857	863	0	TAGAAA	1.09863	0.95175
cg0161265	AFAP1	TFIID [T0	1625	1631	0	TTTTTAA	1.09863	0.95175
cg0161265	AFAP1	GR-alpha [	8	12	0	CCTGT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	82	86	0	CCTGT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	668	672	0	CCTGT	7.8125	7.79817
cg0161265	AFAP1	GR-alpha [	1963	1967	0	CCTGT	7.8125	7.79817
cg0161265	AFAP1	IRF-1 [T0	847	855	0	TTTCCCT	0.00763	0.00712
cg0161265	AFAP1	FOXP3 [T	463	468	0	GTTGTG	1.46484	1.44953
cg0161265	AFAP1	C/EBPbeta	44	47	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	95	98	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	150	153	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	161	164	0	TTGT	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	218	221	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	428	431	0	TTGT	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	438	441	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	464	467	0	TTGT	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	479	482	0	ACAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	495	498	0	ACAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	498	501	0	ACAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	546	549	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	576	579	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	625	628	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	753	756	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	820	823	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	838	841	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	870	873	0	TTGT	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	900	903	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	921	924	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	963	966	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1154	1157	0	TTGC	15.625	15.26275

cg0161265	AFAP1	C/EBPbeta	1156	1159	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1202	1205	0	TTGT	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1263	1266	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1489	1492	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1714	1717	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1725	1728	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1729	1732	0	GCAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1756	1759	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1822	1825	0	ACAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1870	1873	0	TTGC	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1901	1904	0	ACAA	15.625	15.26275
cg0161265	AFAP1	C/EBPbeta	1915	1918	0	TTGC	15.625	15.26275
cg0161265	AFAP1	NF-1 [T00	776	783	0	TGGCCC	0.12207	0.13147
cg0161265	AFAP1	YY1 [T00	21	24	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	223	226	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	326	329	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	356	359	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	358	361	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	394	397	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	409	412	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	411	414	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	421	424	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	702	705	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	830	833	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	903	906	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	924	927	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	960	963	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1055	1058	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1116	1119	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1148	1151	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1223	1226	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1386	1389	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1452	1455	0	ATGG	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1508	1511	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	YY1 [T00	1891	1894	0	CCAT	7.8125	7.79459
cg0161265	AFAP1	TFII-I [T0	1098	1103	0	GGAAAG	1.46484	1.48598
cg0161265	AFAP1	TFII-I [T0	1234	1239	0	CTTTCC	1.46484	1.48598
cg0161265	AFAP1	TFII-I [T0	1419	1424	0	GGACAG	1.46484	1.48598
cg0161265	AFAP1	TFII-I [T0	1426	1431	0	GGACAG	1.46484	1.48598
cg0161265	AFAP1	TFII-I [T0	1741	1746	0	GGAAAG	1.46484	1.48598
cg0161265	AFAP1	ER-alpha [	807	811	0	TGACC	1.95312	1.99744
cg0161265	AFAP1	ER-alpha [	935	939	0	TGACC	1.95312	1.99744
cg0161265	AFAP1	GR [T050	821	827	0	CAAAAA	0.36621	0.33174
cg0161265	AFAP1	c-Myc [T0	614	619	0	CACGTG	0.48828	0.51196
cg0161265	AFAP1	USF1 [T0	610	619	0	GGCCCA	0.00572	0.00652
cg0161265	AFAP1	GATA-1 [	248	253	0	CAGATA	0.97656	0.92541
cg0161265	AFAP1	Pax-5 [T0	170	176	0	GGGCAT	1.09863	1.24633
cg0161265	AFAP1	Pax-5 [T0	376	382	0	CAGGCC	1.09863	1.24633

cg0161265	AFAP1	Pax-5 [T0	1790	1796	0	CAGGCC	1.09863	1.24633
cg0161265	AFAP1	Pax-5 [T0	1842	1848	0	GGGCAG	1.09863	1.24633
cg0161265	AFAP1	Pax-5 [T0	1982	1988	0	CCAGCC	1.09863	1.24633
cg0161265	AFAP1	Pax-5 [T0	1988	1994	0	CCTGCC	1.09863	1.24633
cg0161265	AFAP1	p53 [T006	170	176	0	GGGCAT	0.36621	0.40082
cg0161265	AFAP1	p53 [T006	1842	1848	0	GGGCAG	0.36621	0.40082
cg0161265	AFAP1	p53 [T006	1988	1994	0	CCTGCC	0.36621	0.40082
cg0161265	AFAP1	AP-2alpha	77	82	0	GCCTGC	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	758	763	0	GCAGGC	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	896	901	0	GCCTGC	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	917	922	0	GCCTGC	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	1265	1270	0	GCAGGC	0.97656	1.07867
cg0161265	AFAP1	AP-2alpha	1518	1523	0	GCCTGC	0.97656	1.07867
cg0161265	AFAP1	E2F-1 [T0	1379	1386	0	TTTCCC	0.03052	0.03202
cg0161265	AFAP1	TCF-4 [T0	1923	1932	0	CTTTCA	0.01144	0.01102
cg0161265	AFAP1	IRF-2 [T0	932	937	0	AAGTGA	0.48828	0.46235
cg0161265	AFAP1	IRF-2 [T0	1555	1560	0	AAGTGA	0.48828	0.46235
cg002138	AIFM1	STAT5A [	1440	1452	9.952027	GACTTT	0.01878	0.01703
cg002138	AIFM1	XBP-1 [T	340	345	9.789909	ATGGCT	1.95312	1.94901
cg002138	AIFM1	Elk-1 [T00	1228	1236	9.754368	CTTCCA	0.10681	0.11027
cg002138	AIFM1	PR B [T00	105	111	9.743489	AACACC	1.09863	1.0981
cg002138	AIFM1	PR B [T00	685	691	9.743489	AACACC	1.09863	1.0981
cg002138	AIFM1	PR B [T00	1041	1047	9.743489	CTGTGT	1.09863	1.0981
cg002138	AIFM1	PR A [T01	105	111	9.743489	AACACC	1.09863	1.0981
cg002138	AIFM1	PR A [T01	685	691	9.743489	AACACC	1.09863	1.0981
cg002138	AIFM1	PR A [T01	1041	1047	9.743489	CTGTGT	1.09863	1.0981
cg002138	AIFM1	AhR:Arnt	1217	1226	9.738501	TCCGGC	0.17929	0.20119
cg002138	AIFM1	c-Myb [T0	1056	1063	9.729271	GAACTG	0.36621	0.34746
cg002138	AIFM1	c-Myb [T0	1475	1482	9.729271	TTCAGT	0.36621	0.34746
cg002138	AIFM1	LEF-1 [T0	175	182	9.72404	TGACAA	0.21362	0.21229
cg002138	AIFM1	HNF-4alp	1092	1104	9.675138	GCATCG	0.01109	0.01049
cg002138	AIFM1	HNF-1C [	973	981	9.576203	GTTAAG	0.19836	0.18179
cg002138	AIFM1	NF-AT1 [	286	294	9.557905	GGAAAA	0.16785	0.16528
cg002138	AIFM1	TFIID [T0	86	92	9.552105	TTTGGA	1.46484	1.37777
cg002138	AIFM1	TFIID [T0	175	181	9.552105	TGACAA	1.46484	1.37777
cg002138	AIFM1	TFIID [T0	392	398	9.552105	TTTGGA	1.46484	1.37777
cg002138	AIFM1	TFIID [T0	1255	1261	9.552105	TTTCCC	1.46484	1.37777
cg002138	AIFM1	Pax-5 [T0	1083	1089	9.552105	GTAGCC	1.46484	1.61918
cg002138	AIFM1	NF-1 [T00	766	773	9.535536	TTGGAC	0.73242	0.74634
cg002138	AIFM1	FOXP3 [T	12	17	9.512894	ACCAAC	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	102	107	9.512894	GATAAC	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	254	259	9.512894	GTTCTG	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	494	499	9.512894	GTTGCC	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	1045	1050	9.512894	GTTGGT	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	1054	1059	9.512894	GAGAAC	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	1061	1066	9.512894	GATAAC	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	1244	1249	9.512894	GTTGCC	7.32422	7.22156
cg002138	AIFM1	FOXP3 [T	1262	1267	9.512894	CCCAAC	7.32422	7.22156

cg0021380	AIFM1	FOXP3 [T	1468	1473	9.512894	CAGAAC	7.32422	7.22156
cg0021380	AIFM1	FOXP3 [T	1479	1484	9.512894	GTTATG	7.32422	7.22156
cg0021380	AIFM1	FOXP3 [T	1570	1575	9.512894	CAGAAC	7.32422	7.22156
cg0021380	AIFM1	FOXP3 [T	1672	1677	9.512894	GTTGGG	7.32422	7.22156
cg0021380	AIFM1	FOXP3 [T	1836	1841	9.512894	GTTTAT	7.32422	7.22156
cg0021380	AIFM1	FOXP3 [T	1881	1886	9.512894	GTTTAC	7.32422	7.22156
cg0021380	AIFM1	FOXP3 [T	1892	1897	9.512894	GTTTAT	7.32422	7.22156
cg0021380	AIFM1	FOXP3 [T	1936	1941	9.512894	GTTGGG	7.32422	7.22156
cg0021380	AIFM1	TFII-I [T0	63	68	9.512894	AAATCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	89	94	9.512894	GGAAGG	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	286	291	9.512894	GGAAAA	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	351	356	9.512894	AATTCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	395	400	9.512894	GGAATT	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	484	489	9.512894	GGACTT	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	556	561	9.512894	CGGTCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	650	655	9.512894	CCTTCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	797	802	9.512894	GGAAGG	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	803	808	9.512894	GGAACG	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	876	881	9.512894	GGATTT	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1118	1123	9.512894	GGACAC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1143	1148	9.512894	CCTTCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1178	1183	9.512894	TTTTCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1270	1275	9.512894	GTTTCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1277	1282	9.512894	GGACAA	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1336	1341	9.512894	GTGTCC	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1439	1444	9.512894	GGACTT	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1690	1695	9.512894	GGATGG	7.32422	7.44385
cg0021380	AIFM1	TFII-I [T0	1791	1796	9.512894	GGACTT	7.32422	7.44385
cg0021380	AIFM1	NFI/CTF [	762	769	9.352332	GGCATT	0.54932	0.55369
cg0021380	AIFM1	E2F-1 [T0	354	361	9.261732	TCCTCC	0.15259	0.16832
cg0021380	AIFM1	c-Ets-1 [T	393	399	9.19359	TTGGAA	0.85449	0.84987
cg0021380	AIFM1	NF-AT1 [	653	661	9.18189	TCCCTT	0.22888	0.22581
cg0021380	AIFM1	PXR-1:RX	267	274	9.122407	TGAACA	0.24414	0.24356
cg0021380	AIFM1	USF2 [T0	1356	1365	9.056375	CAGGTG	0.1545	0.16206
cg0021380	AIFM1	E2F-1 [T0	426	433	9.028527	GCGGGG	0.27466	0.30178
cg0021380	AIFM1	c-Ets-1 [T	801	807	9.020687	GGGGAA	0.85449	0.84987
cg0021380	AIFM1	c-Jun [T00	1770	1776	9.013496	CATGTC	0.61035	0.60549
cg0021380	AIFM1	GR [T050	683	689	8.971049	CAAACA	0.61035	0.5928
cg0021380	AIFM1	c-Ets-2 [T	1272	1280	8.912323	TTCCTG	0.27466	0.27171
cg0021380	AIFM1	AP-1 [T00	507	515	8.907204	GGTCAG	0.24414	0.23028
cg0021380	AIFM1	GATA-2 [	1132	1140	8.888889	TGATAC	0.22888	0.22339
cg0021380	AIFM1	NF-kappa	801	811	8.884453	GGGGAA	0.03576	0.03905
cg0021380	AIFM1	c-Jun [T00	326	332	8.832178	AAGGTC	0.61035	0.60549
cg0021380	AIFM1	PR B [T00	981	987	8.827054	ACCTGT	0.36621	0.35051
cg0021380	AIFM1	PR A [T01	981	987	8.827054	ACCTGT	0.36621	0.35051
cg0021380	AIFM1	NFI/CTF [	1642	1649	8.814757	CCTCTT	0.48828	0.48845
cg0021380	AIFM1	c-Ets-1 [T	499	505	8.809329	CTGGAA	0.85449	0.84987
cg0021380	AIFM1	Elk-1 [T00	1299	1307	8.797343	CTTCCC	0.24414	0.26271

cg0021380	AIFM1	NF-1 [T00	384	391	8.790071	TCTGCC	0.24414	0.24339
cg0021380	AIFM1	LEF-1 [T0	907	914	8.759086	TCGCAA	0.54932	0.53171
cg0021380	AIFM1	XBP-1 [T	74	79	8.75604	TCTCAT	2.92969	2.75329
cg0021380	AIFM1	XBP-1 [T	1679	1684	8.75604	ATGAAA	2.92969	2.75329
cg0021380	AIFM1	XBP-1 [T	1756	1761	8.75604	ATGAGA	2.92969	2.75329
cg0021380	AIFM1	STAT1bet	1543	1552	8.695301	AATTGG	0.22316	0.2175
cg0021380	AIFM1	RAR-beta	1261	1270	8.55975	ACCCAA	0.26703	0.27434
cg0021380	AIFM1	RAR-beta	1761	1770	8.55975	ACCTAA	0.26703	0.27434
cg0021380	AIFM1	p53 [T006	1665	1671	8.537081	GGGCTC	0.12207	0.13169
cg0021380	AIFM1	LEF-1 [T0	584	591	8.457856	CTTCAA	0.15259	0.154
cg0021380	AIFM1	c-Myb [T0	1327	1334	8.443873	TTCAGT	0.30518	0.28602
cg0021380	AIFM1	c-Myb [T0	1172	1179	8.412632	TCCAGT	0.30518	0.28602
cg0021380	AIFM1	HNF-3alp	1962	1969	8.343064	TTGAAA	0.27466	0.23078
cg0021380	AIFM1	PR B [T00	43	49	8.338824	TTCTGT	1.09863	1.09384
cg0021380	AIFM1	PR B [T00	149	155	8.338824	TCCTGT	1.09863	1.09384
cg0021380	AIFM1	PR B [T00	269	275	8.338824	AACAGC	1.09863	1.09384
cg0021380	AIFM1	PR B [T00	1064	1070	8.338824	AACAGC	1.09863	1.09384
cg0021380	AIFM1	PR B [T00	1077	1083	8.338824	AACAGC	1.09863	1.09384
cg0021380	AIFM1	PR B [T00	1585	1591	8.338824	GCCTGT	1.09863	1.09384
cg0021380	AIFM1	PR B [T00	1668	1674	8.338824	CTCTGT	1.09863	1.09384
cg0021380	AIFM1	PR A [T01	43	49	8.338824	TTCTGT	1.09863	1.09384
cg0021380	AIFM1	PR A [T01	149	155	8.338824	TCCTGT	1.09863	1.09384
cg0021380	AIFM1	PR A [T01	269	275	8.338824	AACAGC	1.09863	1.09384
cg0021380	AIFM1	PR A [T01	1064	1070	8.338824	AACAGC	1.09863	1.09384
cg0021380	AIFM1	PR A [T01	1077	1083	8.338824	AACAGC	1.09863	1.09384
cg0021380	AIFM1	PR A [T01	1585	1591	8.338824	GCCTGT	1.09863	1.09384
cg0021380	AIFM1	PR A [T01	1668	1674	8.338824	CTCTGT	1.09863	1.09384
cg0021380	AIFM1	ATF3 [T0	1946	1953	8.313799	TGACAT	0.27466	0.27379
cg0021380	AIFM1	GR-alpha [	90	94	8.281568	GAAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	234	238	8.281568	GGAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	325	329	8.281568	GAAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	355	359	8.281568	CCTCC	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	451	455	8.281568	CAAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	480	484	8.281568	CCTCG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	490	494	8.281568	GGAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	536	540	8.281568	CCTCG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	566	570	8.281568	CAAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	606	610	8.281568	CCTCC	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	644	648	8.281568	CCTCC	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	647	651	8.281568	CCTCC	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	650	654	8.281568	CCTTC	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	742	746	8.281568	CCTCC	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	745	749	8.281568	CCTCC	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	798	802	8.281568	GAAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	815	819	8.281568	GGAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	988	992	8.281568	CAAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	991	995	8.281568	GGAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	1143	1147	8.281568	CCTTC	7.8125	8.20394

cg0021380	AIFM1	GR-alpha [	1191	1195	8.281568	CGAGG	7.8125	8.20394
cg0021380	AIFM1	GR-alpha [	1779	1783	8.281568	CGAGG	7.8125	8.20394
cg0021380	AIFM1	GCF [T00	821	829	8.256755	CTACTG	0.09155	0.09762
cg0021380	AIFM1	GCF [T00	1286	1294	8.256755	ATTCTG	0.09155	0.09762
cg0021380	AIFM1	c-Jun [T00	189	195	8.242207	TGACCT	0.48828	0.47447
cg0021380	AIFM1	NFI/CTF [	1263	1270	8.241664	CCAACC	0.18311	0.1922
cg0021380	AIFM1	NF-AT1 [	1251	1259	8.236182	GCTCTT	0.1297	0.12846
cg0021380	AIFM1	ENKTF-1	697	704	8.19852	CCCGGC	0.73242	0.80254
cg0021380	AIFM1	NF-1 [T00	960	967	8.191058	TTGGAC	0.24414	0.24485
cg0021380	AIFM1	LEF-1 [T0	1590	1597	8.117221	TTTCAA	0.12207	0.11275
cg0021380	AIFM1	VDR [T00	263	271	8.079962	TCCCTG	0.24414	0.22992
cg0021380	AIFM1	VDR [T00	312	320	8.079962	GTTCAA	0.24414	0.22992
cg0021380	AIFM1	GR-alpha [	33	37	8.073878	CCTGC	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	135	139	8.073878	GTAGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	474	478	8.073878	CCAGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	498	502	8.073878	CCTGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	516	520	8.073878	CCTGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	601	605	8.073878	CCAGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	783	787	8.073878	CCTGC	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	820	824	8.073878	CCTAC	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	828	832	8.073878	GCAGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	924	928	8.073878	CTAGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1028	1032	8.073878	CCTGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1203	1207	8.073878	CCTGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1274	1278	8.073878	CCTGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1340	1344	8.073878	CCTAG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1355	1359	8.073878	CCAGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1381	1385	8.073878	CCTGC	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1406	1410	8.073878	GCAGG	7.8125	8.20289
cg0021380	AIFM1	GR-alpha [	1488	1492	8.073878	GTAGG	7.8125	8.20289
cg0021380	AIFM1	AR [T000	1118	1126	8.055836	GGACAC	0.19836	0.20641
cg0021380	AIFM1	TFIID [T0	907	913	8.014558	TCGCAA	2.19727	1.99811
cg0021380	AIFM1	TFIID [T0	1415	1421	8.014558	TAGCAA	2.19727	1.99811
cg0021380	AIFM1	TFIID [T0	1545	1551	8.014558	TTGGAA	2.19727	1.99811
cg0021380	AIFM1	TFIID [T0	1590	1596	8.014558	TTTCAA	2.19727	1.99811
cg0021380	AIFM1	TFIID [T0	1678	1684	8.014558	TATGAA	2.19727	1.99811
cg0021380	AIFM1	Pax-5 [T0	138	144	8.014558	GGGCTT	2.19727	2.42766
cg0021380	AIFM1	Pax-5 [T0	445	451	8.014558	GGGCTG	2.19727	2.42766
cg0021380	AIFM1	Pax-5 [T0	540	546	8.014558	GGGCTT	2.19727	2.42766
cg0021380	AIFM1	Pax-5 [T0	569	575	8.014558	GGGCAC	2.19727	2.42766
cg0021380	AIFM1	Pax-5 [T0	692	698	8.014558	TGAGCC	2.19727	2.42766
cg0021380	AIFM1	Pax-5 [T0	1004	1010	8.014558	GGGCCG	2.19727	2.42766
cg0021380	AIFM1	Pax-5 [T0	1498	1504	8.014558	GGGCTG	2.19727	2.42766
cg0021380	AIFM1	C/EBPalp	764	770	8.006685	CATTGG	0.24414	0.23098
cg0021380	AIFM1	C/EBPalp	1577	1583	8.006685	TACAAT	0.24414	0.23098
cg0021380	AIFM1	C/EBPalp	1884	1890	8.006685	TACAAT	0.24414	0.23098
cg0021380	AIFM1	ATF-1 [T0	400	410	7.870358	TCACGT	0.07153	0.07126
cg0021380	AIFM1	c-Ets-2 [	1145	1153	7.84116	TTCCTG	0.32043	0.30792

cg0021380	AIFM1	IRF-1 [T0	1271	1279	7.82345	TTTCCTC	0.25177	0.2462
cg0021380	AIFM1	c-Ets-2 [T	1913	1921	7.76635	ATATAG	0.32043	0.30792
cg0021380	AIFM1	NF-kappa	1690	1700	7.691126	GGATGG	0.04435	0.04858
cg0021380	AIFM1	c-Myb [T0	1854	1861	7.545286	TGCAGT	0.42725	0.40917
cg0021380	AIFM1	GR [T050	587	593	7.527031	CAAAGC	1.83105	1.71535
cg0021380	AIFM1	GR [T050	1008	1014	7.527031	CGCTTTC	1.83105	1.71535
cg0021380	AIFM1	GR [T050	1153	1159	7.527031	TCTTTTG	1.83105	1.71535
cg0021380	AIFM1	GR [T050	1894	1900	7.527031	TTATTTC	1.83105	1.71535
cg0021380	AIFM1	PXR-1:RX	982	989	7.486257	CCTGTTC	0.24414	0.24326
cg0021380	AIFM1	AR [T000	1277	1285	7.467081	GGACAA	0.25177	0.2544
cg0021380	AIFM1	C/EBPalph	1960	1966	7.465744	CATTGA	0.48828	0.45033
cg0021380	AIFM1	CTF [T001	346	357	7.451629	GAGCCA	0.01431	0.0141
cg0021380	AIFM1	c-Myb [T0	1470	1477	7.442719	GAACTT	0.42725	0.40917
cg0021380	AIFM1	HNF-1B [	972	980	7.4296	AGTTAA	0.09155	0.08229
cg0021380	AIFM1	C/EBPalph	1543	1549	7.396431	AATTGG	0.48828	0.45033
cg0021380	AIFM1	C/EBPalph	1727	1733	7.396431	TACAAT	0.48828	0.45033
cg0021380	AIFM1	PXR-1:RX	966	973	7.362674	TGAACG	0.24414	0.24326
cg0021380	AIFM1	E2F-1 [T0	843	850	7.336545	GCTGCC	0.45776	0.49661
cg0021380	AIFM1	E2F-1 [T0	1034	1041	7.336545	GCTGCC	0.45776	0.49661
cg0021380	AIFM1	E2F [T002	1015	1024	7.230283	ATTGGC	0.06866	0.07407
cg0021380	AIFM1	c-Ets-1 [T	1255	1261	7.199436	TTTCCCA	0.73242	0.73732
cg0021380	AIFM1	c-Jun [T00	678	684	7.178905	CGGGTC	0.73242	0.73062
cg0021380	AIFM1	SRY [T00	583	591	7.175614	GCTTCA	0.30518	0.29547
cg0021380	AIFM1	XBP-1 [T	110	115	7.172312	CCTCAT	2.92969	2.7512
cg0021380	AIFM1	XBP-1 [T	192	197	7.172312	CCTCAT	2.92969	2.7512
cg0021380	AIFM1	XBP-1 [T	1184	1189	7.172312	ATGAGT	2.92969	2.7512
cg0021380	AIFM1	XBP-1 [T	1611	1616	7.172312	ATTCAT	2.92969	2.7512
cg0021380	AIFM1	XBP-1 [T	1744	1749	7.172312	ATGATG	2.92969	2.7512
cg0021380	AIFM1	XBP-1 [T	1829	1834	7.172312	ATGATG	2.92969	2.7512
cg0021380	AIFM1	c-Myb [T0	1122	1129	7.127234	ACCAGT	0.18311	0.17765
cg0021380	AIFM1	Ik-1 [T027	747	759	7.122895	TCCCAG	0.01064	0.01145
cg0021380	AIFM1	AhR [T01	663	673	7.102213	CTCACG	0.02289	0.02402
cg0021380	AIFM1	c-Jun [T00	405	411	7.052189	TGACTA	0.73242	0.73062
cg0021380	AIFM1	IRF-1 [T0	657	665	7.044985	TTTCCTC	0.1297	0.12685
cg0021380	AIFM1	HNF-3alph	1317	1324	7.000129	TATTTAT	0.82397	0.71909
cg0021380	AIFM1	HNF-3alph	1546	1553	7.000129	TGGAAA	0.82397	0.71909
cg0021380	AIFM1	HNF-3alph	1625	1632	7.000129	TATTTAT	0.82397	0.71909
cg0021380	AIFM1	HNF-3alph	1895	1902	7.000129	TATTTGC	0.82397	0.71909
cg0021380	AIFM1	IRF-1 [T0	1255	1263	6.968314	TTTCCCA	0.1297	0.12685
cg0021380	AIFM1	NF-1 [T00	561	568	6.948522	CGCACC	0.48828	0.50205
cg0021380	AIFM1	ENKTF-1	341	348	6.942764	TGGCTG	1.46484	1.56616
cg0021380	AIFM1	ENKTF-1	469	476	6.942764	AGGCGC	1.46484	1.56616
cg0021380	AIFM1	ENKTF-1	1017	1024	6.942764	TGGCGG	1.46484	1.56616
cg0021380	AIFM1	ENKTF-1	1524	1531	6.942764	CTCTGCC	1.46484	1.56616
cg0021380	AIFM1	p53 [T006	1004	1010	6.938545	GGGCCG	1.09863	1.22478
cg0021380	AIFM1	VDR [T00	985	993	6.925682	GTTCAA	0.42725	0.41
cg0021380	AIFM1	STAT1bet	1178	1187	6.908963	TTTTCCA	0.103	0.09938
cg0021380	AIFM1	E2F-1 [T0	1197	1204	6.839754	GCGGAA	0.30518	0.33862

cg0021380	AIFM1	c-Ets-1 [T	284	290	6.815175	CGGGAA	0.73242	0.73732
cg0021380	AIFM1	PU.1 [T02	1913	1925	6.801739	ATATAG	0.00337	0.00315
cg0021380	AIFM1	NFI/CTF [	83	90	6.786076	TGGTTT	0.73242	0.74795
cg0021380	AIFM1	NFI/CTF [	1012	1019	6.786076	TTGATT	0.73242	0.74795
cg0021380	AIFM1	p53 [T006	692	698	6.778774	TGAGCC	1.09863	1.22478
cg0021380	AIFM1	p53 [T006	1083	1089	6.775228	GTAGCC	1.09863	1.22478
cg0021380	AIFM1	c-Ets-1 [T	1197	1203	6.693449	GCGGAA	0.48828	0.48842
cg0021380	AIFM1	FOXP3 [T	1112	1117	6.581441	GTTTTA	0.97656	0.904
cg0021380	AIFM1	FOXP3 [T	1805	1810	6.581441	TTCAAC	0.97656	0.904
cg0021380	AIFM1	TFII-I [T0	1941	1946	6.581441	GGAGAT	0.97656	0.9991
cg0021380	AIFM1	NF-kappa	232	242	6.577926	GGGGAG	0.03052	0.03409
cg0021380	AIFM1	c-Ets-1 [T	614	620	6.565361	CCGGAA	0.48828	0.48842
cg0021380	AIFM1	RXR-alpha	1844	1850	6.563693	GGGTAT	0.24414	0.25119
cg0021380	AIFM1	p53 [T006	445	451	6.563521	GGGCTG	0.48828	0.54643
cg0021380	AIFM1	p53 [T006	540	546	6.563521	GGGCTT	0.48828	0.54643
cg0021380	AIFM1	AR [T000	1333	1341	6.50872	TGTGTG	0.19836	0.20813
cg0021380	AIFM1	XBP-1 [T	55	60	6.478682	GGGCAT	0.97656	0.99906
cg0021380	AIFM1	XBP-1 [T	761	766	6.478682	GGGCAT	0.97656	0.99906
cg0021380	AIFM1	c-Ets-1 [T	1545	1551	6.423689	TTGGAA	0.48828	0.48842
cg0021380	AIFM1	C/EBPalp	348	354	6.391486	GCCAAT	0.48828	0.47407
cg0021380	AIFM1	C/EBPalp	387	393	6.391486	GCCAAT	0.48828	0.47407
cg0021380	AIFM1	TCF-4E [T	585	591	6.302385	TTCAAA	0.61035	0.59686
cg0021380	AIFM1	TCF-4E [T	908	914	6.302385	CGCAAA	0.61035	0.59686
cg0021380	AIFM1	TCF-4E [T	1100	1106	6.302385	CTTTGTT	0.61035	0.59686
cg0021380	AIFM1	TCF-4E [T	1591	1597	6.302385	TTCAAA	0.61035	0.59686
cg0021380	AIFM1	c-Ets-1 [T	1179	1185	6.295602	TTTCCAT	0.48828	0.48842
cg0021380	AIFM1	GR-alpha [	23	27	6.263098	CCTTA	3.90625	3.89624
cg0021380	AIFM1	GR-alpha [	110	114	6.263098	CCTCA	3.90625	3.89624
cg0021380	AIFM1	GR-alpha [	192	196	6.263098	CCTCA	3.90625	3.89624
cg0021380	AIFM1	GR-alpha [	294	298	6.263098	CCTCA	3.90625	3.89624
cg0021380	AIFM1	GR-alpha [	467	471	6.263098	TAAGG	3.90625	3.89624
cg0021380	AIFM1	GR-alpha [	975	979	6.263098	TAAGG	3.90625	3.89624
cg0021380	AIFM1	GR-alpha [	1494	1498	6.263098	TGAGG	3.90625	3.89624
cg0021380	AIFM1	GR-alpha [	1709	1713	6.263098	CCTCA	3.90625	3.89624
cg0021380	AIFM1	IRF-1 [T0	282	290	6.203774	CCCGGG	0.16785	0.16217
cg0021380	AIFM1	SRY [T00	174	182	6.176442	ATGACA	0.15259	0.14742
cg0021380	AIFM1	SRY [T00	1589	1597	6.176442	GTTTCA	0.15259	0.14742
cg0021380	AIFM1	c-Myb [T0	1807	1814	6.157321	CAACTT	0.21362	0.2053
cg0021380	AIFM1	c-Jun [T00	175	181	6.152811	TGACAA	0.36621	0.34478
cg0021380	AIFM1	GR-alpha [	129	133	6.055408	TTAGG	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	265	269	6.055408	CCTGA	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	330	334	6.055408	TCAGG	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	371	375	6.055408	TCAGG	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	465	469	6.055408	CCTAA	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	1115	1119	6.055408	TTAGG	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	1147	1151	6.055408	CCTGA	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	1762	1766	6.055408	CCTAA	3.90625	3.89835
cg0021380	AIFM1	GR-alpha [	1841	1845	6.055408	TCAGG	3.90625	3.89835

cg0021380	AIFM1	GCF [T00	1195	1203	5.917256	GCGCGG	0.64087	0.72542
cg0021380	AIFM1	STAT4 [T	89	94	5.882353	GGAAGG	0.48828	0.51201
cg0021380	AIFM1	STAT4 [T	650	655	5.882353	CCTTCC	0.48828	0.51201
cg0021380	AIFM1	STAT4 [T	797	802	5.882353	GGAAGG	0.48828	0.51201
cg0021380	AIFM1	STAT4 [T	1143	1148	5.882353	CCTTCC	0.48828	0.51201
cg0021380	AIFM1	c-Myb [T0	1240	1247	5.841835	ACCAGT	0.21362	0.2053
cg0021380	AIFM1	c-Ets-1 [T	1208	1214	5.814485	CTTCCC	0.36621	0.36174
cg0021380	AIFM1	c-Ets-1 [T	1447	1453	5.814485	TGGGAA	0.36621	0.36174
cg0021380	AIFM1	STAT1bet	1270	1279	5.796867	GTTTCC	0.1545	0.14881
cg0021380	AIFM1	c-Jun [T00	1822	1828	5.783074	TGACTT	0.36621	0.34478
cg0021380	AIFM1	VDR [T00	962	970	5.771401	GGACTG	0.42725	0.41266
cg0021380	AIFM1	VDR [T00	1326	1334	5.771401	GTTCAG	0.42725	0.41266
cg0021380	AIFM1	RXR-alph	105	111	5.715466	AACACC	0.61035	0.65415
cg0021380	AIFM1	ENKTF-1	344	351	5.687009	CTGAGC	0.73242	0.76357
cg0021380	AIFM1	ENKTF-1	950	957	5.687009	TGGCAC	0.73242	0.76357
cg0021380	AIFM1	c-Ets-1 [T	651	657	5.686398	CTTCCC	0.36621	0.38732
cg0021380	AIFM1	HNF-1A [	1863	1870	5.610392	GACTTA	0.24414	0.23087
cg0021380	AIFM1	C/EBPalp	1649	1655	5.565669	GATTGT	0.73242	0.68229
cg0021380	AIFM1	IRF-1 [T0	1179	1187	5.564062	TTTCCAT	0.22888	0.21959
cg0021380	AIFM1	NFI/CTF [	1396	1403	5.558661	GTGCTT	0.54932	0.55504
cg0021380	AIFM1	c-Ets-1 [T	795	801	5.558311	GGGGAA	0.36621	0.38732
cg0021380	AIFM1	TFIID [T0	1114	1120	5.544826	TTTAGG	0.73242	0.65314
cg0021380	AIFM1	TFIID [T0	1237	1243	5.544826	TTTACC	0.73242	0.65314
cg0021380	AIFM1	TFIID [T0	1616	1622	5.544826	TTTAAC	0.73242	0.65314
cg0021380	AIFM1	TFIID [T0	1837	1843	5.544826	TTTATC	0.73242	0.65314
cg0021380	AIFM1	p53 [T006	138	144	5.508538	GGGCTT	0.61035	0.65765
cg0021380	AIFM1	p53 [T006	1498	1504	5.508538	GGGCTG	0.61035	0.65765
cg0021380	AIFM1	C/EBPalp	195	201	5.455853	CATTGC	0.73242	0.68229
cg0021380	AIFM1	c-Ets-1 [T	1299	1305	5.430224	CTTCCC	0.36621	0.38732
cg0021380	AIFM1	RXR-alph	212	218	5.271235	GGGTGG	0.61035	0.65415
cg0021380	AIFM1	RXR-alph	219	225	5.271235	GGGTGG	0.61035	0.65415
cg0021380	AIFM1	RXR-alph	438	444	5.271235	GGGTAG	0.61035	0.65415
cg0021380	AIFM1	RXR-alph	757	763	5.271235	GGGTGG	0.61035	0.65415
cg0021380	AIFM1	RXR-alph	1258	1264	5.271235	CCCACC	0.61035	0.65415
cg0021380	AIFM1	GR [T050	910	916	5.207533	CAAAGA	0.24414	0.24013
cg0021380	AIFM1	c-Ets-2 [T	973	981	5.162974	GTTAAG	0.13733	0.13279
cg0021380	AIFM1	AR [T000	1900	1908	5.106898	GGACAT	0.11444	0.12256
cg0021380	AIFM1	AR [T000	768	776	5.104816	GGACAG	0.11444	0.12256
cg0021380	AIFM1	AP-2alpha	289	294	5.100982	AAAGGC	0.97656	0.97517
cg0021380	AIFM1	RXR-alph	590	596	5.089356	AGCACC	0.48828	0.51407
cg0021380	AIFM1	SRY [T00	1010	1018	5.086565	CTTTGA	0.06104	0.05662
cg0021380	AIFM1	AP-1 [T00	1521	1529	5.059986	TGACTC	0.12207	0.12309
cg0021380	AIFM1	GR-beta [	64	68	5.042296	AATCC	3.90625	3.7093
cg0021380	AIFM1	GR-beta [	876	880	5.042296	GGATT	3.90625	3.7093
cg0021380	AIFM1	GR-beta [	1624	1628	5.042296	GTATT	3.90625	3.7093
cg0021380	AIFM1	GR-beta [	1648	1652	5.042296	GGATT	3.90625	3.7093
cg0021380	AIFM1	GR-beta [	1846	1850	5.042296	GTATT	3.90625	3.7093
cg0021380	AIFM1	c-Ets-1 [T	87	93	5.038739	TTGGAA	0.48828	0.48026

cg0021380	AIFM1	HNF-1A [	973	980	4.972635	GTTAAG	0.36621	0.34064
cg0021380	AIFM1	c-Ets-1 [T	1228	1234	4.910652	CTTCCA	0.48828	0.48026
cg0021380	AIFM1	PXR-1:RX	1801	1808	4.90845	ATGGTT	0.12207	0.11843
cg0021380	AIFM1	XBP-1 [T	227	232	4.894955	ATGCCG	0.97656	0.99839
cg0021380	AIFM1	XBP-1 [T	336	341	4.894955	CGGCAT	0.97656	0.99839
cg0021380	AIFM1	XBP-1 [T	1090	1095	4.894955	CGGCAT	0.97656	0.99839
cg0021380	AIFM1	USF1 [T0	401	410	4.89185	CACGTG	0.04578	0.04763
cg0021380	AIFM1	AP-2alpha	129	134	4.890408	TTAGGC	0.97656	0.97517
cg0021380	AIFM1	AP-2alpha	464	469	4.890408	GCCTAA	0.97656	0.97517
cg0021380	AIFM1	c-Jun [T00	1946	1952	4.883696	TGACAT	0.61035	0.60573
cg0021380	AIFM1	RXR-alph	1675	1681	4.86724	GGGTAT	0.48828	0.51407
cg0021380	AIFM1	GCF [T00	238	246	4.846987	GCGCCG	0.27466	0.31905
cg0021380	AIFM1	HNF-1A [	414	421	4.828753	GTTAAG	0.36621	0.34064
cg0021380	AIFM1	NF-AT1 [	1546	1555	4.823485	TGGAAA	0.07629	0.07281
cg0021380	AIFM1	FOXP3 [T	935	940	4.756447	GTTTTC	2.92969	2.82
cg0021380	AIFM1	FOXP3 [T	1104	1109	4.756447	GTTTTT	2.92969	2.82
cg0021380	AIFM1	FOXP3 [T	1176	1181	4.756447	GTTTTT	2.92969	2.82
cg0021380	AIFM1	FOXP3 [T	1517	1522	4.756447	GTTTTG	2.92969	2.82
cg0021380	AIFM1	FOXP3 [T	1556	1561	4.756447	GTTTTG	2.92969	2.82
cg0021380	AIFM1	FOXP3 [T	1816	1821	4.756447	GTTTTT	2.92969	2.82
cg0021380	AIFM1	TFII-I [T0	501	506	4.756447	GGAATG	2.92969	2.89715
cg0021380	AIFM1	TFII-I [T0	962	967	4.756447	GGACTG	2.92969	2.89715
cg0021380	AIFM1	TFII-I [T0	1547	1552	4.756447	GGAAAT	2.92969	2.89715
cg0021380	AIFM1	TFII-I [T0	1648	1653	4.756447	GGATTG	2.92969	2.89715
cg0021380	AIFM1	TFII-I [T0	1900	1905	4.756447	GGACAT	2.92969	2.89715
cg0021380	AIFM1	VDR [T00	1804	1812	4.617121	GTTCAA	0.37384	0.36855
cg0021380	AIFM1	C/EBPalp	1014	1020	4.560723	GATTGG	0.24414	0.24373
cg0021380	AIFM1	USF1 [T0	397	406	4.464121	AATTCA	0.06866	0.06933
cg0021380	AIFM1	IRF-1 [T0	1543	1551	4.462268	AATTGG	0.05341	0.05056
cg0021380	AIFM1	T3R-beta1	1310	1318	4.462023	TCACCT	0.27466	0.27245
cg0021380	AIFM1	c-Jun [T00	509	515	4.441904	TCAGTC	0.12207	0.11843
cg0021380	AIFM1	AP-2alpha	467	472	4.422424	TAAGGC	0.97656	0.99839
cg0021380	AIFM1	STAT4 [T	501	506	4.411765	GGAATG	1.95312	1.99838
cg0021380	AIFM1	STAT4 [T	803	808	4.411765	GGAACG	1.95312	1.99838
cg0021380	AIFM1	STAT4 [T	1207	1212	4.411765	GCTTCC	1.95312	1.99838
cg0021380	AIFM1	STAT4 [T	1298	1303	4.411765	TCTTCC	1.95312	1.99838
cg0021380	AIFM1	STAT4 [T	1449	1454	4.411765	GGAAGA	1.95312	1.99838
cg0021380	AIFM1	ELF-1 [T0	1913	1925	4.321554	ATATAG	0.0037	0.00365
cg0021380	AIFM1	RAR-beta	1889	1898	4.289108	TGGGTT	0.14496	0.14853
cg0021380	AIFM1	c-Ets-1 [T	352	358	4.282938	ATTCCT	0.85449	0.8381
cg0021380	AIFM1	RXR-alph	1703	1709	4.24113	CTTACC	0.97656	1.02803
cg0021380	AIFM1	AR [T000	1987	1995	4.241082	GGACAG	0.06866	0.06981
cg0021380	AIFM1	AP-2alpha	819	824	4.211849	GCCTAC	0.97656	1.02535
cg0021380	AIFM1	GR-beta [	165	169	4.201913	AATCG	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	634	638	4.201913	CTATT	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	855	859	4.201913	CGATT	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1013	1017	4.201913	TGATT	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1149	1153	4.201913	TGATT	7.8125	7.23274

cg0021380	AIFM1	GR-beta [	1316	1320	4.201913	TTATT	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1320	1324	4.201913	TTATT	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1510	1514	4.201913	AATAA	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1550	1554	4.201913	AATAA	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1628	1632	4.201913	TTATT	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1894	1898	4.201913	TTATT	7.8125	7.23274
cg0021380	AIFM1	GR-beta [	1966	1970	4.201913	AATAA	7.8125	7.23274
cg0021380	AIFM1	NF-Y [T0	1544	1551	4.186615	ATTGGA	0.18311	0.17499
cg0021380	AIFM1	NF-1 [T00	345	352	4.135372	TGAGCC	0.24414	0.25714
cg0021380	AIFM1	p53 [T006	475	481	4.125254	CAGGCC	0.73242	0.82434
cg0021380	AIFM1	p53 [T006	569	575	4.083527	GGGCAC	0.73242	0.82434
cg0021380	AIFM1	TFIID [T0	1319	1325	4.007279	TTTATTA	1.09863	0.94722
cg0021380	AIFM1	TFIID [T0	1741	1747	4.007279	TTTATG	1.09863	0.94722
cg0021380	AIFM1	TFIID [T0	1826	1832	4.007279	TTTATG	1.09863	0.94722
cg0021380	AIFM1	TFIID [T0	1847	1853	4.007279	TATTAA	1.09863	0.94722
cg0021380	AIFM1	TFIID [T0	1882	1888	4.007279	TTTACA	1.09863	0.94722
cg0021380	AIFM1	Pax-5 [T0	55	61	4.007279	GGGCAT	1.09863	1.18533
cg0021380	AIFM1	Pax-5 [T0	761	767	4.007279	GGGCAT	1.09863	1.18533
cg0021380	AIFM1	Pax-5 [T0	1665	1671	4.007279	GGGCTC	1.09863	1.18533
cg0021380	AIFM1	AP-2alpha	451	456	3.970052	CAAGGC	0.97656	1.02535
cg0021380	AIFM1	Elk-1 [T00	1914	1922	3.944668	TATAGG	0.09155	0.08816
cg0021380	AIFM1	c-Fos [T00	1517	1526	3.849714	GTTTTG	0.03815	0.03747
cg0021380	AIFM1	NFI/CTF [	565	572	3.793671	CCAAGG	0.18311	0.19063
cg0021380	AIFM1	GR [T050	1516	1522	3.763516	TGTTTC	0.73242	0.6946
cg0021380	AIFM1	GR [T050	1555	1561	3.763516	TGTTTC	0.73242	0.6946
cg0021380	AIFM1	GR [T050	1593	1599	3.763516	CAAAGA	0.73242	0.6946
cg0021380	AIFM1	AP-2alpha	90	95	3.743866	GAAGGC	0.48828	0.5124
cg0021380	AIFM1	AP-2alpha	1142	1147	3.743866	GCCTTC	0.48828	0.5124
cg0021380	AIFM1	c-Ets-1 [T	976	982	3.71855	AAGGAA	0.61035	0.61936
cg0021380	AIFM1	c-Ets-1 [T	527	533	3.590463	GTTCCT	0.61035	0.61936
cg0021380	AIFM1	C/EBPalph	856	862	3.555778	GATTGG	0.24414	0.23261
cg0021380	AIFM1	E2F-1 [T0	1299	1306	3.55167	CTTCCC	0.15259	0.16507
cg0021380	AIFM1	p53 [T006	55	61	3.516613	GGGCAT	0.73242	0.80362
cg0021380	AIFM1	p53 [T006	761	767	3.516613	GGGCAT	0.73242	0.80362
cg0021380	AIFM1	HNF-3alph	1506	1513	3.500065	TGTAAA	0.27466	0.23175
cg0021380	AIFM1	NF-Y [T0	385	392	3.490142	CTGCCA	0.48828	0.48427
cg0021380	AIFM1	NF-Y [T0	1015	1022	3.490142	ATTGGC	0.48828	0.48427
cg0021380	AIFM1	NF-AT1 [	1175	1184	3.445347	AGTTTT	0.07629	0.07204
cg0021380	AIFM1	PXR-1:RX	309	316	3.395883	TGGGTT	0.12207	0.11883
cg0021380	AIFM1	RXR-alph	1491	1497	3.392904	GGGTGA	1.09863	1.1653
cg0021380	AIFM1	Elk-1 [T00	1144	1152	3.381796	CTTCCT	0.04578	0.04517
cg0021380	AIFM1	GR-beta [	317	321	3.361531	AATCT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [	1596	1600	3.361531	AGATT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [	1609	1613	3.361531	ATATT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [	1872	1876	3.361531	ATATT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [	1969	1973	3.361531	AATAT	3.90625	3.51525
cg0021380	AIFM1	T3R-beta1	513	521	3.332047	TCACCT	0.27466	0.27326
cg0021380	AIFM1	PR B [T00	618	624	3.29756	AACATT	0.24414	0.21408

cg0021380	AIFM1	PR A [T01	618	624	3.29756	AACATT	0.24414	0.21408
cg0021380	AIFM1	c-Jun [T00	1521	1527	3.244843	TGACTC	0.24414	0.2435
cg0021380	AIFM1	RAR-beta	309	318	3.244529	TGGGTT	0.12207	0.12558
cg0021380	AIFM1	RAR-beta	373	382	3.226064	AGGGTT	0.12207	0.12558
cg0021380	AIFM1	RAR-beta	1833	1842	3.207598	TGGGTT	0.12207	0.12558
cg0021380	AIFM1	TCF-4E [T	1010	1016	3.151193	CTTTGA	0.24414	0.23169
cg0021380	AIFM1	TFIID [T0	1155	1161	3.075094	TTTTGC	0.12207	0.11309
cg0021380	AIFM1	c-Jun [T00	505	511	3.049104	TGGGTC	0.24414	0.2435
cg0021380	AIFM1	C/EBPalph	1712	1718	2.981957	CACAAT	0.48828	0.47526
cg0021380	AIFM1	STAT4 [T	526	531	2.941176	GGTTCC	2.92969	2.92382
cg0021380	AIFM1	STAT4 [T	616	621	2.941176	GGAACA	2.92969	2.92382
cg0021380	AIFM1	STAT4 [T	656	661	2.941176	CTTTCC	2.92969	2.92382
cg0021380	AIFM1	STAT4 [T	978	983	2.941176	GGAACC	2.92969	2.92382
cg0021380	AIFM1	STAT4 [T	1199	1204	2.941176	GGAACC	2.92969	2.92382
cg0021380	AIFM1	STAT4 [T	1227	1232	2.941176	ACTTCC	2.92969	2.92382
cg0021380	AIFM1	STAT4 [T	1254	1259	2.941176	CTTTCC	2.92969	2.92382
cg0021380	AIFM1	STAT4 [T	1918	1923	2.941176	GGAAGT	2.92969	2.92382
cg0021380	AIFM1	NF-1 [T00	858	865	2.813149	TTGGTC	0.24414	0.2566
cg0021380	AIFM1	PR B [T00	1552	1558	2.80933	TAATGT	0.73242	0.66711
cg0021380	AIFM1	PR A [T01	1552	1558	2.80933	TAATGT	0.73242	0.66711
cg0021380	AIFM1	TBP [T00	1653	1662	2.807313	GTACTA	0.12207	0.10444
cg0021380	AIFM1	NF-AT2 [	1174	1183	2.800326	CAGTTT	0.03433	0.03159
cg0021380	AIFM1	NF-AT2 [	1547	1556	2.800326	GGAAAT	0.03433	0.03159
cg0021380	AIFM1	RXR-alph	1263	1269	2.726556	CCAACC	0.85449	0.89683
cg0021380	AIFM1	c-Ets-2 [T	353	361	2.715313	TTCCTC	0.07629	0.07844
cg0021380	AIFM1	NFI/CTF [	13	20	2.683003	CCAACC	0.06104	0.06609
cg0021380	AIFM1	NF-Y [T0	765	772	2.673185	ATTGGA	0.21362	0.20842
cg0021380	AIFM1	TCF-4 [T0	1589	1598	2.632973	GTTTCA	0.03433	0.03112
cg0021380	AIFM1	AP-2alpha	293	298	2.550491	GCCTCA	0.48828	0.51216
cg0021380	AIFM1	ENKTF-1	596	603	2.511511	CGCCGC	0.12207	0.13847
cg0021380	AIFM1	C/EBPalph	850	856	2.441016	CATTGC	0.48828	0.47439
cg0021380	AIFM1	GCF [T00	826	834	2.339499	GCGCAG	0.06104	0.06908
cg0021380	AIFM1	T3R-beta1	1044	1052	2.240658	TGTTGG	0.15259	0.15303
cg0021380	AIFM1	GATA-1 [	1869	1874	2.176375	ACGATA	3.90625	3.79558
cg0021380	AIFM1	RAR-beta	1748	1757	2.16302	TGGGTT	0.07629	0.07711
cg0021380	AIFM1	c-Ets-2 [T	528	536	2.142327	TTCCTCT	0.16785	0.16456
cg0021380	AIFM1	NF-Y [T0	346	353	2.12821	GAGCCA	0.21362	0.20748
cg0021380	AIFM1	AP-2alpha	535	540	2.098119	GCCTCG	0.97656	1.07805
cg0021380	AIFM1	AP-2alpha	1191	1196	2.098119	CGAGGC	0.97656	1.07805
cg0021380	AIFM1	LEF-1 [T0	1100	1107	2.004405	CTTTGTT	0.18311	0.17215
cg0021380	AIFM1	NF-AT1 [	1547	1555	1.94698	GGAAAT	0.06866	0.0623
cg0021380	AIFM1	PR B [T00	1513	1519	1.892895	AAGTGT	0.12207	0.1127
cg0021380	AIFM1	PR A [T01	1513	1519	1.892895	AAGTGT	0.12207	0.1127
cg0021380	AIFM1	AP-2alpha	234	239	1.871933	GGAGGC	0.97656	1.07805
cg0021380	AIFM1	AP-2alpha	605	610	1.871933	GCCTCC	0.97656	1.07805
cg0021380	AIFM1	AP-2alpha	815	820	1.871933	GGAGGC	0.97656	1.07805
cg0021380	AIFM1	RXR-alph	506	512	1.696452	GGGTCA	0.48828	0.52093
cg0021380	AIFM1	TCF-4 [T0	583	592	1.687438	GCTTCA	0.04578	0.04304

cg0021380	AIFM1	GR-beta [T	57	61	1.680765	GCATT	3.90625	3.70067
cg0021380	AIFM1	GR-beta [T	351	355	1.680765	AATTC	3.90625	3.70067
cg0021380	AIFM1	GR-beta [T	396	400	1.680765	GAATT	3.90625	3.70067
cg0021380	AIFM1	GR-beta [T	397	401	1.680765	AATTC	3.90625	3.70067
cg0021380	AIFM1	GR-beta [T	763	767	1.680765	GCATT	3.90625	3.70067
cg0021380	AIFM1	GR-beta [T	849	853	1.680765	GCATT	3.90625	3.70067
cg0021380	AIFM1	GR-beta [T	1285	1289	1.680765	AATTC	3.90625	3.70067
cg0021380	AIFM1	GR-beta [T	1852	1856	1.680765	AATGC	3.90625	3.70067
cg0021380	AIFM1	C/EBPbeta	13	16	1.639871	CCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	87	90	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	349	352	1.639871	CCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	388	391	1.639871	CCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	393	396	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	488	491	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	565	568	1.639871	CCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	766	769	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	858	861	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	960	963	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1016	1019	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1046	1049	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1109	1112	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1263	1266	1.639871	CCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1400	1403	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1545	1548	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1559	1562	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1646	1649	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1673	1676	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1898	1901	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1937	1940	1.639871	TTGG	15.625	15.23827
cg0021380	AIFM1	XBP-1 [T0	174	179	1.583727	ATGACA	0.97656	0.94995
cg0021380	AIFM1	XBP-1 [T0	1945	1950	1.583727	ATGACA	0.97656	0.94995
cg0021380	AIFM1	XBP-1 [T0	1957	1962	1.583727	GGTCAT	0.97656	0.94995
cg0021380	AIFM1	TFIID [T0	1178	1184	1.537547	TTTTCCA	0.73242	0.65627
cg0021380	AIFM1	Pax-5 [T0	28	34	1.537547	CTTGCCC	0.73242	0.83087
cg0021380	AIFM1	c-Ets-1 [T	657	663	1.513038	TTTCCTC	0.36621	0.35197
cg0021380	AIFM1	STAT4 [T	286	291	1.470588	GGAAAA	1.95312	1.90161
cg0021380	AIFM1	STAT4 [T	351	356	1.470588	AATTCC	1.95312	1.90161
cg0021380	AIFM1	STAT4 [T	395	400	1.470588	GGAATT	1.95312	1.90161
cg0021380	AIFM1	STAT4 [T	1178	1183	1.470588	TTTTCC	1.95312	1.90161
cg0021380	AIFM1	STAT4 [T	1270	1275	1.470588	GTTTCC	1.95312	1.90161
cg0021380	AIFM1	PR B [T00	955	961	1.404665	CAGTGT	0.36621	0.35143
cg0021380	AIFM1	PR A [T01	955	961	1.404665	CAGTGT	0.36621	0.35143
cg0021380	AIFM1	c-Ets-1 [T	1271	1277	1.384951	TTTCCTC	0.36621	0.35197
cg0021380	AIFM1	C/EBPbeta	61	64	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	163	166	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	188	191	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	296	299	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	314	317	1.366559	TCAA	15.625	15.23827

cg0021380	AIFM1	C/EBPbeta	323	326	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	586	589	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	682	685	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	987	990	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1012	1015	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1131	1134	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1520	1523	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1592	1595	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1631	1634	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1806	1809	1.366559	TCAA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1821	1824	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	C/EBPbeta	1962	1965	1.366559	TTGA	15.625	15.23827
cg0021380	AIFM1	LEF-1 [T0	1010	1017	1.362541	CTTTGA	0.09155	0.08414
cg0021380	AIFM1	AP-2alpha	1305	1310	1.357116	GCCTGT	0.48828	0.51319
cg0021380	AIFM1	AP-2alpha	1585	1590	1.357116	GCCTGT	0.48828	0.51319
cg0021380	AIFM1	C/EBPalp	1629	1635	1.220508	TATTGA	0.24414	0.23153
cg0021380	AIFM1	c-Ets-2 [T	658	666	1.071163	TTCCTCT	0.06104	0.0583
cg0021380	AIFM1	USF2 [T0	510	519	1.048473	CAGTCA	0.01717	0.01798
cg0021380	AIFM1	GATA-1 [	1131	1136	1.038567	TTGATA	1.95312	1.80234
cg0021380	AIFM1	SRY [T00	1100	1108	0.999172	CTTTGTT	0.06104	0.0571
cg0021380	AIFM1	HNF-1A [	1614	1621	0.925521	CATTTA	0.48828	0.45029
cg0021380	AIFM1	TCF-4 [T0	1009	1018	0.925008	GCTTTG	0.05722	0.05422
cg0021380	AIFM1	c-Myb [T0	247	254	0.867346	GCCAGT	0.03052	0.03199
cg0021380	AIFM1	RXR-alpha	374	380	0.848226	GGGTTC	0.48828	0.51313
cg0021380	AIFM1	RXR-alpha	679	685	0.848226	GGGTCA	0.48828	0.51313
cg0021380	AIFM1	RXR-alpha	1763	1769	0.848226	CTAACC	0.48828	0.51313
cg0021380	AIFM1	GR-beta [	112	116	0.840383	TCATT	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	173	177	0.840383	AATGA	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	194	198	0.840383	TCATT	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	350	354	0.840383	CAATT	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	389	393	0.840383	CAATT	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	503	507	0.840383	AATGG	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1284	1288	0.840383	TAATT	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1543	1547	0.840383	AATTG	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1613	1617	0.840383	TCATT	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1715	1719	0.840383	AATGG	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1729	1733	0.840383	CAATT	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1755	1759	0.840383	AATGA	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1887	1891	0.840383	AATGG	7.8125	7.2174
cg0021380	AIFM1	GR-beta [	1959	1963	0.840383	TCATT	7.8125	7.2174
cg0021380	AIFM1	GATA-1 [	1059	1064	0.758539	CTGATA	1.95312	1.80234
cg0021380	AIFM1	GATA-1 [	1839	1844	0.758539	TATCAG	1.95312	1.80234
cg0021380	AIFM1	NF-Y [T0	857	864	0.680578	ATTGGT	0.09155	0.08698
cg0021380	AIFM1	RXR-alpha	1749	1755	0.62611	GGGTTT	0.12207	0.11915
cg0021380	AIFM1	RXR-alpha	1834	1840	0.62611	GGGTTT	0.12207	0.11915
cg0021380	AIFM1	RXR-alpha	1890	1896	0.62611	GGGTTT	0.12207	0.11915
cg0021380	AIFM1	PEA3 [T0	1408	1416	0.597316	AGGATG	0.04578	0.04362
cg0021380	AIFM1	NF-AT1 [	1175	1183	0.479048	AGTTTT	0.02289	0.02115

cg0021380	AIFM1	c-Ets-1 [T	1916	1922	0.384261	TAGGAA	0.24414	0.23743
cg0021380	AIFM1	AP-2alpha	474	479	0.226186	CCAGGC	0.97656	1.07867
cg0021380	AIFM1	AP-2alpha	497	502	0.226186	GCCTGG	0.97656	1.07867
cg0021380	AIFM1	AP-2alpha	601	606	0.226186	CCAGGC	0.97656	1.07867
cg0021380	AIFM1	AP-2alpha	1027	1032	0.226186	GCCTGG	0.97656	1.07867
cg0021380	AIFM1	p53 [T006	28	34	0.211706	CTTGCCC	0.36621	0.40082
cg0021380	AIFM1	GR-alpha [	206	210	0.207689	AAAGG	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	289	293	0.207689	AAAGG	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	442	446	0.207689	AGAGG	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	530	534	0.207689	CCTCT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	655	659	0.207689	CCTTT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	660	664	0.207689	CCTCT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	873	877	0.207689	AGAGG	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	1313	1317	0.207689	CCTTT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	1642	1646	0.207689	CCTCT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	1661	1665	0.207689	AAAGG	7.8125	7.79817
cg0021380	AIFM1	GR-beta [T	390	394	0	AATTT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [T	619	623	0	ACATT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [T	728	732	0	ACATT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [T	1542	1546	0	AAATT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [T	1553	1557	0	AATGT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [T	1580	1584	0	AATGT	3.90625	3.51525
cg0021380	AIFM1	GR-beta [T	1730	1734	0	AATTT	3.90625	3.51525
cg0021380	AIFM1	TFIID [T0	201	207	0	TCTAAA	1.09863	0.95175
cg0021380	AIFM1	TFIID [T0	1657	1663	0	TATAAA	1.09863	0.95175
cg0021380	AIFM1	TFIID [T0	1733	1739	0	TTTTCGA	1.09863	0.95175
cg0021380	AIFM1	TFIID [T0	1818	1824	0	TTTTTGA	1.09863	0.95175
cg0021380	AIFM1	GR-alpha [	150	154	0	CCTGT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	457	461	0	ACAGG	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	982	986	0	CCTGT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	1306	1310	0	CCTGT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	1586	1590	0	CCTGT	7.8125	7.79817
cg0021380	AIFM1	GR-alpha [	1915	1919	0	ATAGG	7.8125	7.79817
cg0021380	AIFM1	FOXP3 [T	8	13	0	CACAAC	1.46484	1.44953
cg0021380	AIFM1	FOXP3 [T	251	256	0	GTTGTT	1.46484	1.44953
cg0021380	AIFM1	FOXP3 [T	1022	1027	0	GTTGTG	1.46484	1.44953
cg0021380	AIFM1	FOXP3 [T	1074	1079	0	CACAAC	1.46484	1.44953
cg0021380	AIFM1	FOXP3 [T	1331	1336	0	GTTGTG	1.46484	1.44953
cg0021380	AIFM1	HNF-3alph	1873	1880	0	TATTTC	0.09155	0.07727
cg0021380	AIFM1	C/EBPbeta	9	12	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	29	32	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	120	123	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	177	180	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	197	200	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	252	255	0	TTGT	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	273	276	0	GCAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	362	365	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	364	367	0	GCAA	15.625	15.26275

cg0021380	AIFM1	C/EBPbeta	450	453	0	GCAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	495	498	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	852	855	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	880	883	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	901	904	0	GCAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	909	912	0	GCAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	947	950	0	TTGT	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1023	1026	0	TTGT	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1075	1078	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1102	1105	0	TTGT	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1157	1160	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1245	1248	0	TTGC	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1279	1282	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1332	1335	0	TTGT	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1417	1420	0	GCAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1578	1581	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1620	1623	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1651	1654	0	TTGT	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1713	1716	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1728	1731	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1885	1888	0	ACAA	15.625	15.26275
cg0021380	AIFM1	C/EBPbeta	1994	1997	0	GCAA	15.625	15.26275
cg0021380	AIFM1	YY1 [T00	67	70	0	CCAT	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	69	72	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	340	343	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	504	507	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1182	1185	0	CCAT	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1231	1234	0	CCAT	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1482	1485	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1692	1695	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1716	1719	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1747	1750	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1769	1772	0	CCAT	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1801	1804	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1832	1835	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	YY1 [T00	1888	1891	0	ATGG	7.8125	7.79459
cg0021380	AIFM1	C/EBPalph	162	168	0	CTCAAT	0.24414	0.24342
cg0021380	AIFM1	TFII-I [T0	656	661	0	CTTTCC	1.46484	1.48598
cg0021380	AIFM1	TFII-I [T0	768	773	0	GGACAG	1.46484	1.48598
cg0021380	AIFM1	TFII-I [T0	1254	1259	0	CTTTCC	1.46484	1.48598
cg0021380	AIFM1	TFII-I [T0	1987	1992	0	GGACAG	1.46484	1.48598
cg0021380	AIFM1	STAT4 [T	1547	1552	0	GGAAAT	0.48828	0.46235
cg0021380	AIFM1	c-Ets-1 [T	1144	1150	0	CTTCCT	0.24414	0.24982
cg0021380	AIFM1	ER-alpha [	189	193	0	TGACC	1.95312	1.99744
cg0021380	AIFM1	ER-alpha [	328	332	0	GGTCA	1.95312	1.99744
cg0021380	AIFM1	ER-alpha [	507	511	0	GGTCA	1.95312	1.99744
cg0021380	AIFM1	ER-alpha [	680	684	0	GGTCA	1.95312	1.99744
cg0021380	AIFM1	ER-alpha [	1957	1961	0	GGTCA	1.95312	1.99744

cg0021380	AIFM1	RXR-alph	310	316	0	GGGTTC	0.24414	0.24342
cg0021380	AIFM1	NFI/CTF [	854	861	0	GCGATT	0.18311	0.191
cg0021380	AIFM1	GR [T050	1105	1111	0	TTTTTTG	0.36621	0.33174
cg0021380	AIFM1	GR [T050	1418	1424	0	CAAAAA	0.36621	0.33174
cg0021380	AIFM1	GR [T050	1817	1823	0	TTTTTTG	0.36621	0.33174
cg0021380	AIFM1	c-Myc [T0	401	406	0	CACGTG	0.48828	0.51196
cg0021380	AIFM1	GATA-1 [	100	105	0	CAGATA	0.97656	0.92541
cg0021380	AIFM1	GATA-1 [	1365	1370	0	CAGATA	0.97656	0.92541
cg0021380	AIFM1	GATA-1 [	1530	1535	0	CAGATA	0.97656	0.92541
cg0021380	AIFM1	GATA-1 [	1971	1976	0	TATCTG	0.97656	0.92541
cg0021380	AIFM1	PXR-1:RX	1323	1330	0	TTAGTT	0.12207	0.11255
cg0021380	AIFM1	Pax-5 [T0	475	481	0	CAGGCC	1.09863	1.24633
cg0021380	AIFM1	AP-2alpha	782	787	0	GCCTGC	0.97656	1.07867
cg0021380	AIFM1	AP-2alpha	828	833	0	GCAGGC	0.97656	1.07867
cg0302000	ALS2CR1	RAR-beta:	896	907	9.97066	TGCCCG	0.06974	0.07677
cg0302000	ALS2CR1	c-Ets-1 [T	479	485	9.969337	TGGGAA	0.24414	0.23698
cg0302000	ALS2CR1	XBP-1 [T	175	180	9.789909	AGCCAT	1.95312	1.94901
cg0302000	ALS2CR1	XBP-1 [T	358	363	9.789909	AGCCAT	1.95312	1.94901
cg0302000	ALS2CR1	NF-1 [T00	282	289	9.761671	GGAACC	0.24414	0.24488
cg0302000	ALS2CR1	Elk-1 [T00	1593	1601	9.754368	CTTCCC	0.10681	0.11027
cg0302000	ALS2CR1	PR B [T00	1745	1751	9.743489	AACACA	1.09863	1.0981
cg0302000	ALS2CR1	PR B [T00	1878	1884	9.743489	AACACA	1.09863	1.0981
cg0302000	ALS2CR1	PR A [T01	1745	1751	9.743489	AACACA	1.09863	1.0981
cg0302000	ALS2CR1	PR A [T01	1878	1884	9.743489	AACACA	1.09863	1.0981
cg0302000	ALS2CR1	AhR:Arnt	1355	1364	9.738501	GCACGC	0.17929	0.20119
cg0302000	ALS2CR1	LEF-1 [T0	270	277	9.72404	TGGCAA	0.21362	0.21229
cg0302000	ALS2CR1	NF-kappa	514	525	9.685431	GGGGAA	0.01776	0.01845
cg0302000	ALS2CR1	ELF-1 [T0	1486	1498	9.604198	TTACTT	0.00417	0.00394
cg0302000	ALS2CR1	NF-AT2 [	1712	1721	9.5654	TACCTT	0.04578	0.04451
cg0302000	ALS2CR1	TFIID [T0	270	276	9.552105	TGGCAA	1.46484	1.37777
cg0302000	ALS2CR1	TFIID [T0	1187	1193	9.552105	TTTCTCA	1.46484	1.37777
cg0302000	ALS2CR1	TFIID [T0	1197	1203	9.552105	TTTCCC	1.46484	1.37777
cg0302000	ALS2CR1	TFIID [T0	1268	1274	9.552105	TTTGGA	1.46484	1.37777
cg0302000	ALS2CR1	TFIID [T0	1541	1547	9.552105	TTTGAC	1.46484	1.37777
cg0302000	ALS2CR1	TFIID [T0	1617	1623	9.552105	TTCCAA	1.46484	1.37777
cg0302000	ALS2CR1	TFIID [T0	1737	1743	9.552105	TTTGGG	1.46484	1.37777
cg0302000	ALS2CR1	Pax-5 [T0	951	957	9.552105	GGGCGT	1.46484	1.61918
cg0302000	ALS2CR1	Pax-5 [T0	1137	1143	9.552105	TGCGCC	1.46484	1.61918
cg0302000	ALS2CR1	Pax-5 [T0	1414	1420	9.552105	TCCGCC	1.46484	1.61918
cg0302000	ALS2CR1	Pax-5 [T0	1422	1428	9.552105	GTAGCC	1.46484	1.61918
cg0302000	ALS2CR1	NF-1 [T00	1138	1145	9.535536	GCGCCC	0.73242	0.74634
cg0302000	ALS2CR1	NF-1 [T00	287	294	9.513281	CAACCC	0.73242	0.74634
cg0302000	ALS2CR1	NF-1 [T00	1099	1106	9.513281	TTGGGG	0.73242	0.74634
cg0302000	ALS2CR1	FOXP3 [T	87	92	9.512894	GTTGGT	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	99	104	9.512894	GTAAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	247	252	9.512894	GTTTAT	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	285	290	9.512894	ACCAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	464	469	9.512894	GTTCTC	7.32422	7.22156

cg0302000	ALS2CR1	FOXP3 [T	545	550	9.512894	GTTGGG	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	617	622	9.512894	ACCAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	729	734	9.512894	ATAAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	913	918	9.512894	GTTCTT	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	919	924	9.512894	GTTCTT	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1066	1071	9.512894	GTTATC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1141	1146	9.512894	CCCAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1388	1393	9.512894	CCCAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1573	1578	9.512894	CATAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1787	1792	9.512894	GCCAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1906	1911	9.512894	GTTCTC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1927	1932	9.512894	CTAAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1936	1941	9.512894	GAGAAC	7.32422	7.22156
cg0302000	ALS2CR1	FOXP3 [T	1961	1966	9.512894	AGCAAC	7.32422	7.22156
cg0302000	ALS2CR1	TFII-I [T0	35	40	9.512894	GGAAAC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	71	76	9.512894	GGAACG	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	177	182	9.512894	CCATCC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	410	415	9.512894	GGAAAC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	481	486	9.512894	GGAATT	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	504	509	9.512894	GGACAC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	720	725	9.512894	GGAATT	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	845	850	9.512894	CGGTCC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	960	965	9.512894	GGACCG	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1044	1049	9.512894	GGACTT	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1196	1201	9.512894	TTTTCC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1411	1416	9.512894	TTGTCC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1716	1721	9.512894	TTTTCC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1741	1746	9.512894	GGACAA	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1803	1808	9.512894	CCATCC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1862	1867	9.512894	TTATCC	7.32422	7.44385
cg0302000	ALS2CR1	TFII-I [T0	1946	1951	9.512894	GGACAC	7.32422	7.44385
cg0302000	ALS2CR1	TCF-4E [T	1267	1273	9.453578	CTTTGG	0.48828	0.46934
cg0302000	ALS2CR1	TCF-4E [T	1540	1546	9.453578	CTTTGA	0.48828	0.46934
cg0302000	ALS2CR1	c-Jun [T00	1795	1801	9.442241	GCTGTC	0.73242	0.7366
cg0302000	ALS2CR1	c-Jun [T00	1984	1990	9.442241	TGACGG	0.73242	0.7366
cg0302000	ALS2CR1	NFI/CTF [	1265	1272	9.352332	AGCTTT	0.54932	0.55369
cg0302000	ALS2CR1	AP-1 [T00	1477	1485	9.3434	TGTCAG	0.09155	0.08441
cg0302000	ALS2CR1	SRY [T00	1540	1548	9.264664	CTTTGA	0.12207	0.11857
cg0302000	ALS2CR1	VDR [T00	377	385	9.234242	GTTCAT	0.12207	0.11552
cg0302000	ALS2CR1	RAR-alph	392	404	9.192562	GGGGTC	0.02065	0.02209
cg0302000	ALS2CR1	E2F-1 [T0	1411	1418	9.140572	TTGTCC	0.27466	0.30178
cg0302000	ALS2CR1	LEF-1 [T0	386	393	9.099721	CTTTGT	0.54932	0.53171
cg0302000	ALS2CR1	LEF-1 [T0	1832	1839	9.099721	CTTTGC	0.54932	0.53171
cg0302000	ALS2CR1	LEF-1 [T0	1540	1547	9.082175	CTTTGA	0.54932	0.53171
cg0302000	ALS2CR1	c-Ets-1 [T	344	350	9.065503	ATGGAA	0.85449	0.84987
cg0302000	ALS2CR1	USF2 [T0	43	52	9.056375	CAGGTG	0.1545	0.16206
cg0302000	ALS2CR1	NFI/CTF [	84	91	9.042931	ACTGTT	0.48828	0.48845
cg0302000	ALS2CR1	NFI/CTF [	1529	1536	9.042931	CCAACA	0.48828	0.48845

cg0302000	ALS2CR1	NF-AT1 [T	1345	1353	9.042733	GGAAAT	0.22888	0.22581
cg0302000	ALS2CR1	c-Ets-1 [T(	514	520	9.020687	GGGGAA	0.85449	0.84987
cg0302000	ALS2CR1	LEF-1 [T0	198	205	8.973041	ACCCAA	0.54932	0.53171
cg0302000	ALS2CR1	LEF-1 [T0	1267	1274	8.973041	CTTTGG/	0.54932	0.53171
cg0302000	ALS2CR1	GR [T050	452	458	8.971049	CAAACA	0.61035	0.5928
cg0302000	ALS2CR1	GR [T050	1652	1658	8.971049	CAAAAT	0.61035	0.5928
cg0302000	ALS2CR1	GR [T050	1896	1902	8.971049	CAAATA	0.61035	0.5928
cg0302000	ALS2CR1	c-Ets-2 [T(	30	38	8.912323	AGTCAG	0.27466	0.27171
cg0302000	ALS2CR1	HOXD9 [T	160	169	8.847863	AATACC	0.04578	0.03831
cg0302000	ALS2CR1	HOXD10 [	160	169	8.847863	AATACC	0.04578	0.03831
cg0302000	ALS2CR1	PR B [T00	41	47	8.827054	AACAGG	0.36621	0.35051
cg0302000	ALS2CR1	PR A [T01	41	47	8.827054	AACAGG	0.36621	0.35051
cg0302000	ALS2CR1	NFI/CTF [	768	775	8.814757	CCAATT(	0.48828	0.48845
cg0302000	ALS2CR1	NFI/CTF [	1095	1102	8.814757	TCTCTTC	0.48828	0.48845
cg0302000	ALS2CR1	NFI/CTF [	1625	1632	8.814757	TCATTTC	0.48828	0.48845
cg0302000	ALS2CR1	NF-1 [T00	1784	1791	8.790071	TCTGCC/	0.24414	0.24339
cg0302000	ALS2CR1	LEF-1 [T0	1948	1955	8.759086	ACACAA	0.54932	0.53171
cg0302000	ALS2CR1	XBP-1 [T(	377	382	8.75604	GTTCAT	2.92969	2.75329
cg0302000	ALS2CR1	XBP-1 [T(	492	497	8.75604	ATGAGA	2.92969	2.75329
cg0302000	ALS2CR1	XBP-1 [T(	992	997	8.75604	ATGATA	2.92969	2.75329
cg0302000	ALS2CR1	XBP-1 [T(	1934	1939	8.75604	ATGAGA	2.92969	2.75329
cg0302000	ALS2CR1	NF-AT1 [T	35	43	8.746017	GGAAAC	0.10681	0.10494
cg0302000	ALS2CR1	RAR-beta	542	551	8.55975	TGGGTT(	0.26703	0.27434
cg0302000	ALS2CR1	NF-AT2 [T	410	419	8.550786	GGAAAC	0.04959	0.04758
cg0302000	ALS2CR1	RAR-beta	284	293	8.541284	AACCAA	0.26703	0.27434
cg0302000	ALS2CR1	c-Ets-1 [T(	1616	1622	8.501115	GTTCCA/	0.24414	0.23702
cg0302000	ALS2CR1	HNF-3alpl	1674	1681	8.343064	CATTTTA	0.27466	0.23078
cg0302000	ALS2CR1	PR B [T00	1886	1892	8.338824	AACAGA	1.09863	1.09384
cg0302000	ALS2CR1	PR B [T00	1964	1970	8.338824	AACAGA	1.09863	1.09384
cg0302000	ALS2CR1	PR A [T01	1886	1892	8.338824	AACAGA	1.09863	1.09384
cg0302000	ALS2CR1	PR A [T01	1964	1970	8.338824	AACAGA	1.09863	1.09384
cg0302000	ALS2CR1	GR-alpha [	142	146	8.281568	CAAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	438	442	8.281568	CAAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	552	556	8.281568	GGAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	556	560	8.281568	GGAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	559	563	8.281568	GGAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	774	778	8.281568	GAAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	823	827	8.281568	CCTCC	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	849	853	8.281568	CCTCC	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	906	910	8.281568	CCTCC	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	972	976	8.281568	CCTCC	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	1175	1179	8.281568	CCTCC	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	1259	1263	8.281568	GGAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	1296	1300	8.281568	GGAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	1342	1346	8.281568	GAAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	1371	1375	8.281568	CAAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	1854	1858	8.281568	GAAGG	7.8125	8.20394
cg0302000	ALS2CR1	GR-alpha [	1991	1995	8.281568	GAAGG	7.8125	8.20394

cg0302000	ALS2CR1	GCF [T00	1157	1165	8.256755	CTACTG	0.09155	0.09762
cg0302000	ALS2CR1	c-Ets-1 [T	1561	1567	8.244941	GTTCCA	0.24414	0.2494
cg0302000	ALS2CR1	NFI/CTF [	286	293	8.241664	CCAACC	0.18311	0.1922
cg0302000	ALS2CR1	NFI/CTF [	542	549	8.241664	TGGGTT	0.18311	0.1922
cg0302000	ALS2CR1	NFI/CTF [	1788	1795	8.241664	CCAACC	0.18311	0.1922
cg0302000	ALS2CR1	p53 [T006	1384	1390	8.208781	GGGGCC	0.48828	0.55336
cg0302000	ALS2CR1	ENKTF-1	172	179	8.19852	CCCAGC	0.73242	0.80254
cg0302000	ALS2CR1	PXR-1:RX	486	493	8.180749	TGAACA	0.12207	0.11255
cg0302000	ALS2CR1	SRY [T00	386	394	8.174786	CTTTGT	0.15259	0.14791
cg0302000	ALS2CR1	HNF-1C [	1581	1589	8.131138	GTTAAT	0.19836	0.18126
cg0302000	ALS2CR1	c-Jun [T00	1639	1645	8.128539	AATGTC	0.48828	0.47447
cg0302000	ALS2CR1	VDR [T00	946	954	8.079962	GTTCAG	0.24414	0.22992
cg0302000	ALS2CR1	GR-alpha [	279	283	8.073878	CTAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	650	654	8.073878	CCTGC	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	672	676	8.073878	CCTAG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	826	830	8.073878	CCAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	834	838	8.073878	CCTGC	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	852	856	8.073878	CCAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	863	867	8.073878	CCAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	909	913	8.073878	CCTGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	927	931	8.073878	GCAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	942	946	8.073878	CCTGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1009	1013	8.073878	GTAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1053	1057	8.073878	CCTGC	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1164	1168	8.073878	GCAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1218	1222	8.073878	CCTAG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1293	1297	8.073878	CCTGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1319	1323	8.073878	CCAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1446	1450	8.073878	CCTGC	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1612	1616	8.073878	GTAGG	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1792	1796	8.073878	CCTGC	7.8125	8.20289
cg0302000	ALS2CR1	GR-alpha [	1978	1982	8.073878	CCTAC	7.8125	8.20289
cg0302000	ALS2CR1	TFIID [T0	319	325	8.014558	TAAGAA	2.19727	1.99811
cg0302000	ALS2CR1	TFIID [T0	643	649	8.014558	TAACAA	2.19727	1.99811
cg0302000	ALS2CR1	Pax-5 [T0	190	196	8.014558	GGGCAT	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	829	835	8.014558	GGTGCC	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	894	900	8.014558	GGTGCC	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	901	907	8.014558	GGTGCC	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	1001	1007	8.014558	GGGCTG	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	1170	1176	8.014558	GCGGCC	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	1238	1244	8.014558	GGGCCC	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	1384	1390	8.014558	GGGGCC	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	1385	1391	8.014558	GGGCCC	2.19727	2.42766
cg0302000	ALS2CR1	Pax-5 [T0	1975	1981	8.014558	GGGCCT	2.19727	2.42766
cg0302000	ALS2CR1	HNF-1C [	638	646	8.002145	CTATGT	0.19836	0.18126
cg0302000	ALS2CR1	MEF-2A [	702	712	7.982343	AAATAA	0.04005	0.03447
cg0302000	ALS2CR1	MEF-2A [	1089	1099	7.982343	TATTTGT	0.04005	0.03447
cg0302000	ALS2CR1	ATF-1 [T0	228	238	7.870358	AAGTCA	0.07153	0.07126

cg0302000	ALS2CR1	c-Ets-2 [T	277	285	7.84116	GACTAG	0.32043	0.30792
cg0302000	ALS2CR1	IRF-1 [T0	31	39	7.82345	GTCAGG	0.25177	0.2462
cg0302000	ALS2CR1	RXR-alph	1032	1038	7.815913	GGGTGG	0.24414	0.26389
cg0302000	ALS2CR1	RXR-alph	1102	1108	7.815913	GGGTGG	0.24414	0.26389
cg0302000	ALS2CR1	c-Ets-2 [T	1879	1887	7.76635	ACACAG	0.32043	0.30792
cg0302000	ALS2CR1	AR [T000	504	512	7.756626	GGACAC	0.19836	0.20641
cg0302000	ALS2CR1	NF-1 [T00	1615	1622	7.693985	GGTTCC	0.24414	0.23756
cg0302000	ALS2CR1	AR [T000	378	386	7.683535	TTCATG	0.25177	0.2544
cg0302000	ALS2CR1	p53 [T006	930	936	7.641867	GGGCCG	0.73242	0.79826
cg0302000	ALS2CR1	p53 [T006	1149	1155	7.641867	ACGGCC	0.73242	0.79826
cg0302000	ALS2CR1	p53 [T006	1372	1378	7.641867	AAGGCC	0.73242	0.79826
cg0302000	ALS2CR1	NFI/CTF [	291	298	7.587343	CCAAAT	0.36621	0.36269
cg0302000	ALS2CR1	NFI/CTF [	784	791	7.587343	GCAATT	0.36621	0.36269
cg0302000	ALS2CR1	NFI/CTF [	1555	1562	7.587343	CCAATT	0.36621	0.36269
cg0302000	ALS2CR1	PU.1 [T02	1486	1498	7.546536	TTACTT	0.01001	0.0098
cg0302000	ALS2CR1	c-Jun [T00	1543	1549	7.538568	TGACAT	0.48828	0.48672
cg0302000	ALS2CR1	GR [T050	1088	1094	7.527031	CTATTT	1.83105	1.71535
cg0302000	ALS2CR1	GR [T050	1265	1271	7.527031	AGCTTT	1.83105	1.71535
cg0302000	ALS2CR1	C/EBPalp	757	763	7.465744	TTCAAT	0.48828	0.45033
cg0302000	ALS2CR1	C/EBPalp	796	802	7.465744	CATTGA	0.48828	0.45033
cg0302000	ALS2CR1	C/EBPalp	1764	1770	7.465744	TGCAAT	0.48828	0.45033
cg0302000	ALS2CR1	PXR-1:RX	880	887	7.362674	CACGTT	0.24414	0.24326
cg0302000	ALS2CR1	c-Ets-1 [T	1197	1203	7.199436	TTTCCCA	0.73242	0.73732
cg0302000	ALS2CR1	SRY [T00	1947	1955	7.175614	GACACA	0.30518	0.29547
cg0302000	ALS2CR1	XBP-1 [T	19	24	7.172312	AATCAT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	213	218	7.172312	AATCAT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	373	378	7.172312	ATGAGT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	402	407	7.172312	ATGAAG	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	416	421	7.172312	CATCAT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	470	475	7.172312	ACTCAT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	1378	1383	7.172312	CCTCAT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	1587	1592	7.172312	ATTCAT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	1623	1628	7.172312	ACTCAT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	1768	1773	7.172312	ATGATT	2.92969	2.7512
cg0302000	ALS2CR1	XBP-1 [T	1775	1780	7.172312	ACTCAT	2.92969	2.7512
cg0302000	ALS2CR1	p53 [T006	1238	1244	7.153797	GGGCCC	1.09863	1.22478
cg0302000	ALS2CR1	p53 [T006	1385	1391	7.153797	GGGCCC	1.09863	1.22478
cg0302000	ALS2CR1	c-Myb [T0	4	11	7.127234	ACCAGT	0.18311	0.17765
cg0302000	ALS2CR1	c-Ets-1 [T	1717	1723	7.071349	TTTCCCT	0.73242	0.73732
cg0302000	ALS2CR1	NFI/CTF [	1389	1396	7.014249	CCAACC	0.73242	0.74795
cg0302000	ALS2CR1	HNF-3alp	156	163	7.000129	TAGAAA	0.82397	0.71909
cg0302000	ALS2CR1	IRF-1 [T0	1197	1205	6.968314	TTTCCCA	0.1297	0.12685
cg0302000	ALS2CR1	RXR-alph	818	824	6.967687	ACCACC	0.36621	0.38841
cg0302000	ALS2CR1	NF-1 [T00	1629	1636	6.948522	TTGGTG	0.48828	0.50205
cg0302000	ALS2CR1	ENKTF-1	131	138	6.942764	TGGCGA	1.46484	1.56616
cg0302000	ALS2CR1	ENKTF-1	270	277	6.942764	TGGCAA	1.46484	1.56616
cg0302000	ALS2CR1	ENKTF-1	839	846	6.942764	TGGCCC	1.46484	1.56616
cg0302000	ALS2CR1	ENKTF-1	1035	1042	6.942764	TGGCGG	1.46484	1.56616

cg0302000	ALS2CR1	ENKTF-1	1319	1326	6.942764	CCAGGC	1.46484	1.56616
cg0302000	ALS2CR1	p53 [T006	1170	1176	6.938545	GCGGCC	1.09863	1.22478
cg0302000	ALS2CR1	VDR [T00	482	490	6.925682	GAATTG	0.42725	0.41
cg0302000	ALS2CR1	STAT1bet	1341	1350	6.908963	AGAAGG	0.103	0.09938
cg0302000	ALS2CR1	NF-AT1 [	409	418	6.890694	TGGAAA	0.01907	0.01836
cg0302000	ALS2CR1	C/EBPalph	483	489	6.85549	AATTGA	0.73242	0.68282
cg0302000	ALS2CR1	C/EBPalph	770	776	6.85549	AATTGA	0.73242	0.68282
cg0302000	ALS2CR1	C/EBPalph	783	789	6.85549	TGCAAT	0.73242	0.68282
cg0302000	ALS2CR1	C/EBPalph	1761	1767	6.85549	AATTGC	0.73242	0.68282
cg0302000	ALS2CR1	E2F-1 [T0	1211	1218	6.839754	CGTGCC	0.30518	0.33862
cg0302000	ALS2CR1	PEA3 [T0	399	407	6.824411	TGGATG	0.22888	0.22744
cg0302000	ALS2CR1	PEA3 [T0	1797	1805	6.824411	TGTCAT	0.22888	0.22744
cg0302000	ALS2CR1	c-Jun [T00	306	312	6.787369	TGACAG	0.73242	0.73062
cg0302000	ALS2CR1	p53 [T006	1422	1428	6.775228	GTAGCC	1.09863	1.22478
cg0302000	ALS2CR1	AR [T000	1946	1954	6.760234	GGACAC	0.23651	0.23986
cg0302000	ALS2CR1	AhR:Arnt	1275	1284	6.698963	GCATGC	0.01717	0.01925
cg0302000	ALS2CR1	c-Ets-2 [T	66	74	6.695187	AAATAG	0.09155	0.08559
cg0302000	ALS2CR1	AR [T000	1408	1416	6.603347	GTCTTGT	0.19836	0.20813
cg0302000	ALS2CR1	FOXP3 [T	108	113	6.581441	TTCAAC	0.97656	0.904
cg0302000	ALS2CR1	TFII-I [T0	94	99	6.581441	GGAGTG	0.97656	0.9991
cg0302000	ALS2CR1	TFII-I [T0	574	579	6.581441	GGAGAT	0.97656	0.9991
cg0302000	ALS2CR1	TFII-I [T0	778	783	6.581441	GGAGAT	0.97656	0.9991
cg0302000	ALS2CR1	TFII-I [T0	1250	1255	6.581441	GGAGTG	0.97656	0.9991
cg0302000	ALS2CR1	p53 [T006	1001	1007	6.563521	GGGCTG	0.48828	0.54643
cg0302000	ALS2CR1	XBP-1 [T	190	195	6.478682	GGGCAT	0.97656	0.99906
cg0302000	ALS2CR1	p53 [T006	1137	1143	6.403751	TGCGCC	0.48828	0.54643
cg0302000	ALS2CR1	C/EBPalph	767	773	6.391486	GCCAAT	0.48828	0.47407
cg0302000	ALS2CR1	C/EBPalph	786	792	6.391486	AATTGG	0.48828	0.47407
cg0302000	ALS2CR1	C/EBPalph	1758	1764	6.391486	GACAAT	0.48828	0.47407
cg0302000	ALS2CR1	TCF-4E [T	271	277	6.302385	GGCAAA	0.61035	0.59686
cg0302000	ALS2CR1	PPAR-alph	1970	1980	6.299891	CACTGG	0.03719	0.04058
cg0302000	ALS2CR1	c-Jun [T00	1687	1693	6.293948	TGACCC	0.61035	0.6179
cg0302000	ALS2CR1	GR-alpha [	139	143	6.263098	CCTCA	3.90625	3.89624
cg0302000	ALS2CR1	GR-alpha [	956	960	6.263098	TAAGG	3.90625	3.89624
cg0302000	ALS2CR1	GR-alpha [	1378	1382	6.263098	CCTCA	3.90625	3.89624
cg0302000	ALS2CR1	GR-alpha [	1427	1431	6.263098	CCTCA	3.90625	3.89624
cg0302000	ALS2CR1	C/EBPalph	1022	1028	6.245236	TGCAAT	0.97656	0.91422
cg0302000	ALS2CR1	GCF [T00	1133	1141	6.116216	TGTCTG	0.64087	0.72542
cg0302000	ALS2CR1	AR [T000	441	449	6.110872	GGACAG	0.24414	0.25115
cg0302000	ALS2CR1	HNF-1B [	1519	1527	6.086797	CGTTAA	0.09918	0.08736
cg0302000	ALS2CR1	GR-alpha [	32	36	6.055408	TCAGG	3.90625	3.89835
cg0302000	ALS2CR1	GR-alpha [	571	575	6.055408	TTAGG	3.90625	3.89835
cg0302000	ALS2CR1	GR-alpha [	583	587	6.055408	CCTAA	3.90625	3.89835
cg0302000	ALS2CR1	GR-alpha [	923	927	6.055408	TTAGG	3.90625	3.89835
cg0302000	ALS2CR1	GR-alpha [	948	952	6.055408	TCAGG	3.90625	3.89835
cg0302000	ALS2CR1	GR-alpha [	1231	1235	6.055408	TCAGG	3.90625	3.89835
cg0302000	ALS2CR1	GR-alpha [	1691	1695	6.055408	CCTAA	3.90625	3.89835
cg0302000	ALS2CR1	GR-alpha [	1732	1736	6.055408	CCTAA	3.90625	3.89835

cg0302000	ALS2CR1	GR-alpha [	1866	1870	6.055408	CCTAA	3.90625	3.89835
cg0302000	ALS2CR1	c-Ets-1 [T	408	414	6.039428	CTGGAA	0.36621	0.36174
cg0302000	ALS2CR1	C/EBPalph	488	494	5.996794	AACAAT	0.97656	0.91422
cg0302000	ALS2CR1	C/EBPalph	1930	1936	5.996794	AACAAT	0.97656	0.91422
cg0302000	ALS2CR1	AR [T000	1039	1047	5.953985	GGACAG	0.24414	0.25115
cg0302000	ALS2CR1	AR [T000	1741	1749	5.8965	GGACAA	0.24414	0.25115
cg0302000	ALS2CR1	p53 [T006	1975	1981	5.883561	GGGCCT	0.61035	0.68483
cg0302000	ALS2CR1	TCF-4 [T0	1539	1548	5.810677	ACTTTG	0.04578	0.04297
cg0302000	ALS2CR1	NF-kappa	514	524	5.806899	GGGGAA	0.04053	0.04443
cg0302000	ALS2CR1	c-Jun [T00	28	34	5.783074	AAAGTC	0.36621	0.34478
cg0302000	ALS2CR1	c-Jun [T00	227	233	5.783074	AAAGTC	0.36621	0.34478
cg0302000	ALS2CR1	c-Jun [T00	392	398	5.703976	GGGGTC	0.48828	0.49294
cg0302000	ALS2CR1	c-Ets-1 [T	1593	1599	5.686398	CTTCCC	0.36621	0.38732
cg0302000	ALS2CR1	IRF-1 [T0	406	414	5.65977	AGCTGG	0.22888	0.21959
cg0302000	ALS2CR1	NF-1 [T00	1048	1055	5.626299	TTGGAC	0.24414	0.25051
cg0302000	ALS2CR1	AhR:Arnt	1206	1215	5.620669	GCGTGC	0.0515	0.05997
cg0302000	ALS2CR1	c-Jun [T00	1475	1481	5.590308	AGTGTC	0.48828	0.49294
cg0302000	ALS2CR1	AP-2alpha	1086	1091	5.568965	GCCTAT	0.48828	0.48642
cg0302000	ALS2CR1	NFI/CTF [	451	458	5.558661	CCAAAC	0.54932	0.55504
cg0302000	ALS2CR1	NFI/CTF [	1619	1626	5.558661	CCAAAC	0.54932	0.55504
cg0302000	ALS2CR1	GATA-2 [	1859	1867	5.555555	CCATTA	0.18311	0.18081
cg0302000	ALS2CR1	TFIID [T0	1338	1344	5.544826	TTTAGA	0.73242	0.65314
cg0302000	ALS2CR1	NF-AT2 [	1192	1201	5.474728	CACATT	0.01144	0.011
cg0302000	ALS2CR1	C/EBPalph	301	307	5.455853	ATCAAT	0.73242	0.68229
cg0302000	ALS2CR1	C/EBPalph	1636	1642	5.455853	AGCAAT	0.73242	0.68229
cg0302000	ALS2CR1	RelA [T00	513	523	5.414465	GGGGGA	0.0124	0.01273
cg0302000	ALS2CR1	p53 [T006	1237	1243	5.39549	CGGGCC	0.61035	0.65765
cg0302000	ALS2CR1	C/EBPalph	1557	1563	5.38654	AATTGT	0.73242	0.68229
cg0302000	ALS2CR1	GR [T050	273	279	5.207533	CAAAGA	0.24414	0.24013
cg0302000	ALS2CR1	p53 [T006	951	957	5.133514	GGGCGT	0.48828	0.53921
cg0302000	ALS2CR1	p53 [T006	1414	1420	5.133514	TCCGCC	0.48828	0.53921
cg0302000	ALS2CR1	AP-2alpha	1082	1087	5.100982	AAAGGC	0.97656	0.97517
cg0302000	ALS2CR1	AP-2alpha	1184	1189	5.100982	GCCTTT	0.97656	0.97517
cg0302000	ALS2CR1	USF2 [T0	853	862	5.052423	CAGGTG	0.103	0.10797
cg0302000	ALS2CR1	GR-beta [	160	164	5.042296	AATAC	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	205	209	5.042296	GGATT	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	315	319	5.042296	GGATT	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	348	352	5.042296	AATAC	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	497	501	5.042296	AATAC	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	746	750	5.042296	GGATT	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	809	813	5.042296	AATCC	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	1013	1017	5.042296	GGATT	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	1823	1827	5.042296	GTATT	3.90625	3.7093
cg0302000	ALS2CR1	GR-beta [	1898	1902	5.042296	AATAC	3.90625	3.7093
cg0302000	ALS2CR1	E2F-1 [T0	1175	1182	5.042045	CCTCCC	0.18311	0.20394
cg0302000	ALS2CR1	c-Ets-1 [T	1269	1275	5.038739	TTGGAA	0.48828	0.48026
cg0302000	ALS2CR1	PXR-1:RX	753	760	5.032032	AGGGTT	0.12207	0.11843
cg0302000	ALS2CR1	PXR-1:RX	799	806	5.032032	TGAACC	0.12207	0.11843

cg0302000	ALS2CR1	NFI/CTF [	200	207	5.021086	CCAAAG	0.24414	0.25666
cg0302000	ALS2CR1	AP-2alpha	923	928	4.890408	TTAGGC	0.97656	0.97517
cg0302000	ALS2CR1	GCF [T00	1168	1176	4.846987	GCGCGG	0.27466	0.31905
cg0302000	ALS2CR1	C/EBPalph	722	728	4.845599	AATTGC	0.97656	0.90302
cg0302000	ALS2CR1	HNF-3alph	1678	1685	4.842999	TTAAAA	0.09155	0.07438
cg0302000	ALS2CR1	c-Ets-1 [T	118	124	4.782565	GTGGAA	0.48828	0.48026
cg0302000	ALS2CR1	FOXP3 [T	446	451	4.756447	GAAAAC	2.92969	2.82
cg0302000	ALS2CR1	FOXP3 [T	1890	1895	4.756447	GAAAAC	2.92969	2.82
cg0302000	ALS2CR1	TFII-I [T0	295	300	4.756447	ATGTCC	2.92969	2.89715
cg0302000	ALS2CR1	TFII-I [T0	381	386	4.756447	ATGTCC	2.92969	2.89715
cg0302000	ALS2CR1	TFII-I [T0	995	1000	4.756447	ATATCC	2.92969	2.89715
cg0302000	ALS2CR1	TFII-I [T0	1345	1350	4.756447	GGAAAT	2.92969	2.89715
cg0302000	ALS2CR1	TFII-I [T0	1525	1530	4.756447	ATATCC	2.92969	2.89715
cg0302000	ALS2CR1	TFII-I [T0	1645	1650	4.756447	ATATCC	2.92969	2.89715
cg0302000	ALS2CR1	PPAR-alph	168	178	4.727619	TTGACC	0.03242	0.03494
cg0302000	ALS2CR1	VDR [T00	756	764	4.617121	GTTCAA	0.37384	0.36855
cg0302000	ALS2CR1	VDR [T00	795	803	4.617121	ACATTG	0.37384	0.36855
cg0302000	ALS2CR1	VDR [T00	883	891	4.617121	GTTCAG	0.37384	0.36855
cg0302000	ALS2CR1	NF-AT1 [	410	418	4.566689	GGAAAC	0.06866	0.06549
cg0302000	ALS2CR1	USF1 [T0	228	237	4.464121	AAGTCA	0.06866	0.06933
cg0302000	ALS2CR1	c-Jun [T00	1479	1485	4.441904	TCAGTC	0.12207	0.11843
cg0302000	ALS2CR1	AP-2alpha	1217	1222	4.438035	GCCTAG	0.97656	0.99839
cg0302000	ALS2CR1	STAT4 [T	71	76	4.411765	GGAACG	1.95312	1.99838
cg0302000	ALS2CR1	STAT4 [T	120	125	4.411765	GGAAGA	1.95312	1.99838
cg0302000	ALS2CR1	STAT4 [T	1271	1276	4.411765	GGAAGC	1.95312	1.99838
cg0302000	ALS2CR1	STAT4 [T	1592	1597	4.411765	TCTTCC	1.95312	1.99838
cg0302000	ALS2CR1	c-Ets-1 [T	718	724	4.411026	AAGGAA	0.85449	0.8381
cg0302000	ALS2CR1	p53 [T006	838	844	4.33696	CTGGCC	0.24414	0.28373
cg0302000	ALS2CR1	HOXD9 [	689	698	4.321431	AATAAA	0.03433	0.02831
cg0302000	ALS2CR1	HOXD9 [	696	705	4.321431	AATAAA	0.03433	0.02831
cg0302000	ALS2CR1	HOXD9 [	709	718	4.321431	AATAAA	0.03433	0.02831
cg0302000	ALS2CR1	HOXD10 [	689	698	4.321431	AATAAA	0.03433	0.02831
cg0302000	ALS2CR1	HOXD10 [	696	705	4.321431	AATAAA	0.03433	0.02831
cg0302000	ALS2CR1	HOXD10 [	709	718	4.321431	AATAAA	0.03433	0.02831
cg0302000	ALS2CR1	PEA3 [T0	370	378	4.30818	AGGATG	0.13733	0.13607
cg0302000	ALS2CR1	c-Ets-1 [T	136	142	4.282938	ATTCCTC	0.85449	0.8381
cg0302000	ALS2CR1	c-Ets-1 [T	1015	1021	4.282938	ATTCCTC	0.85449	0.8381
cg0302000	ALS2CR1	RXR-alpha	1222	1228	4.24113	GTGACC	0.97656	1.02803
cg0302000	ALS2CR1	Sp1 [T007	1412	1421	4.222204	TGTCCG	0.08965	0.10391
cg0302000	ALS2CR1	AP-2alpha	1977	1982	4.211849	GCCTAC	0.97656	1.02535
cg0302000	ALS2CR1	GR-beta [	19	23	4.201913	AATCA	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [	67	71	4.201913	AATAG	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [	134	138	4.201913	CGATT	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [	213	217	4.201913	AATCA	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [	249	253	4.201913	TTATT	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [	260	264	4.201913	CTATT	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [	689	693	4.201913	AATAA	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [	696	700	4.201913	AATAA	7.8125	7.23274

cg0302000	ALS2CR1	GR-beta [T	703	707	4.201913	AATAA	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [T	709	713	4.201913	AATAA	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [T	1025	1029	4.201913	AATAG	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [T	1088	1092	4.201913	CTATT	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [T	1348	1352	4.201913	AATCA	7.8125	7.23274
cg0302000	ALS2CR1	GR-beta [T	1769	1773	4.201913	TGATT	7.8125	7.23274
cg0302000	ALS2CR1	p53 [T006	864	870	4.125254	CAGGCC	0.73242	0.82434
cg0302000	ALS2CR1	PXR-1:RX	943	950	4.090374	CTGGTT	0.12207	0.12474
cg0302000	ALS2CR1	p53 [T006	829	835	4.083527	GGTGCC	0.73242	0.82434
cg0302000	ALS2CR1	p53 [T006	894	900	4.083527	GGTGCC	0.73242	0.82434
cg0302000	ALS2CR1	p53 [T006	901	907	4.083527	GGTGCC	0.73242	0.82434
cg0302000	ALS2CR1	AR [T000	292	300	4.031208	CAAATG	0.06866	0.06981
cg0302000	ALS2CR1	C/EBPalpl	16	22	4.019783	GGCAAT	0.48828	0.46347
cg0302000	ALS2CR1	RXR-alpha	195	201	4.019014	TATACC	0.97656	1.02803
cg0302000	ALS2CR1	TFIID [T0	208	214	4.007279	TTATAA	1.09863	0.94722
cg0302000	ALS2CR1	TFIID [T0	248	254	4.007279	TTTATTA	1.09863	0.94722
cg0302000	ALS2CR1	TFIID [T0	688	694	4.007279	TAATAA	1.09863	0.94722
cg0302000	ALS2CR1	TFIID [T0	1599	1605	4.007279	TCTTAA	1.09863	0.94722
cg0302000	ALS2CR1	TFIID [T0	1657	1663	4.007279	TCTTAA	1.09863	0.94722
cg0302000	ALS2CR1	TFIID [T0	1676	1682	4.007279	TTTTAA	1.09863	0.94722
cg0302000	ALS2CR1	TFIID [T0	1914	1920	4.007279	TTATAA	1.09863	0.94722
cg0302000	ALS2CR1	Pax-5 [T0	930	936	4.007279	GGGCCG	1.09863	1.18533
cg0302000	ALS2CR1	Pax-5 [T0	1149	1155	4.007279	ACGGCC	1.09863	1.18533
cg0302000	ALS2CR1	Pax-5 [T0	1372	1378	4.007279	AAGGCC	1.09863	1.18533
cg0302000	ALS2CR1	Pax-5 [T0	1814	1820	4.007279	ACTGCC	1.09863	1.18533
cg0302000	ALS2CR1	USF2 [T0	827	836	4.003951	CAGGTG	0.01144	0.01199
cg0302000	ALS2CR1	AP-2alpha	1371	1376	3.970052	CAAGGC	0.97656	1.02535
cg0302000	ALS2CR1	c-Ets-1 [T	69	75	3.846637	TAGGAA	0.24414	0.23719
cg0302000	ALS2CR1	c-Ets-1 [T	280	286	3.846637	TAGGAA	0.24414	0.23719
cg0302000	ALS2CR1	USF1 [T0	232	241	3.775819	CACGTG	0.08011	0.08435
cg0302000	ALS2CR1	GR [T050	1951	1957	3.763516	CAAAGA	0.73242	0.6946
cg0302000	ALS2CR1	AP-2alpha	1854	1859	3.743866	GAAGGC	0.48828	0.5124
cg0302000	ALS2CR1	RXR-alpha	975	981	3.574782	CCGACC	1.09863	1.1653
cg0302000	ALS2CR1	p53 [T006	1814	1820	3.516613	ACTGCC	0.73242	0.80362
cg0302000	ALS2CR1	HNF-3alpl	692	699	3.500065	AAAAAA	0.27466	0.23175
cg0302000	ALS2CR1	HNF-3alpl	699	706	3.500065	AAAAAA	0.27466	0.23175
cg0302000	ALS2CR1	VDR [T00	107	115	3.462841	GTTCAA	0.21362	0.21283
cg0302000	ALS2CR1	VDR [T00	1401	1409	3.462841	GTTCAC	0.21362	0.21283
cg0302000	ALS2CR1	c-Ets-1 [T	1882	1888	3.462376	CAGGAA	0.61035	0.61936
cg0302000	ALS2CR1	NF-AT1 [T	1193	1201	3.407861	ACATTT	0.03052	0.02886
cg0302000	ALS2CR1	NF-AT1 [T	1713	1721	3.407861	ACCTTT	0.03052	0.02886
cg0302000	ALS2CR1	RXR-alpha	393	399	3.392904	GGGTCA	1.09863	1.1653
cg0302000	ALS2CR1	RXR-alpha	667	673	3.392904	TGTACC	1.09863	1.1653
cg0302000	ALS2CR1	RXR-alpha	1550	1556	3.392904	TTTACC	1.09863	1.1653
cg0302000	ALS2CR1	GR-beta [T	1467	1471	3.361531	AGATT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1524	1528	3.361531	AATAT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1584	1588	3.361531	AATAT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1585	1589	3.361531	ATATT	3.90625	3.51525

cg0302000	ALS2CR1	GR-beta [T	1655	1659	3.361531	AATCT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1695	1699	3.361531	AATAT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1703	1707	3.361531	AATCT	3.90625	3.51525
cg0302000	ALS2CR1	PR B [T00	1557	1563	3.29756	AATTGTT	0.24414	0.21408
cg0302000	ALS2CR1	PR A [T01	1557	1563	3.29756	AATTGTT	0.24414	0.21408
cg0302000	ALS2CR1	c-Ets-2 [T0	137	145	3.2883	TTCCTCA	0.18311	0.18314
cg0302000	ALS2CR1	NF-Y [T00	765	772	3.263282	GTGCCA	0.48828	0.48427
cg0302000	ALS2CR1	NF-Y [T00	787	794	3.263282	ATTGGCA	0.48828	0.48427
cg0302000	ALS2CR1	TCF-4E [T	1832	1838	3.151193	CTTTGCA	0.24414	0.23169
cg0302000	ALS2CR1	NF-Y [T00	1552	1559	3.051543	TACCCA	0.06104	0.05632
cg0302000	ALS2CR1	c-Jun [T00	169	175	3.049104	TGACCCA	0.24414	0.2435
cg0302000	ALS2CR1	c-Jun [T00	1223	1229	3.049104	TGACCCA	0.24414	0.2435
cg0302000	ALS2CR1	C/EBPalph	114	120	2.981957	CATTGTC	0.48828	0.47526
cg0302000	ALS2CR1	C/EBPalph	265	271	2.981957	CACAATC	0.48828	0.47526
cg0302000	ALS2CR1	c-Ets-2 [T0	715	723	2.945838	AAAAAG	0.06104	0.05567
cg0302000	ALS2CR1	STAT4 [T0	135	140	2.941176	GATTCC	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	282	287	2.941176	GGAACC	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	346	351	2.941176	GGAATA	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	516	521	2.941176	GGAACA	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	1014	1019	2.941176	GATTCC	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	1488	1493	2.941176	ACTTCC	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	1560	1565	2.941176	TGTTCC	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	1615	1620	2.941176	GGTTCC	2.92969	2.92382
cg0302000	ALS2CR1	STAT4 [T0	1884	1889	2.941176	GGAACA	2.92969	2.92382
cg0302000	ALS2CR1	IRF-1 [T00	1341	1349	2.890712	AGAAGG	0.07629	0.07093
cg0302000	ALS2CR1	NF-1 [T00	1385	1392	2.813149	GGGCCCA	0.24414	0.2566
cg0302000	ALS2CR1	PR B [T00	488	494	2.80933	AACAATC	0.73242	0.66711
cg0302000	ALS2CR1	PR B [T00	1662	1668	2.80933	AACATTC	0.73242	0.66711
cg0302000	ALS2CR1	PR B [T00	1930	1936	2.80933	AACAATC	0.73242	0.66711
cg0302000	ALS2CR1	PR A [T01	488	494	2.80933	AACAATC	0.73242	0.66711
cg0302000	ALS2CR1	PR A [T01	1662	1668	2.80933	AACATTC	0.73242	0.66711
cg0302000	ALS2CR1	PR A [T01	1930	1936	2.80933	AACAATC	0.73242	0.66711
cg0302000	ALS2CR1	TBP [T007	220	229	2.807313	CTGCTAT	0.12207	0.10444
cg0302000	ALS2CR1	TBP [T007	724	733	2.807313	TTGCTAT	0.12207	0.10444
cg0302000	ALS2CR1	TBP [T007	1911	1920	2.807313	CACTTAT	0.12207	0.10444
cg0302000	ALS2CR1	RXR-alpha	286	292	2.726556	CCAACCC	0.85449	0.89683
cg0302000	ALS2CR1	RXR-alpha	543	549	2.726556	GGGTTGC	0.85449	0.89683
cg0302000	ALS2CR1	NFI/CTF [	1142	1149	2.683003	CCAACCC	0.06104	0.06609
cg0302000	ALS2CR1	RXR-alpha	606	612	2.544678	GGGTGCA	0.85449	0.89683
cg0302000	ALS2CR1	c-Ets-2 [T0	1340	1348	2.447661	TAGAAG	0.07629	0.07844
cg0302000	ALS2CR1	MAZ [T00	547	559	2.392122	TGGGGG	0.00405	0.00469
cg0302000	ALS2CR1	C/EBPalph	1554	1560	2.371703	CCCAATT	0.48828	0.47439
cg0302000	ALS2CR1	GCF [T00	1162	1170	2.339499	GCGCAG	0.06104	0.06908
cg0302000	ALS2CR1	RXR-alpha	1299	1305	2.322562	GGGTCTC	0.85449	0.89683
cg0302000	ALS2CR1	RXR-alpha	1781	1787	2.322562	GGGTCTC	0.85449	0.89683
cg0302000	ALS2CR1	Elk-1 [T00	1489	1497	2.299314	CTTCCTC	0.09155	0.09306
cg0302000	ALS2CR1	T3R-beta1	816	824	2.259951	TCACCAC	0.03052	0.03203
cg0302000	ALS2CR1	GATA-1 [	1526	1531	2.176375	TATCCA	3.90625	3.79558

cg0302000	ALS2CR1	GATA-1 [	1646	1651	2.176375	TATCCA	3.90625	3.79558
cg0302000	ALS2CR1	GATA-1 [	1863	1868	2.176375	TATCCT	3.90625	3.79558
cg0302000	ALS2CR1	c-Ets-2 [T	1016	1024	2.142327	TTCCTCT	0.16785	0.16456
cg0302000	ALS2CR1	c-Ets-2 [T	1490	1498	2.142327	TTCCTCT	0.16785	0.16456
cg0302000	ALS2CR1	NF-1 [T00	764	771	2.067686	TGTGCC	0.12207	0.12476
cg0302000	ALS2CR1	NF-1 [T00	788	795	2.067686	TTGGCA	0.12207	0.12476
cg0302000	ALS2CR1	NF-1 [T00	1738	1745	2.067686	TTGGGA	0.12207	0.12476
cg0302000	ALS2CR1	GATA-1 [	433	438	2.001358	TATCGC	3.90625	3.79558
cg0302000	ALS2CR1	GATA-1 [	562	567	2.001358	GGGATA	3.90625	3.79558
cg0302000	ALS2CR1	HNF-1C [	1520	1528	1.940349	GTTAAA	0.02289	0.01968
cg0302000	ALS2CR1	GATA-1 [	996	1001	1.896347	TATCCG	3.90625	3.79558
cg0302000	ALS2CR1	AP-2alpha	971	976	1.871933	GCCTCC	0.97656	1.07805
cg0302000	ALS2CR1	AP-2alpha	1259	1264	1.871933	GGAGGC	0.97656	1.07805
cg0302000	ALS2CR1	TBP [T007	205	214	1.871542	GGATTA	0.18311	0.15671
cg0302000	ALS2CR1	TBP [T007	359	368	1.871542	GCCATA	0.18311	0.15671
cg0302000	ALS2CR1	HIF-1 [T0	233	241	1.839875	ACGTGC	0.1297	0.13373
cg0302000	ALS2CR1	TFII-I [T0	51	56	1.824994	GGAGAG	0.48828	0.51201
cg0302000	ALS2CR1	TFII-I [T0	1114	1119	1.824994	CTCTCC	0.48828	0.51201
cg0302000	ALS2CR1	TFII-I [T0	1365	1370	1.824994	GGAGAG	0.48828	0.51201
cg0302000	ALS2CR1	p53 [T006	190	196	1.758307	GGGCAT	0.36621	0.38097
cg0302000	ALS2CR1	AR [T000	1497	1505	1.727468	ACACTG	0.09155	0.09239
cg0302000	ALS2CR1	RXR-alph	1686	1692	1.696452	CTGACC	0.48828	0.52093
cg0302000	ALS2CR1	GR-beta [	482	486	1.680765	GAATT	3.90625	3.70067
cg0302000	ALS2CR1	GR-beta [	568	572	1.680765	GCATT	3.90625	3.70067
cg0302000	ALS2CR1	GR-beta [	721	725	1.680765	GAATT	3.90625	3.70067
cg0302000	ALS2CR1	GR-beta [	1682	1686	1.680765	AATTC	3.90625	3.70067
cg0302000	ALS2CR1	GR-beta [	1919	1923	1.680765	AATGC	3.90625	3.70067
cg0302000	ALS2CR1	c-Ets-1 [T	1343	1349	1.641124	AAGGAA	0.36621	0.35197
cg0302000	ALS2CR1	C/EBPbeta	88	91	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	200	203	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	286	289	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	291	294	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	451	454	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	502	505	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	546	549	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	618	621	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	768	771	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	788	791	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1048	1051	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1099	1102	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1142	1145	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1269	1272	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1389	1392	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1529	1532	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1555	1558	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1619	1622	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1629	1632	1.639871	TTGG	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1738	1741	1.639871	TTGG	15.625	15.23827

cg0302000	ALS2CR1	C/EBPbeta	1788	1791	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1895	1898	1.639871	CCAA	15.625	15.23827
cg0302000	ALS2CR1	XBP-1 [T0	305	310	1.583727	ATGACA	0.97656	0.94995
cg0302000	ALS2CR1	XBP-1 [T0	394	399	1.583727	GGTCAT	0.97656	0.94995
cg0302000	ALS2CR1	XBP-1 [T0	1641	1646	1.583727	TGTCAT	0.97656	0.94995
cg0302000	ALS2CR1	XBP-1 [T0	1797	1802	1.583727	TGTCAT	0.97656	0.94995
cg0302000	ALS2CR1	TFIID [T0	78	84	1.537547	TTTTACA	0.73242	0.65627
cg0302000	ALS2CR1	Pax-5 [T00	838	844	1.537547	CTGGCCC	0.73242	0.83087
cg0302000	ALS2CR1	RXR-alpha	145	151	1.474336	GGGTCTA	0.48828	0.52093
cg0302000	ALS2CR1	STAT4 [T0	35	40	1.470588	GGAAAC	1.95312	1.90161
cg0302000	ALS2CR1	STAT4 [T0	410	415	1.470588	GGAAAC	1.95312	1.90161
cg0302000	ALS2CR1	STAT4 [T0	481	486	1.470588	GGAATT	1.95312	1.90161
cg0302000	ALS2CR1	STAT4 [T0	720	725	1.470588	GGAATT	1.95312	1.90161
cg0302000	ALS2CR1	STAT4 [T0	1196	1201	1.470588	TTTTCC	1.95312	1.90161
cg0302000	ALS2CR1	STAT4 [T0	1716	1721	1.470588	TTTTCC	1.95312	1.90161
cg0302000	ALS2CR1	PR B [T00	454	460	1.404665	AACACTC	0.36621	0.35143
cg0302000	ALS2CR1	PR A [T01	454	460	1.404665	AACACTC	0.36621	0.35143
cg0302000	ALS2CR1	c-Ets-1 [T0	33	39	1.384951	CAGGAA	0.36621	0.35197
cg0302000	ALS2CR1	C/EBPbeta	109	112	1.366559	TCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	141	144	1.366559	TCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	168	171	1.366559	TTGA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	302	305	1.366559	TCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	485	488	1.366559	TTGA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	758	761	1.366559	TCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	772	775	1.366559	TTGA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	798	801	1.366559	TTGA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1070	1073	1.366559	TCAA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1542	1545	1.366559	TTGA	15.625	15.23827
cg0302000	ALS2CR1	C/EBPbeta	1983	1986	1.366559	TTGA	15.625	15.23827
cg0302000	ALS2CR1	AP-2alpha	534	539	1.357116	GCCTGT	0.48828	0.51319
cg0302000	ALS2CR1	AP-2alpha	1130	1135	1.357116	GCCTGT	0.48828	0.51319
cg0302000	ALS2CR1	p53 [T006	937	943	1.270236	CGTGCCC	0.12207	0.13816
cg0302000	ALS2CR1	PEA3 [T00	55	63	1.194633	AGGATG	0.06866	0.06787
cg0302000	ALS2CR1	RAR-beta	753	762	1.08151	AGGGTTC	0.03052	0.03086
cg0302000	ALS2CR1	RAR-beta	797	806	1.08151	ATTGAAC	0.03052	0.03086
cg0302000	ALS2CR1	HNF-1A [	600	607	1.069403	GTTAATC	0.48828	0.45029
cg0302000	ALS2CR1	GATA-1 [	992	997	1.038567	ATGATA	1.95312	1.80234
cg0302000	ALS2CR1	GATA-1 [	1068	1073	1.038567	TATCAA	1.95312	1.80234
cg0302000	ALS2CR1	POU2F2 (	207	217	1.003369	ATTATA	0.00286	0.00234
cg0302000	ALS2CR1	RXR-alpha	168	174	0.848226	TTGACCC	0.48828	0.51313
cg0302000	ALS2CR1	GR-beta [T	13	17	0.840383	AATGG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	21	25	0.840383	TCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	113	117	0.840383	CCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	164	168	0.840383	CCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	182	186	0.840383	CCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	268	272	0.840383	AATGG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	304	308	0.840383	AATGA	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	418	422	0.840383	TCATT	7.8125	7.2174

cg0302000	ALS2CR1	GR-beta [T	483	487	0.840383	AATTG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	491	495	0.840383	AATGA	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	592	596	0.840383	AATGA	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	603	607	0.840383	AATGG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	722	726	0.840383	AATTG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	769	773	0.840383	CAATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	770	774	0.840383	AATTG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	785	789	0.840383	CAATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	786	790	0.840383	AATTG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1324	1328	0.840383	CCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1452	1456	0.840383	CCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1483	1487	0.840383	TCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1556	1560	0.840383	CAATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1557	1561	0.840383	AATTG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1625	1629	0.840383	TCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1734	1738	0.840383	TAATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1760	1764	0.840383	CAATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1761	1765	0.840383	AATTG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1767	1771	0.840383	AATGA	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1845	1849	0.840383	AATGG	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1859	1863	0.840383	CCATT	7.8125	7.2174
cg0302000	ALS2CR1	GR-beta [T	1933	1937	0.840383	AATGA	7.8125	7.2174
cg0302000	ALS2CR1	PXR-1:RX	104	111	0.818075	CTAGTTC	0.12207	0.11843
cg0302000	ALS2CR1	AP-2alpha	1231	1236	0.678558	TCAGGC	0.48828	0.51196
cg0302000	ALS2CR1	HIF-1 [T0	650	658	0.543748	CCTGCAC	0.04578	0.04961
cg0302000	ALS2CR1	AP-2alpha	863	868	0.226186	CCAGGC	0.97656	1.07867
cg0302000	ALS2CR1	AP-2alpha	1292	1297	0.226186	GCCTGG	0.97656	1.07867
cg0302000	ALS2CR1	AP-2alpha	1319	1324	0.226186	CCAGGC	0.97656	1.07867
cg0302000	ALS2CR1	GR-alpha [	53	57	0.207689	AGAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	202	206	0.207689	AAAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	368	372	0.207689	AAAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	385	389	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	717	721	0.207689	AAAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	743	747	0.207689	AAAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	751	755	0.207689	AAAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	804	808	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	812	816	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	980	984	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1018	1022	0.207689	CCTCT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1082	1086	0.207689	AAAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1185	1189	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1336	1340	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1437	1441	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1492	1496	0.207689	CCTCT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1597	1601	0.207689	CCTCT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1606	1610	0.207689	CCTCT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1714	1718	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1721	1725	0.207689	CCTTT	7.8125	7.79817

cg0302000	ALS2CR1	GR-alpha [	1808	1812	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1831	1835	0.207689	CCTTT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1954	1958	0.207689	AGAGG	7.8125	7.79817
cg0302000	ALS2CR1	HNF-1A [	1520	1527	0.143882	GTTAAA	0.24414	0.20853
cg0302000	ALS2CR1	c-Ets-1 [T	1489	1495	0.128087	CTTCCTC	0.24414	0.24982
cg0302000	ALS2CR1	PXR-1:RX	374	381	0.123583	TGAGTT	0.12207	0.11255
cg0302000	ALS2CR1	GATA-1 [	575	580	0.105011	GAGATA	0.97656	0.92541
cg0302000	ALS2CR1	GR-beta [T	294	298	0	AATGT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	325	329	0	AATGT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	586	590	0	AATGT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	760	764	0	AATGT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	795	799	0	ACATT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	985	989	0	AATGT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1193	1197	0	ACATT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1639	1643	0	AATGT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1663	1667	0	ACATT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1673	1677	0	ACATT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1681	1685	0	AAATT	3.90625	3.51525
cg0302000	ALS2CR1	GR-beta [T	1735	1739	0	AATTT	3.90625	3.51525
cg0302000	ALS2CR1	XBP-1 [T	593	598	0	ATGACG	0.97656	0.94838
cg0302000	ALS2CR1	XBP-1 [T	1481	1486	0	AGTCAT	0.97656	0.94838
cg0302000	ALS2CR1	TFIID [T0	24	30	0	TTAAAA	1.09863	0.95175
cg0302000	ALS2CR1	TFIID [T0	363	369	0	TATAAA	1.09863	0.95175
cg0302000	ALS2CR1	TFIID [T0	691	697	0	TAAAAA	1.09863	0.95175
cg0302000	ALS2CR1	TFIID [T0	698	704	0	TAAAAA	1.09863	0.95175
cg0302000	ALS2CR1	TFIID [T0	711	717	0	TAAAAA	1.09863	0.95175
cg0302000	ALS2CR1	TFIID [T0	1677	1683	0	TTTAAA	1.09863	0.95175
cg0302000	ALS2CR1	GR-alpha [	42	46	0	ACAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	68	72	0	ATAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	474	478	0	ATAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	535	539	0	CCTGT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	637	641	0	CCTAT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1041	1045	0	ACAGG	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1087	1091	0	CCTAT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1131	1135	0	CCTGT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1419	1423	0	CCTGT	7.8125	7.79817
cg0302000	ALS2CR1	GR-alpha [	1881	1885	0	ACAGG	7.8125	7.79817
cg0302000	ALS2CR1	IRF-1 [T0	1717	1725	0	TTTCCCT	0.00763	0.00712
cg0302000	ALS2CR1	FOXP3 [T	38	43	0	AACAAC	1.46484	1.44953
cg0302000	ALS2CR1	FOXP3 [T	657	662	0	GTTGTG	1.46484	1.44953
cg0302000	ALS2CR1	FOXP3 [T	1742	1747	0	GACAAC	1.46484	1.44953
cg0302000	ALS2CR1	PR B [T00	83	89	0	CACTGT	0.36621	0.35051
cg0302000	ALS2CR1	PR B [T00	1531	1537	0	AACAGT	0.36621	0.35051
cg0302000	ALS2CR1	PR A [T01	83	89	0	CACTGT	0.36621	0.35051
cg0302000	ALS2CR1	PR A [T01	1531	1537	0	AACAGT	0.36621	0.35051
cg0302000	ALS2CR1	HNF-3alpl	705	712	0	TAAAAA	0.09155	0.07727
cg0302000	ALS2CR1	C/EBPbeta	17	20	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	39	42	0	ACAA	15.625	15.26275

cg0302000	ALS2CR1	C/EBPbeta	116	119	0	TTGT	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	266	269	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	272	275	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	388	391	0	TTGT	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	427	430	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	437	440	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	489	492	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	645	648	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	658	661	0	TTGT	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	724	727	0	TTGC	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	784	787	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	917	920	0	TTGT	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1023	1026	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1092	1095	0	TTGT	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1308	1311	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1316	1319	0	TTGC	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1370	1373	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1411	1414	0	TTGT	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1559	1562	0	TTGT	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1637	1640	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1651	1654	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1743	1746	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1759	1762	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1763	1766	0	TTGC	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1765	1768	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1834	1837	0	TTGC	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1931	1934	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1950	1953	0	ACAA	15.625	15.26275
cg0302000	ALS2CR1	C/EBPbeta	1962	1965	0	GCAA	15.625	15.26275
cg0302000	ALS2CR1	YY1 [T00	14	17	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	113	116	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	164	167	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	177	180	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	182	185	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	254	257	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	269	272	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	299	302	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	342	345	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	344	347	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	360	363	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	398	401	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	415	418	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	604	607	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	623	626	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1110	1113	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1118	1121	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1242	1245	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1324	1327	0	CCAT	7.8125	7.79459

cg0302000	ALS2CR1	YY1 [T00	1382	1385	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1452	1455	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1726	1729	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1779	1782	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1803	1806	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1846	1849	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1859	1862	0	CCAT	7.8125	7.79459
cg0302000	ALS2CR1	YY1 [T00	1944	1947	0	ATGG	7.8125	7.79459
cg0302000	ALS2CR1	TFII-I [T0	441	446	0	GGACAG	1.46484	1.48598
cg0302000	ALS2CR1	TFII-I [T0	563	568	0	GGATAG	1.46484	1.48598
cg0302000	ALS2CR1	TFII-I [T0	1039	1044	0	GGACAG	1.46484	1.48598
cg0302000	ALS2CR1	TFII-I [T0	1500	1505	0	CTGTCC	1.46484	1.48598
cg0302000	ALS2CR1	STAT4 [T	1345	1350	0	GGAAAT	0.48828	0.46235
cg0302000	ALS2CR1	HOXD9 [	703	712	0	AATAAA	0.01144	0.00905
cg0302000	ALS2CR1	HOXD10 [	703	712	0	AATAAA	0.01144	0.00905
cg0302000	ALS2CR1	ER-alpha [	169	173	0	TGACC	1.95312	1.99744
cg0302000	ALS2CR1	ER-alpha [	394	398	0	GGTCA	1.95312	1.99744
cg0302000	ALS2CR1	ER-alpha [	1223	1227	0	TGACC	1.95312	1.99744
cg0302000	ALS2CR1	ER-alpha [	1687	1691	0	TGACC	1.95312	1.99744
cg0302000	ALS2CR1	RXR-alph	754	760	0	GGGTTC	0.24414	0.24342
cg0302000	ALS2CR1	RXR-alph	799	805	0	TGAACC	0.24414	0.24342
cg0302000	ALS2CR1	c-Myc [T0	232	237	0	CACGTG	0.48828	0.51196
cg0302000	ALS2CR1	GATA-1 [	1697	1702	0	TATCTG	0.97656	0.92541
cg0302000	ALS2CR1	PXR-1:RX	1398	1405	0	TTAGTT	0.12207	0.11255
cg0302000	ALS2CR1	Pax-5 [T0	864	870	0	CAGGCC	1.09863	1.24633
cg0302000	ALS2CR1	Pax-5 [T0	937	943	0	CGTGCC	1.09863	1.24633
cg0302000	ALS2CR1	Pax-5 [T0	1053	1059	0	CCTGCC	1.09863	1.24633
cg0302000	ALS2CR1	Pax-5 [T0	1237	1243	0	CGGGCC	1.09863	1.24633
cg0302000	ALS2CR1	p53 [T006	1053	1059	0	CCTGCC	0.36621	0.40082
cg0302000	ALS2CR1	AP-2alpha	1164	1169	0	GCAGGC	0.97656	1.07867
cg0302000	ALS2CR1	GCF [T00	1199	1207	0	TCCCAG	0.09155	0.10999
cg0302000	ALS2CR1	IRF-2 [T0	1910	1915	0	TCACTT	0.48828	0.46235
cg0302000	ALS2CR1	HNF-1A [	1581	1588	0	GTTAAT	0.24414	0.20853
cg0359490	ANKRD11	c-Ets-1 [T	1748	1754	9.969337	TGGGAA	0.24414	0.2459
cg0359490	ANKRD11	c-Myb [T0	1358	1365	9.815171	TCAAGT	0.36621	0.3712
cg0359490	ANKRD11	XBP-1 [T	749	754	9.789909	ATGGCG	1.95312	1.95208
cg0359490	ANKRD11	XBP-1 [T	1646	1651	9.789909	AGACAT	1.95312	1.95208
cg0359490	ANKRD11	CTF [T001	1276	1287	9.754341	GGACAT	0.04292	0.04259
cg0359490	ANKRD11	PR B [T00	263	269	9.743489	AACACC	1.09863	1.10292
cg0359490	ANKRD11	PR B [T00	377	383	9.743489	AACACG	1.09863	1.10292
cg0359490	ANKRD11	PR A [T01	263	269	9.743489	AACACC	1.09863	1.10292
cg0359490	ANKRD11	PR A [T01	377	383	9.743489	AACACG	1.09863	1.10292
cg0359490	ANKRD11	LEF-1 [T0	584	591	9.72404	CTTTGT	0.21362	0.2139
cg0359490	ANKRD11	NF-AT1 [	369	377	9.691726	GGAAAC	0.16785	0.1682
cg0359490	ANKRD11	NF-kappa	956	966	9.668344	GGCTCC	0.02193	0.02152
cg0359490	ANKRD11	RAR-beta	1031	1040	9.622793	CAGAAA	0.21362	0.21243
cg0359490	ANKRD11	Pax-5 [T0	729	735	9.552105	GTTGCC	1.46484	1.43083
cg0359490	ANKRD11	Pax-5 [T0	1288	1294	9.552105	GGGCAA	1.46484	1.43083

cg0359490	ANKRD11	Pax-5 [T0	1531	1537	9.552105	GGGCAA	1.46484	1.43083
cg0359490	ANKRD11	TFIID [T0	1006	1012	9.552105	TTTCTCA	1.46484	1.48472
cg0359490	ANKRD11	TFIID [T0	1129	1135	9.552105	TGGGAA	1.46484	1.48472
cg0359490	ANKRD11	TFIID [T0	1297	1303	9.552105	TTTCTCA	1.46484	1.48472
cg0359490	ANKRD11	TFIID [T0	1553	1559	9.552105	TTTCTCA	1.46484	1.48472
cg0359490	ANKRD11	TFIID [T0	1912	1918	9.552105	TTTGGG	1.46484	1.48472
cg0359490	ANKRD11	NF-1 [T00	1574	1581	9.535536	ATGGCC	0.73242	0.73053
cg0359490	ANKRD11	TFII-I [T0	369	374	9.512894	GGAAAC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	416	421	9.512894	GGAAGG	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	461	466	9.512894	GGACAA	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	629	634	9.512894	CGGTCC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	755	760	9.512894	CGATCC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	812	817	9.512894	CCTTCC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	915	920	9.512894	CCGTCC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	922	927	9.512894	GTGTCC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	936	941	9.512894	GGACAC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	942	947	9.512894	GGATAA	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1131	1136	9.512894	GGAAAA	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1264	1269	9.512894	GGAAAA	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1341	1346	9.512894	GGACAA	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1386	1391	9.512894	GGACAC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1427	1432	9.512894	GGAAAC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1677	1682	9.512894	TTATCC	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1720	1725	9.512894	GGAAAA	7.32422	7.29728
cg0359490	ANKRD11	TFII-I [T0	1791	1796	9.512894	GTTTCC	7.32422	7.29728
cg0359490	ANKRD11	FOXP3 [T	159	164	9.512894	CAGAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	217	222	9.512894	CAGAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	244	249	9.512894	CAGAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	260	265	9.512894	CGCAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	353	358	9.512894	GTTCTC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	452	457	9.512894	GTTCTC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	544	549	9.512894	CTAAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	675	680	9.512894	GCCAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	729	734	9.512894	GTTGCC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1011	1016	9.512894	CAGAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1077	1082	9.512894	AAGAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1085	1090	9.512894	AATAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1118	1123	9.512894	GTAAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1323	1328	9.512894	GGCAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1468	1473	9.512894	CAGAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1577	1582	9.512894	GCCAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1743	1748	9.512894	GTTGGT	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1777	1782	9.512894	GAGAAC	7.32422	7.35678
cg0359490	ANKRD11	FOXP3 [T	1967	1972	9.512894	GCCAAC	7.32422	7.35678
cg0359490	ANKRD11	Ik-1 [T027	818	830	9.497194	TGAGTA	0.02941	0.02907
cg0359490	ANKRD11	TCF-4E [T	1556	1562	9.453578	CTCAAA	0.48828	0.49215
cg0359490	ANKRD11	c-Jun [T00	142	148	9.397655	ATTGTC	0.73242	0.73031
cg0359490	ANKRD11	c-Jun [T00	991	997	9.397655	TGACAA	0.73242	0.73031

cg0359490	ANKRD11	c-Jun [T00	1613	1619	9.397655	ATCGTC	0.73242	0.73031
cg0359490	ANKRD11	NFI/CTF [	1277	1284	9.352332	GACATT	0.54932	0.54821
cg0359490	ANKRD11	c-Myb [T0	382	389	9.29064	GGGAGT	0.36621	0.37054
cg0359490	ANKRD11	c-Myb [T0	1635	1642	9.29064	AAACTA	0.36621	0.37054
cg0359490	ANKRD11	RBP-Jkapp	1744	1755	9.256527	TTGGTG	0.01884	0.01886
cg0359490	ANKRD11	MEF-2A [	863	873	9.220261	TATTTTT	0.07343	0.07563
cg0359490	ANKRD11	NF-AT1 [	1057	1065	9.18189	TCACTT	0.22888	0.22959
cg0359490	ANKRD11	c-Ets-1 [T	1050	1056	9.148774	AGGGAA	0.85449	0.85523
cg0359490	ANKRD11	c-Ets-1 [T	1725	1731	9.148774	AGGGAA	0.85449	0.85523
cg0359490	ANKRD11	LEF-1 [T0	1064	1071	9.099721	CCACAA	0.54932	0.55326
cg0359490	ANKRD11	USF2 [T0	614	623	9.056375	GCCCCA	0.1545	0.15287
cg0359490	ANKRD11	USF2 [T0	1039	1048	9.056375	CACACA	0.1545	0.15287
cg0359490	ANKRD11	LEF-1 [T0	1911	1918	8.973041	CTTTGG	0.54932	0.55326
cg0359490	ANKRD11	GR [T050	375	381	8.971049	CAAACA	0.61035	0.61632
cg0359490	ANKRD11	GR [T050	1365	1371	8.971049	CAAAAG	0.61035	0.61632
cg0359490	ANKRD11	c-Ets-1 [T	483	489	8.937416	ATTCCA	0.85449	0.85523
cg0359490	ANKRD11	T3R-beta1	912	920	8.924046	TCACCG	0.2594	0.25766
cg0359490	ANKRD11	IRF-1 [T0	1061	1069	8.916359	TTTCCA	0.09155	0.09147
cg0359490	ANKRD11	c-Ets-2 [T	814	822	8.912323	TTCCTG	0.27466	0.27495
cg0359490	ANKRD11	NFI/CTF [	1681	1688	8.814757	CCAAAA	0.48828	0.48804
cg0359490	ANKRD11	NFI/CTF [	1856	1863	8.814757	CCAAAA	0.48828	0.48804
cg0359490	ANKRD11	c-Ets-1 [T	1216	1222	8.809329	CTGGAA	0.85449	0.85523
cg0359490	ANKRD11	c-Jun [T00	200	206	8.807683	GTTGTC	0.61035	0.61059
cg0359490	ANKRD11	NF-1 [T00	1913	1920	8.790071	TTGGGA	0.24414	0.24467
cg0359490	ANKRD11	NF-1 [T00	1964	1971	8.790071	CTTGCC	0.24414	0.24467
cg0359490	ANKRD11	NF-AT1 [	1099	1107	8.769753	GGAAAG	0.22888	0.22959
cg0359490	ANKRD11	XBP-1 [T	315	320	8.75604	ATGAAC	2.92969	2.9674
cg0359490	ANKRD11	XBP-1 [T	387	392	8.75604	TTTCAT	2.92969	2.9674
cg0359490	ANKRD11	XBP-1 [T	977	982	8.75604	GTTCAT	2.92969	2.9674
cg0359490	ANKRD11	XBP-1 [T	1238	1243	8.75604	ATGAAA	2.92969	2.9674
cg0359490	ANKRD11	XBP-1 [T	1499	1504	8.75604	ATGAAA	2.92969	2.9674
cg0359490	ANKRD11	STAT1bet	1060	1069	8.695301	CTTTCC	0.22316	0.22446
cg0359490	ANKRD11	IRF-1 [T0	1423	1431	8.661524	GGGAGG	0.20599	0.20664
cg0359490	ANKRD11	IRF-1 [T0	1792	1800	8.661524	TTTCCT	0.20599	0.20664
cg0359490	ANKRD11	IRF-1 [T0	365	373	8.570857	CTGTGG	0.20599	0.20664
cg0359490	ANKRD11	PPAR-alp	576	586	8.543553	AGCTGG	0.02003	0.01963
cg0359490	ANKRD11	RAR-beta	879	888	8.541284	GGGGTT	0.26703	0.26657
cg0359490	ANKRD11	NF-AT1 [	1720	1728	8.532897	GGAAAA	0.10681	0.10725
cg0359490	ANKRD11	NF-kappa	253	263	8.372754	GGGGAC	0.02146	0.02103
cg0359490	ANKRD11	PR B [T00	17	23	8.338824	TCCTGT	1.09863	1.10009
cg0359490	ANKRD11	PR B [T00	547	553	8.338824	AACAGC	1.09863	1.10009
cg0359490	ANKRD11	PR B [T00	1001	1007	8.338824	GTCTGT	1.09863	1.10009
cg0359490	ANKRD11	PR B [T00	1080	1086	8.338824	AACAGA	1.09863	1.10009
cg0359490	ANKRD11	PR B [T00	1396	1402	8.338824	AACAGG	1.09863	1.10009
cg0359490	ANKRD11	PR B [T00	1580	1586	8.338824	AACAGG	1.09863	1.10009
cg0359490	ANKRD11	PR B [T00	1764	1770	8.338824	AACAGC	1.09863	1.10009
cg0359490	ANKRD11	PR A [T01	17	23	8.338824	TCCTGT	1.09863	1.10009
cg0359490	ANKRD11	PR A [T01	547	553	8.338824	AACAGC	1.09863	1.10009

cg0359490	ANKRD11	PR A [T01	1001	1007	8.338824	GTCTGTT	1.09863	1.10009
cg0359490	ANKRD11	PR A [T01	1080	1086	8.338824	AACAGA	1.09863	1.10009
cg0359490	ANKRD11	PR A [T01	1396	1402	8.338824	AACAGG	1.09863	1.10009
cg0359490	ANKRD11	PR A [T01	1580	1586	8.338824	AACAGG	1.09863	1.10009
cg0359490	ANKRD11	PR A [T01	1764	1770	8.338824	AACAGC	1.09863	1.10009
cg0359490	ANKRD11	ATF3 [T01	907	914	8.313799	ATATGT	0.27466	0.27431
cg0359490	ANKRD11	GR-alpha [	62	66	8.281568	GAAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	76	80	8.281568	GGAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	104	108	8.281568	CCTCC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	175	179	8.281568	CCTCC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	233	237	8.281568	CCTCC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	271	275	8.281568	CCTTC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	417	421	8.281568	GAAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	457	461	8.281568	CAAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	512	516	8.281568	CAAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	552	556	8.281568	CCTCC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	570	574	8.281568	GGAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	774	778	8.281568	CCTCC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	780	784	8.281568	CCTCC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	812	816	8.281568	CCTTC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	929	933	8.281568	GAAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	960	964	8.281568	CCTCC	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	1424	1428	8.281568	GGAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	1477	1481	8.281568	GAAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	1709	1713	8.281568	CGAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	1732	1736	8.281568	CCTCG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	1916	1920	8.281568	GGAGG	7.8125	7.72956
cg0359490	ANKRD11	GR-alpha [	1963	1967	8.281568	CCTTG	7.8125	7.72956
cg0359490	ANKRD11	c-Jun [T00	1941	1947	8.242207	GAGGTC	0.48828	0.49076
cg0359490	ANKRD11	ENKTF-1	28	35	8.19852	TGGCGA	0.73242	0.71737
cg0359490	ANKRD11	ENKTF-1	321	328	8.19852	TGGCGG	0.73242	0.71737
cg0359490	ANKRD11	ENKTF-1	1138	1145	8.19852	TGGCTA	0.73242	0.71737
cg0359490	ANKRD11	ENKTF-1	1176	1183	8.19852	TCTCGC	0.73242	0.71737
cg0359490	ANKRD11	ENKTF-1	1963	1970	8.19852	CCTTGC	0.73242	0.71737
cg0359490	ANKRD11	AhR [T01	1890	1900	8.184723	CTCACG	0.04864	0.04833
cg0359490	ANKRD11	SRY [T00	1063	1071	8.174786	TCCACA	0.15259	0.15383
cg0359490	ANKRD11	SRY [T00	1325	1333	8.174786	CAACCA	0.15259	0.15383
cg0359490	ANKRD11	SRY [T00	1378	1386	8.174786	CCAGCA	0.15259	0.15383
cg0359490	ANKRD11	LEF-1 [T0	1555	1562	8.117221	TCTCAA	0.12207	0.1241
cg0359490	ANKRD11	GR-alpha [	10	14	8.073878	CCTAG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	11	15	8.073878	CTAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	46	50	8.073878	CCTGC	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	87	91	8.073878	GCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	182	186	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	239	243	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	301	305	8.073878	CCTGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	308	312	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	430	434	8.073878	CCTGG	7.8125	7.72238

cg0359490	ANKRD11	GR-alpha [	521	525	8.073878	GCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	531	535	8.073878	CCTGC	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	592	596	8.073878	CCTGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	610	614	8.073878	GCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	640	644	8.073878	CCTGC	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	647	651	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	682	686	8.073878	CCTGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	734	738	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	759	763	8.073878	CCTGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	783	787	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	802	806	8.073878	CCTGC	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	888	892	8.073878	CCTGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	953	957	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	1045	1049	8.073878	CCTGC	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	1048	1052	8.073878	GCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	1170	1174	8.073878	CCTAG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	1273	1277	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	1285	1289	8.073878	CCTGG	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	1434	1438	8.073878	CCTGC	7.8125	7.72238
cg0359490	ANKRD11	GR-alpha [	1877	1881	8.073878	CCAGG	7.8125	7.72238
cg0359490	ANKRD11	AR [T000	1341	1349	8.055836	GGACAA	0.19836	0.19634
cg0359490	ANKRD11	Pax-5 [T0	166	172	8.014558	GGGCAG	2.19727	2.14502
cg0359490	ANKRD11	Pax-5 [T0	224	230	8.014558	GGGCAG	2.19727	2.14502
cg0359490	ANKRD11	Pax-5 [T0	395	401	8.014558	GGAGCC	2.19727	2.14502
cg0359490	ANKRD11	Pax-5 [T0	595	601	8.014558	GGGCAC	2.19727	2.14502
cg0359490	ANKRD11	Pax-5 [T0	603	609	8.014558	GGTGCC	2.19727	2.14502
cg0359490	ANKRD11	Pax-5 [T0	665	671	8.014558	TCAGCC	2.19727	2.14502
cg0359490	ANKRD11	Pax-5 [T0	1928	1934	8.014558	GGGCAG	2.19727	2.14502
cg0359490	ANKRD11	TFIID [T0	136	142	8.014558	TCTGAA	2.19727	2.24348
cg0359490	ANKRD11	TFIID [T0	1498	1504	8.014558	TATGAA	2.19727	2.24348
cg0359490	ANKRD11	TFIID [T0	1555	1561	8.014558	TCTCAA	2.19727	2.24348
cg0359490	ANKRD11	TFIID [T0	1952	1958	8.014558	TTTCAG	2.19727	2.24348
cg0359490	ANKRD11	ETF [T002	638	648	7.870358	GCCCTG	0.07153	0.06862
cg0359490	ANKRD11	AR [T000	946	954	7.840422	AAGATG	0.19836	0.19634
cg0359490	ANKRD11	p53 [T006	395	401	7.833758	GGAGCC	0.48828	0.47377
cg0359490	ANKRD11	NF-kappaI	650	660	7.826592	GGGGAC	0.0329	0.03218
cg0359490	ANKRD11	c-Myb [T0	246	253	7.739476	GAACTG	0.42725	0.43114
cg0359490	ANKRD11	c-Jun [T00	654	660	7.686747	ACAGTC	0.48828	0.48775
cg0359490	ANKRD11	c-Jun [T00	1390	1396	7.686747	ACAGTC	0.48828	0.48775
cg0359490	ANKRD11	p53 [T006	580	586	7.641867	GGGCCT	0.73242	0.7186
cg0359490	ANKRD11	NF-AT1 [	368	377	7.579763	TGGAAA	0.00763	0.00769
cg0359490	ANKRD11	GR [T050	856	862	7.527031	AATTTC	1.83105	1.86007
cg0359490	ANKRD11	GR [T050	1188	1194	7.527031	CAAACA	1.83105	1.86007
cg0359490	ANKRD11	GR [T050	1200	1206	7.527031	CAAAAT	1.83105	1.86007
cg0359490	ANKRD11	GR [T050	1291	1297	7.527031	CAAACA	1.83105	1.86007
cg0359490	ANKRD11	GR [T050	1329	1335	7.527031	CAAAGC	1.83105	1.86007
cg0359490	ANKRD11	GR [T050	1534	1540	7.527031	CAAAAG	1.83105	1.86007
cg0359490	ANKRD11	GR [T050	1682	1688	7.527031	CAAAAG	1.83105	1.86007

cg0359490	ANKRD11	GR [T050	1857	1863	7.527031	CAAAAG	1.83105	1.86007
cg0359490	ANKRD11	NF-kappa	1262	1273	7.522319	GGGGAA	0.00727	0.00713
cg0359490	ANKRD11	C/EBPalp	745	751	7.465744	TGCAAT	0.48828	0.49653
cg0359490	ANKRD11	AR [T000	57	65	7.406474	GGACAG	0.25177	0.25079
cg0359490	ANKRD11	AR [T000	1371	1379	7.406474	CTTCTG	0.25177	0.25079
cg0359490	ANKRD11	LEF-1 [T0	189	196	7.396545	GCGCAA	0.21362	0.21302
cg0359490	ANKRD11	IRF-1 [T0	1716	1724	7.387351	GTGGGG	0.14496	0.14449
cg0359490	ANKRD11	PXR-1:RX	506	513	7.362674	CATGTT	0.24414	0.24395
cg0359490	ANKRD11	c-Ets-1 [T	1129	1135	7.199436	TGGGAA	0.73242	0.73099
cg0359490	ANKRD11	SRY [T00	584	592	7.175614	CTTTGT	0.30518	0.30739
cg0359490	ANKRD11	XBP-1 [T	272	277	7.172312	CTTCAT	2.92969	2.97018
cg0359490	ANKRD11	XBP-1 [T	479	484	7.172312	CCTCAT	2.92969	2.97018
cg0359490	ANKRD11	XBP-1 [T	503	508	7.172312	AATCAT	2.92969	2.97018
cg0359490	ANKRD11	XBP-1 [T	1605	1610	7.172312	CATCAT	2.92969	2.97018
cg0359490	ANKRD11	Ik-1 [T027	1121	1133	7.122895	AACGGT	0.01064	0.01049
cg0359490	ANKRD11	p53 [T006	433	439	7.103527	GGGCGA	1.09863	1.07125
cg0359490	ANKRD11	NF-AT1 [	1131	1139	7.095752	GGAAAA	0.15259	0.1548
cg0359490	ANKRD11	Pax-5 [T0	433	439	7.082373	GGGCGA	0.12207	0.12014
cg0359490	ANKRD11	c-Ets-1 [T	1097	1103	7.071349	AGGGAA	0.73242	0.73099
cg0359490	ANKRD11	AR [T000	919	927	7.049779	CCTGTG	0.23651	0.23551
cg0359490	ANKRD11	IRF-1 [T0	1260	1268	7.041849	CTGGGG	0.1297	0.13036
cg0359490	ANKRD11	C/EBPalp	992	998	7.00174	GACAAT	0.73242	0.74337
cg0359490	ANKRD11	C/EBPalp	1279	1285	7.00174	CATTGG	0.73242	0.74337
cg0359490	ANKRD11	HNF-3alp	856	863	7.000129	AATTT	0.82397	0.84946
cg0359490	ANKRD11	HNF-3alp	1754	1761	7.000129	TGTAAA	0.82397	0.84946
cg0359490	ANKRD11	IRF-1 [T0	1127	1135	6.968314	GCTGGG	0.1297	0.13036
cg0359490	ANKRD11	RXR-alph	206	212	6.967687	ACCACC	0.36621	0.36214
cg0359490	ANKRD11	NF-1 [T00	1852	1859	6.948522	AGACCC	0.48828	0.4856
cg0359490	ANKRD11	c-Ets-1 [T	1262	1268	6.943262	GGGGAA	0.73242	0.73099
cg0359490	ANKRD11	c-Ets-1 [T	1718	1724	6.943262	GGGGAA	0.73242	0.73099
cg0359490	ANKRD11	ENKTF-1	671	678	6.942764	CACTGC	1.46484	1.44228
cg0359490	ANKRD11	ENKTF-1	750	757	6.942764	TGGCGC	1.46484	1.44228
cg0359490	ANKRD11	ENKTF-1	1282	1289	6.942764	TGGCCT	1.46484	1.44228
cg0359490	ANKRD11	VDR [T00	312	320	6.925682	GAGATG	0.42725	0.43062
cg0359490	ANKRD11	VDR [T00	509	517	6.925682	GTTCAA	0.42725	0.43062
cg0359490	ANKRD11	VDR [T00	977	985	6.925682	GTTCAT	0.42725	0.43062
cg0359490	ANKRD11	STAT1bet	1095	1104	6.908963	ACAGGG	0.103	0.10372
cg0359490	ANKRD11	p53 [T006	148	154	6.891821	ACCGCC	1.09863	1.07125
cg0359490	ANKRD11	p53 [T006	325	331	6.891821	GGGCGT	1.09863	1.07125
cg0359490	ANKRD11	C/EBPalp	1484	1490	6.85549	TGCAAT	0.73242	0.74337
cg0359490	ANKRD11	C/EBPalp	1626	1632	6.85549	TGCAAT	0.73242	0.74337
cg0359490	ANKRD11	PEA3 [T0	289	297	6.824411	TGTCAT	0.22888	0.22933
cg0359490	ANKRD11	NFI/CTF [	1782	1789	6.786076	CAGTTT	0.73242	0.73214
cg0359490	ANKRD11	T3R-beta1	146	154	6.702681	TCACCG	0.21362	0.21147
cg0359490	ANKRD11	T3R-beta1	1971	1979	6.702681	ACATGG	0.21362	0.21147
cg0359490	ANKRD11	c-Jun [T00	347	353	6.668031	TGACTT	0.61035	0.60769
cg0359490	ANKRD11	T3R-beta1	1656	1664	6.664094	TCACCC	0.21362	0.21147
cg0359490	ANKRD11	AR [T000	1386	1394	6.617912	GGACAC	0.19836	0.19597

cg0359490	ANKRD11	EBF [T054	466	476	6.595238	ACCACA	0.01907	0.01851
cg0359490	ANKRD11	TFII-I [T0	311	316	6.581441	GGAGAT	0.97656	0.97366
cg0359490	ANKRD11	TFII-I [T0	538	543	6.581441	ATCTCC	0.97656	0.97366
cg0359490	ANKRD11	TFII-I [T0	741	746	6.581441	GGAGTG	0.97656	0.97366
cg0359490	ANKRD11	TFII-I [T0	1269	1274	6.581441	ATCTCC	0.97656	0.97366
cg0359490	ANKRD11	FOXP3 [T	329	334	6.581441	GTTGAA	0.97656	0.99397
cg0359490	ANKRD11	FOXP3 [T	1761	1766	6.581441	TAAAAC	0.97656	0.99397
cg0359490	ANKRD11	RXR-alpha	1307	1313	6.563693	AATACC	0.24414	0.2434
cg0359490	ANKRD11	PPAR-alph	396	406	6.51544	GAGCCC	0.03719	0.03639
cg0359490	ANKRD11	AR [T0004	461	469	6.50872	GGACAA	0.19836	0.19597
cg0359490	ANKRD11	XBP-1 [T0	423	428	6.478682	ATGCCA	0.97656	0.97062
cg0359490	ANKRD11	NFI/CTF [	1740	1747	6.476675	CCCGTT	0.06104	0.05991
cg0359490	ANKRD11	AR [T0004	936	944	6.461025	GGACAC	0.19836	0.19597
cg0359490	ANKRD11	RAR-beta	974	983	6.452127	CGGGTT	0.18311	0.183
cg0359490	ANKRD11	c-Myb [T0	1867	1874	6.422836	AAACTG	0.30518	0.3056
cg0359490	ANKRD11	RAR-beta	1976	1985	6.415195	GTGAAA	0.18311	0.183
cg0359490	ANKRD11	RAR-beta	1725	1734	6.39673	AGGGAA	0.18311	0.183
cg0359490	ANKRD11	C/EBPalph	141	147	6.391486	AATTGT	0.48828	0.49071
cg0359490	ANKRD11	TCF-4E [T	190	196	6.302385	CGCAAA	0.61035	0.61344
cg0359490	ANKRD11	TCF-4E [T	1327	1333	6.302385	ACCAAA	0.61035	0.61344
cg0359490	ANKRD11	GR-alpha [	73	77	6.263098	TGAGG	3.90625	3.91061
cg0359490	ANKRD11	GR-alpha [	99	103	6.263098	CCTCA	3.90625	3.91061
cg0359490	ANKRD11	GR-alpha [	250	254	6.263098	TGAGG	3.90625	3.91061
cg0359490	ANKRD11	GR-alpha [	479	483	6.263098	CCTCA	3.90625	3.91061
cg0359490	ANKRD11	GR-alpha [	1229	1233	6.263098	CCTTA	3.90625	3.91061
cg0359490	ANKRD11	GR-alpha [	1795	1799	6.263098	CCTCA	3.90625	3.91061
cg0359490	ANKRD11	GR-alpha [	1922	1926	6.263098	TGAGG	3.90625	3.91061
cg0359490	ANKRD11	GR-alpha [	1940	1944	6.263098	TGAGG	3.90625	3.91061
cg0359490	ANKRD11	c-Ets-1 [T	367	373	6.167515	GTGGAA	0.36621	0.36731
cg0359490	ANKRD11	c-Ets-1 [T	1061	1067	6.167515	TTTCCA	0.36621	0.36731
cg0359490	ANKRD11	GR-alpha [	392	396	6.055408	TCAGG	3.90625	3.9065
cg0359490	ANKRD11	GR-alpha [	543	547	6.055408	CCTAA	3.90625	3.9065
cg0359490	ANKRD11	GR-alpha [	556	560	6.055408	CCTAA	3.90625	3.9065
cg0359490	ANKRD11	GR-alpha [	816	820	6.055408	CCTGA	3.90625	3.9065
cg0359490	ANKRD11	GR-alpha [	926	930	6.055408	CCTGA	3.90625	3.9065
cg0359490	ANKRD11	GR-alpha [	1938	1942	6.055408	CCTGA	3.90625	3.9065
cg0359490	ANKRD11	AR [T0004	91	99	5.953985	GGACAG	0.24414	0.24229
cg0359490	ANKRD11	RXR-alpha	359	365	5.937582	GTCACC	0.73242	0.72249
cg0359490	ANKRD11	RXR-alpha	602	608	5.937582	GGGTGC	0.73242	0.72249
cg0359490	ANKRD11	GCF [T00	184	192	5.917256	AGGCAG	0.64087	0.6219
cg0359490	ANKRD11	GCF [T00	486	494	5.917256	CCACCG	0.64087	0.6219
cg0359490	ANKRD11	STAT4 [T	416	421	5.882353	GGAAGG	0.48828	0.48408
cg0359490	ANKRD11	STAT4 [T	812	817	5.882353	CCTTCC	0.48828	0.48408
cg0359490	ANKRD11	NF-kappaB	1262	1272	5.874059	GGGGAA	0.04053	0.03971
cg0359490	ANKRD11	VDR [T00	1362	1370	5.771401	GTTCAA	0.42725	0.42999
cg0359490	ANKRD11	ENKTF-1	1787	1794	5.687009	TGGCGT	0.73242	0.7249
cg0359490	ANKRD11	c-Ets-1 [T	64	70	5.686398	AGGGAA	0.36621	0.3623
cg0359490	ANKRD11	T3R-beta1	979	987	5.572705	TCATGG	0.21362	0.21287

cg0359490	ANKRD11	NFI/CTF [	374	381	5.558661	CCAAAC	0.54932	0.55038
cg0359490	ANKRD11	GATA-2 [	1674	1682	5.555555	CCTTTAT	0.18311	0.1835
cg0359490	ANKRD11	T3R-beta1	765	773	5.553412	TCACCG	0.21362	0.21287
cg0359490	ANKRD11	Pax-5 [T0	148	154	5.544826	ACCGCC	0.73242	0.72046
cg0359490	ANKRD11	Pax-5 [T0	325	331	5.544826	GGGCGT	0.73242	0.72046
cg0359490	ANKRD11	TFIID [T0	867	873	5.544826	TTTAGT	0.73242	0.75085
cg0359490	ANKRD11	TFIID [T0	1991	1997	5.544826	TACTAA	0.73242	0.75085
cg0359490	ANKRD11	p53 [T006	665	671	5.508538	TCAGCC	0.61035	0.59991
cg0359490	ANKRD11	C/EBPalph	1608	1614	5.455853	CATTGA	0.73242	0.74391
cg0359490	ANKRD11	c-Ets-1 [T	414	420	5.430224	CGGGAA	0.36621	0.3623
cg0359490	ANKRD11	NF-1 [T00	1281	1288	5.377909	TTGGCC	0.24414	0.24258
cg0359490	ANKRD11	c-Myb [T0	161	168	5.137438	GAACTG	0.30518	0.30568
cg0359490	ANKRD11	c-Myb [T0	219	226	5.137438	GAACTG	0.30518	0.30568
cg0359490	ANKRD11	AP-2alpha	582	587	5.100982	GCCTTT	0.97656	0.97567
cg0359490	ANKRD11	AP-2alpha	1673	1678	5.100982	GCCTTT	0.97656	0.97567
cg0359490	ANKRD11	GR-beta [	828	832	5.042296	GGATT	3.90625	3.95351
cg0359490	ANKRD11	GR-beta [	862	866	5.042296	GTATT	3.90625	3.95351
cg0359490	ANKRD11	GR-beta [	1220	1224	5.042296	AATCC	3.90625	3.95351
cg0359490	ANKRD11	GR-beta [	1307	1311	5.042296	AATAC	3.90625	3.95351
cg0359490	ANKRD11	GR-beta [	1514	1518	5.042296	AATCC	3.90625	3.95351
cg0359490	ANKRD11	GR-beta [	1834	1838	5.042296	AATCC	3.90625	3.95351
cg0359490	ANKRD11	GR-beta [	1901	1905	5.042296	AATCC	3.90625	3.95351
cg0359490	ANKRD11	PXR-1:RX	785	792	5.032032	AGGGTT	0.12207	0.12266
cg0359490	ANKRD11	XBP-1 [T	419	424	4.894955	AGGCAT	0.97656	0.96979
cg0359490	ANKRD11	XBP-1 [T	514	519	4.894955	AGGCAT	0.97656	0.96979
cg0359490	ANKRD11	XBP-1 [T	996	1001	4.894955	ATGCCG	0.97656	0.96979
cg0359490	ANKRD11	XBP-1 [T	1479	1484	4.894955	AGGCAT	0.97656	0.96979
cg0359490	ANKRD11	XBP-1 [T	1583	1588	4.894955	AGGCAT	0.97656	0.96979
cg0359490	ANKRD11	c-Jun [T00	908	914	4.883696	TATGTC	0.61035	0.61057
cg0359490	ANKRD11	NF-1 [T00	1071	1078	4.880836	GGTGCC	0.24414	0.24398
cg0359490	ANKRD11	RXR-alpha	1165	1171	4.86724	GAGACC	0.48828	0.484
cg0359490	ANKRD11	C/EBPalph	1700	1706	4.845599	AATTGC	0.97656	0.99332
cg0359490	ANKRD11	TFII-I [T0	482	487	4.756447	CATTCC	2.92969	2.93695
cg0359490	ANKRD11	TFII-I [T0	949	954	4.756447	ATGTCC	2.92969	2.93695
cg0359490	ANKRD11	TFII-I [T0	1276	1281	4.756447	GGACAT	2.92969	2.93695
cg0359490	ANKRD11	TFII-I [T0	1750	1755	4.756447	GGAATG	2.92969	2.93695
cg0359490	ANKRD11	TFII-I [T0	1833	1838	4.756447	CAATCC	2.92969	2.93695
cg0359490	ANKRD11	FOXP3 [T	21	26	4.756447	GTTGAG	2.92969	2.96063
cg0359490	ANKRD11	FOXP3 [T	1132	1137	4.756447	GAAAAC	2.92969	2.96063
cg0359490	ANKRD11	FOXP3 [T	1253	1258	4.756447	GAAAAC	2.92969	2.96063
cg0359490	ANKRD11	FOXP3 [T	1393	1398	4.756447	GTCAAC	2.92969	2.96063
cg0359490	ANKRD11	FOXP3 [T	1525	1530	4.756447	AAAAAC	2.92969	2.96063
cg0359490	ANKRD11	FOXP3 [T	1600	1605	4.756447	CTCAAC	2.92969	2.96063
cg0359490	ANKRD11	FOXP3 [T	1633	1638	4.756447	CAAAAC	2.92969	2.96063
cg0359490	ANKRD11	FOXP3 [T	1800	1805	4.756447	AAAAAC	2.92969	2.96063
cg0359490	ANKRD11	C/EBPalph	1691	1697	4.560723	GACAAT	0.24414	0.24411
cg0359490	ANKRD11	NF-kappa	473	483	4.556008	GGGGAG	0.03242	0.03169
cg0359490	ANKRD11	AP-2alpha	9	14	4.438035	GCCTAG	0.97656	0.96979

cg0359490	ANKRD11	RXR-alpha	198	204	4.423008	GGGTTGT	0.24414	0.24292
cg0359490	ANKRD11	RXR-alpha	932	938	4.423008	GGGTGG	0.24414	0.24292
cg0359490	ANKRD11	TCF-4 [T0	1554	1563	4.412902	TTCTCAA	0.04196	0.04202
cg0359490	ANKRD11	STAT4 [T	66	71	4.411765	GGAAGA	1.95312	1.94235
cg0359490	ANKRD11	STAT4 [T	482	487	4.411765	CATTCC	1.95312	1.94235
cg0359490	ANKRD11	STAT4 [T	1112	1117	4.411765	TCTTCC	1.95312	1.94235
cg0359490	ANKRD11	STAT4 [T	1750	1755	4.411765	GGAATG	1.95312	1.94235
cg0359490	ANKRD11	p53 [T006	1874	1880	4.33696	GGGCCA	0.24414	0.23584
cg0359490	ANKRD11	RXR-alpha	1735	1741	4.24113	CGTACC	0.97656	0.9671
cg0359490	ANKRD11	C/EBPalph	1304	1310	4.235345	AGCAAT	0.48828	0.49358
cg0359490	ANKRD11	PXR-1:RX	974	981	4.213958	CGGGTT	0.12207	0.12119
cg0359490	ANKRD11	GR-beta [T	503	507	4.201913	AATCA	7.8125	7.94607
cg0359490	ANKRD11	GR-beta [T	795	799	4.201913	CGATT	7.8125	7.94607
cg0359490	ANKRD11	GR-beta [T	1085	1089	4.201913	AATAA	7.8125	7.94607
cg0359490	ANKRD11	GR-beta [T	1511	1515	4.201913	AATAA	7.8125	7.94607
cg0359490	ANKRD11	GR-beta [T	1545	1549	4.201913	AATAG	7.8125	7.94607
cg0359490	ANKRD11	GR-beta [T	1669	1673	4.201913	AATAG	7.8125	7.94607
cg0359490	ANKRD11	GR-beta [T	1694	1698	4.201913	AATCA	7.8125	7.94607
cg0359490	ANKRD11	NF-AT1 [T	1057	1066	4.134416	TCACTTT	0.08392	0.08485
cg0359490	ANKRD11	p53 [T006	611	617	4.125254	CAGGCC	0.73242	0.71379
cg0359490	ANKRD11	p53 [T006	595	601	4.083527	GGGCAC	0.73242	0.71379
cg0359490	ANKRD11	p53 [T006	603	609	4.083527	GGTGCC	0.73242	0.71379
cg0359490	ANKRD11	Sp1 [T007	146	155	4.029243	TCACCG	0.08965	0.08686
cg0359490	ANKRD11	RXR-alpha	880	886	4.019014	GGGTTT	0.97656	0.9671
cg0359490	ANKRD11	RXR-alpha	1033	1039	4.019014	GAAACC	0.97656	0.9671
cg0359490	ANKRD11	RXR-alpha	1846	1852	4.019014	GGGTAT	0.97656	0.9671
cg0359490	ANKRD11	RXR-alpha	1978	1984	4.019014	GAAACC	0.97656	0.9671
cg0359490	ANKRD11	Pax-5 [T0	580	586	4.007279	GGGCCT	1.09863	1.07975
cg0359490	ANKRD11	TFIID [T0	707	713	4.007279	TTTAAG	1.09863	1.13456
cg0359490	ANKRD11	USF2 [T0	1932	1941	4.003951	AGATCA	0.01144	0.01129
cg0359490	ANKRD11	AP-2alpha	512	517	3.970052	CAAGGC	0.97656	0.96469
cg0359490	ANKRD11	AP-2alpha	1962	1967	3.970052	GCCTTG	0.97656	0.96469
cg0359490	ANKRD11	E2F [T002	1785	1794	3.793883	TTTGGC	0.04578	0.04588
cg0359490	ANKRD11	GR [T050	1633	1639	3.763516	CAAAAC	0.73242	0.74251
cg0359490	ANKRD11	p53 [T006	635	641	3.750231	CCAGCC	0.73242	0.71379
cg0359490	ANKRD11	AP-2alpha	417	422	3.743866	GAAGGC	0.48828	0.48238
cg0359490	ANKRD11	AP-2alpha	811	816	3.743866	GCCTTC	0.48828	0.48238
cg0359490	ANKRD11	AP-2alpha	1477	1482	3.743866	GAAGGC	0.48828	0.48238
cg0359490	ANKRD11	NF-AT2 [T	1264	1273	3.689016	GGAAAA	0.03433	0.03499
cg0359490	ANKRD11	p53 [T006	891	897	3.586914	GGGCGA	0.73242	0.7189
cg0359490	ANKRD11	HNF-3alph	1806	1813	3.500065	TAAAAA	0.27466	0.28532
cg0359490	ANKRD11	VDR [T00	788	796	3.462841	GTTCAA	0.21362	0.21341
cg0359490	ANKRD11	c-Myb [T0	1134	1141	3.438142	AAACTG	0.12207	0.12203
cg0359490	ANKRD11	RXR-alpha	14	20	3.392904	GGGTCC	1.09863	1.08572
cg0359490	ANKRD11	RXR-alpha	526	532	3.392904	CGCACC	1.09863	1.08572
cg0359490	ANKRD11	RXR-alpha	1727	1733	3.392904	GGAACC	1.09863	1.08572
cg0359490	ANKRD11	Elk-1 [T00	813	821	3.381796	CTTCCTC	0.04578	0.04588
cg0359490	ANKRD11	p53 [T006	845	851	3.375208	CACGCC	0.73242	0.7189

cg0359490	ANKRD11	GR-beta [T	124	128	3.361531	AGATT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [T	134	138	3.361531	AATCT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [T	1268	1272	3.361531	AATCT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [T	1457	1461	3.361531	AGATT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [T	1506	1510	3.361531	AATCT	3.90625	3.99611
cg0359490	ANKRD11	c-Ets-1 [T0	1113	1119	3.359159	CTTCCGT	0.61035	0.60765
cg0359490	ANKRD11	PR B [T00	1293	1299	3.29756	AACATT	0.24414	0.25122
cg0359490	ANKRD11	PR A [T01	1293	1299	3.29756	AACATT	0.24414	0.25122
cg0359490	ANKRD11	TCF-4E [T	1208	1214	3.151193	ATCAAA	0.24414	0.24672
cg0359490	ANKRD11	SRY [T00	1206	1214	3.088221	GGATCA	0.06104	0.06203
cg0359490	ANKRD11	Pax-5 [T0	891	897	3.075094	GGGCGA	0.12207	0.11895
cg0359490	ANKRD11	AR [T000	1276	1284	3.025151	GGACAT	0.06104	0.06058
cg0359490	ANKRD11	p53 [T006	729	735	3.024997	GTTGCC	0.48828	0.47786
cg0359490	ANKRD11	C/EBPalph	1831	1837	3.014837	AGCAAT	0.48828	0.4911
cg0359490	ANKRD11	STAT4 [T	1060	1065	2.941176	CTTTCC	2.92969	2.929
cg0359490	ANKRD11	STAT4 [T	1099	1104	2.941176	GGAAAG	2.92969	2.929
cg0359490	ANKRD11	STAT4 [T	1218	1223	2.941176	GGAATC	2.92969	2.929
cg0359490	ANKRD11	STAT4 [T	1727	1732	2.941176	GGAACC	2.92969	2.929
cg0359490	ANKRD11	p53 [T006	166	172	2.813291	GGGCAG	0.48828	0.47786
cg0359490	ANKRD11	p53 [T006	224	230	2.813291	GGGCAG	0.48828	0.47786
cg0359490	ANKRD11	AP-2alpha	478	483	2.550491	GCCTCA	0.48828	0.48266
cg0359490	ANKRD11	AP-2alpha	1922	1927	2.550491	TGAGGC	0.48828	0.48266
cg0359490	ANKRD11	RXR-alpha	1400	1406	2.544678	GGGTGA	0.85449	0.84796
cg0359490	ANKRD11	RXR-alpha	1655	1661	2.544678	TTCACC	0.85449	0.84796
cg0359490	ANKRD11	AR [T000	1104	1112	2.482011	GGACAG	0.11444	0.11507
cg0359490	ANKRD11	NF-AT1 [T	1264	1272	2.449764	GGAAAA	0.09155	0.0926
cg0359490	ANKRD11	Ik-1 [T027	1903	1915	2.374299	TCCCAG	0.00063	0.00061
cg0359490	ANKRD11	C/EBPalph	1697	1703	2.371703	CACAAT	0.48828	0.49114
cg0359490	ANKRD11	LEF-1 [T0	1379	1386	2.345041	CAGCAA	0.09155	0.09192
cg0359490	ANKRD11	T3R-beta1	101	109	2.259951	TCACCT	0.03052	0.03041
cg0359490	ANKRD11	T3R-beta1	204	212	2.259951	TCACCA	0.03052	0.03041
cg0359490	ANKRD11	T3R-beta1	1935	1943	2.221365	TCACCT	0.15259	0.15262
cg0359490	ANKRD11	LEF-1 [T0	1326	1333	2.21836	AACCAA	0.18311	0.18582
cg0359490	ANKRD11	c-Ets-2 [T0	1793	1801	2.217136	TTCCTCA	0.16785	0.16856
cg0359490	ANKRD11	GATA-1 [	1494	1499	2.176375	TCGATA	3.90625	3.92756
cg0359490	ANKRD11	GATA-1 [	1678	1683	2.176375	TATCCA	3.90625	3.92756
cg0359490	ANKRD11	RAR-beta	785	794	2.16302	AGGGTT	0.07629	0.07625
cg0359490	ANKRD11	TCF-4 [T0	1206	1215	2.160205	GGATCA	0.04196	0.04299
cg0359490	ANKRD11	c-Myb [T0	317	324	2.152744	GAACTG	0.06104	0.06059
cg0359490	ANKRD11	p53 [T006	1288	1294	1.970013	GGGCAA	0.36621	0.36261
cg0359490	ANKRD11	p53 [T006	1531	1537	1.970013	GGGCAA	0.36621	0.36261
cg0359490	ANKRD11	GATA-1 [	941	946	1.896347	CGGATA	3.90625	3.92756
cg0359490	ANKRD11	AP-2alpha	76	81	1.871933	GGAGGC	0.97656	0.95407
cg0359490	ANKRD11	AP-2alpha	174	179	1.871933	GCCTCC	0.97656	0.95407
cg0359490	ANKRD11	AP-2alpha	232	237	1.871933	GCCTCC	0.97656	0.95407
cg0359490	ANKRD11	AP-2alpha	551	556	1.871933	GCCTCC	0.97656	0.95407
cg0359490	ANKRD11	AP-2alpha	570	575	1.871933	GGAGGC	0.97656	0.95407
cg0359490	ANKRD11	AP-2alpha	773	778	1.871933	GCCTCC	0.97656	0.95407

cg0359490	ANKRD11	AP-2alpha	1916	1921	1.871933	GGAGGC	0.97656	0.95407
cg0359490	ANKRD11	C/EBPalph	1810	1816	1.830762	AATTGA	0.48828	0.49438
cg0359490	ANKRD11	RelA [T00	1261	1271	1.825283	TGGGGA	0.00477	0.00477
cg0359490	ANKRD11	TFII-I [T0	686	691	1.824994	GGAGAG	0.48828	0.48408
cg0359490	ANKRD11	p53 [T006	1928	1934	1.758307	GGGCAG	0.36621	0.36261
cg0359490	ANKRD11	NF-Y [T0	1280	1287	1.749852	ATTGGC	0.18311	0.18459
cg0359490	ANKRD11	GR-beta [T	561	565	1.680765	AATGC	3.90625	3.94936
cg0359490	ANKRD11	GR-beta [T	995	999	1.680765	AATGC	3.90625	3.94936
cg0359490	ANKRD11	GR-beta [T	1624	1628	1.680765	AATGC	3.90625	3.94936
cg0359490	ANKRD11	GR-beta [T	1629	1633	1.680765	AATTC	3.90625	3.94936
cg0359490	ANKRD11	c-Ets-2 [T	1422	1430	1.64415	TGGGAG	0.04578	0.04579
cg0359490	ANKRD11	C/EBPbeta	374	377	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	676	679	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1075	1078	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1199	1202	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1223	1226	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1281	1284	1.639871	TTGG	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1328	1331	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1578	1581	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1681	1684	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1744	1747	1.639871	TTGG	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1786	1789	1.639871	TTGG	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1856	1859	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1913	1916	1.639871	TTGG	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1968	1971	1.639871	CCAA	15.625	15.72563
cg0359490	ANKRD11	AR [T000	652	660	1.618276	GGACAG	0.09155	0.09119
cg0359490	ANKRD11	IRF-1 [T0	1095	1103	1.616539	ACAGGG	0.04578	0.04655
cg0359490	ANKRD11	XBP-1 [T	280	285	1.583727	GGTCAT	0.97656	0.98146
cg0359490	ANKRD11	XBP-1 [T	289	294	1.583727	TGTCAT	0.97656	0.98146
cg0359490	ANKRD11	Pax-5 [T0	845	851	1.537547	CACGCC	0.73242	0.71311
cg0359490	ANKRD11	Pax-5 [T0	1874	1880	1.537547	GGGCCA	0.73242	0.71311
cg0359490	ANKRD11	TFIID [T0	858	864	1.537547	TTTTGTA	0.73242	0.75096
cg0359490	ANKRD11	TFIID [T0	967	973	1.537547	TTTTTCA	0.73242	0.75096
cg0359490	ANKRD11	TFIID [T0	1363	1369	1.537547	TTCAAA	0.73242	0.75096
cg0359490	ANKRD11	TFIID [T0	1500	1506	1.537547	TGAAAA	0.73242	0.75096
cg0359490	ANKRD11	TFIID [T0	1631	1637	1.537547	TTCAAA	0.73242	0.75096
cg0359490	ANKRD11	TFIID [T0	1680	1686	1.537547	TCCAAA	0.73242	0.75096
cg0359490	ANKRD11	c-Ets-1 [T	1425	1431	1.513038	GAGGAA	0.36621	0.36952
cg0359490	ANKRD11	c-Ets-1 [T	1792	1798	1.513038	TTTCCTC	0.36621	0.36952
cg0359490	ANKRD11	RXR-alpha	1851	1857	1.474336	TAGACC	0.48828	0.48222
cg0359490	ANKRD11	STAT4 [T	369	374	1.470588	GGAAAC	1.95312	1.96333
cg0359490	ANKRD11	STAT4 [T	1052	1057	1.470588	GGAACT	1.95312	1.96333
cg0359490	ANKRD11	STAT4 [T	1131	1136	1.470588	GGAAAA	1.95312	1.96333
cg0359490	ANKRD11	STAT4 [T	1264	1269	1.470588	GGAAAA	1.95312	1.96333
cg0359490	ANKRD11	STAT4 [T	1427	1432	1.470588	GGAAAC	1.95312	1.96333
cg0359490	ANKRD11	STAT4 [T	1720	1725	1.470588	GGAAAA	1.95312	1.96333
cg0359490	ANKRD11	STAT4 [T	1791	1796	1.470588	GTTTCC	1.95312	1.96333
cg0359490	ANKRD11	PR B [T00	1256	1262	1.404665	AACACT	0.36621	0.37023

cg0359490	ANKRD11	PR A [T01	1256	1262	1.404665	AACACT	0.36621	0.37023
cg0359490	ANKRD11	C/EBPbeta	5	8	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	22	25	1.366559	TTGA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	330	333	1.366559	TTGA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	456	459	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	511	514	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	790	793	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1194	1197	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1209	1212	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1301	1304	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1358	1361	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1364	1367	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1394	1397	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1463	1466	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1521	1524	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1557	1560	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1601	1604	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1610	1613	1.366559	TTGA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1632	1635	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1797	1800	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1812	1815	1.366559	TTGA	15.625	15.72563
cg0359490	ANKRD11	C/EBPbeta	1945	1948	1.366559	TCAA	15.625	15.72563
cg0359490	ANKRD11	AP-2alpha	833	838	1.357116	ACAGGC	0.48828	0.48203
cg0359490	ANKRD11	AP-2alpha	1320	1325	1.357116	ACAGGC	0.48828	0.48203
cg0359490	ANKRD11	AP-2alpha	1581	1586	1.357116	ACAGGC	0.48828	0.48203
cg0359490	ANKRD11	AP-2alpha	1895	1900	1.357116	GCCTGT	0.48828	0.48203
cg0359490	ANKRD11	HNF-3alph	1665	1672	1.342935	TTAAAA	0.03052	0.03194
cg0359490	ANKRD11	PEA3 [T0	1711	1719	1.194633	AGGATG	0.06866	0.06895
cg0359490	ANKRD11	PXR-1:RX	316	323	0.941658	TGAACT	0.12207	0.12266
cg0359490	ANKRD11	HNF-1A [	1486	1493	0.925521	CAATTA	0.48828	0.49664
cg0359490	ANKRD11	GR-beta [T	141	145	0.840383	AATTG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	481	485	0.840383	TCATT	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	748	752	0.840383	AATGG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	855	859	0.840383	TAATT	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1203	1207	0.840383	AATGG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1338	1342	0.840383	AATGG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1346	1350	0.840383	AATGG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1420	1424	0.840383	AATGG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1486	1490	0.840383	CAATT	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1487	1491	0.840383	AATTA	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1573	1577	0.840383	AATGG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1607	1611	0.840383	TCATT	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1628	1632	0.840383	CAATT	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1699	1703	0.840383	CAATT	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1700	1704	0.840383	AATTG	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1758	1762	0.840383	AATTA	7.8125	7.94706
cg0359490	ANKRD11	GR-beta [T	1810	1814	0.840383	AATTG	7.8125	7.94706
cg0359490	ANKRD11	PXR-1:RX	1359	1366	0.818075	CAAGTT	0.12207	0.12266

cg0359490	ANKRD11	PR B [T00	1780	1786	0.48823	AACAGT	0.12207	0.12407
cg0359490	ANKRD11	PR A [T01	1780	1786	0.48823	AACAGT	0.12207	0.12407
cg0359490	ANKRD11	GATA-1 [	904	909	0.280028	TAGATA	0.97656	0.99875
cg0359490	ANKRD11	AP-2alpha	182	187	0.226186	CCAGGC	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	239	244	0.226186	CCAGGC	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	429	434	0.226186	GCCTGG	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	734	739	0.226186	CCAGGC	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	953	958	0.226186	CCAGGC	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	1284	1289	0.226186	GCCTGG	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	1877	1882	0.226186	CCAGGC	0.97656	0.95305
cg0359490	ANKRD11	GR-alpha [	193	197	0.207689	AAAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	583	587	0.207689	CCTTT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	965	969	0.207689	CCTTT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1068	1072	0.207689	AAAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1101	1105	0.207689	AAAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1383	1387	0.207689	AAAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1559	1563	0.207689	AAAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1593	1597	0.207689	AGAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1674	1678	0.207689	CCTTT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1723	1727	0.207689	AAAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	18	22	0	CCTGT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	33	37	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	93	97	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	364	368	0	CCTGT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	469	473	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	620	624	0	CCTGT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	833	837	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	919	923	0	CCTGT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1095	1099	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1320	1324	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1397	1401	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1447	1451	0	CCTGT	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1581	1585	0	ACAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1822	1826	0	ATAGG	7.8125	7.81264
cg0359490	ANKRD11	GR-alpha [	1896	1900	0	CCTGT	7.8125	7.81264
cg0359490	ANKRD11	AP-2alpha	521	526	0	GCAGGC	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	610	615	0	GCAGGC	0.97656	0.95305
cg0359490	ANKRD11	AP-2alpha	1433	1438	0	GCCTGC	0.97656	0.95305
cg0359490	ANKRD11	RXR-alpha	786	792	0	GGGTTC	0.24414	0.2444
cg0359490	ANKRD11	RXR-alpha	975	981	0	GGGTTC	0.24414	0.2444
cg0359490	ANKRD11	Pax-5 [T0	531	537	0	CCTGCC	1.09863	1.06846
cg0359490	ANKRD11	Pax-5 [T0	611	617	0	CAGGCC	1.09863	1.06846
cg0359490	ANKRD11	Pax-5 [T0	635	641	0	CCAGCC	1.09863	1.06846
cg0359490	ANKRD11	Pax-5 [T0	640	646	0	CCTGCC	1.09863	1.06846
cg0359490	ANKRD11	p53 [T006	531	537	0	CCTGCC	0.36621	0.35912
cg0359490	ANKRD11	p53 [T006	640	646	0	CCTGCC	0.36621	0.35912
cg0359490	ANKRD11	TFII-I [T0	57	62	0	GGACAG	1.46484	1.45997
cg0359490	ANKRD11	TFII-I [T0	91	96	0	GGACAG	1.46484	1.45997

cg0359490	ANKRD11	TFII-I [T0	652	657	0	GGACAG	1.46484	1.45997
cg0359490	ANKRD11	TFII-I [T0	1060	1065	0	CTTTCC	1.46484	1.45997
cg0359490	ANKRD11	TFII-I [T0	1099	1104	0	GGAAAG	1.46484	1.45997
cg0359490	ANKRD11	TFII-I [T0	1104	1109	0	GGACAG	1.46484	1.45997
cg0359490	ANKRD11	TFII-I [T0	1374	1379	0	CTGTCC	1.46484	1.45997
cg0359490	ANKRD11	c-Ets-1 [T	813	819	0	CTTCCTC	0.24414	0.2429
cg0359490	ANKRD11	YY1 [T00	2	5	0	CCAT	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	153	156	0	CCAT	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	211	214	0	CCAT	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	518	521	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	536	539	0	CCAT	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	749	752	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	981	984	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1204	1207	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1339	1342	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1347	1350	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1421	1424	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1518	1521	0	CCAT	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1574	1577	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1820	1823	0	CCAT	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1973	1976	0	ATGG	7.8125	7.81711
cg0359490	ANKRD11	YY1 [T00	1984	1987	0	CCAT	7.8125	7.81711
cg0359490	ANKRD11	ER-alpha [	280	284	0	GGTCA	1.95312	1.9404
cg0359490	ANKRD11	ER-alpha [	447	451	0	TGACC	1.95312	1.9404
cg0359490	ANKRD11	ER-alpha [	1943	1947	0	GGTCA	1.95312	1.9404
cg0359490	ANKRD11	C/EBPbeta	143	146	0	TTGT	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	191	194	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	201	204	0	TTGT	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	261	264	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	288	291	0	TTGT	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	351	354	0	TTGT	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	463	466	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	586	589	0	TTGT	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	727	730	0	TTGT	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	730	733	0	TTGC	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	746	749	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	860	863	0	TTGT	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	993	996	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1066	1069	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1187	1190	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1249	1252	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1290	1293	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1305	1308	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1324	1327	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1333	1336	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1343	1346	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1381	1384	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1437	1440	0	GCAA	15.625	15.71349

cg0359490	ANKRD11	C/EBPbeta	1485	1488	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1533	1536	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1570	1573	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1627	1630	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1692	1695	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1698	1701	0	ACAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1702	1705	0	TTGC	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1832	1835	0	GCAA	15.625	15.71349
cg0359490	ANKRD11	C/EBPbeta	1965	1968	0	TTGC	15.625	15.71349
cg0359490	ANKRD11	EBF [T05	644	654	0	CCCCCA	0.00381	0.00364
cg0359490	ANKRD11	TFIID [T0	704	710	0	TTTTTTA	1.09863	1.13474
cg0359490	ANKRD11	TFIID [T0	705	711	0	TTTTTAA	1.09863	1.13474
cg0359490	ANKRD11	TFIID [T0	1521	1527	0	TCAAAA	1.09863	1.13474
cg0359490	ANKRD11	TFIID [T0	1797	1803	0	TCAAAA	1.09863	1.13474
cg0359490	ANKRD11	FOXP3 [T	200	205	0	GTTGTC	1.46484	1.47315
cg0359490	ANKRD11	FOXP3 [T	462	467	0	GACAAC	1.46484	1.47315
cg0359490	ANKRD11	GR-beta [	140	144	0	AAATT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [	856	860	0	AATTT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [	1278	1282	0	ACATT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [	1294	1298	0	ACATT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [	1752	1756	0	AATGT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [	1757	1761	0	AAATT	3.90625	3.99611
cg0359490	ANKRD11	GR-beta [	1809	1813	0	AAATT	3.90625	3.99611
cg0359490	ANKRD11	GR [T050	1334	1340	0	CAAAAA	0.36621	0.37562
cg0359490	ANKRD11	GR [T050	1522	1528	0	CAAAAA	0.36621	0.37562
cg0359490	ANKRD11	GR [T050	1798	1804	0	CAAAAA	0.36621	0.37562
cg0359490	ANKRD11	HNF-3alph	863	870	0	TATTTTT	0.09155	0.09511
cg0359490	ANKRD11	TCF-4E [	1380	1386	0	AGCAAA	0.12207	0.12262
cg0359490	ANKRD11	LEF-1 [T0	1207	1214	0	GATCAA	0.03052	0.03083
cg0359490	ANKRD11	HNF-1A [	1664	1671	0	GTTAAA	0.24414	0.25261
cg0359490	ANKRD11	IRF-2 [T0	1057	1062	0	TCACTT	0.48828	0.49387
cg0359490	ANKRD11	IRF-2 [T0	1651	1656	0	TCACTT	0.48828	0.49387
cg1269862	CCL2	PEA3 [T0	829	837	9.937959	GGGATG	0.18311	0.18382
cg0544082	CCL2	PEA3 [T0	1260	1268	9.937959	GGGATG	0.18311	0.18382
cg1269862	CCL2	HNF-1B [	1173	1181	9.892991	AGTTAA	0.12207	0.11326
cg0544082	CCL2	HNF-1B [	1604	1612	9.892991	AGTTAA	0.12207	0.11326
cg0544082	CCL2	STAT1bet	145	154	9.807397	AAAGGG	0.14877	0.14533
cg1269862	CCL2	XBP-1 [T	144	149	9.789909	AGACAT	1.95312	1.94901
cg1269862	CCL2	XBP-1 [T	462	467	9.789909	AGACAT	1.95312	1.94901
cg1269862	CCL2	XBP-1 [T	597	602	9.789909	AGCCAT	1.95312	1.94901
cg1269862	CCL2	XBP-1 [T	894	899	9.789909	AGCCAT	1.95312	1.94901
cg0544082	CCL2	XBP-1 [T	12	17	9.789909	ATGTCT	1.95312	1.94901
cg0544082	CCL2	XBP-1 [T	575	580	9.789909	AGACAT	1.95312	1.94901
cg0544082	CCL2	XBP-1 [T	893	898	9.789909	AGACAT	1.95312	1.94901
cg0544082	CCL2	XBP-1 [T	1028	1033	9.789909	AGCCAT	1.95312	1.94901
cg0544082	CCL2	XBP-1 [T	1325	1330	9.789909	AGCCAT	1.95312	1.94901
cg1269862	CCL2	NF-AT2 [	184	193	9.787971	GGAAAC	0.08774	0.08205
cg0544082	CCL2	NF-AT2 [	615	624	9.787971	GGAAAC	0.08774	0.08205

cg0544082	CCL2	PR B [T00	358	364	9.743489	AACACA(	1.09863	1.0981
cg0544082	CCL2	PR A [T01	358	364	9.743489	AACACA(	1.09863	1.0981
cg1269862	CCL2	c-Myb [T0	642	649	9.729271	AACAGT'	0.36621	0.34746
cg1269862	CCL2	c-Myb [T0	1307	1314	9.729271	TTCAGT1	0.36621	0.34746
cg1269862	CCL2	c-Myb [T0	1331	1338	9.729271	TACAGT'	0.36621	0.34746
cg0544082	CCL2	c-Myb [T0	192	199	9.729271	TAACTG/	0.36621	0.34746
cg0544082	CCL2	c-Myb [T0	1073	1080	9.729271	AACAGT'	0.36621	0.34746
cg0544082	CCL2	c-Myb [T0	1738	1745	9.729271	TTCAGT1	0.36621	0.34746
cg0544082	CCL2	c-Myb [T0	1762	1769	9.729271	TACAGT'	0.36621	0.34746
cg1269862	CCL2	c-Ets-1 [T(	1160	1166	9.713162	GGGGAA	0.36621	0.37402
cg1269862	CCL2	c-Ets-1 [T(	1954	1960	9.713162	ATTCCC(	0.36621	0.37402
cg0544082	CCL2	c-Ets-1 [T(	1591	1597	9.713162	GGGGAA	0.36621	0.37402
cg1269862	CCL2	NF-AT1 [T	124	132	9.691726	GGAAAC	0.16785	0.16528
cg1269862	CCL2	NF-AT1 [T	998	1006	9.691726	CACGTT1	0.16785	0.16528
cg1269862	CCL2	NF-AT1 [T	1499	1507	9.691726	CTAGTT1	0.16785	0.16528
cg0544082	CCL2	NF-AT1 [T	555	563	9.691726	GGAAAC	0.16785	0.16528
cg0544082	CCL2	NF-AT1 [T	1429	1437	9.691726	CACGTT1	0.16785	0.16528
cg0544082	CCL2	NF-AT1 [T	1930	1938	9.691726	CTAGTT1	0.16785	0.16528
cg1269862	CCL2	RAR-beta	442	451	9.622793	AAGAAA	0.21362	0.22369
cg1269862	CCL2	RAR-beta	673	682	9.622793	TGGGTT1	0.21362	0.22369
cg0544082	CCL2	RAR-beta	873	882	9.622793	AAGAAA	0.21362	0.22369
cg0544082	CCL2	RAR-beta	1104	1113	9.622793	TGGGTT1	0.21362	0.22369
cg1269862	CCL2	HNF-1C [T	1558	1566	9.601936	AAAAAT.	0.19836	0.18179
cg0544082	CCL2	HNF-1C [T	1989	1997	9.601936	AAAAAT.	0.19836	0.18179
cg1269862	CCL2	c-Ets-1 [T(	749	755	9.585075	ATTCCC(	0.36621	0.37402
cg0544082	CCL2	c-Ets-1 [T(	1180	1186	9.585075	ATTCCC(	0.36621	0.37402
cg1269862	CCL2	TFIID [T0	938	944	9.552105	TTTGGA/	1.46484	1.37777
cg1269862	CCL2	Pax-5 [T0(	1778	1784	9.552105	TCCGCC(	1.46484	1.61918
cg1269862	CCL2	Pax-5 [T0(	1915	1921	9.552105	GCCGCC(	1.46484	1.61918
cg0544082	CCL2	TFIID [T0	1369	1375	9.552105	TTTGGA/	1.46484	1.37777
cg1269862	CCL2	NF-1 [T00	1274	1281	9.535536	TTGTCC/	0.73242	0.74634
cg0544082	CCL2	NF-1 [T00	1705	1712	9.535536	TTGTCC/	0.73242	0.74634
cg1269862	CCL2	NF-AT1 [T	1696	1704	9.521781	GGAAAT(	0.16785	0.16528
cg1269862	CCL2	FOXP3 [T	42	47	9.512894	GTTCTC	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	242	247	9.512894	AATAAC	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	274	279	9.512894	GTTGGT	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	821	826	9.512894	CATAAC	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	865	870	9.512894	AGCAAC	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	975	980	9.512894	GGCAAC	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	1059	1064	9.512894	GTTCTG	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	1111	1116	9.512894	GTTGCC	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	1157	1162	9.512894	GTTGGG	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	1318	1323	9.512894	GTTTAC	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	1335	1340	9.512894	GTTCTG	7.32422	7.22156
cg1269862	CCL2	FOXP3 [T	1561	1566	9.512894	AATAAC	7.32422	7.22156
cg1269862	CCL2	TFII-I [T0(	67	72	9.512894	AATTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0(	124	129	9.512894	GGAAAC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0(	184	189	9.512894	GGAAAC	7.32422	7.44385

cg1269862	CCL2	TFII-I [T0	237	242	9.512894	GGACAA	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	748	753	9.512894	AATTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	841	846	9.512894	TTGTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	989	994	9.512894	GGACTT	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1001	1006	9.512894	GTTTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1005	1010	9.512894	CCTTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1162	1167	9.512894	GGAATT	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1274	1279	9.512894	TTGTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1385	1390	9.512894	GGATTT	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1428	1433	9.512894	CCTTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1502	1507	9.512894	GTTTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1514	1519	9.512894	CCTTCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1610	1615	9.512894	CCATCC	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1649	1654	9.512894	GGAAAA	7.32422	7.44385
cg1269862	CCL2	TFII-I [T0	1698	1703	9.512894	AAATCC	7.32422	7.44385
cg0544082	CCL2	FOXP3 [T	381	386	9.512894	GTTGGG	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	416	421	9.512894	CAGAAC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	473	478	9.512894	GTTCTC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	673	678	9.512894	AATAAC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	705	710	9.512894	GTTGGT	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1252	1257	9.512894	CATAAC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1296	1301	9.512894	AGCAAC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1406	1411	9.512894	GGCAAC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1490	1495	9.512894	GTTCTG	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1542	1547	9.512894	GTTGCC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1588	1593	9.512894	GTTGGG	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1749	1754	9.512894	GTTTAC	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1766	1771	9.512894	GTTCTG	7.32422	7.22156
cg0544082	CCL2	FOXP3 [T	1992	1997	9.512894	AATAAC	7.32422	7.22156
cg0544082	CCL2	TFII-I [T0	161	166	9.512894	CGGTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	209	214	9.512894	GTTTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	225	230	9.512894	GGAAAA	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	266	271	9.512894	AATTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	300	305	9.512894	GGAAAC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	318	323	9.512894	GGATAA	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	498	503	9.512894	AATTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	555	560	9.512894	GGAAAC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	615	620	9.512894	GGAAAC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	668	673	9.512894	GGACAA	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1179	1184	9.512894	AATTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1272	1277	9.512894	TTGTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1420	1425	9.512894	GGACTT	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1432	1437	9.512894	GTTTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1436	1441	9.512894	CCTTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1593	1598	9.512894	GGAATT	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1705	1710	9.512894	TTGTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1816	1821	9.512894	GGATTT	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1859	1864	9.512894	CCTTCC	7.32422	7.44385

cg0544082	CCL2	TFII-I [T0	1933	1938	9.512894	GTTTCC	7.32422	7.44385
cg0544082	CCL2	TFII-I [T0	1945	1950	9.512894	CCTTCC	7.32422	7.44385
cg1269862	CCL2	c-Jun [T00	359	365	9.511322	TGACCA	0.73242	0.7366
cg1269862	CCL2	c-Jun [T00	1584	1590	9.511322	GTGGTC	0.73242	0.7366
cg0544082	CCL2	c-Jun [T00	790	796	9.511322	TGACCA	0.73242	0.7366
cg1269862	CCL2	TCF-4E [T	503	509	9.453578	CTTTGTA	0.48828	0.46934
cg0544082	CCL2	TCF-4E [T	934	940	9.453578	CTTTGTA	0.48828	0.46934
cg1269862	CCL2	c-Jun [T00	1396	1402	9.397655	ATTGTCA	0.73242	0.7366
cg0544082	CCL2	c-Jun [T00	1827	1833	9.397655	ATTGTCA	0.73242	0.7366
cg1269862	CCL2	NFI/CTF [	668	675	9.352332	GTCTTTC	0.54932	0.55369
cg1269862	CCL2	NFI/CTF [	1412	1419	9.352332	CCAAAG	0.54932	0.55369
cg0544082	CCL2	NFI/CTF [	1099	1106	9.352332	GTCTTTC	0.54932	0.55369
cg0544082	CCL2	NFI/CTF [	1843	1850	9.352332	CCAAAG	0.54932	0.55369
cg1269862	CCL2	POU2F2 (	1386	1396	9.350233	GATTTA	0.03433	0.03054
cg0544082	CCL2	POU2F2 (	137	147	9.350233	TGGATT	0.03433	0.03054
cg0544082	CCL2	POU2F2 (	1817	1827	9.350233	GATTTA	0.03433	0.03054
cg0544082	CCL2	HNF-1C [	105	113	9.225924	CTTGTTA	0.12207	0.10938
cg1269862	CCL2	c-Ets-1 [T	1449	1455	9.19359	TTGGAA	0.85449	0.84987
cg0544082	CCL2	c-Ets-1 [T	1880	1886	9.19359	TTGGAA	0.85449	0.84987
cg0544082	CCL2	HNF-1B [	106	114	9.183362	TTGTTAA	0.08392	0.07596
cg1269862	CCL2	NF-AT1 [	1679	1687	9.18189	TCCCTTT	0.22888	0.22581
cg0544082	CCL2	c-Myb [T0	276	283	9.142015	CAAAGT	0.39673	0.37851
cg1269862	CCL2	NF-AT1 [	707	715	9.042733	GGAAAT	0.22888	0.22581
cg1269862	CCL2	NF-AT1 [	788	796	9.042733	GGAAAT	0.22888	0.22581
cg0544082	CCL2	NF-AT1 [	1138	1146	9.042733	GGAAAT	0.22888	0.22581
cg0544082	CCL2	NF-AT1 [	1219	1227	9.042733	GGAAAT	0.22888	0.22581
cg1269862	CCL2	c-Jun [T00	1485	1491	9.013496	TGACAT	0.61035	0.60549
cg0544082	CCL2	c-Jun [T00	1916	1922	9.013496	TGACAT	0.61035	0.60549
cg1269862	CCL2	AR [T000	776	784	8.979136	CTCATG	0.04578	0.04758
cg0544082	CCL2	AR [T000	1207	1215	8.979136	CTCATG	0.04578	0.04758
cg1269862	CCL2	LEF-1 [T0	670	677	8.973041	CTTTGG	0.54932	0.53171
cg0544082	CCL2	LEF-1 [T0	1101	1108	8.973041	CTTTGG	0.54932	0.53171
cg0544082	CCL2	GR [T050	356	362	8.971049	CAAACA	0.61035	0.5928
cg1269862	CCL2	c-Myb [T0	244	251	8.947824	TAACTT	0.39673	0.37851
cg1269862	CCL2	c-Myb [T0	834	841	8.947824	GAACTT	0.39673	0.37851
cg0544082	CCL2	c-Myb [T0	675	682	8.947824	TAACTT	0.39673	0.37851
cg0544082	CCL2	c-Myb [T0	1265	1272	8.947824	GAACTT	0.39673	0.37851
cg1269862	CCL2	c-Ets-1 [T	68	74	8.937416	ATTCCA	0.85449	0.84987
cg0544082	CCL2	c-Ets-1 [T	499	505	8.937416	ATTCCA	0.85449	0.84987
cg1269862	CCL2	Elk-1 [T00	1006	1014	8.931691	CTTCCA	0.24414	0.26271
cg0544082	CCL2	Elk-1 [T00	1437	1445	8.931691	CTTCCA	0.24414	0.26271
cg1269862	CCL2	c-Ets-2 [T	119	127	8.912323	CTCCAG	0.27466	0.27171
cg1269862	CCL2	c-Ets-2 [T	1430	1438	8.912323	TTCCTG	0.27466	0.27171
cg0544082	CCL2	c-Ets-2 [T	255	263	8.912323	GCCTAG	0.27466	0.27171
cg0544082	CCL2	c-Ets-2 [T	550	558	8.912323	CTCCAG	0.27466	0.27171
cg0544082	CCL2	c-Ets-2 [T	1861	1869	8.912323	TTCCTG	0.27466	0.27171
cg0544082	CCL2	AP-1 [T00	59	67	8.854325	TGACTA	0.24414	0.23028
cg1269862	CCL2	NFI/CTF [	935	942	8.814757	CCATTT	0.48828	0.48845

cg1269862	CCL2	NFI/CTF [	1627	1634	8.814757	TCATTTC	0.48828	0.48845
cg0544082	CCL2	NFI/CTF [	1366	1373	8.814757	CCATTTC	0.48828	0.48845
cg1269862	CCL2	c-Ets-1 [T	177	183	8.809329	CTGGAA	0.85449	0.84987
cg0544082	CCL2	c-Ets-1 [T	608	614	8.809329	CTGGAA	0.85449	0.84987
cg1269862	CCL2	LEF-1 [T0	503	510	8.759086	CTTTGTA	0.54932	0.53171
cg0544082	CCL2	LEF-1 [T0	273	280	8.759086	ACACAA	0.54932	0.53171
cg0544082	CCL2	LEF-1 [T0	934	941	8.759086	CTTTGTA	0.54932	0.53171
cg1269862	CCL2	XBP-1 [T	141	146	8.75604	ATGAGA	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	485	490	8.75604	ATGAAA	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	623	628	8.75604	TATCAT	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	832	837	8.75604	ATGAAC	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	1128	1133	8.75604	ATGAAA	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	1375	1380	8.75604	ATGAGC	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	1493	1498	8.75604	TTTCAT	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	1625	1630	8.75604	GCTCAT	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	1903	1908	8.75604	ATGAAA	2.92969	2.75329
cg1269862	CCL2	XBP-1 [T	1935	1940	8.75604	GCTCAT	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	172	177	8.75604	GTTCAT	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	338	343	8.75604	ATGAGC	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	572	577	8.75604	ATGAGA	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	916	921	8.75604	ATGAAA	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	1054	1059	8.75604	TATCAT	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	1263	1268	8.75604	ATGAAC	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	1559	1564	8.75604	ATGAAA	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	1806	1811	8.75604	ATGAGC	2.92969	2.75329
cg0544082	CCL2	XBP-1 [T	1924	1929	8.75604	TTTCAT	2.92969	2.75329
cg1269862	CCL2	NF-AT1 [	184	192	8.746017	GGAAAC	0.10681	0.10494
cg0544082	CCL2	NF-AT1 [	615	623	8.746017	GGAAAC	0.10681	0.10494
cg1269862	CCL2	STAT1bet	1682	1691	8.695301	CTTTCCT	0.22316	0.2175
cg1269862	CCL2	IRF-1 [T0	1503	1511	8.661524	TTTCCTC	0.20599	0.20245
cg0544082	CCL2	IRF-1 [T0	1934	1942	8.661524	TTTCCTC	0.20599	0.20245
cg1269862	CCL2	LEF-1 [T0	1410	1417	8.575454	GGCCAA	0.15259	0.154
cg0544082	CCL2	LEF-1 [T0	1841	1848	8.575454	GGCCAA	0.15259	0.154
cg0544082	CCL2	c-Jun [T00	133	139	8.571705	TGACTG	0.12207	0.1249
cg0544082	CCL2	RAR-beta	118	127	8.55975	AGAAAA	0.26703	0.27434
cg1269862	CCL2	NF-AT2 [	738	747	8.550786	CAGGCT	0.04959	0.04758
cg0544082	CCL2	NF-AT2 [	1169	1178	8.550786	CAGGCT	0.04959	0.04758
cg1269862	CCL2	RAR-beta	271	280	8.541284	TGGGTT	0.26703	0.27434
cg0544082	CCL2	RAR-beta	702	711	8.541284	TGGGTT	0.26703	0.27434
cg1269862	CCL2	AP-1 [T00	888	896	8.513775	TGACTT	0.03052	0.02884
cg0544082	CCL2	AP-1 [T00	1319	1327	8.513775	TGACTT	0.03052	0.02884
cg1269862	CCL2	LEF-1 [T0	1272	1279	8.361499	CTTTGTC	0.15259	0.154
cg0544082	CCL2	LEF-1 [T0	1703	1710	8.361499	CTTTGTC	0.15259	0.154
cg0544082	CCL2	c-Ets-2 [T	268	276	8.339336	TTCCTAC	0.13733	0.13927
cg1269862	CCL2	PR B [T00	868	874	8.338824	AACAGC	1.09863	1.09384
cg1269862	CCL2	PR B [T00	1733	1739	8.338824	AACAGC	1.09863	1.09384
cg1269862	CCL2	PR A [T01	868	874	8.338824	AACAGC	1.09863	1.09384
cg1269862	CCL2	PR A [T01	1733	1739	8.338824	AACAGC	1.09863	1.09384

cg0544082	CCL2	PR B [T00	1299	1305	8.338824	AACAGC	1.09863	1.09384
cg0544082	CCL2	PR A [T01	1299	1305	8.338824	AACAGC	1.09863	1.09384
cg1269862	CCL2	IRF-1 [T0	703	711	8.316022	CTGAGG	0.20599	0.20245
cg0544082	CCL2	IRF-1 [T0	1134	1142	8.316022	CTGAGG	0.20599	0.20245
cg1269862	CCL2	ATF3 [T01	308	315	8.313799	GTATGT	0.27466	0.27379
cg1269862	CCL2	ATF3 [T01	1015	1022	8.313799	GTATGT	0.27466	0.27379
cg0544082	CCL2	ATF3 [T01	739	746	8.313799	GTATGT	0.27466	0.27379
cg0544082	CCL2	ATF3 [T01	1446	1453	8.313799	GTATGT	0.27466	0.27379
cg1269862	CCL2	GR-alpha [	281	285	8.281568	GGAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	521	525	8.281568	CAAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	532	536	8.281568	CAAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	541	545	8.281568	GAAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	544	548	8.281568	GGAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	547	551	8.281568	GGAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	763	767	8.281568	CCTCC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	784	788	8.281568	CCTTG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	797	801	8.281568	GAAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	873	877	8.281568	CCTCC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	986	990	8.281568	GGAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1005	1009	8.281568	CCTTC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1069	1073	8.281568	CGAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1077	1081	8.281568	CCTTG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1097	1101	8.281568	CCTTC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1428	1432	8.281568	CCTTC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1440	1444	8.281568	GGAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1447	1451	8.281568	CCTTG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1463	1467	8.281568	GAAGG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1506	1510	8.281568	CCTCG	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1514	1518	8.281568	CCTTC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1614	1618	8.281568	CCTCC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1762	1766	8.281568	CCTCC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1765	1769	8.281568	CCTCC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1895	1899	8.281568	CCTCC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1920	1924	8.281568	CCTTC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1949	1953	8.281568	CCTTC	7.8125	8.20394
cg1269862	CCL2	GR-alpha [	1960	1964	8.281568	CAAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	712	716	8.281568	GGAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	952	956	8.281568	CAAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	963	967	8.281568	CAAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	972	976	8.281568	GAAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	975	979	8.281568	GGAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	978	982	8.281568	GGAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1194	1198	8.281568	CCTCC	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1215	1219	8.281568	CCTTG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1228	1232	8.281568	GAAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1304	1308	8.281568	CCTCC	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1417	1421	8.281568	GGAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1436	1440	8.281568	CCTTC	7.8125	8.20394

cg0544082	CCL2	GR-alpha [	1500	1504	8.281568	CGAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1508	1512	8.281568	CCTTG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1528	1532	8.281568	CCTTC	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1859	1863	8.281568	CCTTC	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1871	1875	8.281568	GGAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1878	1882	8.281568	CCTTG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1894	1898	8.281568	GAAGG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1937	1941	8.281568	CCTCG	7.8125	8.20394
cg0544082	CCL2	GR-alpha [	1945	1949	8.281568	CCTTC	7.8125	8.20394
cg1269862	CCL2	NFI/CTF [	271	278	8.241664	TGGGTT	0.18311	0.1922
cg1269862	CCL2	NFI/CTF [	275	282	8.241664	TTGGTT	0.18311	0.1922
cg0544082	CCL2	NFI/CTF [	378	385	8.241664	CTGGTT	0.18311	0.1922
cg0544082	CCL2	NFI/CTF [	702	709	8.241664	TGGGTT	0.18311	0.1922
cg0544082	CCL2	NFI/CTF [	706	713	8.241664	TTGGTT	0.18311	0.1922
cg1269862	CCL2	ENKTF-1	594	601	8.19852	CCCAGC	0.73242	0.80254
cg1269862	CCL2	ENKTF-1	1434	1441	8.19852	TGGCTG	0.73242	0.80254
cg1269862	CCL2	ENKTF-1	1473	1480	8.19852	TGGCAG	0.73242	0.80254
cg0544082	CCL2	ENKTF-1	1025	1032	8.19852	CCCAGC	0.73242	0.80254
cg0544082	CCL2	ENKTF-1	1865	1872	8.19852	TGGCTG	0.73242	0.80254
cg0544082	CCL2	ENKTF-1	1904	1911	8.19852	TGGCAG	0.73242	0.80254
cg1269862	CCL2	SRY [T00	15	23	8.174786	CAAGCA	0.15259	0.14791
cg0544082	CCL2	SRY [T00	272	280	8.174786	TACACA	0.15259	0.14791
cg0544082	CCL2	SRY [T00	446	454	8.174786	CAAGCA	0.15259	0.14791
cg1269862	CCL2	IRF-1 [T0	784	792	8.151819	CCTTGG	0.25177	0.2462
cg0544082	CCL2	IRF-1 [T0	1215	1223	8.151819	CCTTGG	0.25177	0.2462
cg1269862	CCL2	HNF-1C [	1174	1182	8.131138	GTTAAT	0.19836	0.18126
cg0544082	CCL2	HNF-1C [	1605	1613	8.131138	GTTAAT	0.19836	0.18126
cg1269862	CCL2	IRF-1 [T0	1692	1700	8.078284	TCCTGG	0.25177	0.2462
cg0544082	CCL2	IRF-1 [T0	296	304	8.078284	TCCTGG	0.25177	0.2462
cg1269862	CCL2	GR-alpha [	23	27	8.073878	GCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	55	59	8.073878	CCTGC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	121	125	8.073878	CCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	161	165	8.073878	CCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	192	196	8.073878	CCTGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	291	295	8.073878	GCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	559	563	8.073878	CTAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	805	809	8.073878	CCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	826	830	8.073878	CCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	854	858	8.073878	CCTGC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	972	976	8.073878	GCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1054	1058	8.073878	CCTGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1083	1087	8.073878	GCAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1144	1148	8.073878	CCTAC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1203	1207	8.073878	CCTGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1291	1295	8.073878	CCTAG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1329	1333	8.073878	CCTAC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1341	1345	8.073878	CTAGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1432	1436	8.073878	CCTGG	7.8125	8.20289

cg1269862	CCL2	GR-alpha [	1673	1677	8.073878	CCTGC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1686	1690	8.073878	CCTAC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1693	1697	8.073878	CCTGG	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1768	1772	8.073878	CCTGC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1929	1933	8.073878	CCTGC	7.8125	8.20289
cg1269862	CCL2	GR-alpha [	1975	1979	8.073878	CCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	67	71	8.073878	CCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	113	117	8.073878	CCTAG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	256	260	8.073878	CCTAG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	257	261	8.073878	CTAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	270	274	8.073878	CCTAC	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	297	301	8.073878	CCTGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	454	458	8.073878	GCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	486	490	8.073878	CCTGC	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	552	556	8.073878	CCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	592	596	8.073878	CCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	623	627	8.073878	CCTGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	722	726	8.073878	GCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	990	994	8.073878	CTAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1236	1240	8.073878	CCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1257	1261	8.073878	CCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1285	1289	8.073878	CCTGC	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1403	1407	8.073878	GCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1485	1489	8.073878	CCTGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1514	1518	8.073878	GCAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1575	1579	8.073878	CCTAC	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1634	1638	8.073878	CCTGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1722	1726	8.073878	CCTAG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1760	1764	8.073878	CCTAC	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1772	1776	8.073878	CTAGG	7.8125	8.20289
cg0544082	CCL2	GR-alpha [	1863	1867	8.073878	CCTGG	7.8125	8.20289
cg1269862	CCL2	TFIID [T0	62	68	8.014558	TTTGTA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	80	86	8.014558	TCTGAA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	484	490	8.014558	TATGAA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	630	636	8.014558	TTTGTA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	700	706	8.014558	TTTCTG	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	743	749	8.014558	TTTCCA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	786	792	8.014558	TTGGAA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	1181	1187	8.014558	TTTGTA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	1283	1289	8.014558	TCTGAA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	1683	1689	8.014558	TTTCCTA	2.19727	1.99811
cg1269862	CCL2	TFIID [T0	1870	1876	8.014558	TCTCAA	2.19727	1.99811
cg1269862	CCL2	Pax-5 [T0	508	514	8.014558	TATGCC	2.19727	2.42766
cg1269862	CCL2	Pax-5 [T0	524	530	8.014558	GGGCAC	2.19727	2.42766
cg1269862	CCL2	Pax-5 [T0	590	596	8.014558	TCAGCC	2.19727	2.42766
cg1269862	CCL2	Pax-5 [T0	930	936	8.014558	TCTGCC	2.19727	2.42766
cg1269862	CCL2	Pax-5 [T0	1031	1037	8.014558	GCAGCC	2.19727	2.42766
cg1269862	CCL2	Pax-5 [T0	1048	1054	8.014558	GGGCTG	2.19727	2.42766

cg1269862	CCL2	Pax-5 [T0	1441	1447	8.014558	GAGGCC	2.19727	2.42766
cg1269862	CCL2	Pax-5 [T0	1595	1601	8.014558	GGGCTT	2.19727	2.42766
cg1269862	CCL2	Pax-5 [T0	1793	1799	8.014558	TCTGCC	2.19727	2.42766
cg0544082	CCL2	TFIID [T0	493	499	8.014558	TTTGTA	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	511	517	8.014558	TCTGAA	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	915	921	8.014558	TATGAA	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	1061	1067	8.014558	TTTGTA	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	1131	1137	8.014558	TTTCTG	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	1174	1180	8.014558	TTTCCA	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	1217	1223	8.014558	TTGGAA	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	1612	1618	8.014558	TTTGTA	2.19727	1.99811
cg0544082	CCL2	TFIID [T0	1714	1720	8.014558	TCTGAA	2.19727	1.99811
cg0544082	CCL2	Pax-5 [T0	19	25	8.014558	TAAGCC	2.19727	2.42766
cg0544082	CCL2	Pax-5 [T0	939	945	8.014558	TATGCC	2.19727	2.42766
cg0544082	CCL2	Pax-5 [T0	955	961	8.014558	GGGCAC	2.19727	2.42766
cg0544082	CCL2	Pax-5 [T0	1021	1027	8.014558	TCAGCC	2.19727	2.42766
cg0544082	CCL2	Pax-5 [T0	1361	1367	8.014558	TCTGCC	2.19727	2.42766
cg0544082	CCL2	Pax-5 [T0	1462	1468	8.014558	GCAGCC	2.19727	2.42766
cg0544082	CCL2	Pax-5 [T0	1479	1485	8.014558	GGGCTG	2.19727	2.42766
cg0544082	CCL2	Pax-5 [T0	1872	1878	8.014558	GAGGCC	2.19727	2.42766
cg0544082	CCL2	C/EBPalp	314	320	8.006685	CATTGG	0.24414	0.23098
cg1269862	CCL2	c-Ets-2 [T	159	167	7.84116	TCCCAG	0.32043	0.30792
cg1269862	CCL2	c-Ets-2 [T	1201	1209	7.84116	TTCCTG	0.32043	0.30792
cg1269862	CCL2	c-Ets-2 [T	1691	1699	7.84116	TTCCTG	0.32043	0.30792
cg0544082	CCL2	c-Ets-2 [T	590	598	7.84116	TCCCAG	0.32043	0.30792
cg0544082	CCL2	c-Ets-2 [T	1632	1640	7.84116	TTCCTG	0.32043	0.30792
cg0544082	CCL2	c-Myb [T0	168	175	7.825375	CCAAGT	0.21362	0.20997
cg1269862	CCL2	IRF-1 [T0	120	128	7.82345	TCCAGG	0.25177	0.2462
cg0544082	CCL2	IRF-1 [T0	551	559	7.82345	TCCAGG	0.25177	0.2462
cg1269862	CCL2	IRF-1 [T0	299	307	7.732782	CGCTGG	0.14496	0.14723
cg0544082	CCL2	IRF-1 [T0	730	738	7.732782	CGCTGG	0.14496	0.14723
cg1269862	CCL2	c-Jun [T00	380	386	7.686747	ACAGTC	0.48828	0.48672
cg0544082	CCL2	c-Jun [T00	811	817	7.686747	ACAGTC	0.48828	0.48672
cg1269862	CCL2	p53 [T006	1981	1987	7.641867	AAGGCC	0.73242	0.79826
cg1269862	CCL2	c-Myb [T0	1525	1532	7.545286	TGCAGT	0.42725	0.40917
cg0544082	CCL2	c-Myb [T0	1956	1963	7.545286	TGCAGT	0.42725	0.40917
cg1269862	CCL2	GR [T050	19	25	7.527031	CAAAGC	1.83105	1.71535
cg1269862	CCL2	GR [T050	240	246	7.527031	CAAATA	1.83105	1.71535
cg1269862	CCL2	GR [T050	627	633	7.527031	ATATTT	1.83105	1.71535
cg1269862	CCL2	GR [T050	1178	1184	7.527031	ATATTT	1.83105	1.71535
cg1269862	CCL2	GR [T050	1413	1419	7.527031	CAAAGC	1.83105	1.71535
cg0544082	CCL2	GR [T050	450	456	7.527031	CAAAGC	1.83105	1.71535
cg0544082	CCL2	GR [T050	671	677	7.527031	CAAATA	1.83105	1.71535
cg0544082	CCL2	GR [T050	1058	1064	7.527031	ATATTT	1.83105	1.71535
cg0544082	CCL2	GR [T050	1609	1615	7.527031	ATATTT	1.83105	1.71535
cg0544082	CCL2	GR [T050	1844	1850	7.527031	CAAAGC	1.83105	1.71535
cg1269862	CCL2	RAR-beta	1056	1065	7.47824	TGGGTT	0.24414	0.25121
cg0544082	CCL2	RAR-beta	1487	1496	7.47824	TGGGTT	0.24414	0.25121

cg1269862	CCL2	AR [T000	838	846	7.467081	TTCTTG	0.25177	0.2544
cg0544082	CCL2	AR [T000	1269	1277	7.467081	TTCTTG	0.25177	0.2544
cg1269862	CCL2	C/EBPalp	1312	1318	7.465744	TTCAAT	0.48828	0.45033
cg0544082	CCL2	C/EBPalp	1743	1749	7.465744	TTCAAT	0.48828	0.45033
cg1269862	CCL2	RAR-beta	1848	1857	7.459774	GACTAA	0.24414	0.25121
cg1269862	CCL2	PEA3 [T0	1608	1616	7.421728	CCCCAT	0.34332	0.35389
cg1269862	CCL2	PEA3 [T0	1706	1714	7.421728	AGGATG	0.34332	0.35389
cg1269862	CCL2	C/EBPalp	745	751	7.396431	TCCAAT	0.48828	0.45033
cg1269862	CCL2	C/EBPalp	1864	1870	7.396431	TCCAAT	0.48828	0.45033
cg0544082	CCL2	C/EBPalp	1176	1182	7.396431	TCCAAT	0.48828	0.45033
cg1269862	CCL2	PPAR-alp	156	166	7.370536	TAGTCC	0.04482	0.04884
cg0544082	CCL2	PPAR-alp	587	597	7.370536	TAGTCC	0.04482	0.04884
cg1269862	CCL2	c-Ets-2 [T	1684	1692	7.268173	TTCCTA	0.09155	0.08977
cg1269862	CCL2	p53 [T006	1734	1740	7.266844	ACAGCC	0.73242	0.79826
cg1269862	CCL2	SRY [T00	1272	1280	7.175614	CTTTGT	0.30518	0.29547
cg0544082	CCL2	SRY [T00	1703	1711	7.175614	CTTTGT	0.30518	0.29547
cg1269862	CCL2	XBP-1 [T	49	54	7.172312	CTTCAT	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	137	142	7.172312	CATCAT	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	656	661	7.172312	ATGAAT	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	731	736	7.172312	ATGAAG	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	775	780	7.172312	ACTCAT	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	880	885	7.172312	ACTCAT	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	898	903	7.172312	ATGAGG	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	1351	1356	7.172312	ATGATG	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	1748	1753	7.172312	ACTCAT	2.92969	2.7512
cg1269862	CCL2	XBP-1 [T	1950	1955	7.172312	CTTCAT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	43	48	7.172312	ATGAGT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	221	226	7.172312	ATGAGG	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	242	247	7.172312	ATGAGG	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	311	316	7.172312	ATTCAT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	480	485	7.172312	CTTCAT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	568	573	7.172312	CATCAT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	1087	1092	7.172312	ATGAAT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	1162	1167	7.172312	ATGAAG	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	1206	1211	7.172312	ACTCAT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	1311	1316	7.172312	ACTCAT	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	1329	1334	7.172312	ATGAGG	2.92969	2.7512
cg0544082	CCL2	XBP-1 [T	1782	1787	7.172312	ATGATG	2.92969	2.7512
cg0544082	CCL2	c-Ets-1 [T	147	153	7.071349	AGGGAA	0.73242	0.73732
cg1269862	CCL2	AR [T000	1271	1279	7.049779	CCTTTG	0.23651	0.23986
cg0544082	CCL2	AR [T000	1702	1710	7.049779	CCTTTG	0.23651	0.23986
cg1269862	CCL2	C/EBPalp	1395	1401	7.00174	CATTGT	0.73242	0.68282
cg0544082	CCL2	C/EBPalp	1826	1832	7.00174	CATTGT	0.73242	0.68282
cg1269862	CCL2	HNF-3alp	370	377	7.000129	TAGAAA	0.82397	0.71909
cg1269862	CCL2	HNF-3alp	628	635	7.000129	TATTTG	0.82397	0.71909
cg1269862	CCL2	HNF-3alp	1164	1171	7.000129	AATTTA	0.82397	0.71909
cg1269862	CCL2	HNF-3alp	1179	1186	7.000129	TATTTG	0.82397	0.71909
cg0544082	CCL2	HNF-3alp	801	808	7.000129	TAGAAA	0.82397	0.71909

cg0544082	CCL2	HNF-3alph	1059	1066	7.000129	TATTTGT	0.82397	0.71909
cg0544082	CCL2	HNF-3alph	1595	1602	7.000129	AATTTAC	0.82397	0.71909
cg0544082	CCL2	HNF-3alph	1610	1617	7.000129	TATTTGT	0.82397	0.71909
cg1269862	CCL2	NF-1 [T00	964	971	6.948522	GGACCC	0.48828	0.50205
cg0544082	CCL2	NF-1 [T00	1395	1402	6.948522	GGACCC	0.48828	0.50205
cg0544082	CCL2	c-Ets-1 [T	210	216	6.943262	TTTCCCC	0.73242	0.73732
cg1269862	CCL2	ENKTF-1	891	898	6.942764	CTTAGCC	1.46484	1.56616
cg1269862	CCL2	ENKTF-1	1205	1212	6.942764	TGGCAG	1.46484	1.56616
cg1269862	CCL2	ENKTF-1	1970	1977	6.942764	CTCAGCC	1.46484	1.56616
cg0544082	CCL2	ENKTF-1	1322	1329	6.942764	CTTAGCC	1.46484	1.56616
cg0544082	CCL2	ENKTF-1	1636	1643	6.942764	TGGCAG	1.46484	1.56616
cg1269862	CCL2	p53 [T006	1441	1447	6.938545	GAGGCC	1.09863	1.22478
cg0544082	CCL2	p53 [T006	1872	1878	6.938545	GAGGCC	1.09863	1.22478
cg1269862	CCL2	VDR [T00	1574	1582	6.925682	GTTCAC	0.42725	0.41
cg0544082	CCL2	VDR [T00	172	180	6.925682	GTTCATC	0.42725	0.41
cg0544082	CCL2	C/EBPalph	152	158	6.85549	AATTGA	0.73242	0.68282
cg0544082	CCL2	PEA3 [T0	183	191	6.824411	AGGATG	0.22888	0.22744
cg1269862	CCL2	NFI/CTF [	968	975	6.786076	CCAAGC	0.73242	0.74795
cg0544082	CCL2	NFI/CTF [	1399	1406	6.786076	CCAAGC	0.73242	0.74795
cg1269862	CCL2	AR [T000	237	245	6.760234	GGACAA	0.23651	0.23986
cg0544082	CCL2	AR [T000	668	676	6.760234	GGACAA	0.23651	0.23986
cg1269862	CCL2	NF-1 [T00	516	523	6.722386	TTGGGC	0.24414	0.2565
cg1269862	CCL2	NF-1 [T00	1408	1415	6.722386	CCGGCC	0.24414	0.2565
cg0544082	CCL2	NF-1 [T00	947	954	6.722386	TTGGGC	0.24414	0.2565
cg0544082	CCL2	NF-1 [T00	1839	1846	6.722386	CCGGCC	0.24414	0.2565
cg1269862	CCL2	FOXP3 [T	252	257	6.581441	GTTTTA	0.97656	0.904
cg1269862	CCL2	FOXP3 [T	376	381	6.581441	TAAAAC	0.97656	0.904
cg1269862	CCL2	FOXP3 [T	390	395	6.581441	GTTGAA	0.97656	0.904
cg1269862	CCL2	TFII-I [T0	91	96	6.581441	CACTCC	0.97656	0.9991
cg0544082	CCL2	FOXP3 [T	371	376	6.581441	TTCAAC	0.97656	0.904
cg0544082	CCL2	FOXP3 [T	683	688	6.581441	GTTTTA	0.97656	0.904
cg0544082	CCL2	FOXP3 [T	807	812	6.581441	TAAAAC	0.97656	0.904
cg0544082	CCL2	FOXP3 [T	821	826	6.581441	GTTGAA	0.97656	0.904
cg0544082	CCL2	TFII-I [T0	522	527	6.581441	CACTCC	0.97656	0.9991
cg1269862	CCL2	p53 [T006	1031	1037	6.563521	GCAGCC	0.48828	0.54643
cg1269862	CCL2	p53 [T006	1048	1054	6.563521	GGGCTG	0.48828	0.54643
cg0544082	CCL2	p53 [T006	1462	1468	6.563521	GCAGCC	0.48828	0.54643
cg0544082	CCL2	p53 [T006	1479	1485	6.563521	GGGCTG	0.48828	0.54643
cg1269862	CCL2	XBP-1 [T	349	354	6.478682	ATGCCA	0.97656	0.99906
cg1269862	CCL2	XBP-1 [T	509	514	6.478682	ATGCCC	0.97656	0.99906
cg1269862	CCL2	XBP-1 [T	1236	1241	6.478682	TGGCAT	0.97656	0.99906
cg0544082	CCL2	XBP-1 [T	2	7	6.478682	ATGCCA	0.97656	0.99906
cg0544082	CCL2	XBP-1 [T	780	785	6.478682	ATGCCA	0.97656	0.99906
cg0544082	CCL2	XBP-1 [T	940	945	6.478682	ATGCCC	0.97656	0.99906
cg0544082	CCL2	XBP-1 [T	1667	1672	6.478682	TGGCAT	0.97656	0.99906
cg1269862	CCL2	C/EBPalph	465	471	6.460799	CATTGCC	0.48828	0.47407
cg0544082	CCL2	C/EBPalph	896	902	6.460799	CATTGCC	0.48828	0.47407
cg1269862	CCL2	c-Myb [T0	721	728	6.454077	CAACTG	0.30518	0.30272

cg1269862	CCL2	c-Myb [T0	1107	1114	6.454077	CTCAGT	0.30518	0.30272
cg0544082	CCL2	c-Myb [T0	1152	1159	6.454077	CAACTG	0.30518	0.30272
cg0544082	CCL2	c-Myb [T0	1538	1545	6.454077	CTCAGT	0.30518	0.30272
cg1269862	CCL2	c-Ets-1 [T	743	749	6.423689	TTTCCA	0.48828	0.48842
cg1269862	CCL2	c-Ets-1 [T	786	792	6.423689	TTGGAA	0.48828	0.48842
cg0544082	CCL2	c-Ets-1 [T	1174	1180	6.423689	TTTCCA	0.48828	0.48842
cg0544082	CCL2	c-Ets-1 [T	1217	1223	6.423689	TTGGAA	0.48828	0.48842
cg1269862	CCL2	RAR-beta	1284	1293	6.415195	CTGAAA	0.18311	0.1857
cg0544082	CCL2	RAR-beta	1715	1724	6.415195	CTGAAA	0.18311	0.1857
cg1269862	CCL2	c-Ets-1 [T	182	188	6.295602	ATGGAA	0.48828	0.48842
cg1269862	CCL2	c-Ets-1 [T	1647	1653	6.295602	ATGGAA	0.48828	0.48842
cg0544082	CCL2	c-Ets-1 [T	613	619	6.295602	ATGGAA	0.48828	0.48842
cg1269862	CCL2	c-Jun [T00	476	482	6.293948	TGACCC	0.61035	0.6179
cg0544082	CCL2	c-Jun [T00	907	913	6.293948	TGACCC	0.61035	0.6179
cg1269862	CCL2	GR-alpha	3	7	6.263098	CCTCA	3.90625	3.89624
cg1269862	CCL2	GR-alpha	470	474	6.263098	CCTCA	3.90625	3.89624
cg1269862	CCL2	GR-alpha	610	614	6.263098	CCTCA	3.90625	3.89624
cg1269862	CCL2	GR-alpha	664	668	6.263098	TAAGG	3.90625	3.89624
cg1269862	CCL2	GR-alpha	704	708	6.263098	TGAGG	3.90625	3.89624
cg1269862	CCL2	GR-alpha	714	718	6.263098	TAAGG	3.90625	3.89624
cg1269862	CCL2	GR-alpha	725	729	6.263098	TGAGG	3.90625	3.89624
cg1269862	CCL2	GR-alpha	899	903	6.263098	TGAGG	3.90625	3.89624
cg1269862	CCL2	GR-alpha	950	954	6.263098	TGAGG	3.90625	3.89624
cg1269862	CCL2	GR-alpha	1106	1110	6.263098	CCTCA	3.90625	3.89624
cg1269862	CCL2	GR-alpha	1554	1558	6.263098	CCTTA	3.90625	3.89624
cg1269862	CCL2	GR-alpha	1980	1984	6.263098	TAAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	222	226	6.263098	TGAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	243	247	6.263098	TGAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	332	336	6.263098	TGAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	427	431	6.263098	TAAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	434	438	6.263098	CCTCA	3.90625	3.89624
cg0544082	CCL2	GR-alpha	901	905	6.263098	CCTCA	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1041	1045	6.263098	CCTCA	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1095	1099	6.263098	TAAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1135	1139	6.263098	TGAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1145	1149	6.263098	TAAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1156	1160	6.263098	TGAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1330	1334	6.263098	TGAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1381	1385	6.263098	TGAGG	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1537	1541	6.263098	CCTCA	3.90625	3.89624
cg0544082	CCL2	GR-alpha	1985	1989	6.263098	CCTTA	3.90625	3.89624
cg1269862	CCL2	C/EBPalp	1803	1809	6.245236	TTCAAT	0.97656	0.91422
cg0544082	CCL2	IRF-1 [T0	221	229	6.24301	ATGAGG	0.16785	0.16217
cg1269862	CCL2	c-Fos [T00	1770	1779	6.236188	TGCTTG	0.09155	0.09198
cg1269862	CCL2	p53 [T006	1915	1921	6.188498	GCCGCC	0.61035	0.68483
cg1269862	CCL2	GR-alpha	259	263	6.055408	CCTAA	3.90625	3.89835
cg1269862	CCL2	GR-alpha	324	328	6.055408	CCTGA	3.90625	3.89835
cg1269862	CCL2	GR-alpha	332	336	6.055408	CCTGA	3.90625	3.89835

cg1269862	CCL2	GR-alpha [	737	741	6.055408	TCAGG	3.90625	3.89835
cg1269862	CCL2	GR-alpha [	876	880	6.055408	CCTAA	3.90625	3.89835
cg1269862	CCL2	GR-alpha [	1115	1119	6.055408	CCTGA	3.90625	3.89835
cg1269862	CCL2	GR-alpha [	1400	1404	6.055408	TCAGG	3.90625	3.89835
cg1269862	CCL2	GR-alpha [	1460	1464	6.055408	CCTGA	3.90625	3.89835
cg1269862	CCL2	GR-alpha [	1483	1487	6.055408	CCTGA	3.90625	3.89835
cg1269862	CCL2	GR-alpha [	1665	1669	6.055408	CCTGA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	215	219	6.055408	CCTGA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	411	415	6.055408	TCAGG	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	690	694	6.055408	CCTAA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	755	759	6.055408	CCTGA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	763	767	6.055408	CCTGA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	1168	1172	6.055408	TCAGG	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	1307	1311	6.055408	CCTAA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	1546	1550	6.055408	CCTGA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	1831	1835	6.055408	TCAGG	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	1891	1895	6.055408	CCTGA	3.90625	3.89835
cg0544082	CCL2	GR-alpha [	1914	1918	6.055408	CCTGA	3.90625	3.89835
cg1269862	CCL2	c-Ets-1 [T	301	307	6.039428	CTGGAA	0.36621	0.36174
cg1269862	CCL2	c-Ets-1 [T	1694	1700	6.039428	CTGGAA	0.36621	0.36174
cg0544082	CCL2	c-Ets-1 [T	298	304	6.039428	CTGGAA	0.36621	0.36174
cg0544082	CCL2	c-Ets-1 [T	732	738	6.039428	CTGGAA	0.36621	0.36174
cg1269862	CCL2	C/EBPalph	345	351	5.996794	AACAAT	0.97656	0.91422
cg0544082	CCL2	C/EBPalph	776	782	5.996794	AACAAT	0.97656	0.91422
cg1269862	CCL2	RXR-alpha	1604	1610	5.937582	GGCACC	0.73242	0.78318
cg1269862	CCL2	GCF [T00	293	301	5.917256	AGGCAG	0.64087	0.72542
cg0544082	CCL2	GCF [T00	724	732	5.917256	AGGCAG	0.64087	0.72542
cg1269862	CCL2	STAT4 [T	1005	1010	5.882353	CCTTCC	0.48828	0.51201
cg1269862	CCL2	STAT4 [T	1428	1433	5.882353	CCTTCC	0.48828	0.51201
cg1269862	CCL2	STAT4 [T	1514	1519	5.882353	CCTTCC	0.48828	0.51201
cg0544082	CCL2	STAT4 [T	1436	1441	5.882353	CCTTCC	0.48828	0.51201
cg0544082	CCL2	STAT4 [T	1859	1864	5.882353	CCTTCC	0.48828	0.51201
cg0544082	CCL2	STAT4 [T	1945	1950	5.882353	CCTTCC	0.48828	0.51201
cg1269862	CCL2	IRF-1 [T0	1683	1691	5.823972	TTTCCTA	0.16785	0.16217
cg1269862	CCL2	STAT1bet	120	129	5.796867	TCCAGG	0.1545	0.14881
cg1269862	CCL2	STAT1bet	784	793	5.796867	CCTTGG	0.1545	0.14881
cg0544082	CCL2	STAT1bet	296	305	5.796867	TCCTGG	0.1545	0.14881
cg0544082	CCL2	STAT1bet	551	560	5.796867	TCCAGG	0.1545	0.14881
cg0544082	CCL2	STAT1bet	1215	1224	5.796867	CCTTGG	0.1545	0.14881
cg1269862	CCL2	c-Jun [T00	1667	1673	5.703976	TGACCC	0.48828	0.49294
cg1269862	CCL2	ENKTF-1	347	354	5.687009	CAATGC	0.73242	0.76357
cg0544082	CCL2	ENKTF-1	62	69	5.687009	CTAAGC	0.73242	0.76357
cg0544082	CCL2	ENKTF-1	253	260	5.687009	TGGCCT	0.73242	0.76357
cg0544082	CCL2	ENKTF-1	778	785	5.687009	CAATGC	0.73242	0.76357
cg1269862	CCL2	c-Ets-1 [T	1677	1683	5.686398	CTTCCC	0.36621	0.38732
cg1269862	CCL2	c-Jun [T00	1230	1236	5.590308	TGACAC	0.48828	0.49294
cg0544082	CCL2	c-Jun [T00	1661	1667	5.590308	TGACAC	0.48828	0.49294
cg1269862	CCL2	TFIID [T0	679	685	5.544826	TTTATCA	0.73242	0.65314

cg1269862	CCL2	TFIID [T0	1730	1736	5.544826	TTTAAC	0.73242	0.65314
cg0544082	CCL2	TFIID [T0	177	183	5.544826	TGGTAA	0.73242	0.65314
cg0544082	CCL2	TFIID [T0	1110	1116	5.544826	TTTATC	0.73242	0.65314
cg1269862	CCL2	NF-AT1 [	739	748	5.512555	AGGCTT	0.05913	0.05666
cg1269862	CCL2	NF-AT1 [	1695	1704	5.512555	TGGAAA	0.05913	0.05666
cg0544082	CCL2	NF-AT1 [	1170	1179	5.512555	AGGCTT	0.05913	0.05666
cg1269862	CCL2	p53 [T006	590	596	5.508538	TCAGCC	0.61035	0.65765
cg1269862	CCL2	p53 [T006	1595	1601	5.508538	GGGCTT	0.61035	0.65765
cg0544082	CCL2	p53 [T006	19	25	5.508538	TAAGCC	0.61035	0.65765
cg0544082	CCL2	p53 [T006	1021	1027	5.508538	TCAGCC	0.61035	0.65765
cg0544082	CCL2	C/EBPalp	25	31	5.455853	CATTGA	0.73242	0.68229
cg0544082	CCL2	IRF-1 [T0	210	218	5.42531	TTTCCC	0.22888	0.21959
cg1269862	CCL2	RAR-beta	1090	1099	5.333686	ATTTAA	0.15259	0.15813
cg0544082	CCL2	RAR-beta	1521	1530	5.333686	ATTTAA	0.15259	0.15813
cg1269862	CCL2	IRF-1 [T0	1002	1010	5.309227	TTTCCTT	0.22888	0.21959
cg0544082	CCL2	IRF-1 [T0	1433	1441	5.309227	TTTCCTT	0.22888	0.21959
cg1269862	CCL2	HOXD9 [	374	383	5.275652	AATAAA	0.04578	0.03952
cg1269862	CCL2	HOXD10 [	374	383	5.275652	AATAAA	0.04578	0.03952
cg0544082	CCL2	HOXD9 [	805	814	5.275652	AATAAA	0.04578	0.03952
cg0544082	CCL2	HOXD10 [	805	814	5.275652	AATAAA	0.04578	0.03952
cg1269862	CCL2	RXR-alph	195	201	5.271235	GGGTGG	0.61035	0.65415
cg0544082	CCL2	RXR-alph	626	632	5.271235	GGGTGG	0.61035	0.65415
cg1269862	CCL2	NF-AT2 [	303	312	5.231211	GGAAAG	0.03815	0.03519
cg0544082	CCL2	NF-AT2 [	734	743	5.231211	GGAAAG	0.03815	0.03519
cg1269862	CCL2	GR [T050	501	507	5.207533	GTCTTT	0.24414	0.24013
cg1269862	CCL2	GR [T050	668	674	5.207533	GTCTTT	0.24414	0.24013
cg0544082	CCL2	GR [T050	932	938	5.207533	GTCTTT	0.24414	0.24013
cg0544082	CCL2	GR [T050	1099	1105	5.207533	GTCTTT	0.24414	0.24013
cg1269862	CCL2	c-Jun [T00	491	497	5.193102	GAAGTC	0.61035	0.60573
cg1269862	CCL2	c-Jun [T00	733	739	5.193102	GAAGTC	0.61035	0.60573
cg0544082	CCL2	c-Jun [T00	922	928	5.193102	GAAGTC	0.61035	0.60573
cg0544082	CCL2	c-Jun [T00	1164	1170	5.193102	GAAGTC	0.61035	0.60573
cg1269862	CCL2	p53 [T006	1778	1784	5.133514	TCCGCC	0.48828	0.53921
cg0544082	CCL2	HNF-1A [	108	115	5.116518	GTTAAC	0.36621	0.34064
cg1269862	CCL2	AR [T000	953	961	5.104816	GGACAG	0.11444	0.12256
cg0544082	CCL2	AR [T000	1384	1392	5.104816	GGACAG	0.11444	0.12256
cg1269862	CCL2	AP-2alpha	1270	1275	5.100982	GCCTTT	0.97656	0.97517
cg0544082	CCL2	AP-2alpha	1701	1706	5.100982	GCCTTT	0.97656	0.97517
cg1269862	CCL2	SRY [T00	503	511	5.086565	CTTTGT	0.06104	0.05662
cg0544082	CCL2	SRY [T00	934	942	5.086565	CTTTGT	0.06104	0.05662
cg1269862	CCL2	GR-beta [	114	118	5.042296	GGATT	3.90625	3.7093
cg1269862	CCL2	GR-beta [	394	398	5.042296	AATAC	3.90625	3.7093
cg1269862	CCL2	GR-beta [	757	761	5.042296	AATAC	3.90625	3.7093
cg1269862	CCL2	GR-beta [	1140	1144	5.042296	AATCC	3.90625	3.7093
cg1269862	CCL2	GR-beta [	1326	1330	5.042296	AATCC	3.90625	3.7093
cg1269862	CCL2	GR-beta [	1385	1389	5.042296	GGATT	3.90625	3.7093
cg1269862	CCL2	GR-beta [	1551	1555	5.042296	AATCC	3.90625	3.7093
cg1269862	CCL2	GR-beta [	1699	1703	5.042296	AATCC	3.90625	3.7093

cg0544082	CCL2	GR-beta [T	36	40	5.042296	GGATT	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	138	142	5.042296	GGATT	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	328	332	5.042296	GGATT	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	545	549	5.042296	GGATT	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	825	829	5.042296	AATAC	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	1188	1192	5.042296	AATAC	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	1571	1575	5.042296	AATCC	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	1757	1761	5.042296	AATCC	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	1816	1820	5.042296	GGATT	3.90625	3.7093
cg0544082	CCL2	GR-beta [T	1982	1986	5.042296	AATCC	3.90625	3.7093
cg1269862	CCL2	c-Ets-1 [T	939	945	5.038739	TTGGAA	0.48828	0.48026
cg0544082	CCL2	c-Ets-1 [T	235	241	5.038739	TTGGAA	0.48828	0.48026
cg0544082	CCL2	c-Ets-1 [T	1370	1376	5.038739	TTGGAA	0.48828	0.48026
cg1269862	CCL2	NFI/CTF [	512	519	5.021086	CCCATT	0.24414	0.25666
cg1269862	CCL2	NFI/CTF [	782	789	5.021086	TCCCTT	0.24414	0.25666
cg1269862	CCL2	NFI/CTF [	1445	1452	5.021086	CCCCTT	0.24414	0.25666
cg0544082	CCL2	NFI/CTF [	943	950	5.021086	CCCATT	0.24414	0.25666
cg0544082	CCL2	NFI/CTF [	1213	1220	5.021086	TCCCTT	0.24414	0.25666
cg0544082	CCL2	NFI/CTF [	1876	1883	5.021086	CCCCTT	0.24414	0.25666
cg1269862	CCL2	p53 [T006	26	32	5.020467	GGGCTC	0.48828	0.53921
cg1269862	CCL2	p53 [T006	1963	1969	5.020467	GGGCTC	0.48828	0.53921
cg0544082	CCL2	p53 [T006	457	463	5.020467	GGGCTC	0.48828	0.53921
cg0544082	CCL2	NF-AT2 [T	225	234	4.979362	GGAAAA	0.03815	0.03519
cg1269862	CCL2	AP-1 [T00	326	334	4.955822	TGACTC	0.12207	0.12309
cg0544082	CCL2	AP-1 [T00	757	765	4.955822	TGACTC	0.12207	0.12309
cg1269862	CCL2	AR [T000	1043	1051	4.947929	GGACAG	0.11444	0.12256
cg0544082	CCL2	AR [T000	1474	1482	4.947929	GGACAG	0.11444	0.12256
cg1269862	CCL2	c-Ets-1 [T	1752	1758	4.910652	ATGGAA	0.48828	0.48026
cg1269862	CCL2	XBP-1 [T	607	612	4.894955	ATGCCT	0.97656	0.99839
cg1269862	CCL2	XBP-1 [T	1268	1273	4.894955	ATGCCT	0.97656	0.99839
cg0544082	CCL2	XBP-1 [T	334	339	4.894955	AGGCAT	0.97656	0.99839
cg0544082	CCL2	XBP-1 [T	1038	1043	4.894955	ATGCCT	0.97656	0.99839
cg0544082	CCL2	XBP-1 [T	1699	1704	4.894955	ATGCCT	0.97656	0.99839
cg1269862	CCL2	c-Jun [T00	309	315	4.883696	TATGTC	0.61035	0.60573
cg1269862	CCL2	c-Jun [T00	1016	1022	4.883696	TATGTC	0.61035	0.60573
cg0544082	CCL2	c-Jun [T00	740	746	4.883696	TATGTC	0.61035	0.60573
cg0544082	CCL2	c-Jun [T00	1447	1453	4.883696	TATGTC	0.61035	0.60573
cg1269862	CCL2	HNF-3alp	580	587	4.842999	AATTTT	0.09155	0.07438
cg0544082	CCL2	HNF-3alp	79	86	4.842999	TATTTA	0.09155	0.07438
cg0544082	CCL2	HNF-3alp	1011	1018	4.842999	AATTTT	0.09155	0.07438
cg1269862	CCL2	NF-AT1 [T	302	311	4.823485	TGGAAA	0.07629	0.07281
cg1269862	CCL2	NF-AT1 [T	787	796	4.823485	TGGAAA	0.07629	0.07281
cg0544082	CCL2	NF-AT1 [T	733	742	4.823485	TGGAAA	0.07629	0.07281
cg0544082	CCL2	NF-AT1 [T	1218	1227	4.823485	TGGAAA	0.07629	0.07281
cg1269862	CCL2	C/EBPalp	128	134	4.776286	ACCAAT	0.97656	0.90302
cg0544082	CCL2	C/EBPalp	559	565	4.776286	ACCAAT	0.97656	0.90302
cg1269862	CCL2	FOXP3 [T	34	39	4.756447	GTTGAT	2.92969	2.82
cg1269862	CCL2	FOXP3 [T	342	347	4.756447	CTCAAC	2.92969	2.82

cg1269862	CCL2	FOXP3 [T	432	437	4.756447	GTTTTC	2.92969	2.82
cg1269862	CCL2	FOXP3 [T	676	681	4.756447	GTTTTT	2.92969	2.82
cg1269862	CCL2	FOXP3 [T	1529	1534	4.756447	GTTTTC	2.92969	2.82
cg1269862	CCL2	TFII-I [T0	132	137	4.756447	ATATCC	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	179	184	4.756447	GGAATG	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	284	289	4.756447	GGACTG	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	707	712	4.756447	GGAAAT	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	728	733	4.756447	GGAATG	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	779	784	4.756447	ATGTCC	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	788	793	4.756447	GGAAAT	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	902	907	4.756447	GGAATG	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	1139	1144	4.756447	CAATCC	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	1325	1330	4.756447	CAATCC	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	1451	1456	4.756447	GGAATG	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	1696	1701	4.756447	GGAAAT	2.92969	2.89715
cg1269862	CCL2	TFII-I [T0	1953	1958	4.756447	CATTCC	2.92969	2.89715
cg0544082	CCL2	FOXP3 [T	119	124	4.756447	GAAAAC	2.92969	2.82
cg0544082	CCL2	FOXP3 [T	226	231	4.756447	GAAAAC	2.92969	2.82
cg0544082	CCL2	FOXP3 [T	465	470	4.756447	GTTGAT	2.92969	2.82
cg0544082	CCL2	FOXP3 [T	773	778	4.756447	CTCAAC	2.92969	2.82
cg0544082	CCL2	FOXP3 [T	863	868	4.756447	GTTTTC	2.92969	2.82
cg0544082	CCL2	FOXP3 [T	1107	1112	4.756447	GTTTTT	2.92969	2.82
cg0544082	CCL2	FOXP3 [T	1960	1965	4.756447	GTTTTC	2.92969	2.82
cg0544082	CCL2	TFII-I [T0	149	154	4.756447	GGAAAT	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	328	333	4.756447	GGATTG	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	347	352	4.756447	GGACTG	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	563	568	4.756447	ATATCC	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	610	615	4.756447	GGAATG	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	715	720	4.756447	GGACTG	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1138	1143	4.756447	GGAAAT	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1159	1164	4.756447	GGAATG	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1210	1215	4.756447	ATGTCC	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1219	1224	4.756447	GGAAAT	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1333	1338	4.756447	GGAATG	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1570	1575	4.756447	CAATCC	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1756	1761	4.756447	CAATCC	2.92969	2.89715
cg0544082	CCL2	TFII-I [T0	1882	1887	4.756447	GGAATG	2.92969	2.89715
cg0544082	CCL2	HNF-1A [	106	113	4.684871	TTGTTA	0.12207	0.10966
cg1269862	CCL2	c-Ets-1 [T	1006	1012	4.654478	CTTCCA	0.85449	0.8381
cg0544082	CCL2	c-Ets-1 [T	1437	1443	4.654478	CTTCCA	0.85449	0.8381
cg1269862	CCL2	VDR [T00	646	654	4.617121	GTTCAC	0.37384	0.36855
cg1269862	CCL2	VDR [T00	829	837	4.617121	GGGATG	0.37384	0.36855
cg1269862	CCL2	VDR [T00	1311	1319	4.617121	GTTCAA	0.37384	0.36855
cg0544082	CCL2	VDR [T00	1077	1085	4.617121	GTTCAC	0.37384	0.36855
cg0544082	CCL2	VDR [T00	1260	1268	4.617121	GGGATG	0.37384	0.36855
cg0544082	CCL2	VDR [T00	1742	1750	4.617121	GTTCAA	0.37384	0.36855
cg1269862	CCL2	RAR-alph	1661	1673	4.596281	TCGTCC	0.00376	0.0041
cg1269862	CCL2	c-Ets-2 [T	1512	1520	4.589988	TTCCTTC	0.06866	0.06805

cg0544082	CCL2	c-Ets-2 [T	1943	1951	4.589988	TTCCTTC	0.06866	0.06805
cg1269862	CCL2	AP-1 [T00	1774	1782	4.553988	TGACTC	0.03052	0.03196
cg0544082	CCL2	c-Ets-1 [T	267	273	4.539113	ATTCCT	0.85449	0.8381
cg1269862	CCL2	IRF-1 [T0	743	751	4.462268	TTTCCA	0.05341	0.05056
cg0544082	CCL2	IRF-1 [T0	1174	1182	4.462268	TTTCCA	0.05341	0.05056
cg1269862	CCL2	HNF-1C [	1088	1096	4.443787	CTATTT	0.07629	0.06715
cg0544082	CCL2	HNF-1C [	1519	1527	4.443787	CTATTT	0.07629	0.06715
cg1269862	CCL2	AP-2alpha	1341	1346	4.438035	CTAGGC	0.97656	0.99839
cg0544082	CCL2	AP-2alpha	255	260	4.438035	GCCTAG	0.97656	0.99839
cg0544082	CCL2	AP-2alpha	1772	1777	4.438035	CTAGGC	0.97656	0.99839
cg1269862	CCL2	Sp1 [T007	1913	1922	4.43736	CTGCCG	0.08583	0.0979
cg1269862	CCL2	RXR-alph	397	403	4.423008	ACAACC	0.24414	0.25781
cg0544082	CCL2	RXR-alph	828	834	4.423008	ACAACC	0.24414	0.25781
cg1269862	CCL2	AP-2alpha	714	719	4.422424	TAAGGC	0.97656	0.99839
cg1269862	CCL2	AP-2alpha	1980	1985	4.422424	TAAGGC	0.97656	0.99839
cg0544082	CCL2	AP-2alpha	427	432	4.422424	TAAGGC	0.97656	0.99839
cg0544082	CCL2	AP-2alpha	1145	1150	4.422424	TAAGGC	0.97656	0.99839
cg1269862	CCL2	STAT4 [T	164	169	4.411765	GGAAGA	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	179	184	4.411765	GGAATG	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	728	733	4.411765	GGAATG	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	800	805	4.411765	GGAAGC	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	902	907	4.411765	GGAATG	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	941	946	4.411765	GGAAGA	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	1451	1456	4.411765	GGAATG	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	1510	1515	4.411765	GCTTCC	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	1676	1681	4.411765	GCTTCC	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	1754	1759	4.411765	GGAAGA	1.95312	1.99838
cg1269862	CCL2	STAT4 [T	1953	1958	4.411765	CATTCC	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	237	242	4.411765	GGAAGA	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	260	265	4.411765	GGAAGA	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	595	600	4.411765	GGAAGA	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	610	615	4.411765	GGAATG	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	1159	1164	4.411765	GGAATG	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	1231	1236	4.411765	GGAAGC	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	1333	1338	4.411765	GGAATG	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	1372	1377	4.411765	GGAAGA	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	1882	1887	4.411765	GGAATG	1.95312	1.99838
cg0544082	CCL2	STAT4 [T	1941	1946	4.411765	GCTTCC	1.95312	1.99838
cg0544082	CCL2	HOXD9 [	304	313	4.321431	ACATTT	0.03433	0.02831
cg0544082	CCL2	HOXD10 [	304	313	4.321431	ACATTT	0.03433	0.02831
cg1269862	CCL2	HNF-1C [	1119	1127	4.312587	ATCTAT	0.07629	0.06715
cg0544082	CCL2	HNF-1C [	1550	1558	4.312587	ATCTAT	0.07629	0.06715
cg1269862	CCL2	PEA3 [T0	1859	1867	4.30818	AAACAT	0.13733	0.13607
cg1269862	CCL2	c-Ets-1 [T	726	732	4.282938	GAGGAA	0.85449	0.8381
cg1269862	CCL2	c-Ets-1 [T	900	906	4.282938	GAGGAA	0.85449	0.8381
cg0544082	CCL2	c-Ets-1 [T	1157	1163	4.282938	GAGGAA	0.85449	0.8381
cg0544082	CCL2	c-Ets-1 [T	1331	1337	4.282938	GAGGAA	0.85449	0.8381
cg1269862	CCL2	RXR-alph	475	481	4.24113	GTGACC	0.97656	1.02803

cg0544082	CCL2	RXR-alph	906	912	4.24113	GTGACC	0.97656	1.02803
cg1269862	CCL2	HNF-1B [	1089	1097	4.230295	TATTTA	0.01526	0.01336
cg0544082	CCL2	HNF-1B [	1520	1528	4.230295	TATTTA	0.01526	0.01336
cg1269862	CCL2	GR-beta [	36	40	4.201913	TGATT	7.8125	7.23274
cg1269862	CCL2	GR-beta [	218	222	4.201913	CTATT	7.8125	7.23274
cg1269862	CCL2	GR-beta [	242	246	4.201913	AATAA	7.8125	7.23274
cg1269862	CCL2	GR-beta [	374	378	4.201913	AATAA	7.8125	7.23274
cg1269862	CCL2	GR-beta [	566	570	4.201913	AATCG	7.8125	7.23274
cg1269862	CCL2	GR-beta [	812	816	4.201913	AATAG	7.8125	7.23274
cg1269862	CCL2	GR-beta [	1088	1092	4.201913	CTATT	7.8125	7.23274
cg1269862	CCL2	GR-beta [	1360	1364	4.201913	CTATT	7.8125	7.23274
cg1269862	CCL2	GR-beta [	1561	1565	4.201913	AATAA	7.8125	7.23274
cg1269862	CCL2	GR-beta [	1806	1810	4.201913	AATAA	7.8125	7.23274
cg0544082	CCL2	GR-beta [	28	32	4.201913	TGATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	78	82	4.201913	TTATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	196	200	4.201913	TGATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	309	313	4.201913	TTATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	425	429	4.201913	AATAA	7.8125	7.23274
cg0544082	CCL2	GR-beta [	467	471	4.201913	TGATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	649	653	4.201913	CTATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	673	677	4.201913	AATAA	7.8125	7.23274
cg0544082	CCL2	GR-beta [	805	809	4.201913	AATAA	7.8125	7.23274
cg0544082	CCL2	GR-beta [	997	1001	4.201913	AATCG	7.8125	7.23274
cg0544082	CCL2	GR-beta [	1243	1247	4.201913	AATAG	7.8125	7.23274
cg0544082	CCL2	GR-beta [	1519	1523	4.201913	CTATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	1791	1795	4.201913	CTATT	7.8125	7.23274
cg0544082	CCL2	GR-beta [	1992	1996	4.201913	AATAA	7.8125	7.23274
cg1269862	CCL2	NF-Y [T0	743	750	4.186615	TTTCCA	0.18311	0.17499
cg0544082	CCL2	NF-Y [T0	1174	1181	4.186615	TTTCCA	0.18311	0.17499
cg1269862	CCL2	c-Ets-1 [T	1200	1206	4.154851	ATTCCT	0.24414	0.23719
cg0544082	CCL2	c-Ets-1 [T	1631	1637	4.154851	ATTCCT	0.24414	0.23719
cg0544082	CCL2	NF-AT1 [	299	308	4.134416	TGGAAA	0.08392	0.07965
cg1269862	CCL2	p53 [T006	524	530	4.083527	GGGCAC	0.73242	0.82434
cg0544082	CCL2	p53 [T006	955	961	4.083527	GGGCAC	0.73242	0.82434
cg1269862	CCL2	RXR-alph	444	450	4.019014	GAAACC	0.97656	1.02803
cg1269862	CCL2	RXR-alph	1286	1292	4.019014	GAAACC	0.97656	1.02803
cg0544082	CCL2	RXR-alph	875	881	4.019014	GAAACC	0.97656	1.02803
cg0544082	CCL2	RXR-alph	1717	1723	4.019014	GAAACC	0.97656	1.02803
cg1269862	CCL2	TFIID [T0	411	417	4.007279	TTTACA	1.09863	0.94722
cg1269862	CCL2	TFIID [T0	482	488	4.007279	TTTATG	1.09863	0.94722
cg1269862	CCL2	TFIID [T0	582	588	4.007279	TTTTAA	1.09863	0.94722
cg1269862	CCL2	TFIID [T0	1182	1188	4.007279	TTGTAA	1.09863	0.94722
cg1269862	CCL2	Pax-5 [T0	1734	1740	4.007279	ACAGCC	1.09863	1.18533
cg1269862	CCL2	Pax-5 [T0	1981	1987	4.007279	AAGGCC	1.09863	1.18533
cg0544082	CCL2	TFIID [T0	141	147	4.007279	TTATAA	1.09863	0.94722
cg0544082	CCL2	TFIID [T0	842	848	4.007279	TTTACA	1.09863	0.94722
cg0544082	CCL2	TFIID [T0	913	919	4.007279	TTTATG	1.09863	0.94722
cg0544082	CCL2	TFIID [T0	1013	1019	4.007279	TTTTAA	1.09863	0.94722

cg0544082	CCL2	TFIID [T0	1613	1619	4.007279	TTGTAA	1.09863	0.94722
cg1269862	CCL2	AP-2alpha	532	537	3.970052	CAAGGC	0.97656	1.02535
cg0544082	CCL2	AP-2alpha	963	968	3.970052	CAAGGC	0.97656	1.02535
cg1269862	CCL2	p53 [T006	556	562	3.961937	GGGCTA	0.73242	0.82434
cg0544082	CCL2	p53 [T006	987	993	3.961937	GGGCTA	0.73242	0.82434
cg1269862	CCL2	NF-Y [T0(	1862	1869	3.95898	CATCCA	0.18311	0.17499
cg1269862	CCL2	IRF-1 [T0(	180	188	3.947523	GAATGG	0.1297	0.12468
cg1269862	CCL2	IRF-1 [T0(	1645	1653	3.947523	GAATGG	0.1297	0.12468
cg0544082	CCL2	IRF-1 [T0(	611	619	3.947523	GAATGG	0.1297	0.12468
cg0544082	CCL2	Elk-1 [T00	256	264	3.944668	CCTAGG	0.09155	0.08816
cg1269862	CCL2	NF-AT2 [T	1649	1658	3.814941	GGAAAA	0.01144	0.01081
cg0544082	CCL2	c-Jun [T00	59	65	3.807346	TGACTA	0.24414	0.23729
cg1269862	CCL2	NFI/CTF [	1959	1966	3.793671	CCAAGG	0.18311	0.19063
cg1269862	CCL2	E2F-1 [T0	1912	1919	3.784875	TCTGCC	0.15259	0.15999
cg1269862	CCL2	PEA3 [T0(	49	57	3.710864	CTTCATC	0.09155	0.08745
cg0544082	CCL2	PEA3 [T0(	480	488	3.710864	CTTCATC	0.09155	0.08745
cg1269862	CCL2	c-Ets-1 [T(	1830	1836	3.590463	GAGGAA	0.61035	0.61936
cg1269862	CCL2	Sp1 [T007	1776	1785	3.54287	ACTCCG	0.07439	0.08783
cg1269862	CCL2	c-Ets-2 [T(	795	803	3.518824	AAGAAG	0.18311	0.18314
cg1269862	CCL2	c-Ets-2 [T(	1003	1011	3.518824	TTCCTTC	0.18311	0.18314
cg0544082	CCL2	c-Ets-2 [T(	1226	1234	3.518824	AAGAAG	0.18311	0.18314
cg0544082	CCL2	c-Ets-2 [T(	1434	1442	3.518824	TTCCTTC	0.18311	0.18314
cg1269862	CCL2	HNF-3alpl	1129	1136	3.500065	TGAAAA	0.27466	0.23175
cg0544082	CCL2	HNF-3alpl	1560	1567	3.500065	TGAAAA	0.27466	0.23175
cg1269862	CCL2	RXR-alpha	963	969	3.392904	AGGACC	1.09863	1.1653
cg0544082	CCL2	RXR-alpha	1394	1400	3.392904	AGGACC	1.09863	1.1653
cg0544082	CCL2	T3R-beta1	242	250	3.370634	ATGAGG	0.27466	0.27326
cg1269862	CCL2	GR-beta [T	131	135	3.361531	AATAT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	172	176	3.361531	AGATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	627	631	3.361531	ATATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	710	714	3.361531	AATCT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	913	917	3.361531	AGATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	1177	1181	3.361531	AATAT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	1178	1182	3.361531	ATATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	1197	1201	3.361531	AATAT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	1198	1202	3.361531	ATATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [T	1727	1731	3.361531	AGATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	407	411	3.361531	AGATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	562	566	3.361531	AATAT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	603	607	3.361531	AGATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1058	1062	3.361531	ATATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1141	1145	3.361531	AATCT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1344	1348	3.361531	AGATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1608	1612	3.361531	AATAT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1609	1613	3.361531	ATATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1628	1632	3.361531	AATAT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1629	1633	3.361531	ATATT	3.90625	3.51525
cg0544082	CCL2	PR B [T00	303	309	3.29756	AACATT	0.24414	0.21408

cg0544082	CCL2	PR A [T01	303	309	3.29756	AACATT	0.24414	0.21408
cg1269862	CCL2	c-Ets-2 [T	723	731	3.2883	ACTGAG	0.18311	0.18314
cg1269862	CCL2	c-Ets-2 [T	1504	1512	3.2883	TTCCTC	0.18311	0.18314
cg0544082	CCL2	c-Ets-2 [T	1154	1162	3.2883	ACTGAG	0.18311	0.18314
cg0544082	CCL2	c-Ets-2 [T	1935	1943	3.2883	TTCCTC	0.18311	0.18314
cg1269862	CCL2	AP-2alpha	8	13	3.229049	AGAGGC	0.48828	0.5124
cg1269862	CCL2	AP-2alpha	1810	1815	3.229049	AGAGGC	0.48828	0.5124
cg1269862	CCL2	AP-2alpha	1839	1844	3.229049	AGAGGC	0.48828	0.5124
cg0544082	CCL2	AP-2alpha	439	444	3.229049	AGAGGC	0.48828	0.5124
cg1269862	CCL2	RXR-alph	674	680	3.170788	GGGTTT	0.24414	0.24551
cg0544082	CCL2	RXR-alph	120	126	3.170788	AAAACC	0.24414	0.24551
cg0544082	CCL2	RXR-alph	1105	1111	3.170788	GGGTTT	0.24414	0.24551
cg1269862	CCL2	c-Fos [T00	322	331	3.154982	TACCTG	0.06104	0.06233
cg0544082	CCL2	c-Fos [T00	753	762	3.154982	TACCTG	0.06104	0.06233
cg1269862	CCL2	Elk-1 [T00	1515	1523	3.121991	CTTCCTT	0.07629	0.07518
cg0544082	CCL2	Elk-1 [T00	1946	1954	3.121991	CTTCCTT	0.07629	0.07518
cg1269862	CCL2	NF-AT1 [	739	747	3.098758	AGGCTT	0.03052	0.0304
cg0544082	CCL2	NF-AT1 [	1170	1178	3.098758	AGGCTT	0.03052	0.0304
cg0544082	CCL2	NF-Y [T0	315	322	3.051543	ATTGGA	0.06104	0.05632
cg1269862	CCL2	C/EBPalp	1137	1143	3.014837	AGCAAT	0.48828	0.47526
cg0544082	CCL2	C/EBPalp	1568	1574	3.014837	AGCAAT	0.48828	0.47526
cg1269862	CCL2	C/EBPalp	514	520	2.981957	CATTGG	0.48828	0.47526
cg0544082	CCL2	C/EBPalp	945	951	2.981957	CATTGG	0.48828	0.47526
cg1269862	CCL2	c-Ets-2 [T	1516	1524	2.945838	TTCCTTT	0.06104	0.05567
cg0544082	CCL2	c-Ets-2 [T	1947	1955	2.945838	TTCCTTT	0.06104	0.05567
cg1269862	CCL2	STAT4 [T	303	308	2.941176	GGAAAG	2.92969	2.92382
cg1269862	CCL2	STAT4 [T	742	747	2.941176	CTTTCC	2.92969	2.92382
cg1269862	CCL2	STAT4 [T	1199	1204	2.941176	TATTCC	2.92969	2.92382
cg1269862	CCL2	STAT4 [T	1682	1687	2.941176	CTTTCC	2.92969	2.92382
cg1269862	CCL2	STAT4 [T	1689	1694	2.941176	ACTTCC	2.92969	2.92382
cg1269862	CCL2	STAT4 [T	1832	1837	2.941176	GGAACC	2.92969	2.92382
cg0544082	CCL2	STAT4 [T	734	739	2.941176	GGAAAG	2.92969	2.92382
cg0544082	CCL2	STAT4 [T	1173	1178	2.941176	CTTTCC	2.92969	2.92382
cg0544082	CCL2	STAT4 [T	1630	1635	2.941176	TATTCC	2.92969	2.92382
cg1269862	CCL2	PR B [T00	345	351	2.80933	AACAAT	0.73242	0.66711
cg1269862	CCL2	PR B [T00	903	909	2.80933	GAATGT	0.73242	0.66711
cg1269862	CCL2	PR B [T00	1314	1320	2.80933	CAATGT	0.73242	0.66711
cg1269862	CCL2	PR A [T01	345	351	2.80933	AACAAT	0.73242	0.66711
cg1269862	CCL2	PR A [T01	903	909	2.80933	GAATGT	0.73242	0.66711
cg1269862	CCL2	PR A [T01	1314	1320	2.80933	CAATGT	0.73242	0.66711
cg0544082	CCL2	PR B [T00	776	782	2.80933	AACAAT	0.73242	0.66711
cg0544082	CCL2	PR B [T00	1334	1340	2.80933	GAATGT	0.73242	0.66711
cg0544082	CCL2	PR B [T00	1745	1751	2.80933	CAATGT	0.73242	0.66711
cg0544082	CCL2	PR A [T01	776	782	2.80933	AACAAT	0.73242	0.66711
cg0544082	CCL2	PR A [T01	1334	1340	2.80933	GAATGT	0.73242	0.66711
cg0544082	CCL2	PR A [T01	1745	1751	2.80933	CAATGT	0.73242	0.66711
cg1269862	CCL2	NF-AT1 [	183	192	2.756277	TGGAAA	0.05913	0.05541
cg1269862	CCL2	NF-AT1 [	1648	1657	2.756277	TGGAAA	0.05913	0.05541

cg0544082	CCL2	NF-AT1 [	614	623	2.756277	TGGAAA	0.05913	0.05541
cg1269862	CCL2	RXR-alph	272	278	2.726556	GGGTTG	0.85449	0.89683
cg0544082	CCL2	RXR-alph	703	709	2.726556	GGGTTG	0.85449	0.89683
cg1269862	CCL2	NF-Y [T0	515	522	2.673185	ATTGGG	0.21362	0.20842
cg0544082	CCL2	NF-Y [T0	946	953	2.673185	ATTGGG	0.21362	0.20842
cg1269862	CCL2	c-Jun [T00	326	332	2.654872	TGACTC	0.48828	0.48077
cg1269862	CCL2	c-Jun [T00	1774	1780	2.654872	TGACTC	0.48828	0.48077
cg0544082	CCL2	c-Jun [T00	757	763	2.654872	TGACTC	0.48828	0.48077
cg1269862	CCL2	NF-AT1 [	303	311	2.619709	GGAAAG	0.09155	0.08666
cg0544082	CCL2	NF-AT1 [	734	742	2.619709	GGAAAG	0.09155	0.08666
cg0544082	CCL2	NF-AT1 [	300	308	2.595974	GGAAAC	0.09155	0.08666
cg1269862	CCL2	AP-2alpha	469	474	2.550491	GCCTCA	0.48828	0.51216
cg1269862	CCL2	AP-2alpha	609	614	2.550491	GCCTCA	0.48828	0.51216
cg1269862	CCL2	AP-2alpha	1105	1110	2.550491	GCCTCA	0.48828	0.51216
cg0544082	CCL2	AP-2alpha	332	337	2.550491	TGAGGC	0.48828	0.51216
cg0544082	CCL2	AP-2alpha	900	905	2.550491	GCCTCA	0.48828	0.51216
cg0544082	CCL2	AP-2alpha	1040	1045	2.550491	GCCTCA	0.48828	0.51216
cg0544082	CCL2	AP-2alpha	1536	1541	2.550491	GCCTCA	0.48828	0.51216
cg1269862	CCL2	RXR-alph	1057	1063	2.544678	GGGTTC	0.85449	0.89683
cg1269862	CCL2	RXR-alph	1562	1568	2.544678	ATAACC	0.85449	0.89683
cg0544082	CCL2	RXR-alph	1488	1494	2.544678	GGGTTC	0.85449	0.89683
cg0544082	CCL2	RXR-alph	1993	1999	2.544678	ATAACC	0.85449	0.89683
cg1269862	CCL2	c-Jun [T00	888	894	2.538231	TGACTT	0.48828	0.48077
cg0544082	CCL2	c-Jun [T00	1319	1325	2.538231	TGACTT	0.48828	0.48077
cg1269862	CCL2	PXR-1:RX	833	840	2.454225	TGAACT	0.12207	0.11843
cg0544082	CCL2	PXR-1:RX	1264	1271	2.454225	TGAACT	0.12207	0.11843
cg1269862	CCL2	Elk-1 [T00	160	168	2.299314	CCCAGG	0.09155	0.09306
cg1269862	CCL2	Elk-1 [T00	1690	1698	2.299314	CTTCCT	0.09155	0.09306
cg0544082	CCL2	Elk-1 [T00	591	599	2.299314	CCCAGG	0.09155	0.09306
cg1269862	CCL2	GATA-2 [	1150	1158	2.222222	AGATAA	0.22888	0.21978
cg0544082	CCL2	GATA-2 [	1581	1589	2.222222	AGATAA	0.22888	0.21978
cg1269862	CCL2	c-Ets-2 [T	702	710	2.217136	TCTGAG	0.16785	0.16456
cg1269862	CCL2	c-Ets-2 [T	897	905	2.217136	CATGAG	0.16785	0.16456
cg0544082	CCL2	c-Ets-2 [T	1133	1141	2.217136	TCTGAG	0.16785	0.16456
cg0544082	CCL2	c-Ets-2 [T	1328	1336	2.217136	CATGAG	0.16785	0.16456
cg1269862	CCL2	GATA-1 [	133	138	2.176375	TATCCA	3.90625	3.79558
cg0544082	CCL2	GATA-1 [	317	322	2.176375	TGGATA	3.90625	3.79558
cg0544082	CCL2	GATA-1 [	564	569	2.176375	TATCCA	3.90625	3.79558
cg1269862	CCL2	Elk-1 [T00	1429	1437	2.164966	CTTCCT	0.05341	0.05461
cg0544082	CCL2	Elk-1 [T00	1860	1868	2.164966	CTTCCT	0.05341	0.05461
cg1269862	CCL2	c-Ets-2 [T	1827	1835	2.142327	CCAGAG	0.16785	0.16456
cg1269862	CCL2	LEF-1 [T0	16	23	2.004405	AAGCAA	0.18311	0.17215
cg0544082	CCL2	LEF-1 [T0	447	454	2.004405	AAGCAA	0.18311	0.17215
cg0544082	CCL2	NF-AT1 [	225	233	1.970716	GGAAAA	0.06866	0.0623
cg1269862	CCL2	PR B [T00	428	434	1.892895	AAGTGT	0.12207	0.1127
cg1269862	CCL2	PR A [T01	428	434	1.892895	AAGTGT	0.12207	0.1127
cg0544082	CCL2	PR B [T00	859	865	1.892895	AAGTGT	0.12207	0.1127
cg0544082	CCL2	PR A [T01	859	865	1.892895	AAGTGT	0.12207	0.1127

cg1269862	CCL2	AP-2alpha	547	552	1.871933	GGAGGC	0.97656	1.07805
cg1269862	CCL2	AP-2alpha	872	877	1.871933	GCCTCC	0.97656	1.07805
cg1269862	CCL2	AP-2alpha	1440	1445	1.871933	GGAGGC	0.97656	1.07805
cg1269862	CCL2	AP-2alpha	1894	1899	1.871933	GCCTCC	0.97656	1.07805
cg0544082	CCL2	AP-2alpha	978	983	1.871933	GGAGGC	0.97656	1.07805
cg0544082	CCL2	AP-2alpha	1303	1308	1.871933	GCCTCC	0.97656	1.07805
cg0544082	CCL2	AP-2alpha	1871	1876	1.871933	GGAGGC	0.97656	1.07805
cg1269862	CCL2	TBP [T007	457	466	1.871542	TTTATAC	0.18311	0.15671
cg0544082	CCL2	TBP [T007	138	147	1.871542	GGATTA	0.18311	0.15671
cg0544082	CCL2	TBP [T007	888	897	1.871542	TTTATAC	0.18311	0.15671
cg1269862	CCL2	FOXP3 [T	396	401	1.824994	TACAAC	0.48828	0.46414
cg1269862	CCL2	TFII-I [T0	1786	1791	1.824994	CTCTCC	0.48828	0.51201
cg0544082	CCL2	FOXP3 [T	827	832	1.824994	TACAAC	0.48828	0.46414
cg0544082	CCL2	TFII-I [T0	70	75	1.824994	GGAGAG	0.48828	0.51201
cg1269862	CCL2	c-Ets-1 [T	1683	1689	1.769212	TTTCCTA	0.12207	0.11281
cg1269862	CCL2	PXR-1:RX	643	650	1.759733	ACAGTT	0.06104	0.05771
cg0544082	CCL2	PXR-1:RX	1074	1081	1.759733	ACAGTT	0.06104	0.05771
cg1269862	CCL2	p53 [T006	508	514	1.758307	TATGCC	0.36621	0.38097
cg1269862	CCL2	p53 [T006	930	936	1.758307	TCTGCC	0.36621	0.38097
cg1269862	CCL2	p53 [T006	1793	1799	1.758307	TCTGCC	0.36621	0.38097
cg0544082	CCL2	p53 [T006	939	945	1.758307	TATGCC	0.36621	0.38097
cg0544082	CCL2	p53 [T006	1361	1367	1.758307	TCTGCC	0.36621	0.38097
cg1269862	CCL2	RXR-alpha	1666	1672	1.696452	CTGACC	0.48828	0.52093
cg1269862	CCL2	GR-beta [	67	71	1.680765	AATTC	3.90625	3.70067
cg1269862	CCL2	GR-beta [	336	340	1.680765	AATGC	3.90625	3.70067
cg1269862	CCL2	GR-beta [	348	352	1.680765	AATGC	3.90625	3.70067
cg1269862	CCL2	GR-beta [	454	458	1.680765	GCATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	579	583	1.680765	GAATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	658	662	1.680765	GAATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	659	663	1.680765	AATTC	3.90625	3.70067
cg1269862	CCL2	GR-beta [	748	752	1.680765	AATTC	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1163	1167	1.680765	GAATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1238	1242	1.680765	GCATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1304	1308	1.680765	GAATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1305	1309	1.680765	AATTC	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1367	1371	1.680765	GCATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1391	1395	1.680765	AATGC	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1394	1398	1.680765	GCATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1714	1718	1.680765	GCATT	3.90625	3.70067
cg1269862	CCL2	GR-beta [	1867	1871	1.680765	AATTC	3.90625	3.70067
cg0544082	CCL2	GR-beta [	157	161	1.680765	AATGC	3.90625	3.70067
cg0544082	CCL2	GR-beta [	266	270	1.680765	AATTC	3.90625	3.70067
cg0544082	CCL2	GR-beta [	498	502	1.680765	AATTC	3.90625	3.70067
cg0544082	CCL2	GR-beta [	767	771	1.680765	AATGC	3.90625	3.70067
cg0544082	CCL2	GR-beta [	779	783	1.680765	AATGC	3.90625	3.70067
cg0544082	CCL2	GR-beta [	885	889	1.680765	GCATT	3.90625	3.70067
cg0544082	CCL2	GR-beta [	1010	1014	1.680765	GAATT	3.90625	3.70067
cg0544082	CCL2	GR-beta [	1089	1093	1.680765	GAATT	3.90625	3.70067

cg0544082	CCL2	GR-beta [T	1090	1094	1.680765	AATTC	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1179	1183	1.680765	AATTC	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1594	1598	1.680765	GAATT	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1669	1673	1.680765	GCATT	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1735	1739	1.680765	GAATT	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1736	1740	1.680765	AATTC	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1798	1802	1.680765	GCATT	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1822	1826	1.680765	AATGC	3.90625	3.70067
cg0544082	CCL2	GR-beta [T	1825	1829	1.680765	GCATT	3.90625	3.70067
cg1269862	CCL2	c-Ets-1 [T	1002	1008	1.641124	TTTCCTT	0.36621	0.35197
cg0544082	CCL2	c-Ets-1 [T	1433	1439	1.641124	TTTCCTT	0.36621	0.35197
cg1269862	CCL2	C/EBPbeta	129	132	1.639871	CCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	275	278	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	279	282	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	516	519	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	672	675	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	746	749	1.639871	CCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	786	789	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	939	942	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	968	971	1.639871	CCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	984	987	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1158	1161	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1278	1281	1.639871	CCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1412	1415	1.639871	CCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1449	1452	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1631	1634	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1865	1868	1.639871	CCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1959	1962	1.639871	CCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	168	171	1.639871	CCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	235	238	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	316	319	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	382	385	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	560	563	1.639871	CCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	706	709	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	710	713	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	947	950	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1103	1106	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1177	1180	1.639871	CCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1217	1220	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1370	1373	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1399	1402	1.639871	CCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1415	1418	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1589	1592	1.639871	TTGG	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1709	1712	1.639871	CCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1843	1846	1.639871	CCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1880	1883	1.639871	TTGG	15.625	15.23827
cg1269862	CCL2	XBP-1 [T	1229	1234	1.583727	ATGACA	0.97656	0.94995
cg0544082	CCL2	XBP-1 [T	1660	1665	1.583727	ATGACA	0.97656	0.94995

cg0544082	CCL2	NF-AT2 [T	300	309	1.542196	GGAAAC	0.01717	0.01525
cg1269862	CCL2	TFIID [T0	61	67	1.537547	TTTTGTA	0.73242	0.65627
cg1269862	CCL2	TFIID [T0	410	416	1.537547	TTTTACA	0.73242	0.65627
cg1269862	CCL2	TFIID [T0	1648	1654	1.537547	TGGAAA	0.73242	0.65627
cg1269862	CCL2	Pax-5 [T0	518	524	1.537547	GGGCAA	0.73242	0.83087
cg1269862	CCL2	Pax-5 [T0	556	562	1.537547	GGGCTA	0.73242	0.83087
cg0544082	CCL2	TFIID [T0	492	498	1.537547	TTTTGTA	0.73242	0.65627
cg0544082	CCL2	TFIID [T0	841	847	1.537547	TTTTACA	0.73242	0.65627
cg0544082	CCL2	Pax-5 [T0	949	955	1.537547	GGGCAA	0.73242	0.83087
cg0544082	CCL2	Pax-5 [T0	987	993	1.537547	GGGCTA	0.73242	0.83087
cg1269862	CCL2	c-Ets-1 [T	705	711	1.513038	GAGGAA	0.36621	0.35197
cg1269862	CCL2	c-Ets-1 [T	1503	1509	1.513038	TTTCCTC	0.36621	0.35197
cg0544082	CCL2	c-Ets-1 [T	223	229	1.513038	GAGGAA	0.36621	0.35197
cg0544082	CCL2	c-Ets-1 [T	1136	1142	1.513038	GAGGAA	0.36621	0.35197
cg0544082	CCL2	c-Ets-1 [T	1934	1940	1.513038	TTTCCTC	0.36621	0.35197
cg1269862	CCL2	STAT4 [T	67	72	1.470588	AATTCC	1.95312	1.90161
cg1269862	CCL2	STAT4 [T	124	129	1.470588	GGAAAC	1.95312	1.90161
cg1269862	CCL2	STAT4 [T	184	189	1.470588	GGAAAC	1.95312	1.90161
cg1269862	CCL2	STAT4 [T	748	753	1.470588	AATTCC	1.95312	1.90161
cg1269862	CCL2	STAT4 [T	1001	1006	1.470588	GTTTCC	1.95312	1.90161
cg1269862	CCL2	STAT4 [T	1162	1167	1.470588	GGAATT	1.95312	1.90161
cg1269862	CCL2	STAT4 [T	1502	1507	1.470588	GTTTCC	1.95312	1.90161
cg1269862	CCL2	STAT4 [T	1649	1654	1.470588	GGAAAA	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	209	214	1.470588	GTTTCC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	225	230	1.470588	GGAAAA	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	266	271	1.470588	AATTCC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	300	305	1.470588	GGAAAC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	498	503	1.470588	AATTCC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	555	560	1.470588	GGAAAC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	615	620	1.470588	GGAAAC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	1179	1184	1.470588	AATTCC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	1432	1437	1.470588	GTTTCC	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	1593	1598	1.470588	GGAATT	1.95312	1.90161
cg0544082	CCL2	STAT4 [T	1933	1938	1.470588	GTTTCC	1.95312	1.90161
cg1269862	CCL2	NF-AT1 [T	1649	1657	1.437145	GGAAAA	0.00763	0.00705
cg0544082	CCL2	PR B [T00	374	380	1.404665	AACACT	0.36621	0.35143
cg0544082	CCL2	PR A [T01	374	380	1.404665	AACACT	0.36621	0.35143
cg1269862	CCL2	c-Ets-1 [T	122	128	1.384951	CAGGAA	0.36621	0.35197
cg0544082	CCL2	c-Ets-1 [T	553	559	1.384951	CAGGAA	0.36621	0.35197
cg1269862	CCL2	C/EBPbeta	5	8	1.366559	TCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	35	38	1.366559	TTGA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	149	152	1.366559	TCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	343	346	1.366559	TCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	391	394	1.366559	TTGA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	440	443	1.366559	TCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	612	615	1.366559	TCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1079	1082	1.366559	TTGA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1313	1316	1.366559	TCAA	15.625	15.23827

cg1269862	CCL2	C/EBPbeta	1371	1374	1.366559	TTGA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1419	1422	1.366559	TTGA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1773	1776	1.366559	TTGA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1804	1807	1.366559	TCAA	15.625	15.23827
cg1269862	CCL2	C/EBPbeta	1872	1875	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	27	30	1.366559	TTGA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	154	157	1.366559	TTGA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	331	334	1.366559	TTGA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	372	375	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	436	439	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	466	469	1.366559	TTGA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	580	583	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	774	777	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	822	825	1.366559	TTGA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	871	874	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1043	1046	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1510	1513	1.366559	TTGA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1744	1747	1.366559	TCAA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1802	1805	1.366559	TTGA	15.625	15.23827
cg0544082	CCL2	C/EBPbeta	1850	1853	1.366559	TTGA	15.625	15.23827
cg1269862	CCL2	PEA3 [T0	186	194	1.194633	AAACAT	0.06866	0.06787
cg0544082	CCL2	PEA3 [T0	9	17	1.194633	AGGATG	0.06866	0.06787
cg0544082	CCL2	PEA3 [T0	617	625	1.194633	AAACAT	0.06866	0.06787
cg0544082	CCL2	c-Ets-2 [T	220	228	1.145973	TATGAG	0.06104	0.0583
cg1269862	CCL2	GCF [T00	298	306	1.070269	GCGCTG	0.18311	0.21473
cg0544082	CCL2	GCF [T00	729	737	1.070269	GCGCTG	0.18311	0.21473
cg1269862	CCL2	HNF-1A [	599	606	1.069403	CCATTA	0.48828	0.45029
cg0544082	CCL2	HNF-1A [	1030	1037	1.069403	CCATTA	0.48828	0.45029
cg1269862	CCL2	NF-Y [T0	126	133	1.058936	AAACCA	0.12207	0.11765
cg0544082	CCL2	NF-Y [T0	557	564	1.058936	AAACCA	0.12207	0.11765
cg1269862	CCL2	GATA-1 [	623	628	1.038567	TATCAT	1.95312	1.80234
cg0544082	CCL2	GATA-1 [	1054	1059	1.038567	TATCAT	1.95312	1.80234
cg1269862	CCL2	Elk-1 [T00	796	804	0.957025	AGAAGG	0.03052	0.03046
cg0544082	CCL2	Elk-1 [T00	1227	1235	0.957025	AGAAGG	0.03052	0.03046
cg1269862	CCL2	HNF-1A [	1728	1735	0.925521	GATTTA	0.48828	0.45029
cg1269862	CCL2	GATA-1 [	1744	1749	0.863549	TATCAC	1.95312	1.80234
cg1269862	CCL2	RXR-alpha	1850	1856	0.848226	CTAACC	0.48828	0.51313
cg1269862	CCL2	GR-beta [	66	70	0.840383	TAATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [	85	89	0.840383	AATGG	7.8125	7.2174
cg1269862	CCL2	GR-beta [	181	185	0.840383	AATGG	7.8125	7.2174
cg1269862	CCL2	GR-beta [	352	356	0.840383	CCATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [	384	388	0.840383	TCATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [	513	517	0.840383	CCATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [	599	603	0.840383	CCATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [	655	659	0.840383	AATGA	7.8125	7.2174
cg1269862	CCL2	GR-beta [	730	734	0.840383	AATGA	7.8125	7.2174
cg1269862	CCL2	GR-beta [	747	751	0.840383	CAATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [	791	795	0.840383	AATTA	7.8125	7.2174

cg1269862	CCL2	GR-beta [T	886	890	0.840383	AATGA	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	935	939	0.840383	CCATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1133	1137	0.840383	AATTA	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1374	1378	0.840383	AATGA	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1382	1386	0.840383	AATGG	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1601	1605	0.840383	AATGG	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1619	1623	0.840383	CCATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1627	1631	0.840383	TCATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1646	1650	0.840383	AATGG	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1866	1870	0.840383	CAATT	7.8125	7.2174
cg1269862	CCL2	GR-beta [T	1952	1956	0.840383	TCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	24	28	0.840383	CCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	152	156	0.840383	AATTG	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	313	317	0.840383	TCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	325	329	0.840383	AATGG	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	497	501	0.840383	TAATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	516	520	0.840383	AATGG	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	612	616	0.840383	AATGG	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	783	787	0.840383	CCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	815	819	0.840383	TCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	944	948	0.840383	CCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1030	1034	0.840383	CCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1086	1090	0.840383	AATGA	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1161	1165	0.840383	AATGA	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1178	1182	0.840383	CAATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1222	1226	0.840383	AATTA	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1317	1321	0.840383	AATGA	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1366	1370	0.840383	CCATT	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1564	1568	0.840383	AATTA	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1805	1809	0.840383	AATGA	7.8125	7.2174
cg0544082	CCL2	GR-beta [T	1813	1817	0.840383	AATGG	7.8125	7.2174
cg1269862	CCL2	Elk-1 [T00	1511	1519	0.822677	CTTCCTT	0.03052	0.03046
cg0544082	CCL2	Elk-1 [T00	1942	1950	0.822677	CTTCCTT	0.03052	0.03046
cg0544082	CCL2	PXR-1:RX	169	176	0.818075	CAAGTTC	0.12207	0.11843
cg1269862	CCL2	HNF-1A [	252	259	0.781639	GTTTTAA	0.48828	0.45029
cg0544082	CCL2	HNF-1A [	683	690	0.781639	GTTTTAA	0.48828	0.45029
cg1269862	CCL2	GATA-1 [	681	686	0.758539	TATCAG	1.95312	1.80234
cg0544082	CCL2	GATA-1 [	53	58	0.758539	CTGATA	1.95312	1.80234
cg0544082	CCL2	GATA-1 [	216	221	0.758539	CTGATA	1.95312	1.80234
cg0544082	CCL2	GATA-1 [	1112	1117	0.758539	TATCAG	1.95312	1.80234
cg1269862	CCL2	ELF-1 [T0	1687	1699	0.750936	CTACTTC	0.0006	0.0006
cg1269862	CCL2	AP-2alpha	737	742	0.678558	TCAGGC	0.48828	0.51196
cg1269862	CCL2	AP-2alpha	1114	1119	0.678558	GCCTGA	0.48828	0.51196
cg1269862	CCL2	AP-2alpha	1459	1464	0.678558	GCCTGA	0.48828	0.51196
cg1269862	CCL2	AP-2alpha	1482	1487	0.678558	GCCTGA	0.48828	0.51196
cg0544082	CCL2	AP-2alpha	411	416	0.678558	TCAGGC	0.48828	0.51196
cg0544082	CCL2	AP-2alpha	1168	1173	0.678558	TCAGGC	0.48828	0.51196
cg0544082	CCL2	AP-2alpha	1545	1550	0.678558	GCCTGA	0.48828	0.51196

cg0544082	CCL2	AP-2alpha	1890	1895	0.678558	GCCTGA	0.48828	0.51196
cg0544082	CCL2	AP-2alpha	1913	1918	0.678558	GCCTGA	0.48828	0.51196
cg1269862	CCL2	C/EBPalph	1323	1329	0.540941	CACAAT(	0.24414	0.24432
cg0544082	CCL2	C/EBPalph	1754	1760	0.540941	CACAAT(	0.24414	0.24432
cg1269862	CCL2	PR B [T00	642	648	0.48823	AACAGT'	0.12207	0.11255
cg1269862	CCL2	PR A [T01	642	648	0.48823	AACAGT'	0.12207	0.11255
cg0544082	CCL2	PR B [T00	1073	1079	0.48823	AACAGT'	0.12207	0.11255
cg0544082	CCL2	PR A [T01	1073	1079	0.48823	AACAGT'	0.12207	0.11255
cg0544082	CCL2	c-Ets-1 [T(	258	264	0.384261	TAGGAA(	0.24414	0.23743
cg1269862	CCL2	GATA-1 ['	1149	1154	0.280028	TAGATA	0.97656	0.8795
cg0544082	CCL2	GATA-1 ['	1580	1585	0.280028	TAGATA	0.97656	0.8795
cg1269862	CCL2	c-Ets-1 [T(	798	804	0.256174	AAGGAA	0.24414	0.23743
cg1269862	CCL2	c-Ets-1 [T(	1511	1517	0.256174	CTTCCTT	0.24414	0.23743
cg1269862	CCL2	c-Ets-1 [T(	1515	1521	0.256174	CTTCCTT	0.24414	0.23743
cg0544082	CCL2	c-Ets-1 [T(	1229	1235	0.256174	AAGGAA	0.24414	0.23743
cg0544082	CCL2	c-Ets-1 [T(	1942	1948	0.256174	CTTCCTT	0.24414	0.23743
cg0544082	CCL2	c-Ets-1 [T(	1946	1952	0.256174	CTTCCTT	0.24414	0.23743
cg1269862	CCL2	AP-2alpha	1053	1058	0.226186	GCCTGG	0.97656	1.07867
cg0544082	CCL2	AP-2alpha	1484	1489	0.226186	GCCTGG	0.97656	1.07867
cg1269862	CCL2	p53 [T006'	518	524	0.211706	GGGCAA	0.36621	0.40082
cg0544082	CCL2	p53 [T006'	949	955	0.211706	GGGCAA	0.36621	0.40082
cg1269862	CCL2	GR-alpha [	8	12	0.207689	AGAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	480	484	0.207689	CCTTT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	920	924	0.207689	CCTTT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	961	965	0.207689	AGAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1024	1028	0.207689	AGAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1186	1190	0.207689	AAAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1271	1275	0.207689	CCTTT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1518	1522	0.207689	CCTTT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1567	1571	0.207689	CCTCT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1681	1685	0.207689	CCTTT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1783	1787	0.207689	CCTCT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1791	1795	0.207689	CCTCT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1810	1814	0.207689	AGAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1829	1833	0.207689	AGAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1839	1843	0.207689	AGAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1988	1992	0.207689	CCTCT	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	145	149	0.207689	AAAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	181	185	0.207689	AAAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	205	209	0.207689	AGAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	344	348	0.207689	AGAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	391	395	0.207689	AAAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	439	443	0.207689	AGAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	911	915	0.207689	CCTTT	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	1351	1355	0.207689	CCTTT	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	1392	1396	0.207689	AGAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	1455	1459	0.207689	AGAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	1617	1621	0.207689	AAAGG	7.8125	7.79817

cg0544082	CCL2	GR-alpha [	1702	1706	0.207689	CCTTT	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	1949	1953	0.207689	CCTTT	7.8125	7.79817
cg1269862	CCL2	HNF-1A [	1089	1096	0.143882	TATTTA	0.24414	0.20853
cg0544082	CCL2	HNF-1A [	1520	1527	0.143882	TATTTA	0.24414	0.20853
cg1269862	CCL2	PXR-1:RX	1308	1315	0.123583	TCAGTT	0.12207	0.11255
cg0544082	CCL2	PXR-1:RX	1739	1746	0.123583	TCAGTT	0.12207	0.11255
cg1269862	CCL2	GR-beta [	464	468	0	ACATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [	580	584	0	AATTT	3.90625	3.51525
cg1269862	CCL2	GR-beta [	790	794	0	AAATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [	904	908	0	AATGT	3.90625	3.51525
cg1269862	CCL2	GR-beta [	1132	1136	0	AAATT	3.90625	3.51525
cg1269862	CCL2	GR-beta [	1164	1168	0	AATTT	3.90625	3.51525
cg1269862	CCL2	GR-beta [	1315	1319	0	AATGT	3.90625	3.51525
cg1269862	CCL2	GR-beta [	1453	1457	0	AATGT	3.90625	3.51525
cg1269862	CCL2	XBP-1 [T	382	387	0	AGTCAT	0.97656	0.94838
cg1269862	CCL2	XBP-1 [T	887	892	0	ATGACT	0.97656	0.94838
cg1269862	CCL2	TFIID [T0	1556	1562	0	TTAAAA	1.09863	0.95175
cg1269862	CCL2	GR-alpha [	621	625	0	CCTAT	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1045	1049	0	ACAGG	7.8125	7.79817
cg1269862	CCL2	GR-alpha [	1704	1708	0	ACAGG	7.8125	7.79817
cg1269862	CCL2	FOXP3 [T	639	644	0	GACAAC	1.46484	1.44953
cg1269862	CCL2	FOXP3 [T	719	724	0	CACAAC	1.46484	1.44953
cg1269862	CCL2	PR B [T00	379	385	0	AACAGT	0.36621	0.35051
cg1269862	CCL2	PR A [T01	379	385	0	AACAGT	0.36621	0.35051
cg1269862	CCL2	HNF-3alph	1557	1564	0	TAAAAA	0.09155	0.07727
cg1269862	CCL2	C/EBPbeta	14	17	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	18	21	0	GCAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	40	43	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	63	66	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	239	242	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	346	349	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	388	391	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	397	400	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	414	417	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	467	470	0	TTGC	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	505	508	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	520	523	0	GCAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	531	534	0	GCAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	631	634	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	640	643	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	720	723	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	841	844	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	866	869	0	GCAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	976	979	0	GCAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	993	996	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1112	1115	0	TTGC	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1138	1141	0	GCAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1182	1185	0	TTGT	15.625	15.26275

cg1269862	CCL2	C/EBPbeta	1274	1277	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1324	1327	0	ACAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1379	1382	0	GCAA	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1397	1400	0	TTGT	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1623	1626	0	TTGC	15.625	15.26275
cg1269862	CCL2	C/EBPbeta	1718	1721	0	TTGC	15.625	15.26275
cg1269862	CCL2	YY1 [T00	86	89	0	ATGG	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	95	98	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	136	139	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	182	185	0	ATGG	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	319	322	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	352	355	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	450	453	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	513	516	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	599	602	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	820	823	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	896	899	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	935	938	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	1383	1386	0	ATGG	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	1602	1605	0	ATGG	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	1610	1613	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	1619	1622	0	CCAT	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	1647	1650	0	ATGG	7.8125	7.79459
cg1269862	CCL2	YY1 [T00	1752	1755	0	ATGG	7.8125	7.79459
cg1269862	CCL2	TFII-I [T0	303	308	0	GGAAAG	1.46484	1.48598
cg1269862	CCL2	TFII-I [T0	742	747	0	CTTTCC	1.46484	1.48598
cg1269862	CCL2	TFII-I [T0	953	958	0	GGACAG	1.46484	1.48598
cg1269862	CCL2	TFII-I [T0	1043	1048	0	GGACAG	1.46484	1.48598
cg1269862	CCL2	TFII-I [T0	1682	1687	0	CTTTCC	1.46484	1.48598
cg1269862	CCL2	STAT4 [T	707	712	0	GGAAAT	0.48828	0.46235
cg1269862	CCL2	STAT4 [T	788	793	0	GGAAAT	0.48828	0.46235
cg1269862	CCL2	STAT4 [T	1696	1701	0	GGAAAT	0.48828	0.46235
cg1269862	CCL2	c-Ets-1 [T	162	168	0	CAGGAA	0.24414	0.24982
cg1269862	CCL2	c-Ets-1 [T	1429	1435	0	CTTCCTC	0.24414	0.24982
cg1269862	CCL2	c-Ets-1 [T	1690	1696	0	CTTCCTC	0.24414	0.24982
cg1269862	CCL2	ER-alpha [	359	363	0	TGACC	1.95312	1.99744
cg1269862	CCL2	ER-alpha [	476	480	0	TGACC	1.95312	1.99744
cg1269862	CCL2	ER-alpha [	1586	1590	0	GGTCA	1.95312	1.99744
cg1269862	CCL2	ER-alpha [	1667	1671	0	TGACC	1.95312	1.99744
cg1269862	CCL2	RXR-alpha	1092	1098	0	TTAACC	0.24414	0.24342
cg1269862	CCL2	TCF-4E [T	17	23	0	AGCAAA	0.12207	0.11933
cg1269862	CCL2	GR [T050	59	65	0	CTTTTTG	0.36621	0.33174
cg1269862	CCL2	PXR-1:RX	1571	1578	0	TTAGTT	0.12207	0.11255
cg1269862	CCL2	Pax-5 [T0	26	32	0	GGGCTC	1.09863	1.24633
cg1269862	CCL2	Pax-5 [T0	289	295	0	GGGCAG	1.09863	1.24633
cg1269862	CCL2	Pax-5 [T0	1963	1969	0	GGGCTC	1.09863	1.24633
cg1269862	CCL2	p53 [T006	289	295	0	GGGCAG	0.36621	0.40082
cg1269862	CCL2	AP-2alpha	291	296	0	GCAGGC	0.97656	1.07867

cg1269862	CCL2	AP-2alpha	853	858	0	GCCTGC	0.97656	1.07867
cg1269862	CCL2	AP-2alpha	972	977	0	GCAGGC	0.97656	1.07867
cg1269862	CCL2	AP-2alpha	1083	1088	0	GCAGGC	0.97656	1.07867
cg1269862	CCL2	AP-2alpha	1928	1933	0	GCCTGC	0.97656	1.07867
cg1269862	CCL2	STAT1bet	1692	1701	0	TCCTGG	0.01717	0.01622
cg1269862	CCL2	HNF-1A [	1174	1181	0	GTTAAT	0.24414	0.20853
cg0544082	CCL2	GR-beta [T	151	155	0	AAATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	265	269	0	AAATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	304	308	0	ACATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	895	899	0	ACATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1011	1015	0	AATTT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1221	1225	0	AAATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1335	1339	0	AATGT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1563	1567	0	AAATT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1595	1599	0	AATTT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1746	1750	0	AATGT	3.90625	3.51525
cg0544082	CCL2	GR-beta [T	1884	1888	0	AATGT	3.90625	3.51525
cg0544082	CCL2	XBP-1 [T	58	63	0	ATGACT	0.97656	0.94838
cg0544082	CCL2	XBP-1 [T	132	137	0	ATGACT	0.97656	0.94838
cg0544082	CCL2	XBP-1 [T	813	818	0	AGTCAT	0.97656	0.94838
cg0544082	CCL2	XBP-1 [T	1318	1323	0	ATGACT	0.97656	0.94838
cg0544082	CCL2	TFIID [T0	1987	1993	0	TTAAAA	1.09863	0.95175
cg0544082	CCL2	GR-alpha [	7	11	0	ACAGG	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	1052	1056	0	CCTAT	7.8125	7.79817
cg0544082	CCL2	GR-alpha [	1476	1480	0	ACAGG	7.8125	7.79817
cg0544082	CCL2	IRF-1 [T0	145	153	0	AAAGGG	0.00763	0.00712
cg0544082	CCL2	FOXP3 [T	1070	1075	0	GACAAC	1.46484	1.44953
cg0544082	CCL2	FOXP3 [T	1150	1155	0	CACAAC	1.46484	1.44953
cg0544082	CCL2	PR B [T00	810	816	0	AACAGT	0.36621	0.35051
cg0544082	CCL2	PR A [T01	810	816	0	AACAGT	0.36621	0.35051
cg0544082	CCL2	HNF-3alph	1988	1995	0	TAAAAA	0.09155	0.07727
cg0544082	CCL2	C/EBPbeta	106	109	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	275	278	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	281	284	0	TTGC	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	355	358	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	420	423	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	445	448	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	449	452	0	GCAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	471	474	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	494	497	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	670	673	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	777	780	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	819	822	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	828	831	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	845	848	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	898	901	0	TTGC	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	936	939	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	951	954	0	GCAA	15.625	15.26275

cg0544082	CCL2	C/EBPbeta	962	965	0	GCAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1062	1065	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1071	1074	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1151	1154	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1272	1275	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1297	1300	0	GCAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1407	1410	0	GCAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1424	1427	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1543	1546	0	TTGC	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1569	1572	0	GCAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1613	1616	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1705	1708	0	TTGT	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1755	1758	0	ACAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1810	1813	0	GCAA	15.625	15.26275
cg0544082	CCL2	C/EBPbeta	1828	1831	0	TTGT	15.625	15.26275
cg0544082	CCL2	YY1 [T00	24	27	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	176	179	0	ATGG	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	252	255	0	ATGG	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	326	329	0	ATGG	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	517	520	0	ATGG	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	526	529	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	567	570	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	613	616	0	ATGG	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	750	753	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	783	786	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	881	884	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	944	947	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	1030	1033	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	1251	1254	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	1327	1330	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	1366	1369	0	CCAT	7.8125	7.79459
cg0544082	CCL2	YY1 [T00	1814	1817	0	ATGG	7.8125	7.79459
cg0544082	CCL2	C/EBPalph	329	335	0	GATTGA	0.24414	0.24342
cg0544082	CCL2	TFII-I [T0	734	739	0	GGAAAG	1.46484	1.48598
cg0544082	CCL2	TFII-I [T0	1173	1178	0	CTTTCC	1.46484	1.48598
cg0544082	CCL2	TFII-I [T0	1384	1389	0	GGACAG	1.46484	1.48598
cg0544082	CCL2	TFII-I [T0	1474	1479	0	GGACAG	1.46484	1.48598
cg0544082	CCL2	STAT4 [T	149	154	0	GGAAAT	0.48828	0.46235
cg0544082	CCL2	STAT4 [T	1138	1143	0	GGAAAT	0.48828	0.46235
cg0544082	CCL2	STAT4 [T	1219	1224	0	GGAAAT	0.48828	0.46235
cg0544082	CCL2	c-Ets-1 [T	593	599	0	CAGGAA	0.24414	0.24982
cg0544082	CCL2	c-Ets-1 [T	1860	1866	0	CTTCCT	0.24414	0.24982
cg0544082	CCL2	ER-alpha [	790	794	0	TGACC	1.95312	1.99744
cg0544082	CCL2	ER-alpha [	907	911	0	TGACC	1.95312	1.99744
cg0544082	CCL2	RXR-alpha	1523	1529	0	TTAACC	0.24414	0.24342
cg0544082	CCL2	TCF-4E [T	448	454	0	AGCAAA	0.12207	0.11933
cg0544082	CCL2	GR [T050	490	496	0	CTTTTTG	0.36621	0.33174
cg0544082	CCL2	Pax-5 [T0	457	463	0	GGGCTC	1.09863	1.24633

cg0544082	CCL2	Pax-5 [T0	720	726	0	GGGCAG	1.09863	1.24633
cg0544082	CCL2	p53 [T006	720	726	0	GGGCAG	0.36621	0.40082
cg0544082	CCL2	AP-2alpha	722	727	0	GCAGGC	0.97656	1.07867
cg0544082	CCL2	AP-2alpha	1284	1289	0	GCCTGC	0.97656	1.07867
cg0544082	CCL2	AP-2alpha	1403	1408	0	GCAGGC	0.97656	1.07867
cg0544082	CCL2	AP-2alpha	1514	1519	0	GCAGGC	0.97656	1.07867
cg0544082	CCL2	HNF-1A [	1605	1612	0	GTTAAT	0.24414	0.20853
cg1742692	CREM	NF-AT2 [	1197	1206	9.999272	GGAAAA	0.08774	0.08903
cg1742692	CREM	STAT5A [	933	945	9.952027	CAATTT	0.01878	0.01918
cg1742692	CREM	AhR [T01	995	1005	9.931384	GTAGGC	0.00858	0.00849
cg1742692	CREM	HOXD9 [	1215	1224	9.802084	CAGTCA	0.2327	0.24089
cg1742692	CREM	HOXD9 [	1228	1237	9.802084	GAGTGG	0.2327	0.24089
cg1742692	CREM	HOXD10 [	1215	1224	9.802084	CAGTCA	0.2327	0.24089
cg1742692	CREM	HOXD10 [	1228	1237	9.802084	GAGTGG	0.2327	0.24089
cg1742692	CREM	XBP-1 [T0	320	325	9.789909	ATGGCT	1.95312	1.95208
cg1742692	CREM	XBP-1 [T0	812	817	9.789909	ATGGCT	1.95312	1.95208
cg1742692	CREM	XBP-1 [T0	1413	1418	9.789909	AGCCAT	1.95312	1.95208
cg1742692	CREM	XBP-1 [T0	1495	1500	9.789909	AGCCAT	1.95312	1.95208
cg1742692	CREM	XBP-1 [T0	1703	1708	9.789909	ATGTCT	1.95312	1.95208
cg1742692	CREM	XBP-1 [T0	1962	1967	9.789909	CGCCAT	1.95312	1.95208
cg1742692	CREM	NF-1 [T00	1073	1080	9.761671	GGCACC	0.24414	0.24405
cg1742692	CREM	PR B [T00	13	19	9.743489	TGGTGT	1.09863	1.10292
cg1742692	CREM	PR B [T00	265	271	9.743489	TCGTGT	1.09863	1.10292
cg1742692	CREM	PR B [T00	1725	1731	9.743489	CTGTGT	1.09863	1.10292
cg1742692	CREM	PR B [T00	1811	1817	9.743489	AACACA	1.09863	1.10292
cg1742692	CREM	PR A [T01	13	19	9.743489	TGGTGT	1.09863	1.10292
cg1742692	CREM	PR A [T01	265	271	9.743489	TCGTGT	1.09863	1.10292
cg1742692	CREM	PR A [T01	1725	1731	9.743489	CTGTGT	1.09863	1.10292
cg1742692	CREM	PR A [T01	1811	1817	9.743489	AACACA	1.09863	1.10292
cg1742692	CREM	LEF-1 [T0	171	178	9.72404	AGGCAA	0.21362	0.2139
cg1742692	CREM	LEF-1 [T0	546	553	9.72404	AGACAA	0.21362	0.2139
cg1742692	CREM	EBF [T05	451	461	9.678925	ACACCA	0.06866	0.06676
cg1742692	CREM	HNF-1C [	1254	1262	9.601936	AACAAT	0.19836	0.20229
cg1742692	CREM	Pax-5 [T0	1372	1378	9.552105	GGGCCA	1.46484	1.43083
cg1742692	CREM	TFIID [T0	657	663	9.552105	TTTGGG	1.46484	1.48472
cg1742692	CREM	TFIID [T0	1177	1183	9.552105	TTTGTCA	1.46484	1.48472
cg1742692	CREM	TFIID [T0	1184	1190	9.552105	TTTCTCA	1.46484	1.48472
cg1742692	CREM	TFII-I [T0	393	398	9.512894	GGAAAA	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	399	404	9.512894	GTGTCC	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	474	479	9.512894	GGAATT	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	702	707	9.512894	CCATCC	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	1164	1169	9.512894	GTATCC	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	1197	1202	9.512894	GGAAAA	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	1462	1467	9.512894	CCTTCC	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	1503	1508	9.512894	TTTTCC	7.32422	7.29728
cg1742692	CREM	TFII-I [T0	1611	1616	9.512894	GTGTCC	7.32422	7.29728
cg1742692	CREM	FOXP3 [T	213	218	9.512894	GTTTAC	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	359	364	9.512894	GTTCTG	7.32422	7.35678

cg1742692	CREM	FOXP3 [T	501	506	9.512894	GTTATT	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	514	519	9.512894	CATAAC	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	908	913	9.512894	AAGAAC	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	960	965	9.512894	GTTTAT	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	1257	1262	9.512894	AATAAC	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	1421	1426	9.512894	GTTATT	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	1655	1660	9.512894	GTTGCC	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	1658	1663	9.512894	GCCAAC	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	1722	1727	9.512894	GTTCTG	7.32422	7.35678
cg1742692	CREM	FOXP3 [T	1808	1813	9.512894	ATAAAC	7.32422	7.35678
cg1742692	CREM	Ik-1 [T027	781	793	9.497194	TCCCAG	0.02941	0.02907
cg1742692	CREM	TCF-4E [T	21	27	9.453578	CTCAAA	0.48828	0.49215
cg1742692	CREM	TCF-4E [T	123	129	9.453578	CTTTGA	0.48828	0.49215
cg1742692	CREM	TCF-4E [T	1481	1487	9.453578	CTTTGA	0.48828	0.49215
cg1742692	CREM	NFI/CTF [	8	15	9.352332	ATCATT	0.54932	0.54821
cg1742692	CREM	NFI/CTF [	116	123	9.352332	CCAAGG	0.54932	0.54821
cg1742692	CREM	NFI/CTF [	343	350	9.352332	CCAAAG	0.54932	0.54821
cg1742692	CREM	c-Myb [T0	956	963	9.29064	GGTAGT	0.36621	0.37054
cg1742692	CREM	c-Myb [T0	1016	1023	9.29064	GGTAGT	0.36621	0.37054
cg1742692	CREM	AP-1 [T00	1424	1432	9.256161	ATTCAG	0.09155	0.09305
cg1742692	CREM	VDR [T00	1699	1707	9.234242	GTTCAT	0.12207	0.12335
cg1742692	CREM	MEF-2A [	733	743	9.220261	TACTAA	0.07343	0.07563
cg1742692	CREM	LEF-1 [T0	123	130	9.082175	CTTTGA	0.54932	0.55326
cg1742692	CREM	LEF-1 [T0	1481	1488	9.082175	CTTTGA	0.54932	0.55326
cg1742692	CREM	AhR [T01	852	862	9.058053	ATCACG	0.03242	0.03229
cg1742692	CREM	AhR [T01	1958	1968	9.058053	TTCACG	0.03242	0.03229
cg1742692	CREM	LEF-1 [T0	656	663	8.973041	CTTTGG	0.54932	0.55326
cg1742692	CREM	GR [T050	1078	1084	8.971049	CAAAAG	0.61035	0.61632
cg1742692	CREM	c-Myb [T0	945	952	8.947824	AGAAGT	0.39673	0.40028
cg1742692	CREM	T3R-beta1	713	721	8.924046	AATGGG	0.2594	0.25766
cg1742692	CREM	AP-1 [T00	135	143	8.915609	AGTAAG	0.24414	0.24693
cg1742692	CREM	c-Ets-2 [T	1464	1472	8.912323	TTCCTG	0.27466	0.27495
cg1742692	CREM	AP-1 [T00	106	114	8.862731	TGACTT	0.24414	0.24693
cg1742692	CREM	c-Jun [T00	684	690	8.832178	AAGGTC	0.61035	0.61059
cg1742692	CREM	NFI/CTF [	1667	1674	8.814757	TCATTT	0.48828	0.48804
cg1742692	CREM	c-Ets-1 [T	472	478	8.809329	CTGGAA	0.85449	0.85523
cg1742692	CREM	NF-1 [T00	658	665	8.790071	TTGGGA	0.24414	0.24467
cg1742692	CREM	NF-1 [T00	1300	1307	8.790071	TTGGCA	0.24414	0.24467
cg1742692	CREM	LEF-1 [T0	37	44	8.759086	ACACAA	0.54932	0.55326
cg1742692	CREM	XBP-1 [T	92	97	8.75604	ATGATA	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	429	434	8.75604	ATGAGC	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	584	589	8.75604	TATCAT	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	1293	1298	8.75604	GATCAT	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	1526	1531	8.75604	TATCAT	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	1665	1670	8.75604	TTTCAT	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	1692	1697	8.75604	ATGAGC	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	1699	1704	8.75604	GTTCAT	2.92969	2.9674
cg1742692	CREM	XBP-1 [T	1923	1928	8.75604	ATGATC	2.92969	2.9674

cg1742692	CREM	c-Jun [T00	1214	1220	8.571705	CCAGTC/	0.12207	0.12139
cg1742692	CREM	c-Ets-1 [T(	1045	1051	8.501115	TTGGAA(	0.24414	0.24529
cg1742692	CREM	LEF-1 [T0	20	27	8.457856	CCTCAA/	0.15259	0.15214
cg1742692	CREM	PR B [T00	286	292	8.338824	CTCTGTT	1.09863	1.10009
cg1742692	CREM	PR B [T00	322	328	8.338824	GGCTGT"	1.09863	1.10009
cg1742692	CREM	PR B [T00	1841	1847	8.338824	TGCTGTT	1.09863	1.10009
cg1742692	CREM	PR A [T01	286	292	8.338824	CTCTGTT	1.09863	1.10009
cg1742692	CREM	PR A [T01	322	328	8.338824	GGCTGT"	1.09863	1.10009
cg1742692	CREM	PR A [T01	1841	1847	8.338824	TGCTGTT	1.09863	1.10009
cg1742692	CREM	ATF3 [T01	588	595	8.313799	ATATGT(	0.27466	0.27431
cg1742692	CREM	PXR-1:RX	1445	1452	8.304332	ACCGTT(	0.12207	0.12266
cg1742692	CREM	GR-alpha [	49	53	8.281568	CCTTG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	117	121	8.281568	CAAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	293	297	8.281568	GAAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	419	423	8.281568	CCTTC	7.8125	7.72956
cg1742692	CREM	GR-alpha [	423	427	8.281568	CAAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	661	665	8.281568	GGAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	667	671	8.281568	CAAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	683	687	8.281568	CAAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	794	798	8.281568	GGAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	826	830	8.281568	GGAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1150	1154	8.281568	CCTCC	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1367	1371	8.281568	CCTTC	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1462	1466	8.281568	CCTTC	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1578	1582	8.281568	GGAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1593	1597	8.281568	CCTTG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1761	1765	8.281568	CAAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1910	1914	8.281568	GGAGG	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1949	1953	8.281568	CCTCC	7.8125	7.72956
cg1742692	CREM	GR-alpha [	1981	1985	8.281568	CCTCC	7.8125	7.72956
cg1742692	CREM	NF-AT2 [T	1499	1508	8.21356	ATTTTTT	0.08965	0.09068
cg1742692	CREM	ENKTF-1	619	626	8.19852	TGGCCA(	0.73242	0.71737
cg1742692	CREM	ENKTF-1	765	772	8.19852	TGGCGG(	0.73242	0.71737
cg1742692	CREM	NF-1 [T00	662	669	8.191058	GAGGCC.	0.24414	0.24409
cg1742692	CREM	AhR [T01'	635	645	8.184723	CTCACG(	0.04864	0.04833
cg1742692	CREM	SRY [T00!	36	44	8.174786	CACACA.	0.15259	0.15383
cg1742692	CREM	IRF-1 [T0(	113	121	8.151819	TTTCCA/	0.25177	0.25263
cg1742692	CREM	c-Jun [T00	1110	1116	8.128539	AATGTC/	0.48828	0.49076
cg1742692	CREM	c-Ets-1 [T(	1132	1138	8.116854	GTTCCA(	0.24414	0.2425
cg1742692	CREM	VDR [T00	1448	1456	8.079962	GTTCAG(	0.24414	0.24712
cg1742692	CREM	GR-alpha [	230	234	8.073878	CCTGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	234	238	8.073878	GCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	278	282	8.073878	GTAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	384	388	8.073878	CTAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	454	458	8.073878	CCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	471	475	8.073878	CCTGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	622	626	8.073878	CCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	706	710	8.073878	CCTGG	7.8125	7.72238

cg1742692	CREM	GR-alpha [	804	808	8.073878	GCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	822	826	8.073878	CCTGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	839	843	8.073878	GCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	872	876	8.073878	CCTGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	995	999	8.073878	GTAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1135	1139	8.073878	CCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1168	1172	8.073878	CCTAG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1194	1198	8.073878	GCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1209	1213	8.073878	GTAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1303	1307	8.073878	GCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1390	1394	8.073878	CCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1615	1619	8.073878	CCTGC	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1619	1623	8.073878	CTAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1627	1631	8.073878	GTAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1903	1907	8.073878	CCAGG	7.8125	7.72238
cg1742692	CREM	GR-alpha [	1971	1975	8.073878	CCTGC	7.8125	7.72238
cg1742692	CREM	Pax-5 [T0	338	344	8.014558	TCTGCC	2.19727	2.14502
cg1742692	CREM	Pax-5 [T0	511	517	8.014558	GGGCAT	2.19727	2.14502
cg1742692	CREM	Pax-5 [T0	673	679	8.014558	GGGCAG	2.19727	2.14502
cg1742692	CREM	Pax-5 [T0	769	775	8.014558	GGGCAC	2.19727	2.14502
cg1742692	CREM	Pax-5 [T0	875	881	8.014558	GGGCAG	2.19727	2.14502
cg1742692	CREM	Pax-5 [T0	1072	1078	8.014558	GGGCAC	2.19727	2.14502
cg1742692	CREM	TFIID [T0	2	8	8.014558	TTGGAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	113	119	8.014558	TTTCCA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	222	228	8.014558	TTAGAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	896	902	8.014558	TCTCAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	975	981	8.014558	TAAGAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	1119	1125	8.014558	TCAGAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	1247	1253	8.014558	TAGCAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	1259	1265	8.014558	TAACAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	1433	1439	8.014558	TCAGAA	2.19727	2.24348
cg1742692	CREM	TFIID [T0	1877	1883	8.014558	TTTGAG	2.19727	2.24348
cg1742692	CREM	MEF-2A [	1238	1248	7.982343	ACTTAA	0.04005	0.04149
cg1742692	CREM	p53 [T006	1931	1937	7.853573	GGGCCA	0.48828	0.47377
cg1742692	CREM	RXR-alpha	955	961	7.815913	GGGTAG	0.24414	0.24104
cg1742692	CREM	c-Jun [T00	522	528	7.686747	TGACTG	0.48828	0.48775
cg1742692	CREM	c-Jun [T00	1127	1133	7.686747	TGACTG	0.48828	0.48775
cg1742692	CREM	AR [T000	1383	1391	7.683535	TACATG	0.25177	0.25079
cg1742692	CREM	LEF-1 [T0	341	348	7.6105	GCCCAA	0.21362	0.21302
cg1742692	CREM	NFI/CTF [	1077	1084	7.587343	CCAAAA	0.36621	0.36674
cg1742692	CREM	GR [T050	549	555	7.527031	CAAAGC	1.83105	1.86007
cg1742692	CREM	GR [T050	744	750	7.527031	CAAACA	1.83105	1.86007
cg1742692	CREM	GR [T050	1296	1302	7.527031	CATTTC	1.83105	1.86007
cg1742692	CREM	GR [T050	1572	1578	7.527031	ATATTC	1.83105	1.86007
cg1742692	CREM	GR [T050	1649	1655	7.527031	AGCTTTC	1.83105	1.86007
cg1742692	CREM	GR [T050	1777	1783	7.527031	TATTTC	1.83105	1.86007
cg1742692	CREM	GR [T050	1892	1898	7.527031	CGCTTTC	1.83105	1.86007
cg1742692	CREM	C/EBPalph	1935	1941	7.465744	CATTGCA	0.48828	0.49653

cg1742692	CREM	PEA3 [T0	700	708	7.421728	GACCAT	0.34332	0.34161
cg1742692	CREM	LEF-1 [T0	1037	1044	7.396545	CTTTGTC	0.21362	0.21302
cg1742692	CREM	C/EBPalph	931	937	7.396431	TCCAATT	0.48828	0.49653
cg1742692	CREM	HOXD9 [T	1257	1266	7.270719	AATAAC	0.06866	0.07152
cg1742692	CREM	HOXD9 [T	1819	1828	7.270719	AATATA	0.06866	0.07152
cg1742692	CREM	HOXD10 [	1257	1266	7.270719	AATAAC	0.06866	0.07152
cg1742692	CREM	HOXD10 [	1819	1828	7.270719	AATATA	0.06866	0.07152
cg1742692	CREM	c-Ets-2 [T	1192	1200	7.268173	CAGCAG	0.09155	0.09191
cg1742692	CREM	SRY [T00	545	553	7.175614	GAGACA	0.30518	0.30739
cg1742692	CREM	SRY [T00	1894	1902	7.175614	CTTTGTC	0.30518	0.30739
cg1742692	CREM	XBP-1 [T	7	12	7.172312	AATCAT	2.92969	2.97018
cg1742692	CREM	XBP-1 [T	88	93	7.172312	ACTCAT	2.92969	2.97018
cg1742692	CREM	XBP-1 [T	146	151	7.172312	ATGAAT	2.92969	2.97018
cg1742692	CREM	XBP-1 [T	168	173	7.172312	ATGAGG	2.92969	2.97018
cg1742692	CREM	XBP-1 [T	410	415	7.172312	CCTCAT	2.92969	2.97018
cg1742692	CREM	XBP-1 [T	507	512	7.172312	ATGAGG	2.92969	2.97018
cg1742692	CREM	XBP-1 [T	1519	1524	7.172312	ATTCAT	2.92969	2.97018
cg1742692	CREM	XBP-1 [T	1540	1545	7.172312	ATGAAG	2.92969	2.97018
cg1742692	CREM	NF-AT1 [	393	401	7.095752	GGAAAA	0.15259	0.1548
cg1742692	CREM	TFIID [T0	1746	1752	7.082373	TTTAGC	0.12207	0.12407
cg1742692	CREM	NF-AT1 [	109	117	7.072017	CTTATT	0.15259	0.1548
cg1742692	CREM	IRF-1 [T0	389	397	7.044985	GAGAGG	0.1297	0.13036
cg1742692	CREM	NF-AT2 [	4	13	7.008591	GGAAAT	0.04578	0.04634
cg1742692	CREM	HNF-3alph	54	61	7.000129	AAAAAA	0.82397	0.84946
cg1742692	CREM	HNF-3alph	111	118	7.000129	TATTTCC	0.82397	0.84946
cg1742692	CREM	HNF-3alph	529	536	7.000129	GATTTTT	0.82397	0.84946
cg1742692	CREM	HNF-3alph	1573	1580	7.000129	TATTTGC	0.82397	0.84946
cg1742692	CREM	HNF-3alph	1771	1778	7.000129	GAAAAA	0.82397	0.84946
cg1742692	CREM	HNF-4alph	1029	1041	6.981736	CTTTAGA	0.00626	0.00637
cg1742692	CREM	NF-1 [T00	843	850	6.948522	GGAGCC	0.48828	0.4856
cg1742692	CREM	ENKTF-1	853	860	6.942764	TCACGCC	1.46484	1.44228
cg1742692	CREM	ENKTF-1	1055	1062	6.942764	CTTAGCC	1.46484	1.44228
cg1742692	CREM	ENKTF-1	1410	1417	6.942764	CACAGC	1.46484	1.44228
cg1742692	CREM	ENKTF-1	1959	1966	6.942764	TCACGCC	1.46484	1.44228
cg1742692	CREM	C/EBPalph	183	189	6.85549	TGCAAT	0.73242	0.74337
cg1742692	CREM	C/EBPalph	1684	1690	6.85549	AATTGCA	0.73242	0.74337
cg1742692	CREM	HNF-1B [	1420	1428	6.831535	GGTTATT	0.07629	0.07762
cg1742692	CREM	NFI/CTF [	1375	1382	6.786076	CCAAAC	0.73242	0.73214
cg1742692	CREM	TCF-4 [T0	122	131	6.735684	TCTTTGA	0.04959	0.05016
cg1742692	CREM	TCF-4 [T0	1480	1489	6.735684	TCTTTGA	0.04959	0.05016
cg1742692	CREM	POU2F2 (	1027	1037	6.735173	TGCTTTA	0.04292	0.04408
cg1742692	CREM	NF-1 [T00	339	346	6.722386	CTGCCCA	0.24414	0.24147
cg1742692	CREM	HNF-1C [	1421	1429	6.678556	GTTATTC	0.05341	0.05475
cg1742692	CREM	PXR-1:RX	1726	1733	6.668182	TGTGTTC	0.24414	0.24672
cg1742692	CREM	TFII-I [T0	252	257	6.581441	GGAGTG	0.97656	0.97366
cg1742692	CREM	TFII-I [T0	316	321	6.581441	GGAGAT	0.97656	0.97366
cg1742692	CREM	TFII-I [T0	691	696	6.581441	GGAGAT	0.97656	0.97366
cg1742692	CREM	TFII-I [T0	864	869	6.581441	CACTCC	0.97656	0.97366

cg1742692	CREM	TFII-I [T0	928	933	6.581441	ATCTCC	0.97656	0.97366
cg1742692	CREM	FOXP3 [T	62	67	6.581441	GTTTTA	0.97656	0.99397
cg1742692	CREM	FOXP3 [T	290	295	6.581441	GTTGAA	0.97656	0.99397
cg1742692	CREM	NF-AT1 [	1197	1205	6.562181	GGAAAA	0.03815	0.03835
cg1742692	CREM	PPAR-alp	778	788	6.51544	TAGTCC	0.03719	0.03639
cg1742692	CREM	XBP-1 [T	511	516	6.478682	GGGCAT	0.97656	0.97062
cg1742692	CREM	XBP-1 [T	1919	1924	6.478682	TGGCAT	0.97656	0.97062
cg1742692	CREM	c-Fos [T00	122	131	6.448203	TCTTTGA	0.04578	0.04589
cg1742692	CREM	c-Ets-1 [T	2	8	6.423689	TTGGAA	0.48828	0.48798
cg1742692	CREM	c-Ets-1 [T	113	119	6.423689	TTTCCA	0.48828	0.48798
cg1742692	CREM	RAR-beta	718	727	6.415195	GTGAAA	0.18311	0.183
cg1742692	CREM	p53 [T006	1898	1904	6.400205	GTCGCC	0.48828	0.47541
cg1742692	CREM	TCF-4E [T	172	178	6.302385	GGCAAA	0.61035	0.61344
cg1742692	CREM	TCF-4E [T	1651	1657	6.302385	CTTTGTT	0.61035	0.61344
cg1742692	CREM	TCF-4E [T	1715	1721	6.302385	CTTTGTT	0.61035	0.61344
cg1742692	CREM	GR-alpha [	20	24	6.263098	CCTCA	3.90625	3.91061
cg1742692	CREM	GR-alpha [	169	173	6.263098	TGAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	313	317	6.263098	TGAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	410	414	6.263098	CCTCA	3.90625	3.91061
cg1742692	CREM	GR-alpha [	508	512	6.263098	TGAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	800	804	6.263098	TGAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1002	1006	6.263098	TGAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1013	1017	6.263098	TGAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1087	1091	6.263098	TAAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1102	1106	6.263098	CCTTA	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1283	1287	6.263098	CCTCA	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1600	1604	6.263098	TAAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1782	1786	6.263098	TGAGG	3.90625	3.91061
cg1742692	CREM	GR-alpha [	1975	1979	6.263098	CCTCA	3.90625	3.91061
cg1742692	CREM	TCF-4 [T0	19	28	6.262917	TCCTCA	0.04959	0.05016
cg1742692	CREM	c-Myb [T0	1023	1030	6.259888	TAACTG	0.30518	0.3056
cg1742692	CREM	c-Myb [T0	1359	1366	6.259888	TGCAGT	0.30518	0.3056
cg1742692	CREM	c-Myb [T0	1695	1702	6.259888	AGCAGT	0.30518	0.3056
cg1742692	CREM	SRY [T00	1037	1045	6.176442	CTTTGTC	0.15259	0.15366
cg1742692	CREM	c-Jun [T00	1177	1183	6.152811	TTTGTCA	0.36621	0.37082
cg1742692	CREM	p53 [T006	1372	1378	6.095267	GGGCCA	0.61035	0.594
cg1742692	CREM	IRF-1 [T0	0	8	6.078807	AGTTGG	0.16785	0.16909
cg1742692	CREM	GR-alpha [	301	305	6.055408	TCAGG	3.90625	3.9065
cg1742692	CREM	GR-alpha [	688	692	6.055408	TCAGG	3.90625	3.9065
cg1742692	CREM	GR-alpha [	791	795	6.055408	TCAGG	3.90625	3.9065
cg1742692	CREM	GR-alpha [	973	977	6.055408	CCTAA	3.90625	3.9065
cg1742692	CREM	GR-alpha [	1322	1326	6.055408	TCAGG	3.90625	3.9065
cg1742692	CREM	GR-alpha [	1450	1454	6.055408	TCAGG	3.90625	3.9065
cg1742692	CREM	GR-alpha [	1466	1470	6.055408	CCTGA	3.90625	3.9065
cg1742692	CREM	C/EBPalph	10	16	5.996794	CATTGG	0.97656	0.99
cg1742692	CREM	AR [T000	203	211	5.96855	GGACAG	0.24414	0.24229
cg1742692	CREM	STAT4 [T	1462	1467	5.882353	CCTTCC	0.48828	0.48408
cg1742692	CREM	STAT1bet	0	9	5.796867	AGTTGG	0.1545	0.1557

cg1742692	CREM	STAT1bet	112	121	5.796867	ATTTCC	0.1545	0.1557
cg1742692	CREM	c-Jun [T00	1484	1490	5.783074	TGACTT	0.36621	0.37082
cg1742692	CREM	VDR [T00	814	822	5.771401	GGCTTG	0.42725	0.42999
cg1742692	CREM	AR [T000	1608	1616	5.754178	TCTGTG	0.24414	0.24229
cg1742692	CREM	c-Ets-1 [T	303	309	5.686398	AGGGAA	0.36621	0.3623
cg1742692	CREM	HNF-1A [	348	355	5.610392	GTTAAG	0.24414	0.2469
cg1742692	CREM	T3R-beta1	148	156	5.591999	GAATGG	0.21362	0.21287
cg1742692	CREM	AP-2alpha	196	201	5.568965	GCCTAT	0.48828	0.4878
cg1742692	CREM	AP-2alpha	486	491	5.568965	GCCTAT	0.48828	0.4878
cg1742692	CREM	NFI/CTF [	1041	1048	5.558661	GTGCTT	0.54932	0.55038
cg1742692	CREM	Pax-5 [T0	1931	1937	5.544826	GGGCCA	0.73242	0.72046
cg1742692	CREM	TFIID [T0	533	539	5.544826	TTTATC	0.73242	0.75085
cg1742692	CREM	TFIID [T0	733	739	5.544826	TACTAA	0.73242	0.75085
cg1742692	CREM	TFIID [T0	1030	1036	5.544826	TTTAGA	0.73242	0.75085
cg1742692	CREM	TFIID [T0	1524	1530	5.544826	TTTATC	0.73242	0.75085
cg1742692	CREM	TFIID [T0	1806	1812	5.544826	TGATAA	0.73242	0.75085
cg1742692	CREM	NF-AT1 [	3	12	5.512555	TGGAAA	0.05913	0.05965
cg1742692	CREM	C/EBPalph	1749	1755	5.455853	AGCAAT	0.73242	0.74391
cg1742692	CREM	IRF-1 [T0	1193	1201	5.404935	AGCAGG	0.22888	0.23087
cg1742692	CREM	RAR-beta	1954	1963	5.389083	CGGGTT	0.15259	0.15189
cg1742692	CREM	C/EBPalph	58	64	5.38654	AATTGT	0.73242	0.74391
cg1742692	CREM	C/EBPalph	746	752	5.38654	AACAAT	0.73242	0.74391
cg1742692	CREM	AP-1 [T00	126	134	5.321703	TGACTC	0.09155	0.09214
cg1742692	CREM	GR [T050	121	127	5.207533	GTCTTT	0.24414	0.24606
cg1742692	CREM	GR [T050	237	243	5.207533	GGTTTT	0.24414	0.24606
cg1742692	CREM	GR [T050	1473	1479	5.207533	GGTTTT	0.24414	0.24606
cg1742692	CREM	GR [T050	1479	1485	5.207533	GTCTTT	0.24414	0.24606
cg1742692	CREM	c-Jun [T00	29	35	5.193102	GAAGTC	0.61035	0.61057
cg1742692	CREM	c-Ets-2 [T	1100	1108	5.162974	TTCCTTA	0.13733	0.13828
cg1742692	CREM	NF-AT1 [	1500	1508	5.125037	TTTTTTT	0.05341	0.05402
cg1742692	CREM	AP-2alpha	492	497	5.100982	GCCTTT	0.97656	0.97567
cg1742692	CREM	AP-2alpha	979	984	5.100982	AAAGGC	0.97656	0.97567
cg1742692	CREM	RXR-alph	1764	1770	5.089356	GGGTGC	0.48828	0.484
cg1742692	CREM	GR-beta [	646	650	5.042296	AATCC	3.90625	3.95351
cg1742692	CREM	GR-beta [	740	744	5.042296	AATAC	3.90625	3.95351
cg1742692	CREM	GR-beta [	1233	1237	5.042296	GTATT	3.90625	3.95351
cg1742692	CREM	GR-beta [	1280	1284	5.042296	AATCC	3.90625	3.95351
cg1742692	CREM	GR-beta [	1438	1442	5.042296	AATAC	3.90625	3.95351
cg1742692	CREM	XBP-1 [T	425	430	4.894955	AGGCAT	0.97656	0.96979
cg1742692	CREM	XBP-1 [T	490	495	4.894955	ATGCCT	0.97656	0.96979
cg1742692	CREM	AP-2alpha	972	977	4.890408	GCCTAA	0.97656	0.97567
cg1742692	CREM	c-Jun [T00	589	595	4.883696	TATGTC	0.61035	0.61057
cg1742692	CREM	NF-1 [T00	1045	1052	4.880836	TTGGAA	0.24414	0.24398
cg1742692	CREM	NF-kappa	1334	1344	4.847696	AGAGGC	0.02432	0.02374
cg1742692	CREM	HNF-1A [	918	925	4.828753	GTTAAG	0.36621	0.37179
cg1742692	CREM	C/EBPalph	1254	1260	4.776286	AACAAT	0.97656	0.99332
cg1742692	CREM	TFII-I [T0	4	9	4.756447	GGAAAT	2.92969	2.93695
cg1742692	CREM	TFII-I [T0	112	117	4.756447	ATTTCC	2.92969	2.93695

cg1742692	CREM	TFII-I [T0	1386	1391	4.756447	ATGTCC	2.92969	2.93695
cg1742692	CREM	TFII-I [T0	1675	1680	4.756447	GGACTG	2.92969	2.93695
cg1742692	CREM	FOXP3 [T	225	230	4.756447	GAAAAC	2.92969	2.96063
cg1742692	CREM	FOXP3 [T	238	243	4.756447	GTTTTG	2.92969	2.96063
cg1742692	CREM	FOXP3 [T	269	274	4.756447	GTTTTT	2.92969	2.96063
cg1742692	CREM	FOXP3 [T	1251	1256	4.756447	AAAAAC	2.92969	2.96063
cg1742692	CREM	FOXP3 [T	1474	1479	4.756447	GTTTTG	2.92969	2.96063
cg1742692	CREM	FOXP3 [T	1845	1850	4.756447	GTTTTC	2.92969	2.96063
cg1742692	CREM	Ik-1 [T027	1986	1998	4.748597	CGAGTA	0.00313	0.00308
cg1742692	CREM	IRF-1 [T0	1504	1512	4.626471	TTTCCTC	0.05341	0.05405
cg1742692	CREM	VDR [T00	1729	1737	4.617121	GTTCAA	0.37384	0.37445
cg1742692	CREM	VDR [T00	1957	1965	4.617121	GTTCAC	0.37384	0.37445
cg1742692	CREM	c-Ets-2 [T	1460	1468	4.589988	TTCCTTC	0.06866	0.06881
cg1742692	CREM	USF2 [T0	768	777	4.528187	CGGGCA	0.06866	0.06782
cg1742692	CREM	c-Jun [T00	1426	1432	4.441904	TCAGTC	0.12207	0.12266
cg1742692	CREM	STAT4 [T	45	50	4.411765	TCTTCC	1.95312	1.94235
cg1742692	CREM	STAT4 [T	1458	1463	4.411765	GCTTCC	1.95312	1.94235
cg1742692	CREM	HOXD9 [T	1560	1569	4.321431	TCTTTTT	0.03433	0.03596
cg1742692	CREM	HOXD10 [	1560	1569	4.321431	TCTTTTT	0.03433	0.03596
cg1742692	CREM	c-Ets-1 [T	1579	1585	4.282938	GAGGAA	0.85449	0.85764
cg1742692	CREM	PXR-1:RX	1954	1961	4.213958	CGGGTT	0.12207	0.12119
cg1742692	CREM	AP-2alpha	995	1000	4.211849	GTAGGC	0.97656	0.96469
cg1742692	CREM	AP-2alpha	1209	1214	4.211849	GTAGGC	0.97656	0.96469
cg1742692	CREM	GR-beta [T	7	11	4.201913	AATCA	7.8125	7.94607
cg1742692	CREM	GR-beta [T	110	114	4.201913	TTATT	7.8125	7.94607
cg1742692	CREM	GR-beta [T	502	506	4.201913	TTATT	7.8125	7.94607
cg1742692	CREM	GR-beta [T	528	532	4.201913	TGATT	7.8125	7.94607
cg1742692	CREM	GR-beta [T	603	607	4.201913	AATAA	7.8125	7.94607
cg1742692	CREM	GR-beta [T	609	613	4.201913	AATAA	7.8125	7.94607
cg1742692	CREM	GR-beta [T	1106	1110	4.201913	AATAA	7.8125	7.94607
cg1742692	CREM	GR-beta [T	1245	1249	4.201913	AATAG	7.8125	7.94607
cg1742692	CREM	GR-beta [T	1257	1261	4.201913	AATAA	7.8125	7.94607
cg1742692	CREM	GR-beta [T	1422	1426	4.201913	TTATT	7.8125	7.94607
cg1742692	CREM	GR-beta [T	1565	1569	4.201913	TTATT	7.8125	7.94607
cg1742692	CREM	GR-beta [T	1743	1747	4.201913	TTATT	7.8125	7.94607
cg1742692	CREM	NF-Y [T0	929	936	4.186615	TCTCCA	0.18311	0.1853
cg1742692	CREM	NF-AT1 [T	109	118	4.134416	CTTATTT	0.08392	0.08485
cg1742692	CREM	c-Ets-2 [T	47	55	4.091811	TTCCTTC	0.16022	0.16243
cg1742692	CREM	PXR-1:RX	818	825	4.090374	TGAACC	0.12207	0.12119
cg1742692	CREM	p53 [T006	769	775	4.083527	GGGCAC	0.73242	0.71379
cg1742692	CREM	p53 [T006	1072	1078	4.083527	GGGCAC	0.73242	0.71379
cg1742692	CREM	RXR-alph	720	726	4.019014	GAAACC	0.97656	0.9671
cg1742692	CREM	Pax-5 [T0	1913	1919	4.007279	GGGCAG	1.09863	1.07975
cg1742692	CREM	TFIID [T0	161	167	4.007279	TAGTAA	1.09863	1.13456
cg1742692	CREM	TFIID [T0	214	220	4.007279	TTTACTA	1.09863	1.13456
cg1742692	CREM	TFIID [T0	600	606	4.007279	TTTAATA	1.09863	1.13456
cg1742692	CREM	TFIID [T0	602	608	4.007279	TAATAA	1.09863	1.13456
cg1742692	CREM	TFIID [T0	1105	1111	4.007279	TAATAA	1.09863	1.13456

cg1742692	CREM	TFIID [T0	1537	1543	4.007279	TTTATG	1.09863	1.13456
cg1742692	CREM	TFIID [T0	1564	1570	4.007279	TTTATTA	1.09863	1.13456
cg1742692	CREM	AP-2alpha	423	428	3.970052	CAAGGC	0.97656	0.96469
cg1742692	CREM	NF-AT1 [	4	12	3.917696	GGAAAT	0.07629	0.07734
cg1742692	CREM	PPAR-alp	438	448	3.872523	CTCTGG	0.02575	0.02522
cg1742692	CREM	NFI/CTF [	1760	1767	3.793671	CCAAGG	0.18311	0.18109
cg1742692	CREM	p53 [T006	458	464	3.750231	GGGCTT	0.73242	0.71379
cg1742692	CREM	AP-2alpha	418	423	3.743866	GCCTTC	0.48828	0.48238
cg1742692	CREM	c-Ets-1 [T	294	300	3.71855	AAGGAA	0.61035	0.60765
cg1742692	CREM	c-Ets-1 [T	1099	1105	3.71855	GTTCCT	0.61035	0.60765
cg1742692	CREM	PEA3 [T0	561	569	3.710864	TCACAT	0.09155	0.09258
cg1742692	CREM	c-Ets-1 [T	17	23	3.590463	GTTCCT	0.61035	0.60765
cg1742692	CREM	c-Ets-2 [T	291	299	3.518824	TTGAAG	0.18311	0.18304
cg1742692	CREM	p53 [T006	1913	1919	3.516613	GGGCAG	0.73242	0.7189
cg1742692	CREM	AR [T000	396	404	3.382886	AAAGTG	0.06866	0.06905
cg1742692	CREM	Elk-1 [T00	1463	1471	3.381796	CTTCCT	0.04578	0.04588
cg1742692	CREM	GR-beta [	156	160	3.361531	AATCT	3.90625	3.99611
cg1742692	CREM	GR-beta [	582	586	3.361531	AATAT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1220	1224	3.361531	ATATT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1558	1562	3.361531	AATCT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1572	1576	3.361531	ATATT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1583	1587	3.361531	AATCT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1739	1743	3.361531	AGATT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1775	1779	3.361531	AATAT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1776	1780	3.361531	ATATT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1819	1823	3.361531	AATAT	3.90625	3.99611
cg1742692	CREM	GR-beta [	1826	1830	3.361531	AGATT	3.90625	3.99611
cg1742692	CREM	T3R-beta1	1286	1294	3.332047	CAATGG	0.27466	0.2755
cg1742692	CREM	PR B [T00	58	64	3.29756	AATTGT	0.24414	0.25122
cg1742692	CREM	PR B [T00	746	752	3.29756	AACAAT	0.24414	0.25122
cg1742692	CREM	PR A [T01	58	64	3.29756	AATTGT	0.24414	0.25122
cg1742692	CREM	PR A [T01	746	752	3.29756	AACAAT	0.24414	0.25122
cg1742692	CREM	c-Jun [T00	126	132	3.244843	TGACTC	0.24414	0.24403
cg1742692	CREM	AP-2alpha	365	370	3.229049	GCCTCT	0.48828	0.48238
cg1742692	CREM	AP-2alpha	405	410	3.229049	AGAGGC	0.48828	0.48238
cg1742692	CREM	AP-2alpha	1334	1339	3.229049	AGAGGC	0.48828	0.48238
cg1742692	CREM	Elk-1 [T00	46	54	3.121991	CTTCCT	0.07629	0.07656
cg1742692	CREM	POU2F2 (	61	71	3.116744	TGTTTTA	0.02575	0.0265
cg1742692	CREM	c-Jun [T00	441	447	3.049104	TGGGTC	0.24414	0.24403
cg1742692	CREM	STAT4 [T	16	21	2.941176	TGTTCC	2.92969	2.929
cg1742692	CREM	STAT4 [T	305	310	2.941176	GGAAGT	2.92969	2.929
cg1742692	CREM	STAT4 [T	1047	1052	2.941176	GGAACA	2.92969	2.929
cg1742692	CREM	STAT4 [T	1098	1103	2.941176	TGTTCC	2.92969	2.929
cg1742692	CREM	STAT4 [T	1131	1136	2.941176	TGTTCC	2.92969	2.929
cg1742692	CREM	STAT4 [T	1581	1586	2.941176	GGAATC	2.92969	2.929
cg1742692	CREM	p53 [T006	875	881	2.813291	GGGCAG	0.48828	0.47786
cg1742692	CREM	PR B [T00	1049	1055	2.80933	AACATT	0.73242	0.74818
cg1742692	CREM	PR B [T00	1254	1260	2.80933	AACAAT	0.73242	0.74818

cg1742692	CREM	PR A [T01	1049	1055	2.80933	AACATT	0.73242	0.74818
cg1742692	CREM	PR A [T01	1254	1260	2.80933	AACAAT	0.73242	0.74818
cg1742692	CREM	PXR-1:RX	1696	1703	2.577808	GCAGTT	0.12207	0.12266
cg1742692	CREM	AP-2alpha	169	174	2.550491	TGAGGC	0.48828	0.48266
cg1742692	CREM	AP-2alpha	409	414	2.550491	GCCTCA	0.48828	0.48266
cg1742692	CREM	AP-2alpha	800	805	2.550491	TGAGGC	0.48828	0.48266
cg1742692	CREM	AP-2alpha	1974	1979	2.550491	GCCTCA	0.48828	0.48266
cg1742692	CREM	RXR-alph	716	722	2.544678	GGGTGA	0.85449	0.84796
cg1742692	CREM	RXR-alph	1419	1425	2.544678	GGGTTA	0.85449	0.84796
cg1742692	CREM	RXR-alph	1785	1791	2.544678	GGGTGC	0.85449	0.84796
cg1742692	CREM	c-Jun [T00	106	112	2.538231	TGACTT	0.48828	0.48929
cg1742692	CREM	c-Jun [T00	137	143	2.538231	TAAGTC	0.48828	0.48929
cg1742692	CREM	C/EBPalp	1284	1290	2.441016	CTCAAT	0.48828	0.49114
cg1742692	CREM	Ik-1 [T027	648	660	2.374299	TCCCAG	0.00063	0.00061
cg1742692	CREM	LEF-1 [T0	1651	1658	2.345041	CTTTGTT	0.09155	0.09192
cg1742692	CREM	LEF-1 [T0	1715	1722	2.345041	CTTTGTT	0.09155	0.09192
cg1742692	CREM	GATA-2 [	1084	1092	2.222222	CGATAA	0.22888	0.23091
cg1742692	CREM	T3R-beta1	100	108	2.221365	CACTGG	0.15259	0.15262
cg1742692	CREM	c-Ets-2 [T	18	26	2.217136	TTCCTCA	0.16785	0.16856
cg1742692	CREM	NF-Y [T0	11	18	2.194008	ATTGGT	0.21362	0.21508
cg1742692	CREM	GATA-1 [	263	268	2.176375	TATCGT	3.90625	3.92756
cg1742692	CREM	GATA-1 [	1165	1170	2.176375	TATCCT	3.90625	3.92756
cg1742692	CREM	c-Ets-2 [T	388	396	2.142327	GGAGAG	0.16785	0.16856
cg1742692	CREM	GATA-1 [	1083	1088	2.001358	GCGATA	3.90625	3.92756
cg1742692	CREM	AP-2alpha	661	666	1.871933	GGAGGC	0.97656	0.95407
cg1742692	CREM	AP-2alpha	794	799	1.871933	GGAGGC	0.97656	0.95407
cg1742692	CREM	AP-2alpha	1980	1985	1.871933	GCCTCC	0.97656	0.95407
cg1742692	CREM	TBP [T00	1817	1826	1.871542	GTAATA	0.18311	0.18942
cg1742692	CREM	AR [T000	1138	1146	1.86979	GGACAG	0.03815	0.03818
cg1742692	CREM	TFII-I [T0	388	393	1.824994	GGAGAG	0.48828	0.48408
cg1742692	CREM	p53 [T006	338	344	1.758307	TCTGCC	0.36621	0.36261
cg1742692	CREM	p53 [T006	511	517	1.758307	GGGCAT	0.36621	0.36261
cg1742692	CREM	p53 [T006	673	679	1.758307	GGGCAG	0.36621	0.36261
cg1742692	CREM	RXR-alph	442	448	1.696452	GGGTCA	0.48828	0.48222
cg1742692	CREM	GR-beta [	475	479	1.680765	GAATT	3.90625	3.94936
cg1742692	CREM	GR-beta [	612	616	1.680765	AATTC	3.90625	3.94936
cg1742692	CREM	GR-beta [	1399	1403	1.680765	AATTC	3.90625	3.94936
cg1742692	CREM	GR-beta [	1518	1522	1.680765	AATTC	3.90625	3.94936
cg1742692	CREM	GR-beta [	1752	1756	1.680765	AATGC	3.90625	3.94936
cg1742692	CREM	c-Ets-2 [T	1576	1584	1.64415	TTGGAG	0.04578	0.04579
cg1742692	CREM	C/EBPbeta	2	5	1.639871	TTGG	15.625	15.72563
cg1742692	CREM	C/EBPbeta	12	15	1.639871	TTGG	15.625	15.72563
cg1742692	CREM	C/EBPbeta	116	119	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	343	346	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	658	661	1.639871	TTGG	15.625	15.72563
cg1742692	CREM	C/EBPbeta	666	669	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	847	850	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	932	935	1.639871	CCAA	15.625	15.72563

cg1742692	CREM	C/EBPbeta	1045	1048	1.639871	TTGG	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1077	1080	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1300	1303	1.639871	TTGG	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1375	1378	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1576	1579	1.639871	TTGG	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1659	1662	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1671	1674	1.639871	TTGG	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1760	1763	1.639871	CCAA	15.625	15.72563
cg1742692	CREM	XBP-1 [T	1179	1184	1.583727	TGTCAT	0.97656	0.98146
cg1742692	CREM	TFIID [T0	52	58	1.537547	TGAAAA	0.73242	0.75096
cg1742692	CREM	TFIID [T0	1770	1776	1.537547	TGAAAA	0.73242	0.75096
cg1742692	CREM	c-Ets-1 [T	391	397	1.513038	GAGGAA	0.36621	0.36952
cg1742692	CREM	c-Ets-1 [T	1504	1510	1.513038	TTTCCTC	0.36621	0.36952
cg1742692	CREM	STAT4 [T	296	301	1.470588	GGAACT	1.95312	1.96333
cg1742692	CREM	STAT4 [T	393	398	1.470588	GGAAAA	1.95312	1.96333
cg1742692	CREM	STAT4 [T	474	479	1.470588	GGAATT	1.95312	1.96333
cg1742692	CREM	STAT4 [T	1197	1202	1.470588	GGAAAA	1.95312	1.96333
cg1742692	CREM	STAT4 [T	1503	1508	1.470588	TTTTCC	1.95312	1.96333
cg1742692	CREM	GR [T050	1250	1256	1.444018	CAAAAA	0.12207	0.1245
cg1742692	CREM	PR B [T00	574	580	1.404665	AACACT	0.36621	0.37023
cg1742692	CREM	PR A [T01	574	580	1.404665	AACACT	0.36621	0.37023
cg1742692	CREM	c-Ets-1 [T	1195	1201	1.384951	CAGGAA	0.36621	0.36952
cg1742692	CREM	C/EBPbeta	22	25	1.366559	TCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	51	54	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	125	128	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	132	135	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	241	244	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	291	294	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	422	425	1.366559	TCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	462	465	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	817	820	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	898	901	1.366559	TCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1285	1288	1.366559	TCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1483	1486	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1492	1495	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1731	1734	1.366559	TCAA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1781	1784	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	C/EBPbeta	1878	1881	1.366559	TTGA	15.625	15.72563
cg1742692	CREM	AP-2alpha	640	645	1.357116	GCCTGT	0.48828	0.48203
cg1742692	CREM	c-Ets-2 [T	1505	1513	1.071163	TTCCTCT	0.06104	0.06166
cg1742692	CREM	GATA-1 [	92	97	1.038567	ATGATA	1.95312	1.98662
cg1742692	CREM	GATA-1 [	584	589	1.038567	TATCAT	1.95312	1.98662
cg1742692	CREM	GATA-1 [	1526	1531	1.038567	TATCAT	1.95312	1.98662
cg1742692	CREM	SRY [T00	1651	1659	0.999172	CTTTGTT	0.06104	0.06205
cg1742692	CREM	SRY [T00	1715	1723	0.999172	CTTTGTT	0.06104	0.06205
cg1742692	CREM	TBP [T00	961	970	0.935771	TTTATAC	0.12207	0.12628
cg1742692	CREM	GATA-1 [	353	358	0.863549	GTGATA	1.95312	1.98662
cg1742692	CREM	GATA-1 [	1805	1810	0.863549	GTGATA	1.95312	1.98662

cg1742692	CREM	GR-beta [T	9	13	0.840383	TCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	58	62	0.840383	AATTG	7.8125	7.94706
cg1742692	CREM	GR-beta [T	145	149	0.840383	AATGA	7.8125	7.94706
cg1742692	CREM	GR-beta [T	149	153	0.840383	AATGG	7.8125	7.94706
cg1742692	CREM	GR-beta [T	167	171	0.840383	AATGA	7.8125	7.94706
cg1742692	CREM	GR-beta [T	185	189	0.840383	CAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	186	190	0.840383	AATTA	7.8125	7.94706
cg1742692	CREM	GR-beta [T	219	223	0.840383	TAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	220	224	0.840383	AATTA	7.8125	7.94706
cg1742692	CREM	GR-beta [T	611	615	0.840383	TAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	713	717	0.840383	AATGG	7.8125	7.94706
cg1742692	CREM	GR-beta [T	748	752	0.840383	CAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	749	753	0.840383	AATTA	7.8125	7.94706
cg1742692	CREM	GR-beta [T	811	815	0.840383	AATGG	7.8125	7.94706
cg1742692	CREM	GR-beta [T	933	937	0.840383	CAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1125	1129	0.840383	AATGA	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1181	1185	0.840383	TCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1287	1291	0.840383	AATGG	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1295	1299	0.840383	TCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1398	1402	0.840383	TAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1470	1474	0.840383	AATGG	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1497	1501	0.840383	CCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1517	1521	0.840383	TAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1521	1525	0.840383	TCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1528	1532	0.840383	TCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1667	1671	0.840383	TCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1683	1687	0.840383	TAATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1684	1688	0.840383	AATTG	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1934	1938	0.840383	CCATT	7.8125	7.94706
cg1742692	CREM	GR-beta [T	1964	1968	0.840383	CCATT	7.8125	7.94706
cg1742692	CREM	Elk-1 [T00	1459	1467	0.822677	CTTCCTT	0.03052	0.03057
cg1742692	CREM	GATA-1 [	535	540	0.758539	TATCAG	1.95312	1.98662
cg1742692	CREM	AP-2alpha	1322	1327	0.678558	TCAGGC	0.48828	0.48199
cg1742692	CREM	HNF-1A [	1019	1026	0.431647	AGTTTA	0.24414	0.24974
cg1742692	CREM	GATA-1 [	1170	1175	0.280028	TAGATA	0.97656	0.99875
cg1742692	CREM	GATA-1 [	1569	1574	0.280028	TAGATA	0.97656	0.99875
cg1742692	CREM	c-Ets-1 [T	46	52	0.256174	CTTCCTT	0.24414	0.24569
cg1742692	CREM	c-Ets-1 [T	1459	1465	0.256174	CTTCCTT	0.24414	0.24569
cg1742692	CREM	AP-2alpha	871	876	0.226186	GCCTGG	0.97656	0.95305
cg1742692	CREM	AP-2alpha	1903	1908	0.226186	CCAGGC	0.97656	0.95305
cg1742692	CREM	GR-alpha [	249	253	0.207689	AGAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	366	370	0.207689	CCTCT	7.8125	7.81264
cg1742692	CREM	GR-alpha [	390	394	0.207689	AGAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	405	409	0.207689	AGAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	465	469	0.207689	AAAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	493	497	0.207689	CCTTT	7.8125	7.81264
cg1742692	CREM	GR-alpha [	952	956	0.207689	AGAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	979	983	0.207689	AAAGG	7.8125	7.81264

cg1742692	CREM	GR-alpha [	1266	1270	0.207689	AAAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	1334	1338	0.207689	AGAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	1507	1511	0.207689	CCTCT	7.8125	7.81264
cg1742692	CREM	GATA-1 [	927	932	0.105011	TATCTC	0.97656	0.98738
cg1742692	CREM	GR-alpha [	197	201	0	CCTAT	7.8125	7.81264
cg1742692	CREM	GR-alpha [	200	204	0	ATAGG	7.8125	7.81264
cg1742692	CREM	GR-alpha [	487	491	0	CCTAT	7.8125	7.81264
cg1742692	CREM	GR-alpha [	641	645	0	CCTGT	7.8125	7.81264
cg1742692	CREM	GR-alpha [	774	778	0	CCTGT	7.8125	7.81264
cg1742692	CREM	XBP-1 [T0	139	144	0	AGTCAT	0.97656	0.98127
cg1742692	CREM	XBP-1 [T0	1126	1131	0	ATGACT	0.97656	0.98127
cg1742692	CREM	XBP-1 [T0	1216	1221	0	AGTCAT	0.97656	0.98127
cg1742692	CREM	XBP-1 [T0	1428	1433	0	AGTCAT	0.97656	0.98127
cg1742692	CREM	RXR-alpha	1955	1961	0	GGGTTC	0.24414	0.2444
cg1742692	CREM	Pax-5 [T0	458	464	0	GGGCTT	1.09863	1.06846
cg1742692	CREM	TFII-I [T0	203	208	0	GGACAG	1.46484	1.45997
cg1742692	CREM	TFII-I [T0	1138	1143	0	GGACAG	1.46484	1.45997
cg1742692	CREM	STAT4 [T	4	9	0	GGAAAT	0.48828	0.49387
cg1742692	CREM	STAT4 [T	112	117	0	ATTTCC	0.48828	0.49387
cg1742692	CREM	c-Ets-1 [T	1463	1469	0	CTTCCTC	0.24414	0.2429
cg1742692	CREM	YY1 [T00	150	153	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	320	323	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	702	705	0	CCAT	7.8125	7.81711
cg1742692	CREM	YY1 [T00	714	717	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	812	815	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	913	916	0	CCAT	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1070	1073	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1157	1160	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1288	1291	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1415	1418	0	CCAT	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1417	1420	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1471	1474	0	ATGG	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1497	1500	0	CCAT	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1934	1937	0	CCAT	7.8125	7.81711
cg1742692	CREM	YY1 [T00	1964	1967	0	CCAT	7.8125	7.81711
cg1742692	CREM	ER-alpha [	443	447	0	GGTCA	1.95312	1.9404
cg1742692	CREM	ER-alpha [	686	690	0	GGTCA	1.95312	1.9404
cg1742692	CREM	C/EBPbeta	39	42	0	ACAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	60	63	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	173	176	0	GCAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	184	187	0	GCAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	211	214	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	327	330	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	548	551	0	ACAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	682	685	0	ACAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	743	746	0	ACAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	747	750	0	ACAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	837	840	0	TTGC	15.625	15.71349

cg1742692	CREM	C/EBPbeta	885	888	0	GCAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1039	1042	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1178	1181	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1249	1252	0	GCAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1255	1258	0	ACAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1261	1264	0	ACAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1477	1480	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1555	1558	0	GCAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1595	1598	0	TTGC	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1653	1656	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1656	1659	0	TTGC	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1686	1689	0	TTGC	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1717	1720	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1720	1723	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1750	1753	0	GCAA	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1896	1899	0	TTGT	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1937	1940	0	TTGC	15.625	15.71349
cg1742692	CREM	C/EBPbeta	1939	1942	0	GCAA	15.625	15.71349
cg1742692	CREM	NF-1 [T00	1371	1378	0	CGGGCC	0.12207	0.11983
cg1742692	CREM	TFIID [T0	51	57	0	TTGAAA	1.09863	1.13474
cg1742692	CREM	TFIID [T0	63	69	0	TTTTAG	1.09863	1.13474
cg1742692	CREM	TFIID [T0	223	229	0	TAGAAA	1.09863	1.13474
cg1742692	CREM	TFIID [T0	898	904	0	TCAAAA	1.09863	1.13474
cg1742692	CREM	TFIID [T0	1240	1246	0	TTAAAA	1.09863	1.13474
cg1742692	CREM	TFIID [T0	1875	1881	0	TTTTTGA	1.09863	1.13474
cg1742692	CREM	FOXP3 [T	210	215	0	GTTGTT	1.46484	1.47315
cg1742692	CREM	FOXP3 [T	326	331	0	GTTGTG	1.46484	1.47315
cg1742692	CREM	FOXP3 [T	1719	1724	0	GTTGTT	1.46484	1.47315
cg1742692	CREM	GR-beta [T	57	61	0	AAATT	3.90625	3.99611
cg1742692	CREM	GR-beta [T	476	480	0	AATTT	3.90625	3.99611
cg1742692	CREM	GR-beta [T	597	601	0	ACATT	3.90625	3.99611
cg1742692	CREM	GR-beta [T	934	938	0	AATTT	3.90625	3.99611
cg1742692	CREM	GR-beta [T	1050	1054	0	ACATT	3.90625	3.99611
cg1742692	CREM	GR-beta [T	1110	1114	0	AATGT	3.90625	3.99611
cg1742692	CREM	PR B [T00	517	523	0	AACAGT	0.36621	0.36944
cg1742692	CREM	PR B [T00	987	993	0	CACTGT	0.36621	0.36944
cg1742692	CREM	PR B [T00	1128	1134	0	GACTGT	0.36621	0.36944
cg1742692	CREM	PR A [T01	517	523	0	AACAGT	0.36621	0.36944
cg1742692	CREM	PR A [T01	987	993	0	CACTGT	0.36621	0.36944
cg1742692	CREM	PR A [T01	1128	1134	0	GACTGT	0.36621	0.36944
cg1742692	CREM	GR [T050	899	905	0	CAAAAA	0.36621	0.37562
cg1742692	CREM	GR [T050	1262	1268	0	CAAAAA	0.36621	0.37562
cg1742692	CREM	GR [T050	1874	1880	0	TTTTTTG	0.36621	0.37562
cg1742692	CREM	HNF-3alp	605	612	0	TAAAAA	0.09155	0.09511
cg1742692	CREM	HNF-3alp	736	743	0	TAAAAA	0.09155	0.09511
cg1742692	CREM	HNF-3alp	1241	1248	0	TAAAAA	0.09155	0.09511
cg1742692	CREM	HNF-3alp	1777	1784	0	TATTT	0.09155	0.09511
cg1742692	CREM	IRF-2 [T0	25	30	0	AAGTGA	0.48828	0.49387

cg1742692	CREM	IRF-2 [T0	351	356	0	AAGTGA	0.48828	0.49387
cg1742692	CREM	IRF-2 [T0	1634	1639	0	TCACTT	0.48828	0.49387
cg1742692	CREM	IRF-2 [T0	1712	1717	0	TCACTT	0.48828	0.49387
cg1742692	CREM	HOXD9 [	603	612	0	AATAAA	0.01144	0.01207
cg1742692	CREM	HOXD10 [	603	612	0	AATAAA	0.01144	0.01207
cg2262289	CXorf36	LEF-1 [T0	618	625	9.937995	CTTTGG	0.12207	0.12154
cg2262289	CXorf36	c-Ets-1 [T	1472	1478	9.841249	AGGGAA	0.24414	0.2459
cg2262289	CXorf36	c-Ets-1 [T	1678	1684	9.841249	ATTCCC	0.24414	0.2459
cg2262289	CXorf36	c-Myb [T0	1979	1986	9.815171	ACAAGT	0.36621	0.3712
cg2262289	CXorf36	STAT1bet	167	176	9.807397	CTTTCC	0.14877	0.1495
cg2262289	CXorf36	XBP-1 [T0	868	873	9.789909	AGACAT	1.95312	1.95208
cg2262289	CXorf36	NF-AT2 [	400	409	9.755755	GTTTGT	0.08774	0.08903
cg2262289	CXorf36	Elk-1 [T00	251	259	9.754368	CTTCCC	0.10681	0.10604
cg2262289	CXorf36	PR B [T00	81	87	9.743489	CGGTGT	1.09863	1.10292
cg2262289	CXorf36	PR B [T00	396	402	9.743489	GGGTGT	1.09863	1.10292
cg2262289	CXorf36	PR B [T00	849	855	9.743489	AACACG	1.09863	1.10292
cg2262289	CXorf36	PR B [T00	1769	1775	9.743489	CTGTGT	1.09863	1.10292
cg2262289	CXorf36	PR A [T01	81	87	9.743489	CGGTGT	1.09863	1.10292
cg2262289	CXorf36	PR A [T01	396	402	9.743489	GGGTGT	1.09863	1.10292
cg2262289	CXorf36	PR A [T01	849	855	9.743489	AACACG	1.09863	1.10292
cg2262289	CXorf36	PR A [T01	1769	1775	9.743489	CTGTGT	1.09863	1.10292
cg2262289	CXorf36	AhR:Arnt	1273	1282	9.738501	TGGGGC	0.17929	0.17456
cg2262289	CXorf36	EBF [T05	703	713	9.729328	CCTTCA	0.06866	0.06676
cg2262289	CXorf36	c-Jun [T00	674	680	9.717135	CAGGTC	0.73242	0.73031
cg2262289	CXorf36	c-Ets-1 [T	527	533	9.713162	ATTCCC	0.36621	0.36441
cg2262289	CXorf36	c-Ets-1 [T	1214	1220	9.713162	GGGGAA	0.36621	0.36441
cg2262289	CXorf36	RAR-beta	1200	1209	9.641259	GGGGTT	0.21362	0.21243
cg2262289	CXorf36	ELF-1 [T0	554	566	9.604198	TTACTT	0.00417	0.00423
cg2262289	CXorf36	Pax-5 [T0	709	715	9.552105	GGGCCA	1.46484	1.43083
cg2262289	CXorf36	Pax-5 [T0	860	866	9.552105	GTGGCC	1.46484	1.43083
cg2262289	CXorf36	Pax-5 [T0	1445	1451	9.552105	GGGCCA	1.46484	1.43083
cg2262289	CXorf36	TFIID [T0	259	265	9.552105	TTTCTCA	1.46484	1.48472
cg2262289	CXorf36	TFIID [T0	810	816	9.552105	TTTCAC	1.46484	1.48472
cg2262289	CXorf36	NF-1 [T00	1975	1982	9.535536	TTGGAC	0.73242	0.73053
cg2262289	CXorf36	TFII-I [T0	132	137	9.512894	TTTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	162	167	9.512894	CCTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	189	194	9.512894	CCTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	193	198	9.512894	CCTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	281	286	9.512894	TTTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	318	323	9.512894	GTGTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	338	343	9.512894	GTGTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	404	409	9.512894	GTTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	566	571	9.512894	TTTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	575	580	9.512894	CCTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	752	757	9.512894	CCATCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	785	790	9.512894	GTTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	975	980	9.512894	GGATGG	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	1091	1096	9.512894	CGATCC	7.32422	7.29728

cg2262289	CXorf36	TFII-I [T0	1283	1288	9.512894	GGAAAA	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	1780	1785	9.512894	GGATAA	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	1851	1856	9.512894	TTTTCC	7.32422	7.29728
cg2262289	CXorf36	TFII-I [T0	1977	1982	9.512894	GGACAA	7.32422	7.29728
cg2262289	CXorf36	FOXP3 [T	49	54	9.512894	GTTATT	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	85	90	9.512894	GTTTAT	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	825	830	9.512894	GCCAAC	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	933	938	9.512894	CCCAAC	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	1235	1240	9.512894	GTTGGG	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	1323	1328	9.512894	GTTGGG	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	1773	1778	9.512894	GTTCTT	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	1908	1913	9.512894	AAGAAC	7.32422	7.35678
cg2262289	CXorf36	FOXP3 [T	1960	1965	9.512894	ACCAAC	7.32422	7.35678
cg2262289	CXorf36	c-Jun [T00	1083	1089	9.511322	TGACCA	0.73242	0.73031
cg2262289	CXorf36	Ik-1 [T027	761	773	9.497194	TCCCAG	0.02941	0.02907
cg2262289	CXorf36	TCF-4E [T	664	670	9.453578	CTTTGA	0.48828	0.49215
cg2262289	CXorf36	TCF-4E [T	677	683	9.453578	GTCAAA	0.48828	0.49215
cg2262289	CXorf36	c-Jun [T00	990	996	9.442241	TGACAG	0.73242	0.73031
cg2262289	CXorf36	NFI/CTF [	1971	1978	9.352332	GACCTT	0.54932	0.54821
cg2262289	CXorf36	SRY [T00	675	683	9.264664	AGGTCA	0.12207	0.12265
cg2262289	CXorf36	NF-AT1 [	782	790	9.158155	CCTGTT	0.22888	0.22959
cg2262289	CXorf36	c-Ets-1 [T	309	315	9.148774	GTTCCC	0.85449	0.85523
cg2262289	CXorf36	c-Ets-1 [T	738	744	9.148774	GTTCCC	0.85449	0.85523
cg2262289	CXorf36	COUP-TF	671	683	9.093379	GCACAG	0.01878	0.01865
cg2262289	CXorf36	USF2 [T0	776	785	9.056375	CCCACA	0.1545	0.15287
cg2262289	CXorf36	USF2 [T0	1148	1157	9.056375	CAGGTG	0.1545	0.15287
cg2262289	CXorf36	USF2 [T0	1269	1278	9.056375	CAGGTG	0.1545	0.15287
cg2262289	CXorf36	NFI/CTF [	1232	1239	9.042931	GCTGTT	0.48828	0.48804
cg2262289	CXorf36	NFI/CTF [	1961	1968	9.042931	CCAACT	0.48828	0.48804
cg2262289	CXorf36	MEF-2A [	1892	1902	9.003254	AAAAAA	0.07343	0.07563
cg2262289	CXorf36	GR [T050	398	404	8.971049	GTGTTT	0.61035	0.61632
cg2262289	CXorf36	GR [T050	697	703	8.971049	CAAAGC	0.61035	0.61632
cg2262289	CXorf36	c-Ets-2 [T	636	644	8.912323	TTCCTG	0.27466	0.27495
cg2262289	CXorf36	c-Ets-1 [T	1460	1466	8.8926	CGGGAA	0.85449	0.85523
cg2262289	CXorf36	ETF [T002	1521	1531	8.876947	GAGGGC	0.02384	0.02303
cg2262289	CXorf36	AP-1 [T00	656	664	8.854325	TGACTA	0.24414	0.24693
cg2262289	CXorf36	c-Jun [T00	1970	1976	8.832178	TGACCT	0.61035	0.61059
cg2262289	CXorf36	PR B [T00	45	51	8.827054	AGCTGT	0.36621	0.36944
cg2262289	CXorf36	PR B [T00	781	787	8.827054	ACCTGT	0.36621	0.36944
cg2262289	CXorf36	PR A [T01	45	51	8.827054	AGCTGT	0.36621	0.36944
cg2262289	CXorf36	PR A [T01	781	787	8.827054	ACCTGT	0.36621	0.36944
cg2262289	CXorf36	NFI/CTF [	1483	1490	8.814757	TCTCTTC	0.48828	0.48804
cg2262289	CXorf36	NF-AT2 [	128	137	8.794303	CACCTT	0.05341	0.05386
cg2262289	CXorf36	NF-1 [T00	295	302	8.790071	TCTCCC	0.24414	0.24467
cg2262289	CXorf36	E2F-1 [T0	1342	1349	8.76494	GCGGAG	0.27466	0.26875
cg2262289	CXorf36	LEF-1 [T0	314	321	8.759086	CTTTGT	0.54932	0.55326
cg2262289	CXorf36	LEF-1 [T0	694	701	8.759086	TCACAA	0.54932	0.55326
cg2262289	CXorf36	XBP-1 [T	40	45	8.75604	ATGAGA	2.92969	2.9674

cg2262289	CXorf36	XBP-1 [T	410	415	8.75604	ATGATA	2.92969	2.9674
cg2262289	CXorf36	XBP-1 [T	1477	1482	8.75604	ATGAGC	2.92969	2.9674
cg2262289	CXorf36	XBP-1 [T	1820	1825	8.75604	TCTCAT	2.92969	2.9674
cg2262289	CXorf36	XBP-1 [T	1878	1883	8.75604	ATGAAC	2.92969	2.9674
cg2262289	CXorf36	STAT1bet	1645	1654	8.695301	CCTTGG	0.22316	0.22446
cg2262289	CXorf36	RXR-alph	1326	1332	8.664139	GGGTAG	0.12207	0.12014
cg2262289	CXorf36	LEF-1 [T0	74	81	8.575454	CTTTGG	0.15259	0.15214
cg2262289	CXorf36	RAR-beta	1320	1329	8.55975	GGGGTT	0.26703	0.26657
cg2262289	CXorf36	p53 [T006	1690	1696	8.537081	GGGCTC	0.12207	0.11986
cg2262289	CXorf36	NF-AT1 [	278	286	8.532897	TCCTTTT	0.10681	0.10725
cg2262289	CXorf36	USF2 [T0	26	35	8.532138	CAGGTG	0.103	0.10183
cg2262289	CXorf36	LEF-1 [T0	664	671	8.457856	CTTTGA	0.15259	0.15214
cg2262289	CXorf36	HOXD9 [	45	54	8.402327	AGCTGT	0.02289	0.02363
cg2262289	CXorf36	HOXD10 [	45	54	8.402327	AGCTGT	0.02289	0.02363
cg2262289	CXorf36	PR B [T00	1231	1237	8.338824	TGCTGT	1.09863	1.10009
cg2262289	CXorf36	PR B [T00	1464	1470	8.338824	AACAGA	1.09863	1.10009
cg2262289	CXorf36	PR A [T01	1231	1237	8.338824	TGCTGT	1.09863	1.10009
cg2262289	CXorf36	PR A [T01	1464	1470	8.338824	AACAGA	1.09863	1.10009
cg2262289	CXorf36	AR [T000	1977	1985	8.330815	GGACAA	0.10681	0.10625
cg2262289	CXorf36	GR-alpha [	0	4	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	115	119	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	139	143	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	148	152	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	159	163	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	162	166	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	177	181	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	189	193	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	193	197	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	224	228	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	227	231	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	233	237	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	276	280	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	348	352	8.281568	CCTTG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	451	455	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	575	579	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	592	596	8.281568	CAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	688	692	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	691	695	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	703	707	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	725	729	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	742	746	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	883	887	8.281568	GGAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	905	909	8.281568	GGAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	972	976	8.281568	GGAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1109	1113	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1171	1175	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1210	1214	8.281568	GGAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1317	1321	8.281568	GGAGG	7.8125	7.72956

cg2262289	CXorf36	GR-alpha [	1407	1411	8.281568	GGAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1415	1419	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1470	1474	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1502	1506	8.281568	GGAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1544	1548	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1554	1558	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1645	1649	8.281568	CCTTG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1654	1658	8.281568	GAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1704	1708	8.281568	CCTTC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1883	1887	8.281568	CCTCC	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1913	1917	8.281568	CAAGG	7.8125	7.72956
cg2262289	CXorf36	GR-alpha [	1973	1977	8.281568	CCTTG	7.8125	7.72956
cg2262289	CXorf36	GCF [T00	1012	1020	8.256755	GCGCAG	0.09155	0.09002
cg2262289	CXorf36	HNF-1B [	1904	1912	8.255112	AGTTAA	0.11444	0.11669
cg2262289	CXorf36	c-Jun [T00	352	358	8.242207	GAGGTC	0.48828	0.49076
cg2262289	CXorf36	NFI/CTF [	934	941	8.241664	CCAACC	0.18311	0.1823
cg2262289	CXorf36	ENKTF-1	1131	1138	8.19852	TGGCCA	0.73242	0.71737
cg2262289	CXorf36	ENKTF-1	1365	1372	8.19852	TGGCTG	0.73242	0.71737
cg2262289	CXorf36	ENKTF-1	1681	1688	8.19852	CCCTGC	0.73242	0.71737
cg2262289	CXorf36	NF-1 [T00	376	383	8.191058	TTGGGC	0.24414	0.24409
cg2262289	CXorf36	p53 [T006	1181	1187	8.162057	GGGCGC	0.48828	0.47377
cg2262289	CXorf36	IRF-1 [T0	1645	1653	8.151819	CCTTGG	0.25177	0.25263
cg2262289	CXorf36	NF-AT1 [	1283	1291	8.12076	GGAAAA	0.1297	0.12988
cg2262289	CXorf36	GR-alpha [	14	18	8.073878	CCTGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	25	29	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	124	128	8.073878	CCTGC	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	455	459	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	494	498	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	901	905	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	938	942	8.073878	CCTAG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	951	955	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	969	973	8.073878	GTAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1008	1012	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1095	1099	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1119	1123	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1134	1138	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1140	1144	8.073878	CCTAC	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1147	1151	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1207	1211	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1229	1233	8.073878	CCTGC	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1268	1272	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1291	1295	8.073878	CCTGC	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1294	1298	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1338	1342	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1347	1351	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1499	1503	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1514	1518	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1525	1529	8.073878	GCAGG	7.8125	7.72238

cg2262289	CXorf36	GR-alpha [	1530	1534	8.073878	GCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1640	1644	8.073878	CCTGC	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1665	1669	8.073878	CCAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1682	1686	8.073878	CCTGC	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1802	1806	8.073878	CCTAG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1803	1807	8.073878	CTAGG	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1842	1846	8.073878	CCTAC	7.8125	7.72238
cg2262289	CXorf36	GR-alpha [	1930	1934	8.073878	CCTGC	7.8125	7.72238
cg2262289	CXorf36	Pax-5 [T0	378	384	8.014558	GGGCTC	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	645	651	8.014558	TCGGCC	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	771	777	8.014558	GGGCTC	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	1112	1118	8.014558	GGGCAG	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	1221	1227	8.014558	GGGCAG	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	1333	1339	8.014558	TCTGCC	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	1352	1358	8.014558	GGGCAG	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	1408	1414	8.014558	GAGGCC	2.19727	2.14502
cg2262289	CXorf36	Pax-5 [T0	1489	1495	8.014558	GGGCAG	2.19727	2.14502
cg2262289	CXorf36	TFIID [T0	206	212	8.014558	TTTCTTA	2.19727	2.24348
cg2262289	CXorf36	TFIID [T0	694	700	8.014558	TCACAA	2.19727	2.24348
cg2262289	CXorf36	TFIID [T0	1647	1653	8.014558	TTGGAA	2.19727	2.24348
cg2262289	CXorf36	ETF [T002	1138	1148	7.870358	GCCCTA	0.07153	0.06862
cg2262289	CXorf36	ETF [T002	1411	1421	7.870358	GCCCCC	0.07153	0.06862
cg2262289	CXorf36	p53 [T006	378	384	7.833758	GGGCTC	0.48828	0.47377
cg2262289	CXorf36	p53 [T006	771	777	7.833758	GGGCTC	0.48828	0.47377
cg2262289	CXorf36	T3R-beta1	1026	1034	7.813363	GGTCGG	0.27466	0.27236
cg2262289	CXorf36	NF-AT1 [	164	172	7.744746	TTCCTTT	0.19836	0.19941
cg2262289	CXorf36	NF-AT1 [	401	409	7.72101	TTTGTTT	0.19836	0.19941
cg2262289	CXorf36	LEF-1 [T0	676	683	7.719635	GGTCAA	0.21362	0.21302
cg2262289	CXorf36	p53 [T006	1914	1920	7.641867	AAGGCC	0.73242	0.7186
cg2262289	CXorf36	ELF-1 [T0	632	644	7.608736	CCACTT	0.00846	0.00852
cg2262289	CXorf36	NFI/CTF [	7	14	7.587343	CCAAAT	0.36621	0.36674
cg2262289	CXorf36	c-Myb [T0	984	991	7.587189	GCGAGT	0.42725	0.43114
cg2262289	CXorf36	GR [T050	517	523	7.527031	TTATTT	1.83105	1.86007
cg2262289	CXorf36	C/EBPalp	1626	1632	7.465744	CATTGC	0.48828	0.49653
cg2262289	CXorf36	NF-1 [T00	1777	1784	7.445595	TTGGGA	0.24414	0.24565
cg2262289	CXorf36	PEA3 [T0	974	982	7.421728	AGGATG	0.34332	0.34161
cg2262289	CXorf36	IRF-1 [T0	1279	1287	7.387351	GTGGGG	0.14496	0.14449
cg2262289	CXorf36	p53 [T006	698	704	7.266844	AAAGCC	0.73242	0.7186
cg2262289	CXorf36	PU.1 [T02	632	644	7.265417	CCACTT	0.01001	0.01007
cg2262289	CXorf36	MAZ [T00	1312	1324	7.18478	GGGTGG	0.00918	0.00907
cg2262289	CXorf36	SRY [T00	98	106	7.175614	CTTTGC	0.30518	0.30739
cg2262289	CXorf36	SRY [T00	314	322	7.175614	CTTTGT	0.30518	0.30739
cg2262289	CXorf36	SRY [T00	693	701	7.175614	TTCACA	0.30518	0.30739
cg2262289	CXorf36	XBP-1 [T	63	68	7.172312	AATCAT	2.92969	2.97018
cg2262289	CXorf36	XBP-1 [T	66	71	7.172312	CATCAT	2.92969	2.97018
cg2262289	CXorf36	XBP-1 [T	449	454	7.172312	ATGAAG	2.92969	2.97018
cg2262289	CXorf36	XBP-1 [T	511	516	7.172312	CTTCAT	2.92969	2.97018
cg2262289	CXorf36	XBP-1 [T	1043	1048	7.172312	ATGAAG	2.92969	2.97018

cg2262289	CXorf36	XBP-1 [T	1674	1679	7.172312	ATTCAT	2.92969	2.97018
cg2262289	CXorf36	XBP-1 [T	1735	1740	7.172312	ATGAGG	2.92969	2.97018
cg2262289	CXorf36	p53 [T006	709	715	7.150251	GGGCCA	1.09863	1.07125
cg2262289	CXorf36	p53 [T006	860	866	7.150251	GTGGCC	1.09863	1.07125
cg2262289	CXorf36	p53 [T006	1445	1451	7.150251	GGGCCA	1.09863	1.07125
cg2262289	CXorf36	NF-AT1 [	563	571	7.095752	TTGTTTT	0.15259	0.1548
cg2262289	CXorf36	c-Ets-1 [T	168	174	7.071349	TTTCCCT	0.73242	0.73099
cg2262289	CXorf36	AR [T000	335	343	7.049779	CCTGTGT	0.23651	0.23551
cg2262289	CXorf36	IRF-1 [T0	567	575	7.044985	TTTCCTC	0.1297	0.13036
cg2262289	CXorf36	IRF-1 [T0	786	794	7.044985	TTTCCTC	0.1297	0.13036
cg2262289	CXorf36	NFI/CTF [	1320	1327	7.014249	GGGGTT	0.73242	0.73214
cg2262289	CXorf36	EBF [T05	1358	1368	6.983657	ACCCCT	0.03052	0.02964
cg2262289	CXorf36	TCF-4 [T0	663	672	6.961804	TCTTTG	0.01144	0.01152
cg2262289	CXorf36	c-Ets-1 [T	133	139	6.943262	TTTCCC	0.73242	0.73099
cg2262289	CXorf36	c-Ets-1 [T	1281	1287	6.943262	GGGGAA	0.73242	0.73099
cg2262289	CXorf36	c-Ets-1 [T	1852	1858	6.943262	TTTCCC	0.73242	0.73099
cg2262289	CXorf36	ENKTF-1	1443	1450	6.942764	CGGGGC	1.46484	1.44228
cg2262289	CXorf36	p53 [T006	1408	1414	6.938545	GAGGCC	1.09863	1.07125
cg2262289	CXorf36	STAT1bet	404	413	6.908963	GTTTCC	0.103	0.10372
cg2262289	CXorf36	NF-AT1 [	401	410	6.890694	TTTGTTT	0.01907	0.01922
cg2262289	CXorf36	E2F-1 [T0	1942	1949	6.846071	TTACCC	0.30518	0.29782
cg2262289	CXorf36	AR [T000	315	323	6.760234	TTTGTGT	0.23651	0.23551
cg2262289	CXorf36	NF-1 [T00	76	83	6.722386	TTGGCC	0.24414	0.24147
cg2262289	CXorf36	NF-1 [T00	1487	1494	6.722386	TTGGGC	0.24414	0.24147
cg2262289	CXorf36	c-Myb [T0	1955	1962	6.719843	CAACTA	0.30518	0.3056
cg2262289	CXorf36	c-Jun [T00	1716	1722	6.668031	TGACTT	0.61035	0.60769
cg2262289	CXorf36	TFII-I [T0	369	374	6.581441	GGAGTG	0.97656	0.97366
cg2262289	CXorf36	TFII-I [T0	490	495	6.581441	ATCTCC	0.97656	0.97366
cg2262289	CXorf36	TFII-I [T0	1247	1252	6.581441	GGAGAT	0.97656	0.97366
cg2262289	CXorf36	TFII-I [T0	1297	1302	6.581441	GGAGTG	0.97656	0.97366
cg2262289	CXorf36	TFII-I [T0	1791	1796	6.581441	GGAGAT	0.97656	0.97366
cg2262289	CXorf36	NF-AT1 [	1848	1856	6.562181	CCTTTTT	0.03815	0.03835
cg2262289	CXorf36	PXR-1:RX	1863	1870	6.5446	TGAACA	0.24414	0.24672
cg2262289	CXorf36	XBP-1 [T	833	838	6.478682	ATGCCA	0.97656	0.97062
cg2262289	CXorf36	c-Myb [T0	1962	1969	6.454077	CAACTG	0.30518	0.3056
cg2262289	CXorf36	c-Ets-1 [T	1647	1653	6.423689	TTGGAA	0.48828	0.48798
cg2262289	CXorf36	TCF-4E [T	561	567	6.302385	CTTTGTT	0.61035	0.61344
cg2262289	CXorf36	TCF-4E [T	1865	1871	6.302385	AACAAA	0.61035	0.61344
cg2262289	CXorf36	c-Ets-1 [T	405	411	6.295602	TTTCCAT	0.48828	0.48798
cg2262289	CXorf36	GR-alpha [	236	240	6.263098	CCTCA	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	342	346	6.263098	CCTTA	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	351	355	6.263098	TGAGG	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	500	504	6.263098	CCTTA	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	667	671	6.263098	TGAGG	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	1243	1247	6.263098	TGAGG	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	1255	1259	6.263098	TGAGG	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	1520	1524	6.263098	TGAGG	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	1580	1584	6.263098	CCTCA	3.90625	3.91061

cg2262289	CXorf36	GR-alpha [	1736	1740	6.263098	TGAGG	3.90625	3.91061
cg2262289	CXorf36	GR-alpha [	1921	1925	6.263098	TGAGG	3.90625	3.91061
cg2262289	CXorf36	ETF [T002	1345	1355	6.253495	GAGCAG	0.00954	0.00918
cg2262289	CXorf36	HNF-1C [	1983	1991	6.061796	GTTACT	0.14496	0.14811
cg2262289	CXorf36	GR-alpha [	356	360	6.055408	TCAGG	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	547	551	6.055408	TTAGG	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	638	642	6.055408	CCTGA	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	706	710	6.055408	TCAGG	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	716	720	6.055408	TCAGG	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	846	850	6.055408	CCTAA	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	1081	1085	6.055408	CCTGA	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	1886	1890	6.055408	CCTGA	3.90625	3.9065
cg2262289	CXorf36	GR-alpha [	1919	1923	6.055408	CCTGA	3.90625	3.9065
cg2262289	CXorf36	c-Ets-1 [T	282	288	6.039428	TTTCCAC	0.36621	0.36731
cg2262289	CXorf36	TCF-4 [T0	675	684	6.036797	AGGTCA	0.04578	0.04635
cg2262289	CXorf36	p53 [T006	645	651	5.883561	TCGGCC	0.61035	0.594
cg2262289	CXorf36	STAT4 [T	162	167	5.882353	CCTTCC	0.48828	0.48408
cg2262289	CXorf36	STAT4 [T	189	194	5.882353	CCTTCC	0.48828	0.48408
cg2262289	CXorf36	STAT4 [T	193	198	5.882353	CCTTCC	0.48828	0.48408
cg2262289	CXorf36	STAT4 [T	575	580	5.882353	CCTTCC	0.48828	0.48408
cg2262289	CXorf36	c-Ets-1 [T	1369	1375	5.814485	TGGGAA	0.36621	0.36731
cg2262289	CXorf36	c-Jun [T00	1825	1831	5.783074	TGACTT	0.36621	0.37082
cg2262289	CXorf36	NF-AT1 [	1649	1657	5.77403	GGAAAG	0.06866	0.06922
cg2262289	CXorf36	VDR [T00	1859	1867	5.771401	ATGCTG	0.42725	0.42999
cg2262289	CXorf36	VDR [T00	1875	1883	5.771401	AGCATG	0.42725	0.42999
cg2262289	CXorf36	PXR-1:RX	1879	1886	5.726524	TGAACC	0.06104	0.06104
cg2262289	CXorf36	RXR-alpha	396	402	5.715466	GGGTGT	0.61035	0.6044
cg2262289	CXorf36	c-Jun [T00	330	336	5.703976	TGACCC	0.48828	0.48665
cg2262289	CXorf36	c-Jun [T00	359	365	5.703976	GGGGTC	0.48828	0.48665
cg2262289	CXorf36	c-Jun [T00	928	934	5.703976	TGACCC	0.48828	0.48665
cg2262289	CXorf36	ENKTF-1	707	714	5.687009	CAGGGC	0.73242	0.7249
cg2262289	CXorf36	c-Ets-1 [T	251	257	5.686398	CTTCCCT	0.36621	0.3623
cg2262289	CXorf36	IRF-1 [T0	282	290	5.65977	TTTCCAC	0.22888	0.23087
cg2262289	CXorf36	T3R-beta1	238	246	5.591999	TCACCT	0.21362	0.21287
cg2262289	CXorf36	T3R-beta1	1237	1245	5.572705	TGGGGG	0.21362	0.21287
cg2262289	CXorf36	IRF-1 [T0	405	413	5.564062	TTTCCAT	0.22888	0.23087
cg2262289	CXorf36	NFI/CTF [	372	379	5.558661	GTGATT	0.54932	0.55038
cg2262289	CXorf36	NFI/CTF [	579	586	5.558661	CCAAGC	0.54932	0.55038
cg2262289	CXorf36	Pax-5 [T0	1181	1187	5.544826	GGGCGC	0.73242	0.72046
cg2262289	CXorf36	TFIID [T0	546	552	5.544826	TTTAGG	0.73242	0.75085
cg2262289	CXorf36	TFIID [T0	1888	1894	5.544826	TGATAA	0.73242	0.75085
cg2262289	CXorf36	RXR-alpha	606	612	5.271235	GGGTGG	0.61035	0.6044
cg2262289	CXorf36	RXR-alpha	1312	1318	5.271235	GGGTGG	0.61035	0.6044
cg2262289	CXorf36	RXR-alpha	1397	1403	5.271235	GGGTGG	0.61035	0.6044
cg2262289	CXorf36	RXR-alpha	1402	1408	5.271235	GGGTGG	0.61035	0.6044
cg2262289	CXorf36	RXR-alpha	1617	1623	5.271235	TCTACC	0.61035	0.6044
cg2262289	CXorf36	RXR-alpha	1635	1641	5.271235	CCCACC	0.61035	0.6044
cg2262289	CXorf36	ETF [T002	1174	1184	5.246906	GGGGGC	0.02861	0.02737

cg2262289	CXorf36	GR [T050	96	102	5.207533	GTCTTTC	0.24414	0.24606
cg2262289	CXorf36	AP-2alpha	72	77	5.100982	GCCTTT	0.97656	0.97567
cg2262289	CXorf36	NF-Y [T0	296	303	5.094053	CTCCCA	0.36621	0.36847
cg2262289	CXorf36	GR-beta [	57	61	5.042296	GTATT	3.90625	3.95351
cg2262289	CXorf36	GR-beta [	898	902	5.042296	AATCC	3.90625	3.95351
cg2262289	CXorf36	GR-beta [	1304	1308	5.042296	GGATT	3.90625	3.95351
cg2262289	CXorf36	E2F-1 [T0	753	760	5.042045	CATCCC	0.18311	0.17901
cg2262289	CXorf36	c-Ets-1 [T	576	582	5.038739	CTTCCA	0.48828	0.49031
cg2262289	CXorf36	C/EBPalp	60	66	5.024728	TTCAAT	0.97656	0.99332
cg2262289	CXorf36	IRF-1 [T0	133	141	4.968836	TTTCCCC	0.1297	0.1302
cg2262289	CXorf36	IRF-1 [T0	1852	1860	4.968836	TTTCCCC	0.1297	0.1302
cg2262289	CXorf36	XBP-1 [T	11	16	4.894955	ATGCCT	0.97656	0.96979
cg2262289	CXorf36	XBP-1 [T	70	75	4.894955	ATGCCT	0.97656	0.96979
cg2262289	CXorf36	RXR-alph	1453	1459	4.86724	GAGACC	0.48828	0.484
cg2262289	CXorf36	GCF [T00	1112	1120	4.846987	GGGCAG	0.27466	0.26486
cg2262289	CXorf36	HNF-3alp	388	395	4.842999	TATTTA	0.09155	0.09582
cg2262289	CXorf36	NF-AT1 [	278	287	4.823485	TCCTTTT	0.07629	0.07704
cg2262289	CXorf36	NF-AT1 [	1648	1657	4.823485	TGGAAA	0.07629	0.07704
cg2262289	CXorf36	p53 [T006	1505	1511	4.786849	GGGCAC	0.48828	0.47747
cg2262289	CXorf36	c-Ets-1 [T	1949	1955	4.782565	CTTCCAC	0.48828	0.49031
cg2262289	CXorf36	TFII-I [T0	435	440	4.756447	GGACTG	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	526	531	4.756447	CATTCC	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	541	546	4.756447	GGACAT	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	897	902	4.756447	CAATCC	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	1216	1221	4.756447	GGAATG	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	1304	1309	4.756447	GGATTG	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	1474	1479	4.756447	GGAATG	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	1677	1682	4.756447	CATTCC	2.92969	2.93695
cg2262289	CXorf36	TFII-I [T0	1722	1727	4.756447	GGATAT	2.92969	2.93695
cg2262289	CXorf36	FOXP3 [T	478	483	4.756447	GTTGAC	2.92969	2.96063
cg2262289	CXorf36	FOXP3 [T	565	570	4.756447	GTTTTC	2.92969	2.96063
cg2262289	CXorf36	FOXP3 [T	988	993	4.756447	GTTGAC	2.92969	2.96063
cg2262289	CXorf36	FOXP3 [T	1598	1603	4.756447	GTTTTG	2.92969	2.96063
cg2262289	CXorf36	FOXP3 [T	1753	1758	4.756447	GTTTTT	2.92969	2.96063
cg2262289	CXorf36	c-Myb [T0	91	98	4.754782	TAACTG	0.30518	0.30568
cg2262289	CXorf36	HNF-1A [	1905	1912	4.684871	GTTAAG	0.12207	0.12485
cg2262289	CXorf36	HNF-1C [	86	94	4.656597	TTTATTA	0.07629	0.07843
cg2262289	CXorf36	c-Ets-1 [T	438	444	4.654478	CTGGAA	0.85449	0.85764
cg2262289	CXorf36	c-Ets-2 [T	191	199	4.589988	TTCCTTC	0.06866	0.06881
cg2262289	CXorf36	HNF-1B [	1982	1990	4.569001	AGTTAC	0.05341	0.0549
cg2262289	CXorf36	AP-2alpha	1803	1808	4.438035	CTAGGC	0.97656	0.96979
cg2262289	CXorf36	RXR-alph	1574	1580	4.423008	TCCACC	0.24414	0.24292
cg2262289	CXorf36	STAT4 [T	111	116	4.411765	TCTTCC	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	199	204	4.411765	TCTTCC	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	220	225	4.411765	TCTTCC	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	250	255	4.411765	TCTTCC	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	440	445	4.411765	GGAAGC	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	526	531	4.411765	CATTCC	1.95312	1.94235

cg2262289	CXorf36	STAT4 [T	1216	1221	4.411765	GGAATG	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	1371	1376	4.411765	GGAAGA	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	1474	1479	4.411765	GGAATG	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	1540	1545	4.411765	GGAAGA	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	1677	1682	4.411765	CATTCC	1.95312	1.94235
cg2262289	CXorf36	STAT4 [T	1948	1953	4.411765	GCTTCC	1.95312	1.94235
cg2262289	CXorf36	c-Ets-1 [T	145	151	4.411026	ATTCCTT	0.85449	0.85764
cg2262289	CXorf36	c-Ets-1 [T	1701	1707	4.411026	ATTCCTT	0.85449	0.85764
cg2262289	CXorf36	p53 [T006	1265	1271	4.33696	GGGCCA	0.24414	0.23584
cg2262289	CXorf36	p53 [T006	1378	1384	4.33696	GGGCCA	0.24414	0.23584
cg2262289	CXorf36	EBF [T054	1916	1926	4.334406	GGCCCTC	0.00572	0.00551
cg2262289	CXorf36	RXR-alpha	329	335	4.24113	GTGACC	0.97656	0.9671
cg2262289	CXorf36	RXR-alpha	343	349	4.24113	CTTACC	0.97656	0.9671
cg2262289	CXorf36	GR-beta [T	50	54	4.201913	TTATT	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	63	67	4.201913	AATCA	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	87	91	4.201913	TTATT	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	143	147	4.201913	CTATT	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	373	377	4.201913	TGATT	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	517	521	4.201913	TTATT	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	624	628	4.201913	CTATT	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	1699	1703	4.201913	CGATT	7.8125	7.94607
cg2262289	CXorf36	GR-beta [T	1899	1903	4.201913	AATAG	7.8125	7.94607
cg2262289	CXorf36	p53 [T006	495	501	4.125254	CAGGCC	0.73242	0.71379
cg2262289	CXorf36	p53 [T006	1135	1141	4.125254	CAGGCC	0.73242	0.71379
cg2262289	CXorf36	C/EBPalph	925	931	4.019783	GATTGA	0.48828	0.49358
cg2262289	CXorf36	c-Ets-2 [T	164	172	4.017001	TTCCTTT	0.16022	0.16243
cg2262289	CXorf36	c-Ets-2 [T	558	566	4.017001	TTCCTTT	0.16022	0.16243
cg2262289	CXorf36	Pax-5 [T0	698	704	4.007279	AAAGCC	1.09863	1.07975
cg2262289	CXorf36	Pax-5 [T0	1505	1511	4.007279	GGGCAC	1.09863	1.07975
cg2262289	CXorf36	Pax-5 [T0	1690	1696	4.007279	GGGCTC	1.09863	1.07975
cg2262289	CXorf36	Pax-5 [T0	1914	1920	4.007279	AAGGCC	1.09863	1.07975
cg2262289	CXorf36	TFIID [T0	86	92	4.007279	TTTATTA	1.09863	1.13456
cg2262289	CXorf36	AP-2alpha	1913	1918	3.970052	CAAGGC	0.97656	0.96469
cg2262289	CXorf36	p53 [T006	854	860	3.961937	GGGCTA	0.73242	0.71379
cg2262289	CXorf36	c-Jun [T00	656	662	3.807346	TGACTA	0.24414	0.24526
cg2262289	CXorf36	NFI/CTF [	72	79	3.793671	GCCTTTC	0.18311	0.18109
cg2262289	CXorf36	NFI/CTF [	1643	1650	3.793671	GCCCTTC	0.18311	0.18109
cg2262289	CXorf36	GR [T050	616	622	3.763516	TTCTTTG	0.73242	0.74251
cg2262289	CXorf36	GR [T050	662	668	3.763516	ATCTTTC	0.73242	0.74251
cg2262289	CXorf36	GR [T050	1597	1603	3.763516	AGTTTTC	0.73242	0.74251
cg2262289	CXorf36	GR [T050	1867	1873	3.763516	CAAAGA	0.73242	0.74251
cg2262289	CXorf36	p53 [T006	944	950	3.750231	GGGCTTC	0.73242	0.71379
cg2262289	CXorf36	p53 [T006	1127	1133	3.750231	GGGCTG	0.73242	0.71379
cg2262289	CXorf36	p53 [T006	1836	1842	3.750231	CCAGCC	0.73242	0.71379
cg2262289	CXorf36	AP-2alpha	188	193	3.743866	GCCTTC	0.48828	0.48238
cg2262289	CXorf36	AP-2alpha	451	456	3.743866	GAAGGC	0.48828	0.48238
cg2262289	CXorf36	AP-2alpha	1554	1559	3.743866	GAAGGC	0.48828	0.48238
cg2262289	CXorf36	AP-2alpha	1654	1659	3.743866	GAAGGC	0.48828	0.48238

cg2262289	CXorf36	c-Ets-2 [T	146	154	3.518824	TTCCTTC	0.18311	0.18304
cg2262289	CXorf36	c-Ets-2 [T	1702	1710	3.518824	TTCCTTC	0.18311	0.18304
cg2262289	CXorf36	HNF-3alph	1895	1902	3.500065	AAAAAA	0.27466	0.28532
cg2262289	CXorf36	GCF [T00	1117	1125	3.409768	GCGCAG	0.03052	0.02982
cg2262289	CXorf36	GCF [T00	1145	1153	3.409768	GCGCAG	0.03052	0.02982
cg2262289	CXorf36	NF-AT1 [	129	137	3.407861	ACCTTT	0.03052	0.03089
cg2262289	CXorf36	RXR-alph	610	616	3.392904	GGGTCA	1.09863	1.08572
cg2262289	CXorf36	RXR-alph	980	986	3.392904	GGGTGC	1.09863	1.08572
cg2262289	CXorf36	RXR-alph	1240	1246	3.392904	GGGTGA	1.09863	1.08572
cg2262289	CXorf36	RXR-alph	1941	1947	3.392904	TTTACC	1.09863	1.08572
cg2262289	CXorf36	Elk-1 [T00	635	643	3.381796	CTTCCTC	0.04578	0.04588
cg2262289	CXorf36	p53 [T006	1176	1182	3.375208	GGGCGG	0.73242	0.7189
cg2262289	CXorf36	p53 [T006	1275	1281	3.375208	GGGCGT	0.73242	0.7189
cg2262289	CXorf36	p53 [T006	1440	1446	3.375208	GGGCGG	0.73242	0.7189
cg2262289	CXorf36	GR-beta [	387	391	3.361531	ATATT	3.90625	3.99611
cg2262289	CXorf36	GR-beta [	661	665	3.361531	AATCT	3.90625	3.99611
cg2262289	CXorf36	GR-beta [	924	928	3.361531	AGATT	3.90625	3.99611
cg2262289	CXorf36	NF-Y [T0	375	382	3.353763	ATTGGG	0.48828	0.48904
cg2262289	CXorf36	AP-2alpha	1158	1163	3.229049	AGAGGC	0.48828	0.48238
cg2262289	CXorf36	MAZ [T00	1412	1424	3.189496	CCCCCTC	0.00474	0.00467
cg2262289	CXorf36	Elk-1 [T00	200	208	3.121991	CTTCCT	0.07629	0.07656
cg2262289	CXorf36	Elk-1 [T00	557	565	3.121991	CTTCCT	0.07629	0.07656
cg2262289	CXorf36	TFIID [T0	1599	1605	3.075094	TTTTGC	0.12207	0.12409
cg2262289	CXorf36	c-Jun [T00	609	615	3.049104	TGGGTC	0.24414	0.24403
cg2262289	CXorf36	Elk-1 [T00	163	171	2.987643	CTTCCT	0.07629	0.07656
cg2262289	CXorf36	c-Ets-2 [T	201	209	2.945838	TTCCTTT	0.06104	0.06231
cg2262289	CXorf36	STAT4 [T	144	149	2.941176	TATTCC	2.92969	2.929
cg2262289	CXorf36	STAT4 [T	167	172	2.941176	CTTTCC	2.92969	2.929
cg2262289	CXorf36	STAT4 [T	556	561	2.941176	ACTTCC	2.92969	2.929
cg2262289	CXorf36	STAT4 [T	634	639	2.941176	ACTTCC	2.92969	2.929
cg2262289	CXorf36	STAT4 [T	737	742	2.941176	TGTTCC	2.92969	2.929
cg2262289	CXorf36	STAT4 [T	1462	1467	2.941176	GGAACA	2.92969	2.929
cg2262289	CXorf36	STAT4 [T	1649	1654	2.941176	GGAAAG	2.92969	2.929
cg2262289	CXorf36	STAT4 [T	1700	1705	2.941176	GATTCC	2.92969	2.929
cg2262289	CXorf36	p53 [T006	1112	1118	2.813291	GGGCAG	0.48828	0.47786
cg2262289	CXorf36	p53 [T006	1489	1495	2.813291	GGGCAG	0.48828	0.47786
cg2262289	CXorf36	AR [T000	541	549	2.735606	GGACAT	0.11444	0.11507
cg2262289	CXorf36	RXR-alph	1321	1327	2.726556	GGGTTG	0.85449	0.84796
cg2262289	CXorf36	AP-2alpha	667	672	2.550491	TGAGGC	0.48828	0.48266
cg2262289	CXorf36	AP-2alpha	1255	1260	2.550491	TGAGGC	0.48828	0.48266
cg2262289	CXorf36	AP-2alpha	1736	1741	2.550491	TGAGGC	0.48828	0.48266
cg2262289	CXorf36	AP-2alpha	1921	1926	2.550491	TGAGGC	0.48828	0.48266
cg2262289	CXorf36	RXR-alph	1629	1635	2.544678	TGCACC	0.85449	0.84796
cg2262289	CXorf36	C/EBPalph	298	304	2.371703	CCCAAT	0.48828	0.49114
cg2262289	CXorf36	LEF-1 [T0	98	105	2.345041	CTTTGC	0.09155	0.09192
cg2262289	CXorf36	RXR-alph	1355	1361	2.322562	CAGACC	0.85449	0.84796
cg2262289	CXorf36	Elk-1 [T00	194	202	2.299314	CTTCCTC	0.09155	0.09114
cg2262289	CXorf36	RAR-alph	359	371	2.298141	GGGGTC	0.00107	0.00106

cg2262289	CXorf36	GATA-1 [	1721	1726	2.176375	TGGATA	3.90625	3.92756
cg2262289	CXorf36	Elk-1 [T00	1536	1544	2.164966	GAGAGG	0.05341	0.05317
cg2262289	CXorf36	c-Ets-2 [T	568	576	2.142327	TTCCTCT	0.16785	0.16856
cg2262289	CXorf36	c-Ets-2 [T	787	795	2.142327	TTCCTCT	0.16785	0.16856
cg2262289	CXorf36	c-Ets-2 [T	1535	1543	2.142327	GGAGAG	0.16785	0.16856
cg2262289	CXorf36	LEF-1 [T0	561	568	2.004405	CTTTGTT	0.18311	0.18582
cg2262289	CXorf36	GATA-1 [	747	752	2.001358	TATCCC	3.90625	3.92756
cg2262289	CXorf36	GATA-1 [	1779	1784	2.001358	GGGATA	3.90625	3.92756
cg2262289	CXorf36	AP-2alpha	687	692	1.871933	GCCTCC	0.97656	0.95407
cg2262289	CXorf36	AP-2alpha	905	910	1.871933	GGAGGC	0.97656	0.95407
cg2262289	CXorf36	AP-2alpha	1407	1412	1.871933	GGAGGC	0.97656	0.95407
cg2262289	CXorf36	TBP [T00	1756	1765	1.871542	TTTATAT	0.18311	0.18942
cg2262289	CXorf36	TFII-I [T0	173	178	1.824994	CTCTCC	0.48828	0.48408
cg2262289	CXorf36	TFII-I [T0	181	186	1.824994	CTCTCC	0.48828	0.48408
cg2262289	CXorf36	TFII-I [T0	294	299	1.824994	CTCTCC	0.48828	0.48408
cg2262289	CXorf36	TFII-I [T0	571	576	1.824994	CTCTCC	0.48828	0.48408
cg2262289	CXorf36	TFII-I [T0	887	892	1.824994	GGAGAG	0.48828	0.48408
cg2262289	CXorf36	TFII-I [T0	1154	1159	1.824994	GGAGAG	0.48828	0.48408
cg2262289	CXorf36	TFII-I [T0	1535	1540	1.824994	GGAGAG	0.48828	0.48408
cg2262289	CXorf36	TFII-I [T0	1549	1554	1.824994	GGAGAG	0.48828	0.48408
cg2262289	CXorf36	p53 [T006	1221	1227	1.758307	GGGCAG	0.36621	0.36261
cg2262289	CXorf36	p53 [T006	1333	1339	1.758307	TCTGCCC	0.36621	0.36261
cg2262289	CXorf36	p53 [T006	1352	1358	1.758307	GGGCAG	0.36621	0.36261
cg2262289	CXorf36	RXR-alpha	360	366	1.696452	GGGTCA	0.48828	0.48222
cg2262289	CXorf36	GR-beta [	10	14	1.680765	AATGC	3.90625	3.94936
cg2262289	CXorf36	GR-beta [	504	508	1.680765	AATGC	3.90625	3.94936
cg2262289	CXorf36	GR-beta [	1603	1607	1.680765	GCATT	3.90625	3.94936
cg2262289	CXorf36	GR-beta [	1672	1676	1.680765	GAATT	3.90625	3.94936
cg2262289	CXorf36	GR-beta [	1673	1677	1.680765	AATTC	3.90625	3.94936
cg2262289	CXorf36	GR-beta [	1937	1941	1.680765	GAATT	3.90625	3.94936
cg2262289	CXorf36	HNF-1B [	87	95	1.651022	TTATTA	0.00763	0.00794
cg2262289	CXorf36	c-Ets-2 [T	113	121	1.64415	TTCCTCC	0.04578	0.04579
cg2262289	CXorf36	c-Ets-2 [T	222	230	1.64415	TTCCTCC	0.04578	0.04579
cg2262289	CXorf36	C/EBPbeta	7	10	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	76	79	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	299	302	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	376	379	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	579	582	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	620	623	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	826	829	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	865	868	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	921	924	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	934	937	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1236	1239	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1324	1327	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1487	1490	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1647	1650	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1720	1723	1.639871	TTGG	15.625	15.72563

cg2262289	CXorf36	C/EBPbeta	1777	1780	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1789	1792	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1961	1964	1.639871	CCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1975	1978	1.639871	TTGG	15.625	15.72563
cg2262289	CXorf36	IRF-1 [T0	168	176	1.616539	TTTCCCT	0.04578	0.04655
cg2262289	CXorf36	XBP-1 [T	611	616	1.583727	GGTCAT	0.97656	0.98146
cg2262289	CXorf36	Pax-5 [T0	854	860	1.537547	GGGCTA	0.73242	0.71311
cg2262289	CXorf36	Pax-5 [T0	1176	1182	1.537547	GGGCGG	0.73242	0.71311
cg2262289	CXorf36	Pax-5 [T0	1265	1271	1.537547	GGGCCA	0.73242	0.71311
cg2262289	CXorf36	Pax-5 [T0	1275	1281	1.537547	GGGCGT	0.73242	0.71311
cg2262289	CXorf36	Pax-5 [T0	1378	1384	1.537547	GGGCCA	0.73242	0.71311
cg2262289	CXorf36	Pax-5 [T0	1440	1446	1.537547	GGGCGG	0.73242	0.71311
cg2262289	CXorf36	TFIID [T0	281	287	1.537547	TTTTCCA	0.73242	0.75096
cg2262289	CXorf36	c-Ets-1 [T	567	573	1.513038	TTTCCTC	0.36621	0.36952
cg2262289	CXorf36	c-Ets-1 [T	786	792	1.513038	TTTCCTC	0.36621	0.36952
cg2262289	CXorf36	E2F-1 [T0	182	189	1.490375	TCTCCC	0.06104	0.06008
cg2262289	CXorf36	E2F-1 [T0	1162	1169	1.490375	GCGGGA	0.06104	0.06008
cg2262289	CXorf36	STAT4 [T	132	137	1.470588	TTTTCC	1.95312	1.96333
cg2262289	CXorf36	STAT4 [T	281	286	1.470588	TTTTCC	1.95312	1.96333
cg2262289	CXorf36	STAT4 [T	308	313	1.470588	AGTTCC	1.95312	1.96333
cg2262289	CXorf36	STAT4 [T	404	409	1.470588	GTTTCC	1.95312	1.96333
cg2262289	CXorf36	STAT4 [T	566	571	1.470588	TTTTCC	1.95312	1.96333
cg2262289	CXorf36	STAT4 [T	785	790	1.470588	GTTTCC	1.95312	1.96333
cg2262289	CXorf36	STAT4 [T	1283	1288	1.470588	GGAAAA	1.95312	1.96333
cg2262289	CXorf36	STAT4 [T	1851	1856	1.470588	TTTTCC	1.95312	1.96333
cg2262289	CXorf36	C/EBPbeta	61	64	1.366559	TCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	350	353	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	479	482	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	521	524	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	666	669	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	678	681	1.366559	TCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	896	899	1.366559	TCAA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	927	930	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	989	992	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1254	1257	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	C/EBPbeta	1747	1750	1.366559	TTGA	15.625	15.72563
cg2262289	CXorf36	AP-2alpha	1426	1431	1.357116	ACAGGC	0.48828	0.48203
cg2262289	CXorf36	c-Ets-2 [T	195	203	1.071163	TTCCTCT	0.06104	0.06166
cg2262289	CXorf36	GATA-1 [	410	415	1.038567	ATGATA	1.95312	1.98662
cg2262289	CXorf36	SRY [T00	561	569	0.999172	CTTTGTT	0.06104	0.06205
cg2262289	CXorf36	SRY [T00	1863	1871	0.999172	TGAACA	0.06104	0.06205
cg2262289	CXorf36	GATA-1 [	1725	1730	0.863549	TATCAC	1.95312	1.98662
cg2262289	CXorf36	RXR-alpha	927	933	0.848226	TTGACC	0.48828	0.48333
cg2262289	CXorf36	RXR-alpha	1201	1207	0.848226	GGGTTA	0.48828	0.48333
cg2262289	CXorf36	GR-beta [	39	43	0.840383	AATGA	7.8125	7.94706
cg2262289	CXorf36	GR-beta [	300	304	0.840383	CAATT	7.8125	7.94706
cg2262289	CXorf36	GR-beta [	513	517	0.840383	TCATT	7.8125	7.94706
cg2262289	CXorf36	GR-beta [	525	529	0.840383	CCATT	7.8125	7.94706

cg2262289	CXorf36	GR-beta [T	613	617	0.840383	TCATT	7.8125	7.94706
cg2262289	CXorf36	GR-beta [T	1218	1222	0.840383	AATGG	7.8125	7.94706
cg2262289	CXorf36	GR-beta [T	1476	1480	0.840383	AATGA	7.8125	7.94706
cg2262289	CXorf36	GR-beta [T	1625	1629	0.840383	CCATT	7.8125	7.94706
cg2262289	CXorf36	GR-beta [T	1676	1680	0.840383	TCATT	7.8125	7.94706
cg2262289	CXorf36	Elk-1 [T00	190	198	0.822677	CTTCCTT	0.03052	0.03057
cg2262289	CXorf36	GATA-1 [	1887	1892	0.758539	CTGATA	1.95312	1.98662
cg2262289	CXorf36	AP-2alpha	716	721	0.678558	TCAGGC	0.48828	0.48199
cg2262289	CXorf36	AP-2alpha	1080	1085	0.678558	GCCTGA	0.48828	0.48199
cg2262289	CXorf36	LEF-1 [T0	1864	1871	0.641865	GAACAA	0.06104	0.06131
cg2262289	CXorf36	C/EBPalph	374	380	0.540941	GATTGG	0.24414	0.24507
cg2262289	CXorf36	C/EBPalph	1305	1311	0.540941	GATTGT	0.24414	0.24507
cg2262289	CXorf36	c-Ets-1 [T	163	169	0.256174	CTTCCTT	0.24414	0.24569
cg2262289	CXorf36	c-Ets-1 [T	190	196	0.256174	CTTCCTT	0.24414	0.24569
cg2262289	CXorf36	c-Ets-1 [T	200	206	0.256174	CTTCCTT	0.24414	0.24569
cg2262289	CXorf36	c-Ets-1 [T	557	563	0.256174	CTTCCTT	0.24414	0.24569
cg2262289	CXorf36	AP-2alpha	13	18	0.226186	GCCTGG	0.97656	0.95305
cg2262289	CXorf36	AP-2alpha	494	499	0.226186	CCAGGC	0.97656	0.95305
cg2262289	CXorf36	AP-2alpha	1134	1139	0.226186	CCAGGC	0.97656	0.95305
cg2262289	CXorf36	AP-2alpha	1338	1343	0.226186	CCAGGC	0.97656	0.95305
cg2262289	CXorf36	AP-2alpha	1665	1670	0.226186	CCAGGC	0.97656	0.95305
cg2262289	CXorf36	GR-alpha [	73	77	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	118	122	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	130	134	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	166	170	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	172	176	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	180	184	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	197	201	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	203	207	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	215	219	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	241	245	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	255	259	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	279	283	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	291	295	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	313	317	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	322	326	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	560	564	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	570	574	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	599	603	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	789	793	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	840	844	0.207689	AAAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	880	884	0.207689	AAAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	941	945	0.207689	AGAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1068	1072	0.207689	CCTCT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1158	1162	0.207689	AGAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1374	1378	0.207689	AGAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1537	1541	0.207689	AGAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1568	1572	0.207689	CCTTT	7.8125	7.81264

cg2262289	CXorf36	GR-alpha [	1848	1852	0.207689	CCTTT	7.8125	7.81264
cg2262289	CXorf36	Elk-1 [T00	112	120	0.134348	CTTCCTC	0.06104	0.06047
cg2262289	CXorf36	Elk-1 [T00	221	229	0.134348	CTTCCTC	0.06104	0.06047
cg2262289	CXorf36	c-Ets-1 [T	112	118	0.128087	CTTCCTC	0.24414	0.2429
cg2262289	CXorf36	c-Ets-1 [T	194	200	0.128087	CTTCCTC	0.24414	0.2429
cg2262289	CXorf36	c-Ets-1 [T	221	227	0.128087	CTTCCTC	0.24414	0.2429
cg2262289	CXorf36	c-Ets-1 [T	1538	1544	0.128087	GAGGAA	0.24414	0.2429
cg2262289	CXorf36	GATA-1 [	489	494	0.105011	TATCTC	0.97656	0.98738
cg2262289	CXorf36	GATA-1 [	1792	1797	0.105011	GAGATA	0.97656	0.98738
cg2262289	CXorf36	GR-alpha [	142	146	0	CCTAT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	335	339	0	CCTGT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	532	536	0	CCTGT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	673	677	0	ACAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	745	749	0	CCTAT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	782	786	0	CCTGT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	966	970	0	CCTGT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1361	1365	0	CCTGT	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1426	1430	0	ACAGG	7.8125	7.81264
cg2262289	CXorf36	GR-alpha [	1609	1613	0	CCTGT	7.8125	7.81264
cg2262289	CXorf36	AP-2alpha	1008	1013	0	GCAGGC	0.97656	0.95305
cg2262289	CXorf36	AP-2alpha	1514	1519	0	GCAGGC	0.97656	0.95305
cg2262289	CXorf36	AP-2alpha	1929	1934	0	GCCTGC	0.97656	0.95305
cg2262289	CXorf36	XBP-1 [T	1824	1829	0	ATGACT	0.97656	0.98127
cg2262289	CXorf36	Pax-5 [T0	495	501	0	CAGGCC	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	944	950	0	GGGCTT	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	1127	1133	0	GGGCTG	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	1135	1141	0	CAGGCC	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	1512	1518	0	GGGCAG	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	1523	1529	0	GGGCAG	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	1528	1534	0	GGGCAG	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	1640	1646	0	CCTGCC	1.09863	1.06846
cg2262289	CXorf36	Pax-5 [T0	1836	1842	0	CCAGCC	1.09863	1.06846
cg2262289	CXorf36	p53 [T006	1512	1518	0	GGGCAG	0.36621	0.35912
cg2262289	CXorf36	p53 [T006	1523	1529	0	GGGCAG	0.36621	0.35912
cg2262289	CXorf36	p53 [T006	1528	1534	0	GGGCAG	0.36621	0.35912
cg2262289	CXorf36	p53 [T006	1640	1646	0	CCTGCC	0.36621	0.35912
cg2262289	CXorf36	Sp1 [T007	1175	1184	0	GGGGCG	0.00191	0.00182
cg2262289	CXorf36	Sp1 [T007	1439	1448	0	GGGGCG	0.00191	0.00182
cg2262289	CXorf36	TFII-I [T0	167	172	0	CTTTCC	1.46484	1.45997
cg2262289	CXorf36	TFII-I [T0	746	751	0	CTATCC	1.46484	1.45997
cg2262289	CXorf36	TFII-I [T0	1649	1654	0	GGAAAG	1.46484	1.45997
cg2262289	CXorf36	c-Ets-1 [T	635	641	0	CTTCCTC	0.24414	0.2429
cg2262289	CXorf36	YY1 [T00	394	397	0	ATGG	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	408	411	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	465	468	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	525	528	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	539	542	0	ATGG	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	651	654	0	CCAT	7.8125	7.81711

cg2262289	CXorf36	YY1 [T00	752	755	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	977	980	0	ATGG	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1041	1044	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1219	1222	0	ATGG	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1590	1593	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1625	1628	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1686	1689	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1688	1691	0	ATGG	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1711	1714	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	YY1 [T00	1857	1860	0	CCAT	7.8125	7.81711
cg2262289	CXorf36	ER-alpha [	330	334	0	TGACC	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	354	358	0	GGTCA	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	361	365	0	GGTCA	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	480	484	0	TGACC	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	522	526	0	TGACC	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	611	615	0	GGTCA	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	676	680	0	GGTCA	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	928	932	0	TGACC	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	1083	1087	0	TGACC	1.95312	1.9404
cg2262289	CXorf36	ER-alpha [	1970	1974	0	TGACC	1.95312	1.9404
cg2262289	CXorf36	C/EBPbeta	100	103	0	TTGC	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	316	319	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	402	405	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	471	474	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	476	479	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	563	566	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	591	594	0	GCAA	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	696	699	0	ACAA	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	948	951	0	TTGC	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1019	1022	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1194	1197	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1307	1310	0	TTGT	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1601	1604	0	TTGC	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1628	1631	0	TTGC	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1729	1732	0	ACAA	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1866	1869	0	ACAA	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1912	1915	0	ACAA	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1954	1957	0	ACAA	15.625	15.71349
cg2262289	CXorf36	C/EBPbeta	1979	1982	0	ACAA	15.625	15.71349
cg2262289	CXorf36	NF-1 [T00	861	868	0	TGGCCC	0.12207	0.11983
cg2262289	CXorf36	TFIID [T0	1755	1761	0	TTTTATA	1.09863	1.13474
cg2262289	CXorf36	TFIID [T0	1891	1897	0	TAAAAA	1.09863	1.13474
cg2262289	CXorf36	FOXP3 [T	1728	1733	0	CACAAC	1.46484	1.47315
cg2262289	CXorf36	FOXP3 [T	1953	1958	0	CACAAC	1.46484	1.47315
cg2262289	CXorf36	GR-beta [	301	305	0	AATTT	3.90625	3.99611
cg2262289	CXorf36	GR-beta [	543	547	0	ACATT	3.90625	3.99611
cg2262289	CXorf36	GR-beta [	1938	1942	0	AATTT	3.90625	3.99611
cg2262289	CXorf36	C/EBPalph	895	901	0	CTCAAT	0.24414	0.2444

cg2262289	CXorf36	PR B [T00	734	740	0	TACTGT	0.36621	0.36944
cg2262289	CXorf36	PR A [T01	734	740	0	TACTGT	0.36621	0.36944
cg2262289	CXorf36	TCF-4E [T	98	104	0	CTTTGC	0.12207	0.12262
cg2262289	CXorf36	HNF-1A [	87	94	0	TTATTA	0.24414	0.25261
cg2729146	CYP4X1	c-Ets-1 [T	1030	1036	9.969337	TGGGAA	0.24414	0.2459
cg2729146	CYP4X1	c-Ets-1 [T	1042	1048	9.969337	TGGGAA	0.24414	0.2459
cg2729146	CYP4X1	c-Ets-1 [T	1136	1142	9.969337	TGGGAA	0.24414	0.2459
cg2729146	CYP4X1	MAZ [T00	1398	1410	9.854051	GCCCCT	0.00435	0.00423
cg2729146	CYP4X1	c-Ets-1 [T	452	458	9.841249	AGGGAA	0.24414	0.2459
cg2729146	CYP4X1	STAT1bet	1412	1421	9.807397	CTTTCC	0.14877	0.1495
cg2729146	CYP4X1	XBP-1 [T	1183	1188	9.789909	AGCCAT	1.95312	1.95208
cg2729146	CYP4X1	XBP-1 [T	1552	1557	9.789909	AGCCAT	1.95312	1.95208
cg2729146	CYP4X1	NF-AT2 [	1885	1894	9.787971	TCATTT	0.08774	0.08903
cg2729146	CYP4X1	PR B [T00	1070	1076	9.743489	AACACC	1.09863	1.10292
cg2729146	CYP4X1	PR B [T00	1608	1614	9.743489	TCGTGT	1.09863	1.10292
cg2729146	CYP4X1	PR A [T01	1070	1076	9.743489	AACACC	1.09863	1.10292
cg2729146	CYP4X1	PR A [T01	1608	1614	9.743489	TCGTGT	1.09863	1.10292
cg2729146	CYP4X1	LEF-1 [T0	111	118	9.72404	CTTTGC	0.21362	0.2139
cg2729146	CYP4X1	Elk-1 [T00	1821	1829	9.62002	CTTCCA	0.07629	0.07577
cg2729146	CYP4X1	Pax-5 [T0	267	273	9.552105	TCCGCC	1.46484	1.43083
cg2729146	CYP4X1	Pax-5 [T0	405	411	9.552105	GGGCGG	1.46484	1.43083
cg2729146	CYP4X1	Pax-5 [T0	1683	1689	9.552105	TGCGCC	1.46484	1.43083
cg2729146	CYP4X1	Pax-5 [T0	1769	1775	9.552105	GGGCGG	1.46484	1.43083
cg2729146	CYP4X1	TFIID [T0	283	289	9.552105	TCCCAA	1.46484	1.48472
cg2729146	CYP4X1	TFIID [T0	1143	1149	9.552105	TTTGGT	1.46484	1.48472
cg2729146	CYP4X1	TFIID [T0	1339	1345	9.552105	TTTGGT	1.46484	1.48472
cg2729146	CYP4X1	NF-1 [T00	1719	1726	9.535536	TTGGGC	0.73242	0.73053
cg2729146	CYP4X1	TFII-I [T0	239	244	9.512894	GGATGG	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	397	402	9.512894	GGAATT	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	409	414	9.512894	GGAAGG	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	419	424	9.512894	GGAAGG	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	454	459	9.512894	GGAATT	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	708	713	9.512894	TTTTCC	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	864	869	9.512894	TTATCC	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	934	939	9.512894	GGAATT	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1091	1096	9.512894	GGATAA	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1138	1143	9.512894	GGAATT	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1162	1167	9.512894	GGAAAA	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1278	1283	9.512894	GGACTT	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1355	1360	9.512894	AAATCC	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1523	1528	9.512894	GGAAAC	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1558	1563	9.512894	GGAATT	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1689	1694	9.512894	CCTTCC	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1754	1759	9.512894	GGAAGG	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1824	1829	9.512894	CCATCC	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1889	1894	9.512894	TTTTCC	7.32422	7.29728
cg2729146	CYP4X1	TFII-I [T0	1993	1998	9.512894	GGAAAA	7.32422	7.29728
cg2729146	CYP4X1	FOXP3 [T	446	451	9.512894	GAGAAC	7.32422	7.35678

cg2729146	CYP4X1	FOXP3 [T	474	479	9.512894	GTTTAT	7.32422	7.35678
cg2729146	CYP4X1	FOXP3 [T	715	720	9.512894	GTTATC	7.32422	7.35678
cg2729146	CYP4X1	FOXP3 [T	730	735	9.512894	GTTTAT	7.32422	7.35678
cg2729146	CYP4X1	FOXP3 [T	1054	1059	9.512894	GTAAAC	7.32422	7.35678
cg2729146	CYP4X1	FOXP3 [T	1314	1319	9.512894	GTTGGG	7.32422	7.35678
cg2729146	CYP4X1	FOXP3 [T	1612	1617	9.512894	GTTCTG	7.32422	7.35678
cg2729146	CYP4X1	FOXP3 [T	1979	1984	9.512894	AAGAAC	7.32422	7.35678
cg2729146	CYP4X1	Ik-1 [T027	153	165	9.497194	TGAGTA	0.02941	0.02907
cg2729146	CYP4X1	c-Jun [T00	488	494	9.442241	GCTGTC	0.73242	0.73031
cg2729146	CYP4X1	NFI/CTF [	1950	1957	9.352332	AGCTTT	0.54932	0.54821
cg2729146	CYP4X1	AP-1 [T00	1263	1271	9.3434	TGACTG	0.09155	0.09305
cg2729146	CYP4X1	EBF [T05	1923	1933	9.324368	CCCACA	0.06866	0.06676
cg2729146	CYP4X1	LEF-1 [T0	1952	1959	9.313676	CTTTGG	0.21362	0.2139
cg2729146	CYP4X1	E2F-1 [T0	1771	1778	9.261732	GCGGAG	0.15259	0.14917
cg2729146	CYP4X1	NF-AT1 [	1853	1861	9.248801	GGCCTT	0.22888	0.22959
cg2729146	CYP4X1	c-Ets-1 [T	1556	1562	9.065503	ATGGAA	0.85449	0.85523
cg2729146	CYP4X1	USF2 [T0	650	659	9.056375	TCACCA	0.1545	0.15287
cg2729146	CYP4X1	USF2 [T0	1128	1137	9.056375	CTACCA	0.1545	0.15287
cg2729146	CYP4X1	NFI/CTF [	1272	1279	9.042931	ACTGTT	0.48828	0.48804
cg2729146	CYP4X1	NFI/CTF [	1311	1318	9.042931	GCAGTT	0.48828	0.48804
cg2729146	CYP4X1	GR [T050	668	674	8.971049	CAAATA	0.61035	0.61632
cg2729146	CYP4X1	GR [T050	1306	1312	8.971049	CAAAAG	0.61035	0.61632
cg2729146	CYP4X1	c-Ets-1 [T	932	938	8.937416	GTGGAA	0.85449	0.85523
cg2729146	CYP4X1	Elk-1 [T00	1420	1428	8.931691	CTTCCC	0.24414	0.24034
cg2729146	CYP4X1	c-Ets-2 [T	1518	1526	8.912323	CCCCAG	0.27466	0.27495
cg2729146	CYP4X1	p53 [T006	1445	1451	8.912104	AGGGCC	0.12207	0.11837
cg2729146	CYP4X1	ETF [T002	1762	1772	8.876947	GAGGGA	0.02384	0.02303
cg2729146	CYP4X1	c-Myb [T0	1009	1016	8.872587	GAACTA	0.39673	0.40028
cg2729146	CYP4X1	c-Jun [T00	1933	1939	8.832178	AAGGTC	0.61035	0.61059
cg2729146	CYP4X1	NF-1 [T00	281	288	8.790071	CCTCCC	0.24414	0.24467
cg2729146	CYP4X1	NF-1 [T00	621	628	8.790071	TTGGGA	0.24414	0.24467
cg2729146	CYP4X1	NF-AT1 [	1930	1938	8.769753	GGAAAG	0.22888	0.22959
cg2729146	CYP4X1	XBP-1 [T	495	500	8.75604	ATGAAC	2.92969	2.9674
cg2729146	CYP4X1	XBP-1 [T	560	565	8.75604	ATGAAA	2.92969	2.9674
cg2729146	CYP4X1	XBP-1 [T	773	778	8.75604	ATGAGA	2.92969	2.9674
cg2729146	CYP4X1	XBP-1 [T	875	880	8.75604	TTTCAT	2.92969	2.9674
cg2729146	CYP4X1	XBP-1 [T	1015	1020	8.75604	GCTCAT	2.92969	2.9674
cg2729146	CYP4X1	EBF [T05	325	335	8.453294	CCCCCT	0.03052	0.02952
cg2729146	CYP4X1	c-Myb [T0	1047	1054	8.443873	ATCAGT	0.30518	0.30924
cg2729146	CYP4X1	HNF-3alph	1236	1243	8.343064	TATTTTA	0.27466	0.28528
cg2729146	CYP4X1	PR B [T00	449	455	8.338824	AACAGG	1.09863	1.10009
cg2729146	CYP4X1	PR B [T00	711	717	8.338824	TCCTGT	1.09863	1.10009
cg2729146	CYP4X1	PR A [T01	449	455	8.338824	AACAGG	1.09863	1.10009
cg2729146	CYP4X1	PR A [T01	711	717	8.338824	TCCTGT	1.09863	1.10009
cg2729146	CYP4X1	PXR-1:RX	496	503	8.304332	TGAACA	0.12207	0.12266
cg2729146	CYP4X1	PXR-1:RX	980	987	8.304332	AGTGTT	0.12207	0.12266
cg2729146	CYP4X1	GR-alpha [	148	152	8.281568	CCTCC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	253	257	8.281568	CCTTG	7.8125	7.72956

cg2729146	CYP4X1	GR-alpha [	259	263	8.281568	CCTCG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	275	279	8.281568	CCTCG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	281	285	8.281568	CCTCC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	410	414	8.281568	GAAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	420	424	8.281568	GAAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	429	433	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	599	603	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	762	766	8.281568	CCTTC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	793	797	8.281568	CGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	992	996	8.281568	CCTCG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1115	1119	8.281568	CCTCC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1375	1379	8.281568	CCTCC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1401	1405	8.281568	CCTCC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1416	1420	8.281568	CCTTC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1443	1447	8.281568	CGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1659	1663	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1689	1693	8.281568	CCTTC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1717	1721	8.281568	CCTTG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1729	1733	8.281568	GAAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1740	1744	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1744	1748	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1747	1751	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1751	1755	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1755	1759	8.281568	GAAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1758	1762	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1761	1765	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1765	1769	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1773	1777	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1776	1780	8.281568	GGAGG	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1838	1842	8.281568	CCTCC	7.8125	7.72956
cg2729146	CYP4X1	GR-alpha [	1893	1897	8.281568	CCTTG	7.8125	7.72956
cg2729146	CYP4X1	c-Jun [T00	256	262	8.242207	TGACCT	0.48828	0.49076
cg2729146	CYP4X1	c-Jun [T00	1218	1224	8.242207	TGACCT	0.48828	0.49076
cg2729146	CYP4X1	NF-AT1 [	1409	1417	8.223794	TGCCTTT	0.1297	0.12988
cg2729146	CYP4X1	ENKTF-1	233	240	8.19852	TGGCCA	0.73242	0.71737
cg2729146	CYP4X1	ENKTF-1	351	358	8.19852	ACCCGC	0.73242	0.71737
cg2729146	CYP4X1	AhR [T01	301	311	8.184723	ACAGGC	0.04864	0.04833
cg2729146	CYP4X1	PXR-1:RX	478	485	8.180749	ATTGTT	0.12207	0.12407
cg2729146	CYP4X1	p53 [T006	1696	1702	8.162057	AGCGCC	0.48828	0.47377
cg2729146	CYP4X1	VDR [T00	481	489	8.079962	GTTCAG	0.24414	0.24712
cg2729146	CYP4X1	VDR [T00	797	805	8.079962	GCTCTG	0.24414	0.24712
cg2729146	CYP4X1	IRF-1 [T0	1857	1865	8.078284	TTTCCA	0.25177	0.25263
cg2729146	CYP4X1	GR-alpha [	9	13	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	70	74	8.073878	CCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	138	142	8.073878	CCTGC	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	236	240	8.073878	CCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	328	332	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	387	391	8.073878	GTAGG	7.8125	7.72238

cg2729146	CYP4X1	GR-alpha [	644	648	8.073878	CCTAG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	908	912	8.073878	GCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1077	1081	8.073878	CTAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1081	1085	8.073878	GCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1121	1125	8.073878	CCTAC	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1134	1138	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1297	1301	8.073878	CCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1371	1375	8.073878	CCTGC	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1385	1389	8.073878	CCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1475	1479	8.073878	CCTAC	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1520	1524	8.073878	CCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1566	1570	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1600	1604	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1618	1622	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1624	1628	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1636	1640	8.073878	GCAGG	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1654	1658	8.073878	CCTGC	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1681	1685	8.073878	CCTGC	7.8125	7.72238
cg2729146	CYP4X1	GR-alpha [	1829	1833	8.073878	CCTGG	7.8125	7.72238
cg2729146	CYP4X1	Pax-5 [T0(	757	763	8.014558	TCAGCC(	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1317	1323	8.014558	GGGCCG.	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1395	1401	8.014558	GCTGCC(	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1446	1452	8.014558	GGGCCC.	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1588	1594	8.014558	GCGGCC	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1628	1634	8.014558	GGGCTG	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1721	1727	8.014558	GGGCAC	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1791	1797	8.014558	GGAGCC	2.19727	2.14502
cg2729146	CYP4X1	Pax-5 [T0(	1918	1924	8.014558	GCAGCC	2.19727	2.14502
cg2729146	CYP4X1	TFIID [T0	45	51	8.014558	TTTGAG/	2.19727	2.24348
cg2729146	CYP4X1	TFIID [T0	665	671	8.014558	TTACAA/	2.19727	2.24348
cg2729146	CYP4X1	TFIID [T0	687	693	8.014558	TTTCAA/	2.19727	2.24348
cg2729146	CYP4X1	TFIID [T0	1195	1201	8.014558	TTTGTG/	2.19727	2.24348
cg2729146	CYP4X1	TFIID [T0	1937	1943	8.014558	TCACAA/	2.19727	2.24348
cg2729146	CYP4X1	MAZ [T00	1735	1747	7.968539	AGATGG	0.00915	0.009
cg2729146	CYP4X1	ETF [T002	1398	1408	7.870358	GCCCCT(	0.07153	0.06862
cg2729146	CYP4X1	ETF [T002	1461	1471	7.870358	GTGGGG	0.07153	0.06862
cg2729146	CYP4X1	p53 [T006	1791	1797	7.833758	GGAGCC	0.48828	0.47377
cg2729146	CYP4X1	NF-AT1 [T	1908	1916	7.744746	TTGCTTT	0.19836	0.19941
cg2729146	CYP4X1	c-Jun [T00	916	922	7.686747	TGACTG	0.48828	0.48775
cg2729146	CYP4X1	GR [T050	357	363	7.527031	CAAATA.	1.83105	1.86007
cg2729146	CYP4X1	GR [T050	878	884	7.527031	CATTTC	1.83105	1.86007
cg2729146	CYP4X1	GR [T050	1140	1146	7.527031	AATTTC	1.83105	1.86007
cg2729146	CYP4X1	GR [T050	1336	1342	7.527031	CGCTTC	1.83105	1.86007
cg2729146	CYP4X1	GR [T050	1940	1946	7.527031	CAAAAG	1.83105	1.86007
cg2729146	CYP4X1	GR [T050	1950	1956	7.527031	AGCTTTC	1.83105	1.86007
cg2729146	CYP4X1	PXR-1:RX	973	980	7.486257	CCCGTT(	0.24414	0.24395
cg2729146	CYP4X1	IRF-1 [T0(	1519	1527	7.477948	CCCAGG.	0.14496	0.14449
cg2729146	CYP4X1	PEA3 [T0(	238	246	7.421728	AGGATG	0.34332	0.34161

cg2729146	CYP4X1	PEA3 [T0	1778	1786	7.421728	AGGATG	0.34332	0.34161
cg2729146	CYP4X1	C/EBPalp	456	462	7.396431	AATTGT	0.48828	0.49653
cg2729146	CYP4X1	E2F-1 [T0	407	414	7.336545	GCGGAA	0.45776	0.44878
cg2729146	CYP4X1	p53 [T006	1498	1504	7.266844	AAAGCC	0.73242	0.7186
cg2729146	CYP4X1	SRY [T00	1338	1346	7.175614	CTTTGG	0.30518	0.30739
cg2729146	CYP4X1	XBP-1 [T	532	537	7.172312	ATGAAT	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	540	545	7.172312	ATGAAT	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	544	549	7.172312	ATGAAT	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	556	561	7.172312	ATGAAT	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	763	768	7.172312	CTTCAT	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	892	897	7.172312	ATTCAT	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	945	950	7.172312	ATGATG	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	1104	1109	7.172312	ATGATG	2.92969	2.97018
cg2729146	CYP4X1	XBP-1 [T	1883	1888	7.172312	CATCAT	2.92969	2.97018
cg2729146	CYP4X1	p53 [T006	1446	1452	7.153797	GGGCCC	1.09863	1.07125
cg2729146	CYP4X1	NF-AT1 [	1162	1170	7.095752	GGAAAA	0.15259	0.1548
cg2729146	CYP4X1	TFIID [T0	1228	1234	7.082373	TTTAGC	0.12207	0.12407
cg2729146	CYP4X1	c-Ets-1 [T	1928	1934	7.071349	AGGGAA	0.73242	0.73099
cg2729146	CYP4X1	HNF-3alp	547	554	7.000129	AATAAA	0.82397	0.84946
cg2729146	CYP4X1	HNF-3alp	666	673	7.000129	TACAAA	0.82397	0.84946
cg2729146	CYP4X1	HNF-3alp	872	879	7.000129	CATTTC	0.82397	0.84946
cg2729146	CYP4X1	HNF-3alp	1246	1253	7.000129	TATAAA	0.82397	0.84946
cg2729146	CYP4X1	RXR-alph	3	9	6.967687	ACCACC	0.36621	0.36214
cg2729146	CYP4X1	NF-1 [T00	776	783	6.948522	AGACCC	0.48828	0.4856
cg2729146	CYP4X1	ENKTF-1	86	93	6.942764	TGGCGC	1.46484	1.44228
cg2729146	CYP4X1	ENKTF-1	174	181	6.942764	GCGCGC	1.46484	1.44228
cg2729146	CYP4X1	ENKTF-1	231	238	6.942764	CTTGGC	1.46484	1.44228
cg2729146	CYP4X1	ENKTF-1	1180	1187	6.942764	CATAGC	1.46484	1.44228
cg2729146	CYP4X1	p53 [T006	1588	1594	6.938545	GCGGCC	1.09863	1.07125
cg2729146	CYP4X1	VDR [T00	492	500	6.925682	TCAATG	0.42725	0.43062
cg2729146	CYP4X1	VDR [T00	983	991	6.925682	GTTCAG	0.42725	0.43062
cg2729146	CYP4X1	STAT1bet	1926	1935	6.908963	ACAGGG	0.103	0.10372
cg2729146	CYP4X1	E2F-1 [T0	349	356	6.846071	TTACCC	0.30518	0.29782
cg2729146	CYP4X1	c-Ets-1 [T	1912	1918	6.815175	TTTCCC	0.73242	0.73099
cg2729146	CYP4X1	STAT5A [	460	472	6.810722	GTAGCA	0.01341	0.01369
cg2729146	CYP4X1	c-Jun [T00	63	69	6.787369	TCTGTC	0.73242	0.73173
cg2729146	CYP4X1	c-Jun [T00	834	840	6.787369	TCTGTC	0.73242	0.73173
cg2729146	CYP4X1	C/EBPalp	1241	1247	6.786177	TACAAT	0.73242	0.74337
cg2729146	CYP4X1	NFI/CTF [	617	624	6.786076	CAGCTT	0.73242	0.73214
cg2729146	CYP4X1	NFI/CTF [	780	787	6.786076	CCAAGC	0.73242	0.73214
cg2729146	CYP4X1	POU2F2 (	1051	1061	6.735173	GTTGTA	0.04292	0.04408
cg2729146	CYP4X1	NF-1 [T00	232	239	6.722386	TTGGCC	0.24414	0.24147
cg2729146	CYP4X1	Elk-1 [T00	405	413	6.598007	GGGCGG	0.06104	0.05967
cg2729146	CYP4X1	TFII-I [T0	77	82	6.581441	GGAGTG	0.97656	0.97366
cg2729146	CYP4X1	FOXP3 [T	675	680	6.581441	TAAAAC	0.97656	0.99397
cg2729146	CYP4X1	c-Ets-1 [T	1066	1072	6.565361	CCGGAA	0.48828	0.48798
cg2729146	CYP4X1	p53 [T006	1628	1634	6.563521	GGGCTG	0.48828	0.47541
cg2729146	CYP4X1	p53 [T006	1918	1924	6.563521	GCAGCC	0.48828	0.47541

cg2729146	CYP4X1	IRF-1 [T0	1912	1920	6.549276	TTTCCC	0.19073	0.19127
cg2729146	CYP4X1	PPAR-alp	1623	1633	6.51544	CCCTGG	0.03719	0.03639
cg2729146	CYP4X1	XBP-1 [T	745	750	6.478682	TGGCAT	0.97656	0.97062
cg2729146	CYP4X1	XBP-1 [T	769	774	6.478682	GGGCAT	0.97656	0.97062
cg2729146	CYP4X1	XBP-1 [T	1152	1157	6.478682	ATGCCA	0.97656	0.97062
cg2729146	CYP4X1	NF-kappa	607	617	6.465662	GGGGAG	0.03052	0.02976
cg2729146	CYP4X1	C/EBPalp	491	497	6.460799	GTCAAT	0.48828	0.49071
cg2729146	CYP4X1	C/EBPalp	570	576	6.460799	GGCAAT	0.48828	0.49071
cg2729146	CYP4X1	RAR-beta	218	227	6.415195	GGGGTT	0.18311	0.183
cg2729146	CYP4X1	p53 [T006	1683	1689	6.403751	TGCGCC	0.48828	0.47541
cg2729146	CYP4X1	p53 [T006	1468	1474	6.400205	GGGCGA	0.48828	0.47541
cg2729146	CYP4X1	HNF-1C [	664	672	6.400146	GTTACA	0.05341	0.05475
cg2729146	CYP4X1	MAZ [T00	1760	1772	6.395959	AGGAGG	0.00316	0.00309
cg2729146	CYP4X1	TCF-4E [	111	117	6.302385	CTTTGC	0.61035	0.61344
cg2729146	CYP4X1	TCF-4E [	1338	1344	6.302385	CTTTGG	0.61035	0.61344
cg2729146	CYP4X1	c-Ets-1 [T	1160	1166	6.295602	ATGGAA	0.48828	0.48798
cg2729146	CYP4X1	c-Ets-1 [T	1991	1997	6.295602	ATGGAA	0.48828	0.48798
cg2729146	CYP4X1	GR-alpha	142	146	6.263098	CCTCA	3.90625	3.91061
cg2729146	CYP4X1	GR-alpha	394	398	6.263098	TAAGG	3.90625	3.91061
cg2729146	CYP4X1	GR-alpha	1202	1206	6.263098	TAAGG	3.90625	3.91061
cg2729146	CYP4X1	GR-alpha	1221	1225	6.263098	CCTCA	3.90625	3.91061
cg2729146	CYP4X1	NF-AT2 [	704	713	6.245826	TACATT	0.04196	0.04255
cg2729146	CYP4X1	NF-AT1 [	1161	1170	6.201624	TGGAAA	0.03815	0.03846
cg2729146	CYP4X1	AP-1 [T00	1425	1433	6.13358	CGCGAG	0.09155	0.09072
cg2729146	CYP4X1	RXR-alph	1470	1476	6.119461	GCGACC	0.73242	0.72249
cg2729146	CYP4X1	GCF [T00	1541	1549	6.116216	GCGCTG	0.64087	0.6219
cg2729146	CYP4X1	GCF [T00	1546	1554	6.116216	GCGCAG	0.64087	0.6219
cg2729146	CYP4X1	GR-alpha	151	155	6.055408	CCTGA	3.90625	3.9065
cg2729146	CYP4X1	GR-alpha	523	527	6.055408	CCTAA	3.90625	3.9065
cg2729146	CYP4X1	GR-alpha	629	633	6.055408	TCAGG	3.90625	3.9065
cg2729146	CYP4X1	GR-alpha	656	660	6.055408	CCTGA	3.90625	3.9065
cg2729146	CYP4X1	GR-alpha	914	918	6.055408	CCTGA	3.90625	3.9065
cg2729146	CYP4X1	GR-alpha	1036	1040	6.055408	TCAGG	3.90625	3.9065
cg2729146	CYP4X1	GR-alpha	1390	1394	6.055408	CCTGA	3.90625	3.9065
cg2729146	CYP4X1	GR-alpha	1984	1988	6.055408	CCTGA	3.90625	3.9065
cg2729146	CYP4X1	c-Ets-1 [T	1857	1863	6.039428	TTTCCA	0.36621	0.36731
cg2729146	CYP4X1	C/EBPalp	1213	1219	5.996794	AACAAT	0.97656	0.99
cg2729146	CYP4X1	GCF [T00	312	320	5.917256	CCACCG	0.64087	0.6219
cg2729146	CYP4X1	GCF [T00	1536	1544	5.917256	GTTCGG	0.64087	0.6219
cg2729146	CYP4X1	p53 [T006	1317	1323	5.883561	GGGCCG	0.61035	0.594
cg2729146	CYP4X1	STAT4 [T	409	414	5.882353	GGAAGG	0.48828	0.48408
cg2729146	CYP4X1	STAT4 [T	419	424	5.882353	GGAAGG	0.48828	0.48408
cg2729146	CYP4X1	STAT4 [T	1689	1694	5.882353	CCTTCC	0.48828	0.48408
cg2729146	CYP4X1	STAT4 [T	1754	1759	5.882353	GGAAGG	0.48828	0.48408
cg2729146	CYP4X1	c-Ets-1 [T	622	628	5.814485	TGGGAA	0.36621	0.36731
cg2729146	CYP4X1	c-Ets-1 [T	1690	1696	5.814485	CTTCCC	0.36621	0.36731
cg2729146	CYP4X1	AR [T000	593	601	5.811663	GGACAG	0.24414	0.24229
cg2729146	CYP4X1	STAT1bet	1911	1920	5.796867	CTTTCC	0.1545	0.1557

cg2729146	CYP4X1	VDR [T00	976	984	5.771401	GTTCAG	0.42725	0.42999
cg2729146	CYP4X1	ENKTF-1	1549	1556	5.687009	CAGAGC	0.73242	0.7249
cg2729146	CYP4X1	ENKTF-1	1602	1609	5.687009	TGGCGT	0.73242	0.7249
cg2729146	CYP4X1	ENKTF-1	1620	1627	5.687009	TGGCCC	0.73242	0.7249
cg2729146	CYP4X1	c-Ets-2 [T	710	718	5.624023	TTCCTG	0.01526	0.0156
cg2729146	CYP4X1	HNF-1A [	500	507	5.610392	CACTTA	0.24414	0.2469
cg2729146	CYP4X1	T3R-beta1	67	75	5.591999	TCACCA	0.21362	0.21287
cg2729146	CYP4X1	AP-2alpha	576	581	5.568965	GCCTAT	0.48828	0.4878
cg2729146	CYP4X1	c-Ets-1 [T	417	423	5.558311	GGGGAA	0.36621	0.3623
cg2729146	CYP4X1	c-Ets-1 [T	969	975	5.558311	CTTCCC	0.36621	0.3623
cg2729146	CYP4X1	GATA-2 [	1091	1099	5.555555	GGATAA	0.18311	0.1835
cg2729146	CYP4X1	Pax-5 [T0	569	575	5.544826	GGGCAA	0.73242	0.72046
cg2729146	CYP4X1	Pax-5 [T0	1696	1702	5.544826	AGCGCC	0.73242	0.72046
cg2729146	CYP4X1	TFIID [T0	197	203	5.544826	TTTAGT	0.73242	0.75085
cg2729146	CYP4X1	TFIID [T0	672	678	5.544826	TACTAA	0.73242	0.75085
cg2729146	CYP4X1	p53 [T006	757	763	5.508538	TCAGCC	0.61035	0.59991
cg2729146	CYP4X1	E2F-1 [T0	415	422	5.476857	GCGGGG	0.03052	0.02989
cg2729146	CYP4X1	C/EBPalph	528	534	5.455853	ATCAAT	0.73242	0.74391
cg2729146	CYP4X1	c-Ets-1 [T	1420	1426	5.430224	CTTCCC	0.36621	0.3623
cg2729146	CYP4X1	C/EBPalph	847	853	5.38654	AATTGT	0.73242	0.74391
cg2729146	CYP4X1	AP-1 [T00	751	759	5.374582	CTAGAG	0.09155	0.09214
cg2729146	CYP4X1	IRF-1 [T0	1890	1898	5.309227	TTTCCTT	0.22888	0.23087
cg2729146	CYP4X1	COUP-TF	1930	1942	5.282214	GGAAAG	0.00477	0.00473
cg2729146	CYP4X1	RXR-alpha	1039	1045	5.271235	GGGTGG	0.61035	0.6044
cg2729146	CYP4X1	RXR-alpha	1464	1470	5.271235	GGGTGG	0.61035	0.6044
cg2729146	CYP4X1	RXR-alpha	1502	1508	5.271235	CCCACC	0.61035	0.6044
cg2729146	CYP4X1	RXR-alpha	1703	1709	5.271235	CCCACC	0.61035	0.6044
cg2729146	CYP4X1	ETF [T002	1699	1709	5.246906	GCCCCC	0.02861	0.02737
cg2729146	CYP4X1	c-Jun [T00	625	631	5.193102	GAAGTC	0.61035	0.61057
cg2729146	CYP4X1	c-Ets-2 [T	392	400	5.162974	CTTAAG	0.13733	0.13828
cg2729146	CYP4X1	c-Ets-2 [T	1715	1723	5.162974	TTCCTTC	0.13733	0.13828
cg2729146	CYP4X1	c-Ets-2 [T	1891	1899	5.162974	TTCCTTC	0.13733	0.13828
cg2729146	CYP4X1	p53 [T006	267	273	5.133514	TCCGCC	0.48828	0.47747
cg2729146	CYP4X1	p53 [T006	405	411	5.133514	GGGCGG	0.48828	0.47747
cg2729146	CYP4X1	p53 [T006	1769	1775	5.133514	GGGCGG	0.48828	0.47747
cg2729146	CYP4X1	NF-AT1 [	1886	1894	5.125037	CATTTTT	0.05341	0.05402
cg2729146	CYP4X1	AP-2alpha	1410	1415	5.100982	GCCTTT	0.97656	0.97567
cg2729146	CYP4X1	AP-2alpha	1854	1859	5.100982	GCCTTT	0.97656	0.97567
cg2729146	CYP4X1	NF-Y [T0	400	407	5.094053	ATTGGG	0.36621	0.36847
cg2729146	CYP4X1	GR-beta [	163	167	5.042296	GGATT	3.90625	3.95351
cg2729146	CYP4X1	GR-beta [	296	300	5.042296	GGATT	3.90625	3.95351
cg2729146	CYP4X1	GR-beta [	670	674	5.042296	AATAC	3.90625	3.95351
cg2729146	CYP4X1	GR-beta [	1356	1360	5.042296	AATCC	3.90625	3.95351
cg2729146	CYP4X1	E2F-1 [T0	1356	1363	5.042045	AATCCC	0.18311	0.17901
cg2729146	CYP4X1	C/EBPalph	105	111	5.024728	TGCAAT	0.97656	0.99332
cg2729146	CYP4X1	c-Myb [T0	1310	1317	4.974489	AGCAGT	0.30518	0.30568
cg2729146	CYP4X1	c-Ets-1 [T	1821	1827	4.910652	CTTCCA	0.48828	0.49031
cg2729146	CYP4X1	XBP-1 [T	510	515	4.894955	ATGCCT	0.97656	0.96979

cg2729146	CYP4X1	XBP-1 [T	574	579	4.894955	ATGCCT	0.97656	0.96979
cg2729146	CYP4X1	AP-2alpha	522	527	4.890408	GCCTAA	0.97656	0.97567
cg2729146	CYP4X1	RXR-alpha	775	781	4.86724	GAGACC	0.48828	0.484
cg2729146	CYP4X1	GCF [T00	1586	1594	4.846987	GCGCGG	0.27466	0.26486
cg2729146	CYP4X1	C/EBPalph	288	294	4.845599	AATTGC	0.97656	0.99332
cg2729146	CYP4X1	C/EBPalph	1906	1912	4.845599	AATTGC	0.97656	0.99332
cg2729146	CYP4X1	HNF-3alph	1973	1980	4.842999	TATTTA	0.09155	0.09582
cg2729146	CYP4X1	NF-AT1 [	1853	1862	4.823485	GGCCTT	0.07629	0.07704
cg2729146	CYP4X1	EBF [T05	1826	1836	4.802704	ATCCCT	0.02289	0.02224
cg2729146	CYP4X1	p53 [T006	987	993	4.786849	AGTGCC	0.48828	0.47747
cg2729146	CYP4X1	C/EBPalph	477	483	4.776286	TATTGT	0.97656	0.99332
cg2729146	CYP4X1	FOXP3 [T	860	865	4.756447	GTTTTT	2.92969	2.96063
cg2729146	CYP4X1	FOXP3 [T	1210	1215	4.756447	AAAAAC	2.92969	2.96063
cg2729146	CYP4X1	FOXP3 [T	1268	1273	4.756447	GAAAAC	2.92969	2.96063
cg2729146	CYP4X1	Ik-1 [T027	286	298	4.748597	CAAATT	0.00313	0.00308
cg2729146	CYP4X1	PPAR-alph	588	598	4.727619	TGCTGG	0.03242	0.03183
cg2729146	CYP4X1	HNF-1C [	851	859	4.656597	GTTAAT	0.07629	0.07843
cg2729146	CYP4X1	p53 [T006	316	322	4.645444	CGCGCC	0.24414	0.23584
cg2729146	CYP4X1	p53 [T006	1514	1520	4.645444	CGCGCC	0.24414	0.23584
cg2729146	CYP4X1	p53 [T006	1584	1590	4.645444	GGGCGC	0.24414	0.23584
cg2729146	CYP4X1	VDR [T00	648	656	4.617121	GTTCAC	0.37384	0.37445
cg2729146	CYP4X1	VDR [T00	1004	1012	4.617121	AGCTTG	0.37384	0.37445
cg2729146	CYP4X1	NF-kappaI	1832	1842	4.600708	GGGGAC	0.03242	0.03169
cg2729146	CYP4X1	E2F-1 [T0	1675	1682	4.545253	GCGGGA	0.15259	0.14941
cg2729146	CYP4X1	T3R-beta1	224	232	4.481316	TCACCA	0.27466	0.27551
cg2729146	CYP4X1	c-Jun [T00	1263	1269	4.441904	TGACTG	0.12207	0.12266
cg2729146	CYP4X1	AP-2alpha	1077	1082	4.438035	CTAGGC	0.97656	0.96979
cg2729146	CYP4X1	HNF-1B [	850	858	4.435774	TGTTAA	0.05341	0.0549
cg2729146	CYP4X1	STAT4 [T	968	973	4.411765	TCTTCC	1.95312	1.94235
cg2729146	CYP4X1	STAT4 [T	1205	1210	4.411765	GGAAGA	1.95312	1.94235
cg2729146	CYP4X1	STAT4 [T	1419	1424	4.411765	TCTTCC	1.95312	1.94235
cg2729146	CYP4X1	STAT4 [T	1820	1825	4.411765	TCTTCC	1.95312	1.94235
cg2729146	CYP4X1	STAT4 [T	1947	1952	4.411765	GGAAGC	1.95312	1.94235
cg2729146	CYP4X1	c-Ets-1 [T	395	401	4.411026	AAGGAA	0.85449	0.85764
cg2729146	CYP4X1	c-Ets-1 [T	1096	1102	4.411026	AAGGAA	0.85449	0.85764
cg2729146	CYP4X1	p53 [T006	1619	1625	4.33696	CTGGCC	0.24414	0.23584
cg2729146	CYP4X1	Sp1 [T007	265	274	4.333247	GATCCG	0.08583	0.08339
cg2729146	CYP4X1	RAR-beta	121	130	4.326039	CGGGTT	0.14496	0.1447
cg2729146	CYP4X1	HOXD9 [	359	368	4.321431	AATAAA	0.03433	0.03596
cg2729146	CYP4X1	HOXD10 [	359	368	4.321431	AATAAA	0.03433	0.03596
cg2729146	CYP4X1	RAR-beta	799	808	4.307573	TCTGAA	0.14496	0.1447
cg2729146	CYP4X1	RAR-beta	471	480	4.289108	TGGGTT	0.14496	0.1447
cg2729146	CYP4X1	RXR-alpha	348	354	4.24113	CTTACC	0.97656	0.9671
cg2729146	CYP4X1	RXR-alpha	1833	1839	4.24113	GGGACC	0.97656	0.9671
cg2729146	CYP4X1	PXR-1:RX	121	128	4.213958	CGGGTT	0.12207	0.12119
cg2729146	CYP4X1	AP-2alpha	387	392	4.211849	GTAGGC	0.97656	0.96469
cg2729146	CYP4X1	Elk-1 [T00	1201	1209	4.204473	ATAAGG	0.09155	0.09227
cg2729146	CYP4X1	GR-beta [	131	135	4.201913	CGATT	7.8125	7.94607

cg2729146	CYP4X1	GR-beta [T	343	347	4.201913	AATCA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	359	363	4.201913	AATAA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	476	480	4.201913	TTATT	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	527	531	4.201913	AATCA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	535	539	4.201913	AATAA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	547	551	4.201913	AATAA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	551	555	4.201913	AATAA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	694	698	4.201913	TTATT	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	732	736	4.201913	TTATT	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	854	858	4.201913	AATAA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	1034	1038	4.201913	AATCA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	1046	1050	4.201913	AATCA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	1100	1104	4.201913	AATAA	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	1235	1239	4.201913	TTATT	7.8125	7.94607
cg2729146	CYP4X1	GR-beta [T	1972	1976	4.201913	CTATT	7.8125	7.94607
cg2729146	CYP4X1	c-Jun [T00	1427	1433	4.1298	CGAGTC	0.24414	0.24526
cg2729146	CYP4X1	p53 [T006	13	19	4.125254	GGGCCT	0.73242	0.71379
cg2729146	CYP4X1	p53 [T006	321	327	4.125254	CCGGCC	0.73242	0.71379
cg2729146	CYP4X1	p53 [T006	909	915	4.125254	CAGGCC	0.73242	0.71379
cg2729146	CYP4X1	c-Ets-2 [T	1200	1208	4.091811	GATAAG	0.16022	0.16243
cg2729146	CYP4X1	p53 [T006	1721	1727	4.083527	GGGCAC	0.73242	0.71379
cg2729146	CYP4X1	RXR-alpha	219	225	4.019014	GGGTTT	0.97656	0.9671
cg2729146	CYP4X1	c-Ets-2 [T	1093	1101	4.017001	ATAAAG	0.16022	0.16243
cg2729146	CYP4X1	Pax-5 [T0	987	993	4.007279	AGTGCC	1.09863	1.07975
cg2729146	CYP4X1	Pax-5 [T0	1445	1451	4.007279	AGGGCC	1.09863	1.07975
cg2729146	CYP4X1	Pax-5 [T0	1498	1504	4.007279	AAAGCC	1.09863	1.07975
cg2729146	CYP4X1	TFIID [T0	699	705	4.007279	TTTACTA	1.09863	1.13456
cg2729146	CYP4X1	TFIID [T0	853	859	4.007279	TAATAA	1.09863	1.13456
cg2729146	CYP4X1	TFIID [T0	894	900	4.007279	TCATAA	1.09863	1.13456
cg2729146	CYP4X1	TFIID [T0	1052	1058	4.007279	TTGTAA	1.09863	1.13456
cg2729146	CYP4X1	TFIID [T0	1188	1194	4.007279	TTTATAA	1.09863	1.13456
cg2729146	CYP4X1	TFIID [T0	1239	1245	4.007279	TTTACA	1.09863	1.13456
cg2729146	CYP4X1	IRF-1 [T0	1158	1166	3.947523	GAATGG	0.1297	0.13087
cg2729146	CYP4X1	IRF-1 [T0	709	717	3.788396	TTTCCTC	0.1297	0.13087
cg2729146	CYP4X1	E2F-1 [T0	1783	1790	3.784875	GCGGCA	0.15259	0.15068
cg2729146	CYP4X1	GR [T050	109	115	3.763516	ATCTTTC	0.73242	0.74251
cg2729146	CYP4X1	p53 [T006	1860	1866	3.750231	CCAGCC	0.73242	0.71379
cg2729146	CYP4X1	p53 [T006	1958	1964	3.750231	GGGCTG	0.73242	0.71379
cg2729146	CYP4X1	NF-Y [T0	469	476	3.732121	ATTGGG	0.48828	0.48904
cg2729146	CYP4X1	p53 [T006	569	575	3.728319	GGGCAA	0.73242	0.7189
cg2729146	CYP4X1	c-Ets-1 [T	1714	1720	3.71855	GTTCCTT	0.61035	0.60765
cg2729146	CYP4X1	Sp1 [T007	404	413	3.623596	GGGGCG	0.07439	0.07186
cg2729146	CYP4X1	E2F-1 [T0	1420	1427	3.55167	CTTCCCC	0.15259	0.14974
cg2729146	CYP4X1	c-Ets-2 [T	1414	1422	3.518824	TTCCTTC	0.18311	0.18304
cg2729146	CYP4X1	VDR [T00	124	132	3.462841	GTTCAA	0.21362	0.21341
cg2729146	CYP4X1	NF-AT1 [T	705	713	3.407861	ACATTTT	0.03052	0.03089
cg2729146	CYP4X1	PXR-1:RX	801	808	3.395883	TGAACC	0.12207	0.12271
cg2729146	CYP4X1	p53 [T006	183	189	3.375208	CACGCC	0.73242	0.7189

cg2729146	CYP4X1	p53 [T006	413	419	3.375208	GGGCGG	0.73242	0.7189
cg2729146	CYP4X1	p53 [T006	1489	1495	3.375208	GGGCGG	0.73242	0.7189
cg2729146	CYP4X1	GR-beta [T	108	112	3.361531	AATCT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	364	368	3.361531	AATCT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	584	588	3.361531	AGATT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	890	894	3.361531	AGATT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	1171	1175	3.361531	AATCT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	1244	1248	3.361531	AATAT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	1988	1992	3.361531	AATAT	3.90625	3.99611
cg2729146	CYP4X1	PR B [T00	847	853	3.29756	AATTGT	0.24414	0.25122
cg2729146	CYP4X1	PR A [T01	847	853	3.29756	AATTGT	0.24414	0.25122
cg2729146	CYP4X1	c-Jun [T00	753	759	3.244843	AGAGTC	0.24414	0.24403
cg2729146	CYP4X1	c-Ets-1 [T	407	413	3.231072	GCGGAA	0.24414	0.23981
cg2729146	CYP4X1	AP-2alpha	115	120	3.229049	GCCTCT	0.48828	0.48238
cg2729146	CYP4X1	AP-2alpha	1454	1459	3.229049	AGAGGC	0.48828	0.48238
cg2729146	CYP4X1	c-Fos [T00	754	763	3.154982	GAGTCA	0.06104	0.06065
cg2729146	CYP4X1	IRF-1 [T0	1989	1997	3.145547	ATATGG	0.07629	0.07756
cg2729146	CYP4X1	TFIID [T0	880	886	3.075094	TTTTGCA	0.12207	0.12409
cg2729146	CYP4X1	C/EBPalpl	585	591	3.014837	GATTGC	0.48828	0.4911
cg2729146	CYP4X1	HOXD9 [T	1244	1253	2.949288	AATATA	0.02289	0.02401
cg2729146	CYP4X1	HOXD10 [	1244	1253	2.949288	AATATA	0.02289	0.02401
cg2729146	CYP4X1	STAT4 [T	624	629	2.941176	GGAAGT	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1032	1037	2.941176	GGAATC	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1044	1049	2.941176	GGAATC	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1068	1073	2.941176	GGAACA	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1098	1103	2.941176	GGAATA	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1412	1417	2.941176	CTTTCC	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1713	1718	2.941176	GGTTCC	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1856	1861	2.941176	CTTTCC	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1911	1916	2.941176	CTTTCC	2.92969	2.929
cg2729146	CYP4X1	STAT4 [T	1930	1935	2.941176	GGAAAG	2.92969	2.929
cg2729146	CYP4X1	IRF-1 [T0	1413	1421	2.890712	TTTCCTT	0.07629	0.07756
cg2729146	CYP4X1	p53 [T006	1395	1401	2.813291	GCTGCC	0.48828	0.47786
cg2729146	CYP4X1	AhR:Arnt	1362	1371	2.810335	GCACGC	0.01717	0.01648
cg2729146	CYP4X1	PR B [T00	477	483	2.80933	TATTGT	0.73242	0.74818
cg2729146	CYP4X1	PR B [T00	1213	1219	2.80933	AACAAT	0.73242	0.74818
cg2729146	CYP4X1	PR A [T01	477	483	2.80933	TATTGT	0.73242	0.74818
cg2729146	CYP4X1	PR A [T01	1213	1219	2.80933	AACAAT	0.73242	0.74818
cg2729146	CYP4X1	TBP [T007	575	584	2.807313	TGCCTA	0.12207	0.12635
cg2729146	CYP4X1	c-Ets-2 [T	1749	1757	2.715313	AGGGAG	0.07629	0.07593
cg2729146	CYP4X1	MAZ [T00	424	436	2.669271	GTGGGG	0.00405	0.00399
cg2729146	CYP4X1	AP-2alpha	141	146	2.550491	GCCTCA	0.48828	0.48266
cg2729146	CYP4X1	Sp1 [T007	1768	1777	2.491373	GGGGCG	0.04005	0.03892
cg2729146	CYP4X1	Sp1 [T007	1488	1497	2.418403	CGGGCG	0.04005	0.03892
cg2729146	CYP4X1	C/EBPalpl	399	405	2.371703	AATTGG	0.48828	0.49114
cg2729146	CYP4X1	C/EBPalpl	468	474	2.371703	AATTGG	0.48828	0.49114
cg2729146	CYP4X1	GCF [T00	1679	1687	2.339499	GACCTG	0.06104	0.05925
cg2729146	CYP4X1	Elk-1 [T00	1943	1951	2.299314	AAGAGG	0.09155	0.09114

cg2729146	CYP4X1	T3R-beta1	1	9	2.259951	TCACCA	0.03052	0.03041
cg2729146	CYP4X1	T3R-beta1	650	658	2.259951	TCACCA	0.03052	0.03041
cg2729146	CYP4X1	GATA-2 [	439	447	2.222222	TGATAG	0.22888	0.23091
cg2729146	CYP4X1	GATA-2 [	1199	1207	2.222222	TGATAA	0.22888	0.23091
cg2729146	CYP4X1	LEF-1 [T0	1338	1345	2.21836	CTTTGG	0.18311	0.18582
cg2729146	CYP4X1	GATA-1 [	1090	1095	2.176375	AGGATA	3.90625	3.92756
cg2729146	CYP4X1	GCF [T00	1510	1518	2.140539	CTCCCG	0.09155	0.08882
cg2729146	CYP4X1	AP-2alpha	274	279	2.098119	GCCTCG	0.97656	0.95407
cg2729146	CYP4X1	AP-2alpha	793	798	2.098119	CGAGGC	0.97656	0.95407
cg2729146	CYP4X1	GATA-1 [	865	870	2.001358	TATCCC	3.90625	3.92756
cg2729146	CYP4X1	GATA-1 [	997	1002	1.896347	TATCGG	3.90625	3.92756
cg2729146	CYP4X1	PR B [T00	498	504	1.892895	AACACT	0.12207	0.12429
cg2729146	CYP4X1	PR A [T01	498	504	1.892895	AACACT	0.12207	0.12429
cg2729146	CYP4X1	AP-2alpha	147	152	1.871933	GCCTCC	0.97656	0.95407
cg2729146	CYP4X1	AP-2alpha	280	285	1.871933	GCCTCC	0.97656	0.95407
cg2729146	CYP4X1	AP-2alpha	1374	1379	1.871933	GCCTCC	0.97656	0.95407
cg2729146	CYP4X1	AP-2alpha	1659	1664	1.871933	GGAGGC	0.97656	0.95407
cg2729146	CYP4X1	TBP [T00	1188	1197	1.871542	TTTATA	0.18311	0.18942
cg2729146	CYP4X1	TBP [T00	1242	1251	1.871542	ACAATA	0.18311	0.18942
cg2729146	CYP4X1	TFII-I [T0	1379	1384	1.824994	CTCTCC	0.48828	0.48408
cg2729146	CYP4X1	TFII-I [T0	1508	1513	1.824994	CTCTCC	0.48828	0.48408
cg2729146	CYP4X1	TFII-I [T0	1964	1969	1.824994	GGAGAG	0.48828	0.48408
cg2729146	CYP4X1	FOXP3 [T	1051	1056	1.824994	GTTGTA	0.48828	0.49451
cg2729146	CYP4X1	GR-beta [	398	402	1.680765	GAATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	455	459	1.680765	GAATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	573	577	1.680765	AATGC	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	846	850	1.680765	GAATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	871	875	1.680765	GCATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	935	939	1.680765	GAATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	1139	1143	1.680765	GAATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	1151	1155	1.680765	AATGC	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	1232	1236	1.680765	GCATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	1250	1254	1.680765	AATTC	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	1559	1563	1.680765	GAATT	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	1560	1564	1.680765	AATTC	3.90625	3.94936
cg2729146	CYP4X1	GR-beta [	1905	1909	1.680765	GAATT	3.90625	3.94936
cg2729146	CYP4X1	c-Ets-1 [T	1413	1419	1.641124	TTTCCTT	0.36621	0.36952
cg2729146	CYP4X1	c-Ets-1 [T	1890	1896	1.641124	TTTCCTT	0.36621	0.36952
cg2729146	CYP4X1	C/EBPbeta	232	235	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	285	288	1.639871	CCAA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	356	359	1.639871	CCAA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	401	404	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	470	473	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	621	624	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	780	783	1.639871	CCAA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	1144	1147	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	1276	1279	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	1315	1318	1.639871	TTGG	15.625	15.72563

cg2729146	CYP4X1	C/EBPbeta	1340	1343	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	1719	1722	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	1954	1957	1.639871	TTGG	15.625	15.72563
cg2729146	CYP4X1	IRF-1 [T0	1926	1934	1.616539	ACAGGG	0.04578	0.04655
cg2729146	CYP4X1	XBP-1 [T	836	841	1.583727	TGTCAT	0.97656	0.98146
cg2729146	CYP4X1	XBP-1 [T	1217	1222	1.583727	ATGACC	0.97656	0.98146
cg2729146	CYP4X1	EBF [T05	1621	1631	1.581175	GGCCCT	0.00381	0.00363
cg2729146	CYP4X1	Pax-5 [T0	183	189	1.537547	CACGCC	0.73242	0.71311
cg2729146	CYP4X1	Pax-5 [T0	316	322	1.537547	CGCGCC	0.73242	0.71311
cg2729146	CYP4X1	Pax-5 [T0	413	419	1.537547	GGGCGG	0.73242	0.71311
cg2729146	CYP4X1	Pax-5 [T0	1489	1495	1.537547	GGGCGG	0.73242	0.71311
cg2729146	CYP4X1	Pax-5 [T0	1514	1520	1.537547	CGCGCC	0.73242	0.71311
cg2729146	CYP4X1	Pax-5 [T0	1584	1590	1.537547	GGGCGC	0.73242	0.71311
cg2729146	CYP4X1	Pax-5 [T0	1619	1625	1.537547	CTGGCC	0.73242	0.71311
cg2729146	CYP4X1	TFIID [T0	1161	1167	1.537547	TGGAAA	0.73242	0.75096
cg2729146	CYP4X1	TFIID [T0	1238	1244	1.537547	TTTTACA	0.73242	0.75096
cg2729146	CYP4X1	TFIID [T0	1992	1998	1.537547	TGGAAA	0.73242	0.75096
cg2729146	CYP4X1	E2F-1 [T0	865	872	1.490375	TATCCC	0.06104	0.06008
cg2729146	CYP4X1	E2F-1 [T0	1491	1498	1.490375	GCGGGA	0.06104	0.06008
cg2729146	CYP4X1	E2F-1 [T0	1509	1516	1.490375	TCTCCC	0.06104	0.06008
cg2729146	CYP4X1	EBF [T05	6	16	1.477196	ACCCCT	0.00381	0.00363
cg2729146	CYP4X1	STAT4 [T	397	402	1.470588	GGAATT	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	454	459	1.470588	GGAATT	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	708	713	1.470588	TTTTCC	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	934	939	1.470588	GGAATT	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	1138	1143	1.470588	GGAATT	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	1162	1167	1.470588	GGAAAA	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	1523	1528	1.470588	GGAAAC	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	1558	1563	1.470588	GGAATT	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	1889	1894	1.470588	TTTTCC	1.95312	1.96333
cg2729146	CYP4X1	STAT4 [T	1993	1998	1.470588	GGAAAA	1.95312	1.96333
cg2729146	CYP4X1	PR B [T00	979	985	1.404665	CAGTGT	0.36621	0.37023
cg2729146	CYP4X1	PR A [T01	979	985	1.404665	CAGTGT	0.36621	0.37023
cg2729146	CYP4X1	Sp1 [T007	412	421	1.388285	AGGGCG	0.03242	0.03129
cg2729146	CYP4X1	c-Ets-1 [T	709	715	1.384951	TTTCCTC	0.36621	0.36952
cg2729146	CYP4X1	c-Ets-1 [T	1521	1527	1.384951	CAGGAA	0.36621	0.36952
cg2729146	CYP4X1	C/EBPbeta	46	49	1.366559	TTGA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	126	129	1.366559	TCAA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	247	250	1.366559	TTGA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	255	258	1.366559	TTGA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	492	495	1.366559	TCAA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	529	532	1.366559	TCAA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	689	692	1.366559	TCAA	15.625	15.72563
cg2729146	CYP4X1	C/EBPbeta	1007	1010	1.366559	TTGA	15.625	15.72563
cg2729146	CYP4X1	AP-2alpha	15	20	1.357116	GCCTGT	0.48828	0.48203
cg2729146	CYP4X1	AP-2alpha	168	173	1.357116	ACAGGC	0.48828	0.48203
cg2729146	CYP4X1	AP-2alpha	301	306	1.357116	ACAGGC	0.48828	0.48203
cg2729146	CYP4X1	AP-2alpha	334	339	1.357116	GCCTGT	0.48828	0.48203

cg2729146	CYP4X1	AP-2alpha	512	517	1.357116	GCCTGT	0.48828	0.48203
cg2729146	CYP4X1	AP-2alpha	1868	1873	1.357116	GCCTGT	0.48828	0.48203
cg2729146	CYP4X1	E2F [T002	351	360	1.31691	ACCCGC(	0.00763	0.00754
cg2729146	CYP4X1	c-Ets-2 [T(	1942	1950	1.071163	AAAGAG	0.06104	0.06166
cg2729146	CYP4X1	AR [T000	433	441	0.863734	GGACAG	0.03815	0.03779
cg2729146	CYP4X1	GATA-1 [	438	443	0.863549	GTGATA	1.95312	1.98662
cg2729146	CYP4X1	GATA-1 [	1198	1203	0.863549	GTGATA	1.95312	1.98662
cg2729146	CYP4X1	GR-beta [T	193	197	0.840383	TAATT	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	288	292	0.840383	AATTG	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	399	403	0.840383	AATTG	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	456	460	0.840383	AATTG	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	468	472	0.840383	AATTG	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	494	498	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	531	535	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	539	543	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	543	547	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	555	559	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	559	563	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	692	696	0.840383	AATTA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	829	833	0.840383	AATGG	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	847	851	0.840383	AATTG	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	877	881	0.840383	TCATT	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	899	903	0.840383	AATTA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	936	940	0.840383	AATTA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1059	1063	0.840383	CCATT	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1103	1107	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1159	1163	0.840383	AATGG	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1185	1189	0.840383	CCATT	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1192	1196	0.840383	TAATT	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1216	1220	0.840383	AATGA	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1641	1645	0.840383	CCATT	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1885	1889	0.840383	TCATT	7.8125	7.94706
cg2729146	CYP4X1	GR-beta [T	1906	1910	0.840383	AATTG	7.8125	7.94706
cg2729146	CYP4X1	PXR-1:RX	645	652	0.818075	CTAGTT(	0.12207	0.12266
cg2729146	CYP4X1	PXR-1:RX	1008	1015	0.818075	TGAACT	0.12207	0.12266
cg2729146	CYP4X1	GATA-1 [	657	662	0.758539	CTGATA	1.95312	1.98662
cg2729146	CYP4X1	AP-2alpha	629	634	0.678558	TCAGGC	0.48828	0.48199
cg2729146	CYP4X1	AP-2alpha	1389	1394	0.678558	GCCTGA	0.48828	0.48199
cg2729146	CYP4X1	RXR-alpha	472	478	0.62611	GGGTTT	0.12207	0.12313
cg2729146	CYP4X1	PR B [T00	1271	1277	0.48823	AACTGT	0.12207	0.12407
cg2729146	CYP4X1	PR A [T01	1271	1277	0.48823	AACTGT	0.12207	0.12407
cg2729146	CYP4X1	GATA-1 [	966	971	0.280028	TATCTT	0.97656	0.99875
cg2729146	CYP4X1	c-Ets-1 [T(	1203	1209	0.256174	AAGGAA	0.24414	0.24569
cg2729146	CYP4X1	AP-2alpha	70	75	0.226186	CCAGGC	0.97656	0.95305
cg2729146	CYP4X1	AP-2alpha	1385	1390	0.226186	CCAGGC	0.97656	0.95305
cg2729146	CYP4X1	AP-2alpha	1617	1622	0.226186	GCCTGG	0.97656	0.95305
cg2729146	CYP4X1	c-Fos [T00	1428	1437	0.212015	GAGTCA(	0.01144	0.01142
cg2729146	CYP4X1	GR-alpha [	116	120	0.207689	CCTCT	7.8125	7.81264

cg2729146	CYP4X1	GR-alpha [	1095	1099	0.207689	AAAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1125	1129	0.207689	CCTCT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1287	1291	0.207689	AGAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1378	1382	0.207689	CCTCT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1411	1415	0.207689	CCTTT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1454	1458	0.207689	AGAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1507	1511	0.207689	CCTCT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1593	1597	0.207689	CCTTT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1788	1792	0.207689	AGAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1855	1859	0.207689	CCTTT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1932	1936	0.207689	AAAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1944	1948	0.207689	AGAGG	7.8125	7.81264
cg2729146	CYP4X1	c-Ets-1 [T(	1752	1758	0.128087	GAGGAA	0.24414	0.2429
cg2729146	CYP4X1	c-Ets-1 [T(	1945	1951	0.128087	GAGGAA	0.24414	0.2429
cg2729146	CYP4X1	GR-alpha [	16	20	0	CCTGT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	168	172	0	ACAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	301	305	0	ACAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	335	339	0	CCTGT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	441	445	0	ATAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	450	454	0	ACAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	513	517	0	CCTGT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	577	581	0	CCTAT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	595	599	0	ACAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	712	716	0	CCTGT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	924	928	0	CCTGT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1088	1092	0	ACAGG	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1869	1873	0	CCTGT	7.8125	7.81264
cg2729146	CYP4X1	GR-alpha [	1926	1930	0	ACAGG	7.8125	7.81264
cg2729146	CYP4X1	AP-2alpha	908	913	0	GCAGGC	0.97656	0.95305
cg2729146	CYP4X1	AP-2alpha	1081	1086	0	GCAGGC	0.97656	0.95305
cg2729146	CYP4X1	AP-2alpha	1370	1375	0	GCCTGC	0.97656	0.95305
cg2729146	CYP4X1	AP-2alpha	1636	1641	0	GCAGGC	0.97656	0.95305
cg2729146	CYP4X1	RXR-alpha	122	128	0	GGGTTC/	0.24414	0.2444
cg2729146	CYP4X1	RXR-alpha	801	807	0	TGAACC(	0.24414	0.2444
cg2729146	CYP4X1	Pax-5 [T0(	13	19	0	GGGCCT(	1.09863	1.06846
cg2729146	CYP4X1	Pax-5 [T0(	321	327	0	CCGGCC(	1.09863	1.06846
cg2729146	CYP4X1	Pax-5 [T0(	769	775	0	GGGCAT(	1.09863	1.06846
cg2729146	CYP4X1	Pax-5 [T0(	909	915	0	CAGGCC(	1.09863	1.06846
cg2729146	CYP4X1	Pax-5 [T0(	1860	1866	0	CCAGCC(	1.09863	1.06846
cg2729146	CYP4X1	Pax-5 [T0(	1958	1964	0	GGGCTG(	1.09863	1.06846
cg2729146	CYP4X1	p53 [T006	769	775	0	GGGCAT(	0.36621	0.35912
cg2729146	CYP4X1	ENKTF-1	1476	1483	0	CTACGC(	0.12207	0.1201
cg2729146	CYP4X1	E2F-1 [T0	1912	1919	0	TTTCCCC	0.03052	0.03017
cg2729146	CYP4X1	TFII-I [T0(	433	438	0	GGACAG	1.46484	1.45997
cg2729146	CYP4X1	TFII-I [T0(	593	598	0	GGACAG	1.46484	1.45997
cg2729146	CYP4X1	TFII-I [T0(	1412	1417	0	CTTTCC	1.46484	1.45997
cg2729146	CYP4X1	TFII-I [T0(	1856	1861	0	CTTTCC	1.46484	1.45997
cg2729146	CYP4X1	TFII-I [T0(	1911	1916	0	CTTTCC	1.46484	1.45997

cg2729146	CYP4X1	TFII-I [T0	1930	1935	0	GGAAAG	1.46484	1.45997
cg2729146	CYP4X1	YY1 [T00	216	219	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	227	230	0	CCAT	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	241	244	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	680	683	0	CCAT	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	767	770	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	830	833	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	948	951	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1019	1022	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1059	1062	0	CCAT	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1107	1110	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1160	1163	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1185	1188	0	CCAT	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1554	1557	0	CCAT	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1556	1559	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1641	1644	0	CCAT	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1737	1740	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1824	1827	0	CCAT	7.8125	7.81711
cg2729146	CYP4X1	YY1 [T00	1991	1994	0	ATGG	7.8125	7.81711
cg2729146	CYP4X1	Elk-1 [T00	1750	1758	0	GGGAGG	0.06104	0.06047
cg2729146	CYP4X1	GCF [T00	1579	1587	0	GCGCTG	0.09155	0.08765
cg2729146	CYP4X1	GCF [T00	1692	1700	0	TCCCAG	0.09155	0.08765
cg2729146	CYP4X1	ER-alpha [	256	260	0	TGACC	1.95312	1.9404
cg2729146	CYP4X1	ER-alpha [	1218	1222	0	TGACC	1.95312	1.9404
cg2729146	CYP4X1	ER-alpha [	1935	1939	0	GGTCA	1.95312	1.9404
cg2729146	CYP4X1	GATA-1 [	717	722	0	TATCTG	0.97656	0.98738
cg2729146	CYP4X1	C/EBPbeta	106	109	0	GCAA	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	113	116	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	290	293	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	458	461	0	TTGT	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	479	482	0	TTGT	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	571	574	0	GCAA	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	587	590	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	635	638	0	TTGT	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	667	670	0	ACAA	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	849	852	0	TTGT	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	882	885	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1052	1055	0	TTGT	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1177	1180	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1196	1199	0	TTGT	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1214	1217	0	ACAA	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1242	1245	0	ACAA	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1305	1308	0	GCAA	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1846	1849	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1895	1898	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1908	1911	0	TTGC	15.625	15.71349
cg2729146	CYP4X1	C/EBPbeta	1939	1942	0	ACAA	15.625	15.71349
cg2729146	CYP4X1	NF-1 [T00	1315	1322	0	TTGGGC	0.12207	0.11983

cg2729146	CYP4X1	TFIID [T0	43	49	0	TTTTTGA	1.09863	1.13474
cg2729146	CYP4X1	GR-beta [T	194	198	0	AATTT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	287	291	0	AAATT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	467	471	0	AAATT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	564	568	0	AATGT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	691	695	0	AAATT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	705	709	0	ACATT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	898	902	0	AAATT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	1140	1144	0	AATTT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	1193	1197	0	AATTT	3.90625	3.99611
cg2729146	CYP4X1	GR-beta [T	1249	1253	0	AAATT	3.90625	3.99611
cg2729146	CYP4X1	PR B [T00	202	208	0	TACTGT	0.36621	0.36944
cg2729146	CYP4X1	PR A [T01	202	208	0	TACTGT	0.36621	0.36944
cg2729146	CYP4X1	GR [T050	42	48	0	TTTTTTG	0.36621	0.37562
cg2729146	CYP4X1	HNF-3alph	695	702	0	TATTTTT	0.09155	0.09511
cg2729146	CYP4X1	HNF-1A [	851	858	0	GTTAAT	0.24414	0.25261
cg2729146	CYP4X1	IRF-2 [T01	345	350	0	TCACTT	0.48828	0.49387
cg2729146	CYP4X1	IRF-2 [T01	683	688	0	TCACTT	0.48828	0.49387
cg0191319	DCAF12L	HNF-1B [	1577	1585	9.892991	AGTTAA	0.12207	0.12399
cg0191319	DCAF12L	HNF-1C [	1845	1853	9.805024	GTTACA	0.10681	0.10839
cg0191319	DCAF12L	XBP-1 [T0	331	336	9.789909	CGCCAT	1.95312	1.95208
cg0191319	DCAF12L	XBP-1 [T0	395	400	9.789909	CGCCAT	1.95312	1.95208
cg0191319	DCAF12L	XBP-1 [T0	636	641	9.789909	ATGGCT	1.95312	1.95208
cg0191319	DCAF12L	XBP-1 [T0	1176	1181	9.789909	AGACAT	1.95312	1.95208
cg0191319	DCAF12L	XBP-1 [T0	1275	1280	9.789909	ATGTCT	1.95312	1.95208
cg0191319	DCAF12L	NF-1 [T00	204	211	9.761671	TTGGTG	0.24414	0.24405
cg0191319	DCAF12L	PR B [T00	193	199	9.743489	GCGTGT	1.09863	1.10292
cg0191319	DCAF12L	PR A [T01	193	199	9.743489	GCGTGT	1.09863	1.10292
cg0191319	DCAF12L	c-Myb [T0	1841	1848	9.729271	TTCAGT	0.36621	0.37054
cg0191319	DCAF12L	c-Ets-1 [T0	148	154	9.713162	GGGGAA	0.36621	0.36441
cg0191319	DCAF12L	RAR-beta	38	47	9.641259	GGGGTT	0.21362	0.21243
cg0191319	DCAF12L	Pax-5 [T0	317	323	9.552105	GTAGCC	1.46484	1.43083
cg0191319	DCAF12L	Pax-5 [T0	554	560	9.552105	GGGCGG	1.46484	1.43083
cg0191319	DCAF12L	Pax-5 [T0	710	716	9.552105	GGGCGG	1.46484	1.43083
cg0191319	DCAF12L	Pax-5 [T0	818	824	9.552105	GGGCGG	1.46484	1.43083
cg0191319	DCAF12L	Pax-5 [T0	1389	1395	9.552105	TTGGCC	1.46484	1.43083
cg0191319	DCAF12L	Pax-5 [T0	1605	1611	9.552105	GGCGCC	1.46484	1.43083
cg0191319	DCAF12L	TFIID [T0	1433	1439	9.552105	TGAGAA	1.46484	1.48472
cg0191319	DCAF12L	NF-1 [T00	1606	1613	9.535536	GCGCCC	0.73242	0.73053
cg0191319	DCAF12L	E2F-1 [T0	721	728	9.529774	GCGGTG	0.15259	0.14917
cg0191319	DCAF12L	TFII-I [T0	453	458	9.512894	CCGTCC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	520	525	9.512894	GTTTCC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	634	639	9.512894	GGATGG	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	684	689	9.512894	GGACCG	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1019	1024	9.512894	GGACAA	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1044	1049	9.512894	AAATCC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1156	1161	9.512894	GGACAC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1195	1200	9.512894	GGATGG	7.32422	7.29728

cg0191319	DCAF12L	TFII-I [T0	1303	1308	9.512894	TTTTCC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1370	1375	9.512894	AAATCC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1531	1536	9.512894	GGAAGG	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1654	1659	9.512894	GGATTT	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1679	1684	9.512894	CGTTCC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1703	1708	9.512894	GGATAC	7.32422	7.29728
cg0191319	DCAF12L	TFII-I [T0	1766	1771	9.512894	TTATCC	7.32422	7.29728
cg0191319	DCAF12L	FOXP3 [T	35	40	9.512894	GTTGGG	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	109	114	9.512894	GTTGGT	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	277	282	9.512894	GTTGGC	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	583	588	9.512894	GTTGGT	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1669	1674	9.512894	GAGAAC	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1674	1679	9.512894	CATAAC	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1692	1697	9.512894	GGCAAC	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1719	1724	9.512894	GTTTAG	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1727	1732	9.512894	GTTCTG	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1739	1744	9.512894	AATAAC	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1762	1767	9.512894	GTTCTT	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1773	1778	9.512894	GTTCTG	7.32422	7.35678
cg0191319	DCAF12L	FOXP3 [T	1879	1884	9.512894	GAGAAC	7.32422	7.35678
cg0191319	DCAF12L	TCF-4E [	1499	1505	9.453578	CTTTGA	0.48828	0.49215
cg0191319	DCAF12L	NFI/CTF [	1627	1634	9.352332	GACCTT	0.54932	0.54821
cg0191319	DCAF12L	POU2F2 (	1276	1286	9.350233	TGTCTT	0.03433	0.03518
cg0191319	DCAF12L	SRY [T00	1499	1507	9.264664	CTTTGA	0.12207	0.12265
cg0191319	DCAF12L	VDR [T00	1753	1761	9.234242	GTTCAT	0.12207	0.12335
cg0191319	DCAF12L	PPAR-alp	1374	1384	9.158357	CCCTGG	0.0515	0.04986
cg0191319	DCAF12L	c-Myb [T0	1183	1190	9.110773	AAACTT	0.39673	0.40028
cg0191319	DCAF12L	MAZ [T00	1920	1932	9.056677	AAGCGG	0.01413	0.01385
cg0191319	DCAF12L	NFI/CTF [	32	39	9.042931	GCTGTT	0.48828	0.48804
cg0191319	DCAF12L	GR [T050	1488	1494	8.971049	GTGTTT	0.61035	0.61632
cg0191319	DCAF12L	c-Myb [T0	1741	1748	8.947824	TAACTT	0.39673	0.40028
cg0191319	DCAF12L	T3R-beta1	450	458	8.924046	TCACCG	0.2594	0.25766
cg0191319	DCAF12L	T3R-beta1	898	906	8.924046	GCGGGG	0.2594	0.25766
cg0191319	DCAF12L	p53 [T006	964	970	8.912104	AGGGCC	0.12207	0.11837
cg0191319	DCAF12L	PR B [T00	530	536	8.827054	ACCTGT	0.36621	0.36944
cg0191319	DCAF12L	PR B [T00	1023	1029	8.827054	AACAGC	0.36621	0.36944
cg0191319	DCAF12L	PR A [T01	530	536	8.827054	ACCTGT	0.36621	0.36944
cg0191319	DCAF12L	PR A [T01	1023	1029	8.827054	AACAGC	0.36621	0.36944
cg0191319	DCAF12L	c-Jun [T00	1590	1596	8.807683	GTTGTC	0.61035	0.61059
cg0191319	DCAF12L	Elk-1 [T00	741	749	8.797343	GGCGGG	0.24414	0.24034
cg0191319	DCAF12L	NF-1 [T00	1187	1194	8.790071	TTGGCA	0.24414	0.24467
cg0191319	DCAF12L	XBP-1 [T0	1753	1758	8.75604	GTTCAT	2.92969	2.9674
cg0191319	DCAF12L	RXR-alph	933	939	8.664139	GGGTAG	0.12207	0.12014
cg0191319	DCAF12L	RXR-alph	1009	1015	8.664139	GCTACC	0.12207	0.12014
cg0191319	DCAF12L	c-Jun [T00	1793	1799	8.571705	CCAGTC	0.12207	0.12139
cg0191319	DCAF12L	p53 [T006	1510	1516	8.537081	AGAGCC	0.12207	0.11986
cg0191319	DCAF12L	USF2 [T0	214	223	8.532138	ACACCA	0.103	0.10183
cg0191319	DCAF12L	EBF [T05	1619	1629	8.430724	GTCCCT	0.03052	0.02952

cg0191319	DCAF12L	EBF [T054	340	350	8.349314	AGCCCT	0.03052	0.02952
cg0191319	DCAF12L	HNF-3alp	1041	1048	8.343064	TTAAAA	0.27466	0.28528
cg0191319	DCAF12L	PR B [T00	31	37	8.338824	GGCTGT	1.09863	1.10009
cg0191319	DCAF12L	PR B [T00	105	111	8.338824	CCCTGT	1.09863	1.10009
cg0191319	DCAF12L	PR B [T00	1586	1592	8.338824	CCCTGT	1.09863	1.10009
cg0191319	DCAF12L	PR A [T01	31	37	8.338824	GGCTGT	1.09863	1.10009
cg0191319	DCAF12L	PR A [T01	105	111	8.338824	CCCTGT	1.09863	1.10009
cg0191319	DCAF12L	PR A [T01	1586	1592	8.338824	CCCTGT	1.09863	1.10009
cg0191319	DCAF12L	E2F-1 [T0	559	566	8.336446	GCGGGC	0.15259	0.14963
cg0191319	DCAF12L	EBF [T054	1372	1382	8.326745	ATCCCT	0.03052	0.02952
cg0191319	DCAF12L	ATF3 [T01	1232	1239	8.313799	ATATGT	0.27466	0.27431
cg0191319	DCAF12L	GR-alpha [	8	12	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	71	75	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	253	257	8.281568	CCTTG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	373	377	8.281568	CCTCC	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	382	386	8.281568	CCTTC	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	499	503	8.281568	CCTCG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	577	581	8.281568	CAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	656	660	8.281568	CCTTC	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	738	742	8.281568	GAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	814	818	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	822	826	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	832	836	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	905	909	8.281568	GAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	913	917	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	923	927	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	928	932	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	947	951	8.281568	CAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	962	966	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1036	1040	8.281568	CCTTC	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1098	1102	8.281568	GAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1162	1166	8.281568	CCTTC	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1191	1195	8.281568	CAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1308	1312	8.281568	CCTCC	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1346	1350	8.281568	CCTTG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1430	1434	8.281568	CCTTG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1461	1465	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1484	1488	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1532	1536	8.281568	GAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1629	1633	8.281568	CCTTG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1689	1693	8.281568	GAAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1909	1913	8.281568	CGAGG	7.8125	7.72956
cg0191319	DCAF12L	GR-alpha [	1925	1929	8.281568	GGAGG	7.8125	7.72956
cg0191319	DCAF12L	MAZ [T00	809	821	8.259303	GAGTGG	0.00525	0.00516
cg0191319	DCAF12L	MAZ [T00	908	920	8.232074	GGCTGG	0.00915	0.009
cg0191319	DCAF12L	NF-AT1 [	1912	1920	8.223794	GGAAAG	0.1297	0.12988
cg0191319	DCAF12L	p53 [T006	356	362	8.208781	GGGGCC	0.48828	0.47377
cg0191319	DCAF12L	p53 [T006	357	363	8.208781	GGGCCC	0.48828	0.47377

cg0191319	DCAF12L	ENKTF-1	25	32	8.19852	TGGCCA	0.73242	0.71737
cg0191319	DCAF12L	ENKTF-1	328	335	8.19852	GCTCGC	0.73242	0.71737
cg0191319	DCAF12L	ENKTF-1	461	468	8.19852	TGCCGC	0.73242	0.71737
cg0191319	DCAF12L	ENKTF-1	637	644	8.19852	TGGCTG	0.73242	0.71737
cg0191319	DCAF12L	ENKTF-1	756	763	8.19852	TGGCCG	0.73242	0.71737
cg0191319	DCAF12L	ENKTF-1	1188	1195	8.19852	TGGCAA	0.73242	0.71737
cg0191319	DCAF12L	p53 [T006	509	515	8.162057	GGGCGC	0.48828	0.47377
cg0191319	DCAF12L	c-Ets-1 [T	645	651	8.116854	CTGGAA	0.24414	0.2425
cg0191319	DCAF12L	c-Ets-1 [T	1680	1686	8.116854	GTTCCA	0.24414	0.2425
cg0191319	DCAF12L	GR-alpha [	4	8	8.073878	CCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	28	32	8.073878	CCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	115	119	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	125	129	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	220	224	8.073878	CCTGC	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	224	228	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	343	347	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	350	354	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	369	373	8.073878	CCTAC	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	472	476	8.073878	CCTGC	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	524	528	8.073878	CCTGC	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	731	735	8.073878	CCTAG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	732	736	8.073878	CTAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	838	842	8.073878	GCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	850	854	8.073878	GCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	959	963	8.073878	CTAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	976	980	8.073878	CCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1049	1053	8.073878	CCTAC	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1071	1075	8.073878	CCTAC	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1106	1110	8.073878	CCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1152	1156	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1214	1218	8.073878	GCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1242	1246	8.073878	CCTGC	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1375	1379	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1443	1447	8.073878	GTAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1622	1626	8.073878	CCTGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1804	1808	8.073878	GCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1949	1953	8.073878	GCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1961	1965	8.073878	GCAGG	7.8125	7.72238
cg0191319	DCAF12L	GR-alpha [	1993	1997	8.073878	CCTGC	7.8125	7.72238
cg0191319	DCAF12L	AR [T000	1019	1027	8.055836	GGACAA	0.19836	0.19634
cg0191319	DCAF12L	Ik-1 [T027	1369	1381	8.033887	CAAATC	0.00355	0.00346
cg0191319	DCAF12L	Pax-5 [T0	11	17	8.014558	GGGCAG	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	101	107	8.014558	GCAGCC	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	299	305	8.014558	GGGCAG	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	338	344	8.014558	GAAGCC	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	356	362	8.014558	GGGGCC	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	357	363	8.014558	GGGCCC	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	442	448	8.014558	GCGGCC	2.19727	2.14502

cg0191319	DCAF12L	Pax-5 [T0	804	810	8.014558	GGGCCG	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	950	956	8.014558	GGGCAG	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	1101	1107	8.014558	GGAGCC	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	1260	1266	8.014558	TCAGCC	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	1817	1823	8.014558	GGGCAT	2.19727	2.14502
cg0191319	DCAF12L	Pax-5 [T0	1929	1935	8.014558	GGGCTG	2.19727	2.14502
cg0191319	DCAF12L	TFIID [T0	1064	1070	8.014558	TCTGAA	2.19727	2.24348
cg0191319	DCAF12L	TFIID [T0	1288	1294	8.014558	TTTCAA	2.19727	2.24348
cg0191319	DCAF12L	C/EBPalph	1706	1712	8.006685	TACAAT	0.24414	0.24674
cg0191319	DCAF12L	c-Myb [T0	1029	1036	8.005241	TAACTA	0.21362	0.21454
cg0191319	DCAF12L	ETF [T002	359	369	7.870358	GCCCCA	0.07153	0.06862
cg0191319	DCAF12L	ETF [T002	811	821	7.870358	GTGGGA	0.07153	0.06862
cg0191319	DCAF12L	ETF [T002	1922	1932	7.870358	GCGGGA	0.07153	0.06862
cg0191319	DCAF12L	p53 [T006	544	550	7.853573	GGGCCA	0.48828	0.47377
cg0191319	DCAF12L	p53 [T006	1101	1107	7.833758	GGAGCC	0.48828	0.47377
cg0191319	DCAF12L	RXR-alpha	1031	1037	7.815913	ACTACC	0.24414	0.24104
cg0191319	DCAF12L	GATA-2 [	1075	1083	7.777778	CGATAT	0.30518	0.30758
cg0191319	DCAF12L	E2F-1 [T0	44	51	7.771357	TTCGCC	0.30518	0.3
cg0191319	DCAF12L	c-Myb [T0	1824	1831	7.739476	CTCAGT	0.42725	0.43114
cg0191319	DCAF12L	MAZ [T00	918	930	7.686328	GACAGG	0.00641	0.00633
cg0191319	DCAF12L	NFI/CTF [	200	207	7.587343	ACACTT	0.36621	0.36674
cg0191319	DCAF12L	NFI/CTF [	1138	1145	7.587343	GCACTT	0.36621	0.36674
cg0191319	DCAF12L	NFI/CTF [	1362	1369	7.587343	CCAAAT	0.36621	0.36674
cg0191319	DCAF12L	NFI/CTF [	1385	1392	7.587343	ACATTT	0.36621	0.36674
cg0191319	DCAF12L	NFI/CTF [	1412	1419	7.587343	ACACTT	0.36621	0.36674
cg0191319	DCAF12L	GR [T050	532	538	7.527031	CTGTTT	1.83105	1.86007
cg0191319	DCAF12L	GR [T050	1291	1297	7.527031	CAAACA	1.83105	1.86007
cg0191319	DCAF12L	GR [T050	1295	1301	7.527031	CAAATA	1.83105	1.86007
cg0191319	DCAF12L	p53 [T006	1605	1611	7.458735	GGCGCC	0.73242	0.7186
cg0191319	DCAF12L	AR [T000	1156	1164	7.372454	GGACAC	0.25177	0.25079
cg0191319	DCAF12L	E2F-1 [T0	95	102	7.336545	GATGCC	0.45776	0.44878
cg0191319	DCAF12L	E2F-1 [T0	459	466	7.336545	GCTGCC	0.45776	0.44878
cg0191319	DCAF12L	E2F-1 [T0	673	680	7.336545	GCGGCA	0.45776	0.44878
cg0191319	DCAF12L	E2F-1 [T0	999	1006	7.336545	GCGGCA	0.45776	0.44878
cg0191319	DCAF12L	p53 [T006	1475	1481	7.266844	GGGCTT	0.73242	0.7186
cg0191319	DCAF12L	E2F [T002	461	470	7.198598	TGCCGC	0.06866	0.06749
cg0191319	DCAF12L	SRY [T00	1570	1578	7.175614	GAAGCA	0.30518	0.30739
cg0191319	DCAF12L	XBP-1 [T	1710	1715	7.172312	ATGATG	2.92969	2.97018
cg0191319	DCAF12L	XBP-1 [T	1736	1741	7.172312	ATGAAT	2.92969	2.97018
cg0191319	DCAF12L	c-Myb [T0	1769	1776	7.127234	TCCAGT	0.18311	0.18399
cg0191319	DCAF12L	c-Ets-1 [T	1304	1310	7.071349	TTTCCCT	0.73242	0.73099
cg0191319	DCAF12L	c-Jun [T00	1079	1085	7.052189	ATAGTC	0.73242	0.73173
cg0191319	DCAF12L	HNF-3alph	1655	1662	7.000129	GATTTC	0.82397	0.84946
cg0191319	DCAF12L	GCF [T00	671	679	6.987525	GCGCGG	0.45776	0.44706
cg0191319	DCAF12L	NF-1 [T00	278	285	6.948522	TTGGCG	0.48828	0.4856
cg0191319	DCAF12L	NF-1 [T00	1421	1428	6.948522	TTGGTG	0.48828	0.4856
cg0191319	DCAF12L	ENKTF-1	88	95	6.942764	TGGCAT	1.46484	1.44228
cg0191319	DCAF12L	ENKTF-1	588	595	6.942764	TGGCGG	1.46484	1.44228

cg0191319	DCAF12L	ENKTF-1	604	611	6.942764	TGGCTC	1.46484	1.44228
cg0191319	DCAF12L	ENKTF-1	680	687	6.942764	TGGCGG	1.46484	1.44228
cg0191319	DCAF12L	ENKTF-1	1106	1113	6.942764	CCAGGC	1.46484	1.44228
cg0191319	DCAF12L	p53 [T006	442	448	6.938545	GCGGCC	1.09863	1.07125
cg0191319	DCAF12L	E2F-1 [T0	206	213	6.839754	GGTGCC	0.30518	0.29782
cg0191319	DCAF12L	E2F [T002	277	286	6.807413	GTTGGC	0.06866	0.06749
cg0191319	DCAF12L	c-Jun [T00	285	291	6.787369	TCCGTC	0.73242	0.73173
cg0191319	DCAF12L	NFI/CTF [	1417	1424	6.786076	TGGTTT	0.73242	0.73214
cg0191319	DCAF12L	NFI/CTF [	1610	1617	6.786076	CCAAGC	0.73242	0.73214
cg0191319	DCAF12L	RXR-alph	1828	1834	6.785809	GTTACC	0.36621	0.36214
cg0191319	DCAF12L	p53 [T006	317	323	6.775228	GTAGCC	1.09863	1.07125
cg0191319	DCAF12L	PPAR-alph	540	550	6.755733	TGCTGG	0.01431	0.01397
cg0191319	DCAF12L	LEF-1 [T0	1499	1506	6.75468	CTTTGA	0.06104	0.06131
cg0191319	DCAF12L	AR [T000	1634	1642	6.675397	GGACAG	0.19836	0.19597
cg0191319	DCAF12L	TFII-I [T0	1526	1531	6.581441	GGAGTG	0.97656	0.97366
cg0191319	DCAF12L	TFII-I [T0	1561	1566	6.581441	CACTCC	0.97656	0.97366
cg0191319	DCAF12L	RXR-alph	1157	1163	6.563693	GACACC	0.24414	0.2434
cg0191319	DCAF12L	p53 [T006	101	107	6.563521	GCAGCC	0.48828	0.47541
cg0191319	DCAF12L	p53 [T006	338	344	6.563521	GAAGCC	0.48828	0.47541
cg0191319	DCAF12L	PPAR-alph	1595	1605	6.51544	CAGTCC	0.03719	0.03639
cg0191319	DCAF12L	XBP-1 [T	88	93	6.478682	TGGCAT	0.97656	0.97062
cg0191319	DCAF12L	XBP-1 [T	1817	1822	6.478682	GGGCAT	0.97656	0.97062
cg0191319	DCAF12L	c-Jun [T00	242	248	6.475265	TGACGC	0.61035	0.60769
cg0191319	DCAF12L	c-Myb [T0	1267	1274	6.454077	CTCAGT	0.30518	0.3056
cg0191319	DCAF12L	GATA-3 [	385	396	6.358354	TCAGAT	0.01049	0.01054
cg0191319	DCAF12L	TCF-4E [T	1882	1888	6.302385	AACAAA	0.61035	0.61344
cg0191319	DCAF12L	GR-alpha [	130	134	6.263098	CCTCA	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	448	452	6.263098	CCTCA	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	667	671	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	692	696	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	878	882	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	889	893	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1014	1018	6.263098	CCTCA	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1251	1255	6.263098	CCTCA	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1266	1270	6.263098	CCTCA	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1311	1315	6.263098	CCTCA	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1319	1323	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1349	1353	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1471	1475	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1506	1510	6.263098	CCTCA	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1517	1521	6.263098	TAAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1933	1937	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	GR-alpha [	1972	1976	6.263098	TGAGG	3.90625	3.91061
cg0191319	DCAF12L	C/EBPalph	1054	1060	6.245236	TTCAAT	0.97656	0.99
cg0191319	DCAF12L	IRF-1 [T0	1908	1916	6.24301	ACGAGG	0.16785	0.16909
cg0191319	DCAF12L	c-Ets-2 [T	522	530	6.19701	TTCCTG	0.01526	0.01543
cg0191319	DCAF12L	p53 [T006	554	560	6.188498	GGGCGG	0.61035	0.594
cg0191319	DCAF12L	p53 [T006	710	716	6.188498	GGGCGG	0.61035	0.594

cg0191319	DCAF12L	SRY [T00	769	777	6.176442	AGAGCA	0.15259	0.15366
cg0191319	DCAF12L	c-Myb [T0	1715	1722	6.12608	GCAAGT	0.21362	0.21535
cg0191319	DCAF12L	GCF [T00	637	645	6.116216	TGGCTG	0.64087	0.6219
cg0191319	DCAF12L	p53 [T006	1389	1395	6.095267	TTGGCC	0.61035	0.594
cg0191319	DCAF12L	GR-alpha [	168	172	6.055408	CCTGA	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	876	880	6.055408	CCTGA	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	1016	1020	6.055408	TCAGG	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	1469	1473	6.055408	CCTGA	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	1515	1519	6.055408	CCTAA	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	1539	1543	6.055408	CCTGA	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	1565	1569	6.055408	CCTGA	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	1797	1801	6.055408	TCAGG	3.90625	3.9065
cg0191319	DCAF12L	GR-alpha [	1970	1974	6.055408	CCTGA	3.90625	3.9065
cg0191319	DCAF12L	RXR-alph	871	877	5.937582	GGGTGC	0.73242	0.72249
cg0191319	DCAF12L	GCF [T00	594	602	5.917256	TTGCAG	0.64087	0.6219
cg0191319	DCAF12L	GCF [T00	1207	1215	5.917256	CGGCAG	0.64087	0.6219
cg0191319	DCAF12L	HNF-1B [	1737	1745	5.903284	TGAATA	0.09918	0.10196
cg0191319	DCAF12L	p53 [T006	804	810	5.883561	GGGCCG	0.61035	0.594
cg0191319	DCAF12L	STAT4 [T	1531	1536	5.882353	GGAAGG	0.48828	0.48408
cg0191319	DCAF12L	E2F-1 [T0	573	580	5.846171	GCGGCA	0.18311	0.18044
cg0191319	DCAF12L	USF1 [T0	1657	1666	5.845905	TTTTCAC	0.01526	0.01523
cg0191319	DCAF12L	c-Myb [T0	273	280	5.841835	TCCAGT	0.21362	0.21535
cg0191319	DCAF12L	c-Ets-1 [T	1941	1947	5.814485	TGGGAA	0.36621	0.36731
cg0191319	DCAF12L	AR [T000	917	925	5.811663	GGACAG	0.24414	0.24229
cg0191319	DCAF12L	STAT1bet	1908	1917	5.796867	ACGAGG	0.1545	0.1557
cg0191319	DCAF12L	c-Jun [T00	774	780	5.783074	AAAGTC	0.36621	0.37082
cg0191319	DCAF12L	c-Jun [T00	1885	1891	5.783074	AAAGTC	0.36621	0.37082
cg0191319	DCAF12L	PPAR-alp	114	124	5.741676	TCCTGG	0.03529	0.03451
cg0191319	DCAF12L	ENKTF-1	116	123	5.687009	CTGGGC	0.73242	0.7249
cg0191319	DCAF12L	ENKTF-1	279	286	5.687009	TGGCGC	0.73242	0.7249
cg0191319	DCAF12L	ENKTF-1	392	399	5.687009	GTGCGC	0.73242	0.7249
cg0191319	DCAF12L	ENKTF-1	542	549	5.687009	CTGGGC	0.73242	0.7249
cg0191319	DCAF12L	NF-1 [T00	110	117	5.626299	TTGGTC	0.24414	0.24258
cg0191319	DCAF12L	AhR:Arnt	626	635	5.620669	GGCGGC	0.0515	0.04981
cg0191319	DCAF12L	C/EBPalp	1356	1362	5.565669	TACAAT	0.73242	0.74391
cg0191319	DCAF12L	NFI/CTF [	466	473	5.558661	CCAAGC	0.54932	0.55038
cg0191319	DCAF12L	c-Ets-1 [T	1555	1561	5.558311	CTTCCC	0.36621	0.3623
cg0191319	DCAF12L	Pax-5 [T0	509	515	5.544826	GGGCGC	0.73242	0.72046
cg0191319	DCAF12L	Pax-5 [T0	544	550	5.544826	GGGCCA	0.73242	0.72046
cg0191319	DCAF12L	p53 [T006	1260	1266	5.508538	TCAGCC	0.61035	0.59991
cg0191319	DCAF12L	p53 [T006	1929	1935	5.508538	GGGCTG	0.61035	0.59991
cg0191319	DCAF12L	c-Ets-1 [T	743	749	5.430224	CGGGAA	0.36621	0.3623
cg0191319	DCAF12L	IRF-1 [T0	521	529	5.404935	TTTCCTC	0.22888	0.23087
cg0191319	DCAF12L	p53 [T006	965	971	5.39549	GGGCCC	0.61035	0.59991
cg0191319	DCAF12L	RXR-alph	361	367	5.271235	CCCACC	0.61035	0.6044
cg0191319	DCAF12L	RXR-alph	1245	1251	5.271235	GCAACC	0.61035	0.6044
cg0191319	DCAF12L	AR [T000	1898	1906	5.247138	GGACAG	0.11444	0.11247
cg0191319	DCAF12L	ETF [T002	554	564	5.246906	GGGCGG	0.02861	0.02737

cg0191319	DCAF12L	USF1 [T0	1661	1670	5.206903	CACGTG	0.04578	0.04527
cg0191319	DCAF12L	p53 [T006	818	824	5.133514	GGGCGG	0.48828	0.47747
cg0191319	DCAF12L	RXR-alpha	1982	1988	5.089356	GGGTGC	0.48828	0.484
cg0191319	DCAF12L	USF2 [T0	1798	1807	5.052423	CAGGTG	0.103	0.10178
cg0191319	DCAF12L	USF2 [T0	1987	1996	5.052423	CTGACA	0.103	0.10178
cg0191319	DCAF12L	GR-beta [T	75	79	5.042296	GGATT	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	661	665	5.042296	GGATT	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	1045	1049	5.042296	AATCC	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	1149	1153	5.042296	AATCC	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	1202	1206	5.042296	GGATT	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	1359	1363	5.042296	AATCC	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	1371	1375	5.042296	AATCC	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	1466	1470	5.042296	AATCC	3.90625	3.95351
cg0191319	DCAF12L	GR-beta [T	1654	1658	5.042296	GGATT	3.90625	3.95351
cg0191319	DCAF12L	E2F-1 [T0	1922	1929	5.042045	GCGGGA	0.18311	0.17901
cg0191319	DCAF12L	c-Jun [T00	1988	1994	5.000337	TGACAC	0.61035	0.61057
cg0191319	DCAF12L	XBP-1 [T	96	101	4.894955	ATGCCG	0.97656	0.96979
cg0191319	DCAF12L	XBP-1 [T	1000	1005	4.894955	CGGCAT	0.97656	0.96979
cg0191319	DCAF12L	c-Jun [T00	1233	1239	4.883696	TATGTC	0.61035	0.61057
cg0191319	DCAF12L	c-Ets-1 [T	1529	1535	4.782565	GTGGAA	0.48828	0.49031
cg0191319	DCAF12L	TFII-I [T0	150	155	4.756447	GGAATG	2.92969	2.93695
cg0191319	DCAF12L	TFII-I [T0	1341	1346	4.756447	CAGTCC	2.92969	2.93695
cg0191319	DCAF12L	TFII-I [T0	1358	1363	4.756447	CAATCC	2.92969	2.93695
cg0191319	DCAF12L	TFII-I [T0	1582	1587	4.756447	ATATCC	2.92969	2.93695
cg0191319	DCAF12L	TFII-I [T0	1595	1600	4.756447	CAGTCC	2.92969	2.93695
cg0191319	DCAF12L	FOXP3 [T	41	46	4.756447	GTTTTC	2.92969	2.96063
cg0191319	DCAF12L	FOXP3 [T	257	262	4.756447	GTTGAC	2.92969	2.96063
cg0191319	DCAF12L	FOXP3 [T	1271	1276	4.756447	GTTGAT	2.92969	2.96063
cg0191319	DCAF12L	c-Ets-1 [T	515	521	4.74411	TTTCCGT	0.85449	0.85764
cg0191319	DCAF12L	PPAR-alph	1151	1161	4.727619	TCCTGG	0.03242	0.03183
cg0191319	DCAF12L	TCF-4 [T0	1498	1507	4.639022	CCTTTG	0.04196	0.04202
cg0191319	DCAF12L	VDR [T00	230	238	4.617121	GTTCAG	0.37384	0.37445
cg0191319	DCAF12L	AP-1 [T00	170	178	4.606866	TGACTC	0.03052	0.03019
cg0191319	DCAF12L	T3R-beta1	1394	1402	4.442729	CCATGG	0.27466	0.27551
cg0191319	DCAF12L	AP-2alpha	732	737	4.438035	CTAGGC	0.97656	0.96979
cg0191319	DCAF12L	STAT4 [T	150	155	4.411765	GGAATG	1.95312	1.94235
cg0191319	DCAF12L	STAT4 [T	1494	1499	4.411765	GCTTCC	1.95312	1.94235
cg0191319	DCAF12L	STAT4 [T	1554	1559	4.411765	TCTTCC	1.95312	1.94235
cg0191319	DCAF12L	STAT4 [T	1679	1684	4.411765	CGTTCC	1.95312	1.94235
cg0191319	DCAF12L	STAT4 [T	1943	1948	4.411765	GGAAGA	1.95312	1.94235
cg0191319	DCAF12L	p53 [T006	118	124	4.33696	GGGCCA	0.24414	0.23584
cg0191319	DCAF12L	HOXD9 [T	1057	1066	4.321431	AATAAA	0.03433	0.03596
cg0191319	DCAF12L	HOXD10 [	1057	1066	4.321431	AATAAA	0.03433	0.03596
cg0191319	DCAF12L	c-Ets-1 [T	1462	1468	4.282938	GAGGAA	0.85449	0.85764
cg0191319	DCAF12L	RXR-alpha	1378	1384	4.24113	GGGACC	0.97656	0.9671
cg0191319	DCAF12L	AP-2alpha	368	373	4.211849	GCCTAC	0.97656	0.96469
cg0191319	DCAF12L	AP-2alpha	1443	1448	4.211849	GTAGGC	0.97656	0.96469
cg0191319	DCAF12L	GR-beta [T	1057	1061	4.201913	AATAA	7.8125	7.94607

cg0191319	DCAF12L	GR-beta [T	1739	1743	4.201913	AATAA	7.8125	7.94607
cg0191319	DCAF12L	GR-beta [T	1837	1841	4.201913	TGATT	7.8125	7.94607
cg0191319	DCAF12L	NF-Y [T0	1860	1867	4.186615	ATTGGG	0.18311	0.1853
cg0191319	DCAF12L	HNF-1C [	1736	1744	4.175118	ATGAAT	0.04578	0.04699
cg0191319	DCAF12L	E2F-1 [T0	309	316	4.052917	TGTACC	0.15259	0.15068
cg0191319	DCAF12L	IRF-1 [T0	1304	1312	4.035054	TTTCCCT	0.1297	0.13087
cg0191319	DCAF12L	RXR-alpha	1975	1981	4.019014	GGGTGT	0.97656	0.9671
cg0191319	DCAF12L	Pax-5 [T0	761	767	4.007279	GGGCAG	1.09863	1.07975
cg0191319	DCAF12L	Pax-5 [T0	964	970	4.007279	AGGGCC	1.09863	1.07975
cg0191319	DCAF12L	Pax-5 [T0	1475	1481	4.007279	GGGCTT	1.09863	1.07975
cg0191319	DCAF12L	Pax-5 [T0	1510	1516	4.007279	AGAGCC	1.09863	1.07975
cg0191319	DCAF12L	Pax-5 [T0	1872	1878	4.007279	GGGCAG	1.09863	1.07975
cg0191319	DCAF12L	TFIID [T0	1039	1045	4.007279	TCTTAA	1.09863	1.13456
cg0191319	DCAF12L	TFIID [T0	1278	1284	4.007279	TCTTAA	1.09863	1.13456
cg0191319	DCAF12L	TFIID [T0	1755	1761	4.007279	TCATAA	1.09863	1.13456
cg0191319	DCAF12L	AP-2alpha	577	582	3.970052	CAAGGC	0.97656	0.96469
cg0191319	DCAF12L	AP-2alpha	1429	1434	3.970052	GCCTTG	0.97656	0.96469
cg0191319	DCAF12L	p53 [T006	1092	1098	3.961937	GGGCTA	0.73242	0.71379
cg0191319	DCAF12L	p53 [T006	467	473	3.750231	CAAGCC	0.73242	0.71379
cg0191319	DCAF12L	AP-2alpha	655	660	3.743866	GCCTTC	0.48828	0.48238
cg0191319	DCAF12L	AP-2alpha	738	743	3.743866	GAAGGC	0.48828	0.48238
cg0191319	DCAF12L	AP-2alpha	905	910	3.743866	GAAGGC	0.48828	0.48238
cg0191319	DCAF12L	AP-2alpha	1689	1694	3.743866	GAAGGC	0.48828	0.48238
cg0191319	DCAF12L	p53 [T006	561	567	3.586914	GGGCGA	0.73242	0.7189
cg0191319	DCAF12L	NF-AT2 [	1299	1308	3.571424	TATTTTT	0.03433	0.03499
cg0191319	DCAF12L	E2F-1 [T0	742	749	3.55167	GCGGGA	0.15259	0.14974
cg0191319	DCAF12L	p53 [T006	761	767	3.516613	GGGCAG	0.73242	0.7189
cg0191319	DCAF12L	p53 [T006	1872	1878	3.516613	GGGCAG	0.73242	0.7189
cg0191319	DCAF12L	HNF-3alph	1299	1306	3.500065	TATTTTT	0.27466	0.28532
cg0191319	DCAF12L	Sp1 [T007	553	562	3.440764	TGGGCG	0.07439	0.07186
cg0191319	DCAF12L	RXR-alpha	689	695	3.392904	GGGTGA	1.09863	1.08572
cg0191319	DCAF12L	RXR-alpha	1225	1231	3.392904	TTTACC	1.09863	1.08572
cg0191319	DCAF12L	p53 [T006	896	902	3.375208	GGGCGG	0.73242	0.7189
cg0191319	DCAF12L	GR-beta [T	1062	1066	3.361531	AATCT	3.90625	3.99611
cg0191319	DCAF12L	GR-beta [T	1171	1175	3.361531	AGATT	3.90625	3.99611
cg0191319	DCAF12L	GR-beta [T	1297	1301	3.361531	AATAT	3.90625	3.99611
cg0191319	DCAF12L	GR-beta [T	1298	1302	3.361531	ATATT	3.90625	3.99611
cg0191319	DCAF12L	GR-beta [T	1581	1585	3.361531	AATAT	3.90625	3.99611
cg0191319	DCAF12L	Sp1 [T007	709	718	3.305137	AGGGCG	0.07439	0.07186
cg0191319	DCAF12L	AP-2alpha	304	309	3.229049	GCCTCT	0.48828	0.48238
cg0191319	DCAF12L	AP-2alpha	421	426	3.229049	GCCTCT	0.48828	0.48238
cg0191319	DCAF12L	AP-2alpha	427	432	3.229049	GCCTCT	0.48828	0.48238
cg0191319	DCAF12L	AP-2alpha	1602	1607	3.229049	AGAGGC	0.48828	0.48238
cg0191319	DCAF12L	AP-2alpha	1645	1650	3.229049	AGAGGC	0.48828	0.48238
cg0191319	DCAF12L	RXR-alpha	39	45	3.170788	GGGTTT	0.24414	0.24522
cg0191319	DCAF12L	c-Fos [T00	166	175	3.154982	GGCCTG	0.06104	0.06065
cg0191319	DCAF12L	Elk-1 [T00	1495	1503	3.121991	CTTCCTT	0.07629	0.07656
cg0191319	DCAF12L	Pax-5 [T0	561	567	3.075094	GGGCGA	0.12207	0.11895

cg0191319	DCAF12L	C/EBPalph	1859	1865	2.981957	CATTGG	0.48828	0.4911
cg0191319	DCAF12L	c-Ets-2 [T	1496	1504	2.945838	TTCCTTT	0.06104	0.06231
cg0191319	DCAF12L	STAT4 [T	514	519	2.941176	CTTTCC	2.92969	2.929
cg0191319	DCAF12L	STAT4 [T	647	652	2.941176	GGAACC	2.92969	2.929
cg0191319	DCAF12L	STAT4 [T	745	750	2.941176	GGAAGT	2.92969	2.929
cg0191319	DCAF12L	STAT4 [T	1464	1469	2.941176	GGAATC	2.92969	2.929
cg0191319	DCAF12L	STAT4 [T	1912	1917	2.941176	GGAAAG	2.92969	2.929
cg0191319	DCAF12L	p53 [T006	11	17	2.813291	GGGCAG	0.48828	0.47786
cg0191319	DCAF12L	p53 [T006	299	305	2.813291	GGGCAG	0.48828	0.47786
cg0191319	DCAF12L	c-Ets-2 [T	1459	1467	2.715313	GGGGAG	0.07629	0.07593
cg0191319	DCAF12L	c-Jun [T00	170	176	2.654872	TGACTC	0.48828	0.48929
cg0191319	DCAF12L	PXR-1:RX	227	234	2.577808	GGAGTT	0.12207	0.12266
cg0191319	DCAF12L	AP-2alpha	129	134	2.550491	GCCTCA	0.48828	0.48266
cg0191319	DCAF12L	AP-2alpha	667	672	2.550491	TGAGGC	0.48828	0.48266
cg0191319	DCAF12L	AP-2alpha	889	894	2.550491	TGAGGC	0.48828	0.48266
cg0191319	DCAF12L	AP-2alpha	1505	1510	2.550491	GCCTCA	0.48828	0.48266
cg0191319	DCAF12L	AP-2alpha	1933	1938	2.550491	TGAGGC	0.48828	0.48266
cg0191319	DCAF12L	RXR-alpha	901	907	2.544678	GGGTGA	0.85449	0.84796
cg0191319	DCAF12L	ENKTF-1	352	359	2.511511	TGGCGG	0.12207	0.11894
cg0191319	DCAF12L	ENKTF-1	622	629	2.511511	TGGCGG	0.12207	0.11894
cg0191319	DCAF12L	Sp1 [T007	817	826	2.491373	GGGGCG	0.04005	0.03892
cg0191319	DCAF12L	MAZ [T00	923	935	2.378507	GGAGGG	0.00405	0.00399
cg0191319	DCAF12L	c-Ets-2 [T	1907	1915	2.217136	CACGAG	0.16785	0.16856
cg0191319	DCAF12L	GATA-1 [	1074	1079	2.176375	ACGATA	3.90625	3.92756
cg0191319	DCAF12L	GATA-1 [	1702	1707	2.176375	TGGATA	3.90625	3.92756
cg0191319	DCAF12L	GATA-1 [	1767	1772	2.176375	TATCCA	3.90625	3.92756
cg0191319	DCAF12L	GCF [T00	700	708	2.140539	GCGCGG	0.09155	0.08882
cg0191319	DCAF12L	AP-2alpha	498	503	2.098119	GCCTCG	0.97656	0.95407
cg0191319	DCAF12L	NF-1 [T00	1631	1638	2.067686	TTGGGA	0.12207	0.12133
cg0191319	DCAF12L	LEF-1 [T0	1571	1578	2.004405	AAGCAA	0.18311	0.18582
cg0191319	DCAF12L	GATA-1 [	404	409	2.001358	GCGATA	3.90625	3.92756
cg0191319	DCAF12L	GATA-1 [	1583	1588	2.001358	TATCCC	3.90625	3.92756
cg0191319	DCAF12L	PR B [T00	1411	1417	1.892895	AACACT	0.12207	0.12429
cg0191319	DCAF12L	PR A [T01	1411	1417	1.892895	AACACT	0.12207	0.12429
cg0191319	DCAF12L	AP-2alpha	822	827	1.871933	GGAGGC	0.97656	0.95407
cg0191319	DCAF12L	C/EBPalph	1316	1322	1.830762	AATTGA	0.48828	0.49438
cg0191319	DCAF12L	TFII-I [T0	705	710	1.824994	GGAGAG	0.48828	0.48408
cg0191319	DCAF12L	TFII-I [T0	1520	1525	1.824994	GGAGAG	0.48828	0.48408
cg0191319	DCAF12L	TFII-I [T0	1865	1870	1.824994	GGAGAG	0.48828	0.48408
cg0191319	DCAF12L	PXR-1:RX	1750	1757	1.759733	AGAGTT	0.06104	0.06168
cg0191319	DCAF12L	p53 [T006	950	956	1.758307	GGGCAG	0.36621	0.36261
cg0191319	DCAF12L	p53 [T006	1817	1823	1.758307	GGGCAT	0.36621	0.36261
cg0191319	DCAF12L	GR-beta [	152	156	1.680765	AATGC	3.90625	3.94936
cg0191319	DCAF12L	GR-beta [	1002	1006	1.680765	GCATT	3.90625	3.94936
cg0191319	DCAF12L	GR-beta [	1365	1369	1.680765	AATGC	3.90625	3.94936
cg0191319	DCAF12L	C/EBPbeta	36	39	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	69	72	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	110	113	1.639871	TTGG	15.625	15.72563

cg0191319	DCAF12L	C/EBPbeta	204	207	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	278	281	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	466	469	1.639871	CCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	584	587	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	984	987	1.639871	CCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1142	1145	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1187	1190	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1362	1365	1.639871	CCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1389	1392	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1416	1419	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1421	1424	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1482	1485	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1610	1613	1.639871	CCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1631	1634	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1861	1864	1.639871	TTGG	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1918	1921	1.639871	CCAA	15.625	15.72563
cg0191319	DCAF12L	Pax-5 [T0	118	124	1.537547	GGGCCA	0.73242	0.71311
cg0191319	DCAF12L	Pax-5 [T0	896	902	1.537547	GGGCGG	0.73242	0.71311
cg0191319	DCAF12L	Pax-5 [T0	1092	1098	1.537547	GGGCTA	0.73242	0.71311
cg0191319	DCAF12L	TFIID [T0	1480	1486	1.537547	TTTTGG	0.73242	0.75096
cg0191319	DCAF12L	IRF-1 [T0	515	523	1.529008	TTTCCG	0.04578	0.04655
cg0191319	DCAF12L	Sp1 [T007	895	904	1.523913	CGGGCG	0.03242	0.03129
cg0191319	DCAF12L	c-Ets-1 [T	1910	1916	1.513038	GAGGAA	0.36621	0.36952
cg0191319	DCAF12L	E2F-1 [T0	702	709	1.490375	GCGGGA	0.06104	0.06008
cg0191319	DCAF12L	RXR-alph	1639	1645	1.474336	GGGTCT	0.48828	0.48222
cg0191319	DCAF12L	STAT4 [T	520	525	1.470588	GTTTCC	1.95312	1.96333
cg0191319	DCAF12L	STAT4 [T	1303	1308	1.470588	TTTTCC	1.95312	1.96333
cg0191319	DCAF12L	c-Ets-1 [T	521	527	1.384951	TTTCCT	0.36621	0.36952
cg0191319	DCAF12L	C/EBPbeta	258	261	1.366559	TTGA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	432	435	1.366559	TTGA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1055	1058	1.366559	TCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1083	1086	1.366559	TCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1253	1256	1.366559	TCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1272	1275	1.366559	TTGA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1290	1293	1.366559	TCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1313	1316	1.366559	TCAA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1318	1321	1.366559	TTGA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1348	1351	1.366559	TTGA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1432	1435	1.366559	TTGA	15.625	15.72563
cg0191319	DCAF12L	C/EBPbeta	1501	1504	1.366559	TTGA	15.625	15.72563
cg0191319	DCAF12L	p53 [T006	263	269	1.270236	CGTGCC	0.12207	0.11849
cg0191319	DCAF12L	GCF [T00	1212	1220	1.26923	GCGCAG	0.03052	0.02943
cg0191319	DCAF12L	ENKTF-1	719	726	1.255756	TGGCGG	0.24414	0.23904
cg0191319	DCAF12L	NFI/CTF [	1918	1925	1.227415	CCAAGC	0.18311	0.18127
cg0191319	DCAF12L	GATA-2 [	387	395	1.111111	AGATAG	0.09155	0.09208
cg0191319	DCAF12L	GCF [T00	642	650	1.070269	GCGCTG	0.18311	0.17647
cg0191319	DCAF12L	E2F-1 [T0	136	143	0.993583	TGTCCC	0.03052	0.02978
cg0191319	DCAF12L	AR [T000	132	140	0.863734	TCACTG	0.03815	0.03779

cg0191319	DCAF12L	GATA-1 [	1399	1404	0.863549	GTGATA	1.95312	1.98662
cg0191319	DCAF12L	GATA-1 [	1853	1858	0.863549	GTGATA	1.95312	1.98662
cg0191319	DCAF12L	GR-beta [T	1316	1320	0.840383	AATTG	7.8125	7.94706
cg0191319	DCAF12L	GR-beta [T	1439	1443	0.840383	AATGG	7.8125	7.94706
cg0191319	DCAF12L	GR-beta [T	1455	1459	0.840383	AATGG	7.8125	7.94706
cg0191319	DCAF12L	GR-beta [T	1709	1713	0.840383	AATGA	7.8125	7.94706
cg0191319	DCAF12L	HIF-1 [T0	1662	1670	0.83452	ACGTGC	0.09918	0.0975
cg0191319	DCAF12L	GATA-1 [	989	994	0.758539	TATCAG	1.95312	1.98662
cg0191319	DCAF12L	GATA-1 [	1403	1408	0.758539	TATCAG	1.95312	1.98662
cg0191319	DCAF12L	AP-2alpha	167	172	0.678558	GCCTGA	0.48828	0.48199
cg0191319	DCAF12L	AP-2alpha	875	880	0.678558	GCCTGA	0.48828	0.48199
cg0191319	DCAF12L	AP-2alpha	1969	1974	0.678558	GCCTGA	0.48828	0.48199
cg0191319	DCAF12L	LEF-1 [T0	770	777	0.641865	GAGCAA	0.06104	0.06131
cg0191319	DCAF12L	LEF-1 [T0	1881	1888	0.641865	GAACAA	0.06104	0.06131
cg0191319	DCAF12L	PR B [T00	1283	1289	0.48823	AACAGT	0.12207	0.12407
cg0191319	DCAF12L	PR A [T01	1283	1289	0.48823	AACAGT	0.12207	0.12407
cg0191319	DCAF12L	POU2F1 [	1363	1373	0.269172	CAAATG	0.00715	0.00734
cg0191319	DCAF12L	c-Ets-1 [T	1495	1501	0.256174	CTTCCTT	0.24414	0.24569
cg0191319	DCAF12L	AP-2alpha	28	33	0.226186	CCAGGC	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	124	129	0.226186	GCCTGG	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	223	228	0.226186	GCCTGG	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	349	354	0.226186	GCCTGG	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	1106	1111	0.226186	CCAGGC	0.97656	0.95305
cg0191319	DCAF12L	GR-alpha [	145	149	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	305	309	0.207689	CCTCT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	422	426	0.207689	CCTCT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	428	432	0.207689	CCTCT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	707	711	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1223	1227	0.207689	CCTTT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1498	1502	0.207689	CCTTT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1522	1526	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1543	1547	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1552	1556	0.207689	CCTCT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1602	1606	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1645	1649	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1651	1655	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1723	1727	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1869	1873	0.207689	AGAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	106	110	0	CCTGT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	531	535	0	CCTGT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	919	923	0	ACAGG	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1587	1591	0	CCTGT	7.8125	7.81264
cg0191319	DCAF12L	GR-alpha [	1636	1640	0	ACAGG	7.8125	7.81264
cg0191319	DCAF12L	AP-2alpha	838	843	0	GCAGGC	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	850	855	0	GCAGGC	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	1804	1809	0	GCAGGC	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	1949	1954	0	GCAGGC	0.97656	0.95305
cg0191319	DCAF12L	AP-2alpha	1961	1966	0	GCAGGC	0.97656	0.95305

cg0191319	DCAF12L	Pax-5 [T0	263	269	0	CGTGCC	1.09863	1.06846
cg0191319	DCAF12L	Pax-5 [T0	467	473	0	CAAGCC	1.09863	1.06846
cg0191319	DCAF12L	Pax-5 [T0	848	854	0	GGGCAG	1.09863	1.06846
cg0191319	DCAF12L	Pax-5 [T0	965	971	0	GGGCCC	1.09863	1.06846
cg0191319	DCAF12L	Pax-5 [T0	1959	1965	0	GGGCAG	1.09863	1.06846
cg0191319	DCAF12L	p53 [T006	848	854	0	GGGCAG	0.36621	0.35912
cg0191319	DCAF12L	p53 [T006	1959	1965	0	GGGCAG	0.36621	0.35912
cg0191319	DCAF12L	TFII-I [T0	135	140	0	CTGTCC	1.46484	1.45997
cg0191319	DCAF12L	TFII-I [T0	514	519	0	CTTTCC	1.46484	1.45997
cg0191319	DCAF12L	TFII-I [T0	917	922	0	GGACAG	1.46484	1.45997
cg0191319	DCAF12L	TFII-I [T0	1634	1639	0	GGACAG	1.46484	1.45997
cg0191319	DCAF12L	TFII-I [T0	1898	1903	0	GGACAG	1.46484	1.45997
cg0191319	DCAF12L	TFII-I [T0	1912	1917	0	GGAAAG	1.46484	1.45997
cg0191319	DCAF12L	YY1 [T00	24	27	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	87	90	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	92	95	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	333	336	0	CCAT	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	397	400	0	CCAT	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	547	550	0	CCAT	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	549	552	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	636	639	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	1197	1200	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	1230	1233	0	CCAT	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	1394	1397	0	CCAT	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	1396	1399	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	1440	1443	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	YY1 [T00	1456	1459	0	ATGG	7.8125	7.81711
cg0191319	DCAF12L	ER-alpha [	259	263	0	TGACC	1.95312	1.9404
cg0191319	DCAF12L	GATA-1 [	386	391	0	CAGATA	0.97656	0.98738
cg0191319	DCAF12L	C/EBPbeta	142	145	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	255	258	0	TTGT	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	536	539	0	TTGC	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	576	579	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	594	597	0	TTGC	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	772	775	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	858	861	0	TTGT	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	946	949	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	971	974	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1021	1024	0	ACAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1190	1193	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1245	1248	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1294	1297	0	ACAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1357	1360	0	ACAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1368	1371	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1492	1495	0	TTGC	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1573	1576	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1591	1594	0	TTGT	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1693	1696	0	GCAA	15.625	15.71349

cg0191319	DCAF12L	C/EBPbeta	1696	1699	0	ACAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1707	1710	0	ACAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1715	1718	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1810	1813	0	GCAA	15.625	15.71349
cg0191319	DCAF12L	C/EBPbeta	1883	1886	0	ACAA	15.625	15.71349
cg0191319	DCAF12L	NF-1 [T00	1389	1396	0	TTGGCC	0.12207	0.11983
cg0191319	DCAF12L	FOXP3 [T	857	862	0	GTTGTG	1.46484	1.47315
cg0191319	DCAF12L	FOXP3 [T	1020	1025	0	GACAAC	1.46484	1.47315
cg0191319	DCAF12L	FOXP3 [T	1590	1595	0	GTTGTC	1.46484	1.47315
cg0191319	DCAF12L	FOXP3 [T	1695	1700	0	AACAAC	1.46484	1.47315
cg0191319	DCAF12L	GR-beta [	1178	1182	0	ACATT	3.90625	3.99611
cg0191319	DCAF12L	GR-beta [	1315	1319	0	AAATT	3.90625	3.99611
cg0191319	DCAF12L	GR-beta [	1385	1389	0	ACATT	3.90625	3.99611
cg0191319	DCAF12L	GR-beta [	1858	1862	0	ACATT	3.90625	3.99611
cg0191319	DCAF12L	NF-AT1 [	1300	1308	0	ATTTTTT	0.01526	0.01569
cg0191319	DCAF12L	GR [T050	1478	1484	0	CTTTTTG	0.36621	0.37562
cg0191319	DCAF12L	SRY [T00	1880	1888	0	AGAACA	0.03052	0.03101
cg0191319	DCAF12L	TCF-4E [T	771	777	0	AGCAAA	0.12207	0.12262
cg0191319	DCAF12L	TCF-4E [T	1572	1578	0	AGCAAA	0.12207	0.12262
cg0191319	DCAF12L	HNF-1A [	1578	1585	0	GTTAAT	0.24414	0.25261
cg0191319	DCAF12L	c-Myc [T0	1661	1666	0	CACGTG	0.48828	0.48199
cg1494300	DDB2	Elk-1 [T00	428	436	9.979803	CTTCCG	0.10681	0.11027
cg1494300	DDB2	c-Ets-1 [T	104	110	9.969337	ATTCCC	0.24414	0.23698
cg1494300	DDB2	LEF-1 [T0	695	702	9.937995	CTTTGG	0.12207	0.1238
cg1494300	DDB2	STAT1bet	1396	1405	9.807397	AGAGGG	0.14877	0.14533
cg1494300	DDB2	STAT1bet	1510	1519	9.807397	TTTTCCC	0.14877	0.14533
cg1494300	DDB2	XBP-1 [T	177	182	9.789909	ATGGCG	1.95312	1.94901
cg1494300	DDB2	XBP-1 [T	181	186	9.789909	CGCCAT	1.95312	1.94901
cg1494300	DDB2	XBP-1 [T	864	869	9.789909	AGCCAT	1.95312	1.94901
cg1494300	DDB2	XBP-1 [T	1572	1577	9.789909	ATGTCT	1.95312	1.94901
cg1494300	DDB2	NF-1 [T00	342	349	9.761671	TTGGAT	0.24414	0.24488
cg1494300	DDB2	NF-1 [T00	1335	1342	9.761671	TTGGTT	0.24414	0.24488
cg1494300	DDB2	PR B [T00	614	620	9.743489	TTGTGTT	1.09863	1.0981
cg1494300	DDB2	PR B [T00	1069	1075	9.743489	AACACA	1.09863	1.0981
cg1494300	DDB2	PR A [T01	614	620	9.743489	TTGTGTT	1.09863	1.0981
cg1494300	DDB2	PR A [T01	1069	1075	9.743489	AACACA	1.09863	1.0981
cg1494300	DDB2	LEF-1 [T0	819	826	9.72404	CTTTGT	0.21362	0.21229
cg1494300	DDB2	LEF-1 [T0	1777	1784	9.72404	CTTTGC	0.21362	0.21229
cg1494300	DDB2	RAR-beta	763	772	9.641259	TCAGAA	0.21362	0.22369
cg1494300	DDB2	TFIID [T0	470	476	9.552105	TGGCAA	1.46484	1.37777
cg1494300	DDB2	TFIID [T0	1274	1280	9.552105	TTTGGA	1.46484	1.37777
cg1494300	DDB2	TFIID [T0	1376	1382	9.552105	TTTGGG	1.46484	1.37777
cg1494300	DDB2	TFIID [T0	1778	1784	9.552105	TTTGCC	1.46484	1.37777
cg1494300	DDB2	Pax-5 [T0	200	206	9.552105	GGGCAA	1.46484	1.61918
cg1494300	DDB2	Pax-5 [T0	1312	1318	9.552105	GTGGCC	1.46484	1.61918
cg1494300	DDB2	NF-1 [T00	697	704	9.513281	TTGGCT	0.73242	0.74634
cg1494300	DDB2	FOXP3 [T	32	37	9.512894	GCCAAC	7.32422	7.22156
cg1494300	DDB2	FOXP3 [T	201	206	9.512894	GGCAAC	7.32422	7.22156

cg1494300	DDB2	FOXP3 [T	764	769	9.512894	CAGAAC	7.32422	7.22156
cg1494300	DDB2	FOXP3 [T	867	872	9.512894	CATAAC	7.32422	7.22156
cg1494300	DDB2	FOXP3 [T	964	969	9.512894	GTTATT	7.32422	7.22156
cg1494300	DDB2	FOXP3 [T	1023	1028	9.512894	GGCAAC	7.32422	7.22156
cg1494300	DDB2	FOXP3 [T	1193	1198	9.512894	GTTCTC	7.32422	7.22156
cg1494300	DDB2	FOXP3 [T	1235	1240	9.512894	GTTCTG	7.32422	7.22156
cg1494300	DDB2	FOXP3 [T	1845	1850	9.512894	GTTTAC	7.32422	7.22156
cg1494300	DDB2	TFII-I [T0	103	108	9.512894	AATTCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	193	198	9.512894	CCATCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	303	308	9.512894	GGAATT	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	467	472	9.512894	GGATGG	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	491	496	9.512894	GGATTT	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	621	626	9.512894	TTTTCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	834	839	9.512894	GGACTT	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	894	899	9.512894	TTATCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	899	904	9.512894	CCATCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	914	919	9.512894	GGACGG	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	1154	1159	9.512894	GGAACG	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	1176	1181	9.512894	GGACGG	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	1240	1245	9.512894	GTGTCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	1510	1515	9.512894	TTTTCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	1618	1623	9.512894	GTTTCC	7.32422	7.44385
cg1494300	DDB2	TFII-I [T0	1942	1947	9.512894	GGAAGG	7.32422	7.44385
cg1494300	DDB2	c-Jun [T00	1132	1138	9.511322	GTGGTC	0.73242	0.7366
cg1494300	DDB2	c-Jun [T00	1495	1501	9.511322	TGACCA	0.73242	0.7366
cg1494300	DDB2	c-Jun [T00	1816	1822	9.511322	TGACCA	0.73242	0.7366
cg1494300	DDB2	TCF-4E [T	1273	1279	9.453578	CTTTGG	0.48828	0.46934
cg1494300	DDB2	NFI/CTF [	333	340	9.352332	AGCATT	0.54932	0.55369
cg1494300	DDB2	NFI/CTF [	1271	1278	9.352332	AGCTTT	0.54932	0.55369
cg1494300	DDB2	EBF [T05	358	368	9.324368	CCCGCA	0.06866	0.07687
cg1494300	DDB2	RelA [T00	1508	1518	9.314493	GGTTTT	0.02813	0.02907
cg1494300	DDB2	c-Ets-1 [T	1577	1583	9.276861	TGGGAA	0.36621	0.37402
cg1494300	DDB2	SRY [T00	1273	1281	9.264664	CTTTGG	0.12207	0.11857
cg1494300	DDB2	c-Ets-1 [T	1275	1281	9.19359	TTGGAA	0.85449	0.84987
cg1494300	DDB2	LEF-1 [T0	1584	1591	9.099721	CTTTGTC	0.54932	0.53171
cg1494300	DDB2	USF2 [T0	1243	1252	9.056375	TCCCCA	0.1545	0.16206
cg1494300	DDB2	NF-AT1 [	263	271	9.042733	TTGATT	0.22888	0.22581
cg1494300	DDB2	c-Myb [T0	512	519	9.024874	AAACTG	0.39673	0.37851
cg1494300	DDB2	c-Ets-1 [T	1152	1158	9.020687	GGGGAA	0.85449	0.84987
cg1494300	DDB2	PXR-1:RX	1638	1645	8.998824	GTTGTTC	0.24414	0.24356
cg1494300	DDB2	LEF-1 [T0	1273	1280	8.973041	CTTTGG	0.54932	0.53171
cg1494300	DDB2	Elk-1 [T00	1904	1912	8.931691	CTTCCA	0.24414	0.26271
cg1494300	DDB2	c-Ets-2 [T	1339	1347	8.912323	TTCCTGC	0.27466	0.27171
cg1494300	DDB2	AP-1 [T00	1007	1015	8.907204	GGTTAG	0.24414	0.23028
cg1494300	DDB2	HNF-4alph	1769	1781	8.87767	GCTTTTC	0.01502	0.01406
cg1494300	DDB2	c-Myb [T0	328	335	8.872587	TAACTA	0.39673	0.37851
cg1494300	DDB2	NF-1 [T00	116	123	8.790071	TTGGGA	0.24414	0.24339
cg1494300	DDB2	NF-1 [T00	1560	1567	8.790071	TCTGCC	0.24414	0.24339

cg1494300 DDB2	XBP-1 [T0	1968	1973	8.75604	GATCAT	2.92969	2.75329
cg1494300 DDB2	STAT1bet	621	630	8.695301	TTTTCCC	0.22316	0.2175
cg1494300 DDB2	NF-AT1 [T	1507	1515	8.599808	GGGTTTT	0.10681	0.10494
cg1494300 DDB2	LEF-1 [T0	711	718	8.575454	CTTTGG	0.15259	0.154
cg1494300 DDB2	USF2 [T0	1448	1457	8.532138	CAGGTG	0.103	0.10815
cg1494300 DDB2	PR B [T00	675	681	8.338824	AACAGG	1.09863	1.09384
cg1494300 DDB2	PR A [T01	675	681	8.338824	AACAGG	1.09863	1.09384
cg1494300 DDB2	ATF3 [T0	1304	1311	8.313799	TGACGC	0.27466	0.27379
cg1494300 DDB2	PXR-1:RX	630	637	8.304332	AGTGTT	0.12207	0.11843
cg1494300 DDB2	GR-alpha [	119	123	8.281568	GGAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	151	155	8.281568	GGAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	411	415	8.281568	CAAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	561	565	8.281568	CCTCC	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	573	577	8.281568	CCTCC	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	638	642	8.281568	GAAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	753	757	8.281568	GGAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1082	1086	8.281568	CCTCC	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1199	1203	8.281568	CGAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1215	1219	8.281568	CCTCC	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1230	1234	8.281568	CCTCG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1352	1356	8.281568	CCTCC	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1693	1697	8.281568	GGAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1716	1720	8.281568	GAAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1725	1729	8.281568	CAAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1755	1759	8.281568	CCTTC	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1925	1929	8.281568	CAAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1943	1947	8.281568	GAAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1956	1960	8.281568	GAAGG	7.8125	8.20394
cg1494300 DDB2	GR-alpha [	1959	1963	8.281568	GGAGG	7.8125	8.20394
cg1494300 DDB2	c-Jun [T00	6	12	8.242207	GAGGTC	0.48828	0.47447
cg1494300 DDB2	NF-AT1 [T	1207	1215	8.223794	TGCCTTT	0.1297	0.12846
cg1494300 DDB2	NF-AT1 [T	1400	1408	8.223794	GGAAAG	0.1297	0.12846
cg1494300 DDB2	ENKTF-1	28	35	8.19852	CCTGGC	0.73242	0.80254
cg1494300 DDB2	ENKTF-1	861	868	8.19852	CCCAGC	0.73242	0.80254
cg1494300 DDB2	ENKTF-1	1341	1348	8.19852	CCTGGC	0.73242	0.80254
cg1494300 DDB2	SRY [T00	819	827	8.174786	CTTTGTC	0.15259	0.14791
cg1494300 DDB2	VDR [T00	1315	1323	8.079962	GCCCTG	0.24414	0.22992
cg1494300 DDB2	IRF-1 [T0	1619	1627	8.078284	TTTCCAC	0.25177	0.2462
cg1494300 DDB2	GR-alpha [	28	32	8.073878	CCTGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	91	95	8.073878	GTAGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	148	152	8.073878	CCAGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	197	201	8.073878	CCTGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	348	352	8.073878	CCTGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	361	365	8.073878	GCAGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	394	398	8.073878	GCAGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	418	422	8.073878	CCAGG	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	445	449	8.073878	CCTGC	7.8125	8.20289
cg1494300 DDB2	GR-alpha [	543	547	8.073878	GCAGG	7.8125	8.20289

cg1494300	DDB2	GR-alpha [	564	568	8.073878	CCTAG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	609	613	8.073878	CCTGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	682	686	8.073878	CCAGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	784	788	8.073878	GCAGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	855	859	8.073878	CCTGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	943	947	8.073878	CTAGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1104	1108	8.073878	CCTGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1164	1168	8.073878	CCTGC	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1205	1209	8.073878	CCTGC	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1341	1345	8.073878	CCTGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1383	1387	8.073878	CCTGC	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1389	1393	8.073878	CCAGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1447	1451	8.073878	GCAGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1476	1480	8.073878	CCTGC	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1485	1489	8.073878	CCTGC	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1707	1711	8.073878	CCTGC	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1710	1714	8.073878	GCAGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1721	1725	8.073878	CCTGC	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1730	1734	8.073878	CCAGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1874	1878	8.073878	CCTGG	7.8125	8.20289
cg1494300	DDB2	GR-alpha [	1983	1987	8.073878	GCAGG	7.8125	8.20289
cg1494300	DDB2	TFIID [T0	222	228	8.014558	TCTCAA	2.19727	1.99811
cg1494300	DDB2	TFIID [T0	494	500	8.014558	TTTGAG	2.19727	1.99811
cg1494300	DDB2	TFIID [T0	502	508	8.014558	TTTGAG	2.19727	1.99811
cg1494300	DDB2	TFIID [T0	881	887	8.014558	TTTCTGA	2.19727	1.99811
cg1494300	DDB2	Pax-5 [T0	92	98	8.014558	TAGGCC	2.19727	2.42766
cg1494300	DDB2	Pax-5 [T0	643	649	8.014558	GGGCAG	2.19727	2.42766
cg1494300	DDB2	Pax-5 [T0	857	863	8.014558	TGGGCC	2.19727	2.42766
cg1494300	DDB2	Pax-5 [T0	858	864	8.014558	GGGCCC	2.19727	2.42766
cg1494300	DDB2	Pax-5 [T0	885	891	8.014558	TGAGCC	2.19727	2.42766
cg1494300	DDB2	Pax-5 [T0	1803	1809	8.014558	GGAGCC	2.19727	2.42766
cg1494300	DDB2	Pax-5 [T0	1988	1994	8.014558	TCTGCC	2.19727	2.42766
cg1494300	DDB2	C/EBPalph	335	341	8.006685	CATTGG	0.24414	0.23098
cg1494300	DDB2	c-Jun [T00	565	571	7.937147	CTAGTC	0.48828	0.47447
cg1494300	DDB2	HNF-1C [	1008	1016	7.930275	GTTAGT	0.19836	0.18126
cg1494300	DDB2	EBF [T05	1760	1770	7.884197	AGCTCA	0.04196	0.04563
cg1494300	DDB2	c-Ets-2 [T	941	949	7.84116	CACTAG	0.32043	0.30792
cg1494300	DDB2	p53 [T006	1803	1809	7.833758	GGAGCC	0.48828	0.55336
cg1494300	DDB2	T3R-beta1	1895	1903	7.79407	TCACCG	0.27466	0.28753
cg1494300	DDB2	NF-AT1 [	1663	1671	7.744746	TTCCTTT	0.19836	0.19379
cg1494300	DDB2	EBF [T05	295	305	7.659914	CTCCCT	0.01144	0.0122
cg1494300	DDB2	NFI/CTF [	398	405	7.587343	GCAATT	0.36621	0.36269
cg1494300	DDB2	PPAR-alph	1873	1883	7.529496	CCCTGG	0.04482	0.04884
cg1494300	DDB2	GR [T050	473	479	7.527031	CAAAAG	1.83105	1.71535
cg1494300	DDB2	GR [T050	817	823	7.527031	AGCTTT	1.83105	1.71535
cg1494300	DDB2	GR [T050	981	987	7.527031	CAAATA	1.83105	1.71535
cg1494300	DDB2	GR [T050	1271	1277	7.527031	AGCTTT	1.83105	1.71535
cg1494300	DDB2	GR [T050	1363	1369	7.527031	CAAACA	1.83105	1.71535

cg1494300	DDB2	RAR-beta	1506	1515	7.47824	GGGGTT	0.24414	0.25121
cg1494300	DDB2	C/EBPalph	184	190	7.465744	CATTGC	0.48828	0.45033
cg1494300	DDB2	RAR-beta	1005	1014	7.459774	TGGGTT	0.24414	0.25121
cg1494300	DDB2	PEA3 [T0	1432	1440	7.421728	AGGCAT	0.34332	0.35389
cg1494300	DDB2	C/EBPalph	400	406	7.396431	AATTGG	0.48828	0.45033
cg1494300	DDB2	IRF-1 [T0	622	630	7.387351	TTTCCC	0.14496	0.14723
cg1494300	DDB2	PXR-1:RX	1169	1176	7.362674	TGAACA	0.24414	0.24326
cg1494300	DDB2	E2F-1 [T0	1422	1429	7.336545	GCTGCC	0.45776	0.49661
cg1494300	DDB2	IRF-1 [T0	1667	1675	7.299819	TTTCCG	0.14496	0.14723
cg1494300	DDB2	c-Ets-2 [T	443	451	7.268173	TTCCTG	0.09155	0.08977
cg1494300	DDB2	p53 [T006	351	357	7.266844	GGGCTG	0.73242	0.79826
cg1494300	DDB2	p53 [T006	1645	1651	7.266844	ACAGCC	0.73242	0.79826
cg1494300	DDB2	p53 [T006	1767	1773	7.266844	GGGCTT	0.73242	0.79826
cg1494300	DDB2	MAZ [T00	1688	1700	7.18478	GAGTGG	0.00918	0.01018
cg1494300	DDB2	SRY [T00	1584	1592	7.175614	CTTTGT	0.30518	0.29547
cg1494300	DDB2	XBP-1 [T	367	372	7.172312	ATGAGG	2.92969	2.7512
cg1494300	DDB2	XBP-1 [T	458	463	7.172312	ATTCAT	2.92969	2.7512
cg1494300	DDB2	XBP-1 [T	967	972	7.172312	ATTCAT	2.92969	2.7512
cg1494300	DDB2	XBP-1 [T	971	976	7.172312	ATTCAT	2.92969	2.7512
cg1494300	DDB2	XBP-1 [T	1466	1471	7.172312	CCTCAT	2.92969	2.7512
cg1494300	DDB2	XBP-1 [T	1972	1977	7.172312	ATGAGG	2.92969	2.7512
cg1494300	DDB2	p53 [T006	857	863	7.153797	TGGGCC	1.09863	1.22478
cg1494300	DDB2	p53 [T006	858	864	7.153797	GGGCCC	1.09863	1.22478
cg1494300	DDB2	p53 [T006	1312	1318	7.150251	GTGGCC	1.09863	1.22478
cg1494300	DDB2	c-Jun [T00	289	295	7.096776	TGACTG	0.73242	0.73062
cg1494300	DDB2	c-Ets-1 [T	1211	1217	7.071349	TTTCCCT	0.73242	0.73732
cg1494300	DDB2	c-Ets-1 [T	1398	1404	7.071349	AGGGAA	0.73242	0.73732
cg1494300	DDB2	c-Ets-1 [T	1511	1517	7.071349	TTTCCCT	0.73242	0.73732
cg1494300	DDB2	HNF-3alph	69	76	7.000129	AAAAAA	0.82397	0.71909
cg1494300	DDB2	HNF-3alph	238	245	7.000129	AAAAAA	0.82397	0.71909
cg1494300	DDB2	HNF-3alph	985	992	7.000129	TATTTAT	0.82397	0.71909
cg1494300	DDB2	HNF-3alph	1033	1040	7.000129	AGTAAA	0.82397	0.71909
cg1494300	DDB2	HNF-3alph	1626	1633	7.000129	AATTTTT	0.82397	0.71909
cg1494300	DDB2	c-Ets-1 [T	622	628	6.943262	TTTCCC	0.73242	0.73732
cg1494300	DDB2	ENKTF-1	178	185	6.942764	TGGCGC	1.46484	1.56616
cg1494300	DDB2	ENKTF-1	1589	1596	6.942764	TGGCTG	1.46484	1.56616
cg1494300	DDB2	ENKTF-1	1777	1784	6.942764	CTTTGC	1.46484	1.56616
cg1494300	DDB2	VDR [T00	633	641	6.925682	GTTCAG	0.42725	0.41
cg1494300	DDB2	VDR [T00	1247	1255	6.925682	CACCTG	0.42725	0.41
cg1494300	DDB2	HNF-1B [	1007	1015	6.831535	GGTTAG	0.07629	0.07044
cg1494300	DDB2	PEA3 [T0	191	199	6.824411	CTCCAT	0.22888	0.22744
cg1494300	DDB2	NFI/CTF [	338	345	6.786076	TGGATT	0.73242	0.74795
cg1494300	DDB2	NFI/CTF [	1564	1571	6.786076	CCAAGC	0.73242	0.74795
cg1494300	DDB2	p53 [T006	885	891	6.778774	TGAGCC	1.09863	1.22478
cg1494300	DDB2	NF-1 [T00	29	36	6.722386	CTGGCC	0.24414	0.2565
cg1494300	DDB2	T3R-beta1	36	44	6.702681	ACATGG	0.21362	0.2251
cg1494300	DDB2	NF-kappa	1506	1517	6.673038	GGGGTT	0.00405	0.00452
cg1494300	DDB2	T3R-beta1	1013	1021	6.664094	TCACCG	0.21362	0.2251

cg1494300	DDB2	FOXP3 [T	976	981	6.581441	TTCAAC	0.97656	0.904
cg1494300	DDB2	TFII-I [T0	189	194	6.581441	CACTCC	0.97656	0.9991
cg1494300	DDB2	TFII-I [T0	371	376	6.581441	GGAGTG	0.97656	0.9991
cg1494300	DDB2	TFII-I [T0	1687	1692	6.581441	GGAGTG	0.97656	0.9991
cg1494300	DDB2	XBP-1 [T	995	1000	6.478682	ATGCCC	0.97656	0.99906
cg1494300	DDB2	RAR-beta	41	50	6.415195	GTGAAA	0.18311	0.1857
cg1494300	DDB2	NF-kappaB	1595	1605	6.321969	TGGCTG	0.03052	0.03409
cg1494300	DDB2	TCF-4E [T	1180	1186	6.302385	GGCAAA	0.61035	0.59686
cg1494300	DDB2	TCF-4E [T	1777	1783	6.302385	CTTTGCC	0.61035	0.59686
cg1494300	DDB2	GR-alpha [	5	9	6.263098	TGAGG	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	300	304	6.263098	TGAGG	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	312	316	6.263098	TGAGG	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	368	372	6.263098	TGAGG	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	591	595	6.263098	TGAGG	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	670	674	6.263098	TGAGG	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	793	797	6.263098	CCTCA	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	938	942	6.263098	CCTCA	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	1219	1223	6.263098	CCTCA	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	1466	1470	6.263098	CCTCA	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	1515	1519	6.263098	CCTCA	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	1893	1897	6.263098	CCTCA	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	1913	1917	6.263098	CCTCA	3.90625	3.89624
cg1494300	DDB2	GR-alpha [	1973	1977	6.263098	TGAGG	3.90625	3.89624
cg1494300	DDB2	C/EBPalph	989	995	6.245236	TATTGA	0.97656	0.91422
cg1494300	DDB2	c-Fos [T00	279	288	6.236188	GCCGTG	0.09155	0.09198
cg1494300	DDB2	ATF-2 [T0	1531	1540	6.203442	ACTACG	0.11826	0.11557
cg1494300	DDB2	NF-AT1 [T	263	272	6.201624	TTGATTT	0.03815	0.03661
cg1494300	DDB2	NF-AT1 [T	618	626	6.150044	GTTTTTT	0.06866	0.06621
cg1494300	DDB2	MAZ [T00	1212	1224	6.11881	TTCCCTC	0.00393	0.00438
cg1494300	DDB2	GR-alpha [	3	7	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	10	14	6.055408	TCAGG	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	298	302	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	551	555	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	717	721	6.055408	CCTAA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	795	799	6.055408	TCAGG	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	830	834	6.055408	TCAGG	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	840	844	6.055408	TTAGG	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	1249	1253	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	1317	1321	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	1550	1554	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	1763	1767	6.055408	TCAGG	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	1814	1818	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	GR-alpha [	1880	1884	6.055408	CCTGA	3.90625	3.89835
cg1494300	DDB2	c-Ets-1 [T	267	273	6.039428	TTTCCAC	0.36621	0.36174
cg1494300	DDB2	c-Ets-1 [T	1619	1625	6.039428	TTTCCAC	0.36621	0.36174
cg1494300	DDB2	RXR-alpha	1701	1707	5.937582	AGTACC	0.73242	0.78318
cg1494300	DDB2	HNF-1B [	963	971	5.903284	AGTTAT	0.09918	0.08736
cg1494300	DDB2	p53 [T006	92	98	5.883561	TAGGCC	0.61035	0.68483

cg1494300	DDB2	STAT4 [T	1942	1947	5.882353	GGAAGG	0.48828	0.51201
cg1494300	DDB2	AR [T000	1595	1603	5.859358	TGGCTG	0.24414	0.25115
cg1494300	DDB2	C/EBPalp	397	403	5.850545	GGCAAT	0.97656	0.91422
cg1494300	DDB2	E2F-1 [T0	1021	1028	5.846171	GCGGCA	0.18311	0.19383
cg1494300	DDB2	E2F-1 [T0	1666	1673	5.846171	CTTTCC	0.18311	0.19383
cg1494300	DDB2	c-Ets-1 [T	1855	1861	5.814485	CTTCCC	0.36621	0.36174
cg1494300	DDB2	c-Ets-1 [T	1940	1946	5.814485	TGGGAA	0.36621	0.36174
cg1494300	DDB2	STAT1bet	266	275	5.796867	ATTTCC	0.1545	0.14881
cg1494300	DDB2	VDR [T00	1641	1649	5.771401	GTTCAC	0.42725	0.41266
cg1494300	DDB2	AR [T000	1237	1245	5.754178	TCTGTG	0.24414	0.25115
cg1494300	DDB2	ENKTF-1	677	684	5.687009	CAGGGC	0.73242	0.76357
cg1494300	DDB2	ENKTF-1	1313	1320	5.687009	TGGCCC	0.73242	0.76357
cg1494300	DDB2	ENKTF-1	1725	1732	5.687009	CAAGGC	0.73242	0.76357
cg1494300	DDB2	IRF-1 [T0	267	275	5.65977	TTTCCA	0.22888	0.21959
cg1494300	DDB2	EBF [T05	1871	1881	5.623365	CCCCCT	0.01907	0.0226
cg1494300	DDB2	T3R-beta1	1221	1229	5.572705	TCACCC	0.21362	0.21789
cg1494300	DDB2	T3R-beta1	1924	1932	5.572705	TCAAGG	0.21362	0.21789
cg1494300	DDB2	C/EBPalp	340	346	5.565669	GATTGG	0.73242	0.68229
cg1494300	DDB2	NFI/CTF [	1331	1338	5.558661	GTGATT	0.54932	0.55504
cg1494300	DDB2	GATA-2 [	891	899	5.555555	CCATTA	0.18311	0.18081
cg1494300	DDB2	TFIID [T0	839	845	5.544826	TTTAGG	0.73242	0.65314
cg1494300	DDB2	NF-AT1 [	1615	1624	5.512555	TGAGTT	0.05913	0.05666
cg1494300	DDB2	AP-1 [T00	283	291	5.496182	TGACTC	0.09155	0.08822
cg1494300	DDB2	NF-1 [T00	713	720	5.377909	TTGGCC	0.24414	0.25051
cg1494300	DDB2	ETF [T002	775	785	5.246906	GTGTGG	0.02861	0.03569
cg1494300	DDB2	GR [T050	1094	1100	5.207533	GGTTTT	0.24414	0.24013
cg1494300	DDB2	AR [T000	1047	1055	5.104816	TCTCTG	0.11444	0.12256
cg1494300	DDB2	AP-2alpha	475	480	5.100982	AAAGGC	0.97656	0.97517
cg1494300	DDB2	AP-2alpha	1208	1213	5.100982	GCCTTT	0.97656	0.97517
cg1494300	DDB2	RXR-alph	315	321	5.089356	GGGTGC	0.48828	0.51407
cg1494300	DDB2	RXR-alph	556	562	5.089356	AGCACC	0.48828	0.51407
cg1494300	DDB2	GR-beta [	64	68	5.042296	AATAC	3.90625	3.7093
cg1494300	DDB2	GR-beta [	250	254	5.042296	AATAC	3.90625	3.7093
cg1494300	DDB2	GR-beta [	339	343	5.042296	GGATT	3.90625	3.7093
cg1494300	DDB2	GR-beta [	491	495	5.042296	GGATT	3.90625	3.7093
cg1494300	DDB2	GR-beta [	688	692	5.042296	AATCC	3.90625	3.7093
cg1494300	DDB2	GR-beta [	948	952	5.042296	AATCC	3.90625	3.7093
cg1494300	DDB2	E2F-1 [T0	1883	1890	5.042045	GATCCC	0.18311	0.20394
cg1494300	DDB2	NFI/CTF [	709	716	5.021086	TCCTTT	0.24414	0.25666
cg1494300	DDB2	AR [T000	351	359	4.995624	GGGCTG	0.11444	0.12256
cg1494300	DDB2	ATF3 [T0	1532	1539	4.941398	CTACGT	0.09155	0.08959
cg1494300	DDB2	XBP-1 [T	1432	1437	4.894955	AGGCAT	0.97656	0.99839
cg1494300	DDB2	AP-2alpha	716	721	4.890408	GCCTAA	0.97656	0.97517
cg1494300	DDB2	c-Jun [T00	1533	1539	4.883696	TACGTC	0.61035	0.60573
cg1494300	DDB2	NF-1 [T00	1377	1384	4.880836	TTGGGA	0.24414	0.24345
cg1494300	DDB2	c-Ets-1 [T	1522	1528	4.782565	GTGGAA	0.48828	0.48026
cg1494300	DDB2	C/EBPalp	61	67	4.776286	AACAAT	0.97656	0.90302
cg1494300	DDB2	FOXP3 [T	510	515	4.756447	AAAAAC	2.92969	2.82

cg1494300	DDB2	FOXP3 [T	618	623	4.756447	GTTTTT	2.92969	2.82
cg1494300	DDB2	FOXP3 [T	1095	1100	4.756447	GTTTTG	2.92969	2.82
cg1494300	DDB2	FOXP3 [T	1441	1446	4.756447	GTCAAC	2.92969	2.82
cg1494300	DDB2	FOXP3 [T	1509	1514	4.756447	GTTTTC	2.92969	2.82
cg1494300	DDB2	TFII-I [T0	266	271	4.756447	ATTTCC	2.92969	2.89715
cg1494300	DDB2	TFII-I [T0	339	344	4.756447	GGATTG	2.92969	2.89715
cg1494300	DDB2	TFII-I [T0	578	583	4.756447	CAGTCC	2.92969	2.89715
cg1494300	DDB2	TFII-I [T0	687	692	4.756447	CAATCC	2.92969	2.89715
cg1494300	DDB2	TFII-I [T0	1456	1461	4.756447	ATATCC	2.92969	2.89715
cg1494300	DDB2	TFII-I [T0	1793	1798	4.756447	CAGTCC	2.92969	2.89715
cg1494300	DDB2	TFII-I [T0	1865	1870	4.756447	GGACTG	2.92969	2.89715
cg1494300	DDB2	c-Myb [T0	960	967	4.754782	GACAGT	0.30518	0.30087
cg1494300	DDB2	c-Ets-1 [T	1904	1910	4.654478	CTTCCAC	0.85449	0.8381
cg1494300	DDB2	VDR [T00	1165	1173	4.617121	CTGCTGA	0.37384	0.36855
cg1494300	DDB2	c-Ets-1 [T	1667	1673	4.616023	TTTCCGC	0.85449	0.8381
cg1494300	DDB2	c-Ets-2 [T	1753	1761	4.589988	TTCCTTC	0.06866	0.06805
cg1494300	DDB2	c-Ets-1 [T	944	950	4.539113	TAGGAA	0.85449	0.8381
cg1494300	DDB2	GATA-2 [	1552	1560	4.444445	TGATAGC	0.24414	0.23857
cg1494300	DDB2	STAT4 [T	427	432	4.411765	TCTTCC	1.95312	1.99838
cg1494300	DDB2	STAT4 [T	441	446	4.411765	TCTTCC	1.95312	1.99838
cg1494300	DDB2	STAT4 [T	1154	1159	4.411765	GGAACG	1.95312	1.99838
cg1494300	DDB2	STAT4 [T	1409	1414	4.411765	GCTTCC	1.95312	1.99838
cg1494300	DDB2	STAT4 [T	1524	1529	4.411765	GGAAGC	1.95312	1.99838
cg1494300	DDB2	STAT4 [T	1661	1666	4.411765	TCTTCC	1.95312	1.99838
cg1494300	DDB2	STAT4 [T	1854	1859	4.411765	GCTTCC	1.95312	1.99838
cg1494300	DDB2	p53 [T006	679	685	4.33696	GGGCCA	0.24414	0.28373
cg1494300	DDB2	PEA3 [T0	1106	1114	4.30818	TGGATGT	0.13733	0.13607
cg1494300	DDB2	RAR-beta	1317	1326	4.307573	CCTGAAC	0.14496	0.14853
cg1494300	DDB2	c-Ets-1 [T	301	307	4.282938	GAGGAA	0.85449	0.8381
cg1494300	DDB2	CREB [T0	1531	1539	4.261795	ACTACGT	0.04578	0.0464
cg1494300	DDB2	EBF [T05	792	802	4.230426	GCCTCAC	0.0248	0.02839
cg1494300	DDB2	AP-2alpha	91	96	4.211849	GTAGGC	0.97656	1.02535
cg1494300	DDB2	GR-beta [T	136	140	4.201913	AATCG	7.8125	7.23274
cg1494300	DDB2	GR-beta [T	264	268	4.201913	TGATT	7.8125	7.23274
cg1494300	DDB2	GR-beta [T	389	393	4.201913	AATCA	7.8125	7.23274
cg1494300	DDB2	GR-beta [T	539	543	4.201913	AATAG	7.8125	7.23274
cg1494300	DDB2	GR-beta [T	965	969	4.201913	TTATT	7.8125	7.23274
cg1494300	DDB2	GR-beta [T	988	992	4.201913	TTATT	7.8125	7.23274
cg1494300	DDB2	GR-beta [T	1037	1041	4.201913	AATAG	7.8125	7.23274
cg1494300	DDB2	GR-beta [T	1332	1336	4.201913	TGATT	7.8125	7.23274
cg1494300	DDB2	HNF-1C [	964	972	4.175118	GTTATTC	0.04578	0.04045
cg1494300	DDB2	p53 [T006	1877	1883	4.125254	GGGCCTC	0.73242	0.82434
cg1494300	DDB2	SRY [T00	261	269	4.087393	CTTTGAT	0.12207	0.11312
cg1494300	DDB2	IRF-1 [T0	1211	1219	4.035054	TTTCCCT	0.1297	0.12468
cg1494300	DDB2	IRF-1 [T0	1511	1519	4.035054	TTTCCCT	0.1297	0.12468
cg1494300	DDB2	C/EBPalph	685	691	4.019783	GGCAATC	0.48828	0.46347
cg1494300	DDB2	RXR-alpha	43	49	4.019014	GAAACC	0.97656	1.02803
cg1494300	DDB2	RXR-alpha	773	779	4.019014	GGGTGTC	0.97656	1.02803

cg1494300	DDB2	RXR-alpha	1916	1922	4.019014	CACACC	0.97656	1.02803
cg1494300	DDB2	c-Ets-2 [T	1663	1671	4.017001	TTCCTTT	0.16022	0.15061
cg1494300	DDB2	Pax-5 [T0	351	357	4.007279	GGGCTG	1.09863	1.18533
cg1494300	DDB2	Pax-5 [T0	994	1000	4.007279	AATGCC	1.09863	1.18533
cg1494300	DDB2	Pax-5 [T0	1645	1651	4.007279	ACAGCC	1.09863	1.18533
cg1494300	DDB2	Pax-5 [T0	1767	1773	4.007279	GGGCTT	1.09863	1.18533
cg1494300	DDB2	Pax-5 [T0	1867	1873	4.007279	ACTGCC	1.09863	1.18533
cg1494300	DDB2	AP-2alpha	411	416	3.970052	CAAGGC	0.97656	1.02535
cg1494300	DDB2	AP-2alpha	1725	1730	3.970052	CAAGGC	0.97656	1.02535
cg1494300	DDB2	c-Jun [T00	1009	1015	3.807346	TTAGTC	0.24414	0.23729
cg1494300	DDB2	E2F-1 [T0	427	434	3.784875	TCTTCC	0.15259	0.15999
cg1494300	DDB2	GR [T050	693	699	3.763516	CTCTTTC	0.73242	0.6946
cg1494300	DDB2	GR [T050	1182	1188	3.763516	CAAAGA	0.73242	0.6946
cg1494300	DDB2	p53 [T006	798	804	3.750231	GGGCTT	0.73242	0.82434
cg1494300	DDB2	p53 [T006	1743	1749	3.750231	GGGCTT	0.73242	0.82434
cg1494300	DDB2	AP-2alpha	1716	1721	3.743866	GAAGGC	0.48828	0.5124
cg1494300	DDB2	NF-Y [T0	336	343	3.732121	ATTGGA	0.48828	0.48427
cg1494300	DDB2	NF-Y [T0	341	348	3.732121	ATTGGA	0.48828	0.48427
cg1494300	DDB2	c-Ets-1 [T	1752	1758	3.71855	GTTCCTT	0.61035	0.61936
cg1494300	DDB2	c-Ets-1 [T	671	677	3.590463	GAGGAA	0.61035	0.61936
cg1494300	DDB2	c-Ets-1 [T	935	941	3.590463	GTTCCTC	0.61035	0.61936
cg1494300	DDB2	C/EBPalph	1333	1339	3.555778	GATTGG	0.24414	0.23261
cg1494300	DDB2	p53 [T006	994	1000	3.516613	AATGCC	0.73242	0.80362
cg1494300	DDB2	p53 [T006	1867	1873	3.516613	ACTGCC	0.73242	0.80362
cg1494300	DDB2	HNF-3alph	1370	1377	3.500065	TGAAAA	0.27466	0.23175
cg1494300	DDB2	VDR [T00	139	147	3.462841	CGCTTG	0.21362	0.21283
cg1494300	DDB2	c-Ets-1 [T	1338	1344	3.462376	GTTCCTC	0.61035	0.61936
cg1494300	DDB2	PXR-1:RX	143	150	3.395883	TGAACC	0.12207	0.11883
cg1494300	DDB2	PXR-1:RX	1251	1258	3.395883	TGAACC	0.12207	0.11883
cg1494300	DDB2	PXR-1:RX	1319	1326	3.395883	TGAACC	0.12207	0.11883
cg1494300	DDB2	RXR-alpha	1220	1226	3.392904	CTCACC	1.09863	1.1653
cg1494300	DDB2	RXR-alpha	1544	1550	3.392904	TTTACCC	1.09863	1.1653
cg1494300	DDB2	RXR-alpha	1888	1894	3.392904	CGCACC	1.09863	1.1653
cg1494300	DDB2	p53 [T006	81	87	3.375208	GGGCGT	0.73242	0.80362
cg1494300	DDB2	T3R-beta1	1656	1664	3.370634	TCACCTC	0.27466	0.27326
cg1494300	DDB2	GR-beta [	216	220	3.361531	AATCT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	439	443	3.361531	AATCT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	456	460	3.361531	ATATT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	878	882	3.361531	AGATT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	983	987	3.361531	AATAT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	984	988	3.361531	ATATT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	1061	1065	3.361531	AATCT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	1279	1283	3.361531	AATCT	3.90625	3.51525
cg1494300	DDB2	GR-beta [	1652	1656	3.361531	AGATT	3.90625	3.51525
cg1494300	DDB2	c-Ets-2 [T	298	306	3.2883	CCTGAG	0.18311	0.18314
cg1494300	DDB2	c-Ets-2 [T	936	944	3.2883	TTCCTCA	0.18311	0.18314
cg1494300	DDB2	c-Jun [T00	283	289	3.244843	TGACTC	0.24414	0.2435
cg1494300	DDB2	RAR-beta	141	150	3.244529	CTTGAA	0.12207	0.12558

cg1494300	DDB2	c-Ets-1 [T	428	434	3.231072	CTTCCG	0.24414	0.26272
cg1494300	DDB2	RXR-alph	323	329	3.170788	GGGTGT	0.24414	0.24551
cg1494300	DDB2	RXR-alph	1507	1513	3.170788	GGGTTT	0.24414	0.24551
cg1494300	DDB2	TCF-4E [	261	267	3.151193	CTTTGA	0.24414	0.23169
cg1494300	DDB2	NF-Y [T0	401	408	3.051543	ATTGGA	0.06104	0.05632
cg1494300	DDB2	p53 [T006	200	206	3.024997	GGGCAA	0.48828	0.53227
cg1494300	DDB2	Elk-1 [T00	1662	1670	2.987643	CTTCCT	0.07629	0.07518
cg1494300	DDB2	STAT4 [T	673	678	2.941176	GGAACA	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	934	939	2.941176	TGTTCC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	946	951	2.941176	GGAATC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1210	1215	2.941176	CTTTCC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1277	1282	2.941176	GGAATC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1337	1342	2.941176	GGTTCC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1400	1405	2.941176	GGAAAG	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1579	1584	2.941176	GGAACC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1666	1671	2.941176	CTTTCC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1751	1756	2.941176	GGTTCC	2.92969	2.92382
cg1494300	DDB2	STAT4 [T	1903	1908	2.941176	ACTTCC	2.92969	2.92382
cg1494300	DDB2	PR B [T00	61	67	2.80933	AACAAT	0.73242	0.66711
cg1494300	DDB2	PR B [T00	931	937	2.80933	GAATGT	0.73242	0.66711
cg1494300	DDB2	PR A [T01	61	67	2.80933	AACAAT	0.73242	0.66711
cg1494300	DDB2	PR A [T01	931	937	2.80933	GAATGT	0.73242	0.66711
cg1494300	DDB2	AP-2alpha	792	797	2.550491	GCCTCA	0.48828	0.51216
cg1494300	DDB2	AP-2alpha	1973	1978	2.550491	TGAGGC	0.48828	0.51216
cg1494300	DDB2	RXR-alph	723	729	2.544678	GGGTGA	0.85449	0.89683
cg1494300	DDB2	RXR-alph	765	771	2.544678	AGAACC	0.85449	0.89683
cg1494300	DDB2	Ik-1 [T027	106	118	2.374299	TCCCAG	0.00063	0.00068
cg1494300	DDB2	c-Jun [T00	1304	1310	2.345465	TGACGC	0.48828	0.48077
cg1494300	DDB2	GCF [T00	1381	1389	2.339499	GACCTG	0.06104	0.06908
cg1494300	DDB2	RXR-alph	1480	1486	2.322562	CAGACC	0.85449	0.89683
cg1494300	DDB2	Elk-1 [T00	1410	1418	2.299314	CTTCCT	0.09155	0.09306
cg1494300	DDB2	T3R-beta1	0	8	2.221365	TCACCT	0.15259	0.15303
cg1494300	DDB2	c-Ets-2 [T	668	676	2.217136	TCTGAG	0.16785	0.16456
cg1494300	DDB2	GATA-1 [	403	408	2.176375	TGGATA	3.90625	3.79558
cg1494300	DDB2	TCF-4 [T0	260	269	2.160205	ACTTTG	0.04196	0.03736
cg1494300	DDB2	c-Ets-2 [T	1411	1419	2.142327	TTCCTC	0.16785	0.16456
cg1494300	DDB2	GATA-1 [	895	900	2.001358	TATCCC	3.90625	3.79558
cg1494300	DDB2	GATA-1 [	1457	1462	2.001358	TATCCC	3.90625	3.79558
cg1494300	DDB2	AP-2alpha	119	124	1.871933	GGAGGC	0.97656	1.07805
cg1494300	DDB2	AP-2alpha	151	156	1.871933	GGAGGC	0.97656	1.07805
cg1494300	DDB2	AP-2alpha	572	577	1.871933	GCCTCC	0.97656	1.07805
cg1494300	DDB2	AP-2alpha	753	758	1.871933	GGAGGC	0.97656	1.07805
cg1494300	DDB2	AP-2alpha	1351	1356	1.871933	GCCTCC	0.97656	1.07805
cg1494300	DDB2	AP-2alpha	1959	1964	1.871933	GGAGGC	0.97656	1.07805
cg1494300	DDB2	FOXP3 [T	1066	1071	1.824994	TACAAC	0.48828	0.46414
cg1494300	DDB2	TFII-I [T0	738	743	1.824994	GGAGAG	0.48828	0.51201
cg1494300	DDB2	TFII-I [T0	1077	1082	1.824994	CTCTCC	0.48828	0.51201
cg1494300	DDB2	TFII-I [T0	1472	1477	1.824994	CTCTCC	0.48828	0.51201

cg1494300	DDB2	TFII-I [T0	1697	1702	1.824994	GGAGAG	0.48828	0.51201
cg1494300	DDB2	p53 [T006	643	649	1.758307	GGGCAG	0.36621	0.38097
cg1494300	DDB2	p53 [T006	1988	1994	1.758307	TCTGCCC	0.36621	0.38097
cg1494300	DDB2	GR-beta [T	103	107	1.680765	AATTC	3.90625	3.70067
cg1494300	DDB2	GR-beta [T	304	308	1.680765	GAATT	3.90625	3.70067
cg1494300	DDB2	GR-beta [T	334	338	1.680765	GCATT	3.90625	3.70067
cg1494300	DDB2	GR-beta [T	994	998	1.680765	AATGC	3.90625	3.70067
cg1494300	DDB2	GR-beta [T	1287	1291	1.680765	AATGC	3.90625	3.70067
cg1494300	DDB2	GR-beta [T	1625	1629	1.680765	GAATT	3.90625	3.70067
cg1494300	DDB2	C/EBPbeta	33	36	1.639871	CCAA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	116	119	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	337	340	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	342	345	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	402	405	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	697	700	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	713	716	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1056	1059	1.639871	CCAA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1275	1278	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1335	1338	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1377	1380	1.639871	TTGG	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1564	1567	1.639871	CCAA	15.625	15.23827
cg1494300	DDB2	IRF-1 [T0	1396	1404	1.616539	AGAGGG	0.04578	0.04268
cg1494300	DDB2	TFIID [T0	66	72	1.537547	TACAAA	0.73242	0.65627
cg1494300	DDB2	TFIID [T0	1096	1102	1.537547	TTTTGTA	0.73242	0.65627
cg1494300	DDB2	Pax-5 [T0	81	87	1.537547	GGGCGT	0.73242	0.83087
cg1494300	DDB2	Pax-5 [T0	679	685	1.537547	GGGCCA	0.73242	0.83087
cg1494300	DDB2	STAT4 [T	103	108	1.470588	AATTCC	1.95312	1.90161
cg1494300	DDB2	STAT4 [T	303	308	1.470588	GGAATT	1.95312	1.90161
cg1494300	DDB2	STAT4 [T	621	626	1.470588	TTTTCC	1.95312	1.90161
cg1494300	DDB2	STAT4 [T	1510	1515	1.470588	TTTTCC	1.95312	1.90161
cg1494300	DDB2	STAT4 [T	1618	1623	1.470588	GTTTCC	1.95312	1.90161
cg1494300	DDB2	PR B [T00	629	635	1.404665	CAGTGT	0.36621	0.35143
cg1494300	DDB2	PR A [T01	629	635	1.404665	CAGTGT	0.36621	0.35143
cg1494300	DDB2	C/EBPbeta	142	145	1.366559	TTGA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	224	227	1.366559	TCAA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	263	266	1.366559	TTGA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	450	453	1.366559	TTGA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	495	498	1.366559	TTGA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	503	506	1.366559	TTGA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	590	593	1.366559	TTGA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	977	980	1.366559	TCAA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	991	994	1.366559	TTGA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1362	1365	1.366559	TCAA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1442	1445	1.366559	TCAA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1537	1540	1.366559	TCAA	15.625	15.23827
cg1494300	DDB2	C/EBPbeta	1924	1927	1.366559	TCAA	15.625	15.23827
cg1494300	DDB2	LEF-1 [T0	261	268	1.362541	CTTTGA	0.09155	0.08414
cg1494300	DDB2	AP-2alpha	1430	1435	1.357116	ACAGGC	0.48828	0.51319

cg1494300	DDB2	AP-2alpha	1488	1493	1.357116	GCCTGT	0.48828	0.51319
cg1494300	DDB2	ENKTF-1	1934	1941	1.255756	TGGCGG	0.24414	0.27027
cg1494300	DDB2	AhR:Arnt	784	793	1.078293	GCAGGC	0.00191	0.00221
cg1494300	DDB2	NF-Y [T0	1334	1341	1.058936	ATTGGT	0.12207	0.11765
cg1494300	DDB2	E2F-1 [T0	355	362	0.993583	TGTCCC	0.03052	0.03367
cg1494300	DDB2	GATA-1 [	1453	1458	0.863549	GTGATA	1.95312	1.80234
cg1494300	DDB2	RXR-alph	1006	1012	0.848226	GGGTTA	0.48828	0.51313
cg1494300	DDB2	GR-beta [	73	77	0.840383	AATTA	7.8125	7.2174
cg1494300	DDB2	GR-beta [	102	106	0.840383	TAATT	7.8125	7.2174
cg1494300	DDB2	GR-beta [	183	187	0.840383	CCATT	7.8125	7.2174
cg1494300	DDB2	GR-beta [	242	246	0.840383	AATTA	7.8125	7.2174
cg1494300	DDB2	GR-beta [	305	309	0.840383	AATTA	7.8125	7.2174
cg1494300	DDB2	GR-beta [	399	403	0.840383	CAATT	7.8125	7.2174
cg1494300	DDB2	GR-beta [	400	404	0.840383	AATTG	7.8125	7.2174
cg1494300	DDB2	GR-beta [	891	895	0.840383	CCATT	7.8125	7.2174
cg1494300	DDB2	GR-beta [	969	973	0.840383	TCATT	7.8125	7.2174
cg1494300	DDB2	GR-beta [	973	977	0.840383	TCATT	7.8125	7.2174
cg1494300	DDB2	GR-beta [	1128	1132	0.840383	AATGG	7.8125	7.2174
cg1494300	DDB2	GATA-1 [	1551	1556	0.758539	CTGATA	1.95312	1.80234
cg1494300	DDB2	AP-2alpha	1879	1884	0.678558	GCCTGA	0.48828	0.51196
cg1494300	DDB2	GATA-1 [	453	458	0.280028	AAGATA	0.97656	0.8795
cg1494300	DDB2	c-Ets-1 [T	1662	1668	0.256174	CTTCCTT	0.24414	0.23743
cg1494300	DDB2	AP-2alpha	27	32	0.226186	GCCTGG	0.97656	1.07867
cg1494300	DDB2	AP-2alpha	418	423	0.226186	CCAGGC	0.97656	1.07867
cg1494300	DDB2	AP-2alpha	682	687	0.226186	CCAGGC	0.97656	1.07867
cg1494300	DDB2	AP-2alpha	1103	1108	0.226186	GCCTGG	0.97656	1.07867
cg1494300	DDB2	GR-alpha	157	161	0.207689	AGAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	475	479	0.207689	AAAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	692	696	0.207689	CCTCT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	710	714	0.207689	CCTTT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	720	724	0.207689	AAAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	735	739	0.207689	AAAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	750	754	0.207689	AAAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	905	909	0.207689	CCTCT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1185	1189	0.207689	AGAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1209	1213	0.207689	CCTTT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1396	1400	0.207689	AGAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1413	1417	0.207689	CCTCT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1542	1546	0.207689	CCTTT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1583	1587	0.207689	CCTTT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1659	1663	0.207689	CCTCT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1665	1669	0.207689	CCTTT	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1684	1688	0.207689	AGAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha	1740	1744	0.207689	AGAGG	7.8125	7.79817
cg1494300	DDB2	Elk-1 [T00	442	450	0.134348	CTTCCTC	0.06104	0.06399
cg1494300	DDB2	c-Ets-1 [T	1410	1416	0.128087	CTTCCTC	0.24414	0.24982
cg1494300	DDB2	GATA-1 [	220	225	0.105011	TATCTC	0.97656	0.92541
cg1494300	DDB2	GATA-1 [	1045	1050	0.105011	TATCTC	0.97656	0.92541

cg1494300	DDB2	GR-beta [T	72	76	0	AAATT	3.90625	3.51525
cg1494300	DDB2	GR-beta [T	241	245	0	AAATT	3.90625	3.51525
cg1494300	DDB2	GR-beta [T	932	936	0	AATGT	3.90625	3.51525
cg1494300	DDB2	GR-beta [T	1373	1377	0	AAATT	3.90625	3.51525
cg1494300	DDB2	GR-beta [T	1374	1378	0	AATTT	3.90625	3.51525
cg1494300	DDB2	GR-beta [T	1626	1630	0	AATTT	3.90625	3.51525
cg1494300	DDB2	ENKTF-1	1384	1391	0	CTGCGC	0.12207	0.13179
cg1494300	DDB2	TFIID [T0	224	230	0	TCAAAA	1.09863	0.95175
cg1494300	DDB2	TFIID [T0	655	661	0	TTTTCTA	1.09863	0.95175
cg1494300	DDB2	GR-alpha [	98	102	0	CCTGT	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	462	466	0	ATAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	676	680	0	ACAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	1038	1042	0	ATAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	1138	1142	0	ACAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	1430	1434	0	ACAGG	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	1438	1442	0	CCTGT	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	1489	1493	0	CCTGT	7.8125	7.79817
cg1494300	DDB2	GR-alpha [	1675	1679	0	CCTGT	7.8125	7.79817
cg1494300	DDB2	FOXP3 [T	613	618	0	GTTGTG	1.46484	1.44953
cg1494300	DDB2	FOXP3 [T	1144	1149	0	GACAAC	1.46484	1.44953
cg1494300	DDB2	FOXP3 [T	1635	1640	0	GTTGTT	1.46484	1.44953
cg1494300	DDB2	FOXP3 [T	1638	1643	0	GTTGTT	1.46484	1.44953
cg1494300	DDB2	PR B [T00	1026	1032	0	AACAGT	0.36621	0.35051
cg1494300	DDB2	PR B [T00	1365	1371	0	AACAGT	0.36621	0.35051
cg1494300	DDB2	PR A [T01	1026	1032	0	AACAGT	0.36621	0.35051
cg1494300	DDB2	PR A [T01	1365	1371	0	AACAGT	0.36621	0.35051
cg1494300	DDB2	C/EBPbeta	62	65	0	ACAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	67	70	0	ACAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	129	132	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	162	165	0	TTGC	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	186	189	0	TTGC	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	202	205	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	205	208	0	ACAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	386	389	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	398	401	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	410	413	0	ACAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	433	436	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	472	475	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	614	617	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	686	689	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	702	705	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	759	762	0	TTGC	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	802	805	0	TTGC	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	821	824	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	956	959	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	980	983	0	ACAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1024	1027	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1067	1070	0	ACAA	15.625	15.26275

cg1494300	DDB2	C/EBPbeta	1098	1101	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1145	1148	0	ACAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1181	1184	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1292	1295	0	ACAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1586	1589	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1633	1636	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1636	1639	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1639	1642	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1724	1727	0	GCAA	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1747	1750	0	TTGT	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1779	1782	0	TTGC	15.625	15.26275
cg1494300	DDB2	C/EBPbeta	1787	1790	0	TTGT	15.625	15.26275
cg1494300	DDB2	YY1 [T00	38	41	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	50	53	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	177	180	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	183	186	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	193	196	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	469	472	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	489	492	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	809	812	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	866	869	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	891	894	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	899	902	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	1129	1132	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	1174	1177	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	1324	1327	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	1604	1607	0	CCAT	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	1801	1804	0	ATGG	7.8125	7.79459
cg1494300	DDB2	YY1 [T00	1921	1924	0	CCAT	7.8125	7.79459
cg1494300	DDB2	TFII-I [T0	354	359	0	CTGTCC	1.46484	1.48598
cg1494300	DDB2	TFII-I [T0	404	409	0	GGATAG	1.46484	1.48598
cg1494300	DDB2	TFII-I [T0	1050	1055	0	CTGTCC	1.46484	1.48598
cg1494300	DDB2	TFII-I [T0	1210	1215	0	CTTTCC	1.46484	1.48598
cg1494300	DDB2	TFII-I [T0	1400	1405	0	GGAAAG	1.46484	1.48598
cg1494300	DDB2	TFII-I [T0	1598	1603	0	CTGTCC	1.46484	1.48598
cg1494300	DDB2	TFII-I [T0	1666	1671	0	CTTTCC	1.46484	1.48598
cg1494300	DDB2	STAT4 [T	266	271	0	ATTTCC	0.48828	0.46235
cg1494300	DDB2	c-Ets-1 [T	442	448	0	CTTCCTC	0.24414	0.24982
cg1494300	DDB2	ER-alpha [	8	12	0	GGTCA	1.95312	1.99744
cg1494300	DDB2	ER-alpha [	1134	1138	0	GGTCA	1.95312	1.99744
cg1494300	DDB2	ER-alpha [	1495	1499	0	TGACC	1.95312	1.99744
cg1494300	DDB2	ER-alpha [	1816	1820	0	TGACC	1.95312	1.99744
cg1494300	DDB2	RXR-alpha	143	149	0	TGAACC	0.24414	0.24342
cg1494300	DDB2	RXR-alpha	1319	1325	0	TGAACC	0.24414	0.24342
cg1494300	DDB2	GR [T050	68	74	0	CAAAAA	0.36621	0.33174
cg1494300	DDB2	GR [T050	225	231	0	CAAAAA	0.36621	0.33174
cg1494300	DDB2	GR [T050	1293	1299	0	CAAAAA	0.36621	0.33174
cg1494300	DDB2	GR [T050	1629	1635	0	TTTTTTG	0.36621	0.33174

cg1494300	DDB2	Pax-5 [T0	782	788	0	GGGCAG	1.09863	1.24633
cg1494300	DDB2	Pax-5 [T0	798	804	0	GGGCTT	1.09863	1.24633
cg1494300	DDB2	Pax-5 [T0	1743	1749	0	GGGCTT	1.09863	1.24633
cg1494300	DDB2	Pax-5 [T0	1877	1883	0	GGGCCT	1.09863	1.24633
cg1494300	DDB2	p53 [T006	782	788	0	GGGCAG	0.36621	0.40082
cg1494300	DDB2	AP-2alpha	394	399	0	GCAGGC	0.97656	1.07867
cg1494300	DDB2	AP-2alpha	784	789	0	GCAGGC	0.97656	1.07867
cg1494300	DDB2	AP-2alpha	1720	1725	0	GCCTGC	0.97656	1.07867
cg1494300	DDB2	IRF-2 [T0	258	263	0	TCACTT	0.48828	0.46235
cg1494300	DDB2	IRF-2 [T0	309	314	0	AAGTGA	0.48828	0.46235
cg1494300	DDB2	IRF-2 [T0	1301	1306	0	AAGTGA	0.48828	0.46235
cg1494300	DDB2	IRF-2 [T0	1774	1779	0	TCACTT	0.48828	0.46235
cg1494300	DDB2	IRF-2 [T0	1901	1906	0	TCACTT	0.48828	0.46235
cg1850382	DIP2C	RAR-beta:	1891	1902	9.97066	GGGATC	0.06974	0.07677
cg1493188	DIP2C	RAR-beta:	113	124	9.97066	GGGCTC	0.06974	0.07677
cg1493188	DIP2C	RAR-beta:	811	822	9.97066	GGGCTC	0.06974	0.07677
cg0545033	DIP2C	RAR-beta:	1931	1942	9.97066	GGGATC	0.06974	0.07677
cg1850223	DIP2C	PEA3 [T0	230	238	9.937959	GGGATG	0.18311	0.18382
cg1146814	DIP2C	PEA3 [T0	290	298	9.937959	TGGATG	0.18311	0.18382
cg1850223	DIP2C	NF-AT2 [	680	689	9.905562	ACAAAT	0.08774	0.08205
cg1850223	DIP2C	c-Ets-1 [T	1221	1227	9.841249	ATTCCC	0.24414	0.23698
cg1850223	DIP2C	HNF-1B [	1320	1328	9.830287	TGTTACT	0.12207	0.11326
cg1850382	DIP2C	HNF-1B [	647	655	9.830287	TGAGTA	0.12207	0.11326
cg1006492	DIP2C	HNF-1B [	757	765	9.830287	TGAGTA	0.12207	0.11326
cg0545033	DIP2C	HNF-1B [	687	695	9.830287	TGAGTA	0.12207	0.11326
cg1850223	DIP2C	Egr-3 [T0	1523	1535	9.828903	ATCACC	0.02503	0.02648
cg0270010	DIP2C	XBP-1 [T	1170	1175	9.789909	AGCCAT	1.95312	1.94901
cg1850223	DIP2C	XBP-1 [T	522	527	9.789909	AGACAT	1.95312	1.94901
cg1850382	DIP2C	XBP-1 [T	148	153	9.789909	ATGTCT	1.95312	1.94901
cg1850382	DIP2C	XBP-1 [T	542	547	9.789909	CGCCAT	1.95312	1.94901
cg1850382	DIP2C	XBP-1 [T	964	969	9.789909	ATGGCT	1.95312	1.94901
cg1850382	DIP2C	XBP-1 [T	1274	1279	9.789909	AGCCAT	1.95312	1.94901
cg1850382	DIP2C	XBP-1 [T	1786	1791	9.789909	ATGTCT	1.95312	1.94901
cg1493188	DIP2C	XBP-1 [T	1587	1592	9.789909	CGCCAT	1.95312	1.94901
cg1146814	DIP2C	XBP-1 [T	1761	1766	9.789909	AGCCAT	1.95312	1.94901
cg1006492	DIP2C	XBP-1 [T	258	263	9.789909	ATGTCT	1.95312	1.94901
cg1006492	DIP2C	XBP-1 [T	652	657	9.789909	CGCCAT	1.95312	1.94901
cg1006492	DIP2C	XBP-1 [T	1074	1079	9.789909	ATGGCT	1.95312	1.94901
cg1006492	DIP2C	XBP-1 [T	1384	1389	9.789909	AGCCAT	1.95312	1.94901
cg1006492	DIP2C	XBP-1 [T	1896	1901	9.789909	ATGTCT	1.95312	1.94901
cg0545033	DIP2C	XBP-1 [T	188	193	9.789909	ATGTCT	1.95312	1.94901
cg0545033	DIP2C	XBP-1 [T	582	587	9.789909	CGCCAT	1.95312	1.94901
cg0545033	DIP2C	XBP-1 [T	1004	1009	9.789909	ATGGCT	1.95312	1.94901
cg0545033	DIP2C	XBP-1 [T	1314	1319	9.789909	AGCCAT	1.95312	1.94901
cg0545033	DIP2C	XBP-1 [T	1826	1831	9.789909	ATGTCT	1.95312	1.94901
cg0270010	DIP2C	NF-1 [T00	158	165	9.761671	GGCTCC	0.24414	0.24488
cg1850223	DIP2C	NF-1 [T00	853	860	9.761671	AGCACC	0.24414	0.24488
cg1850223	DIP2C	NF-1 [T00	1915	1922	9.761671	AGCACC	0.24414	0.24488

cg1493188	DIP2C	NF-1 [T00	1870	1877	9.761671	TTGGTT	0.24414	0.24488
cg1146814	DIP2C	NF-1 [T00	749	756	9.761671	GGCTCC	0.24414	0.24488
cg0270010	DIP2C	PR B [T00	25	31	9.743489	AACACG	1.09863	1.0981
cg0270010	DIP2C	PR B [T00	60	66	9.743489	AACACA	1.09863	1.0981
cg0270010	DIP2C	PR B [T00	551	557	9.743489	GTGTGT	1.09863	1.0981
cg0270010	DIP2C	PR B [T00	1613	1619	9.743489	AACACA	1.09863	1.0981
cg0270010	DIP2C	PR B [T00	1777	1783	9.743489	AACACC	1.09863	1.0981
cg0270010	DIP2C	PR B [T00	1936	1942	9.743489	TGGTGT	1.09863	1.0981
cg0270010	DIP2C	PR B [T00	1962	1968	9.743489	CGGTGT	1.09863	1.0981
cg0270010	DIP2C	PR A [T01	25	31	9.743489	AACACG	1.09863	1.0981
cg0270010	DIP2C	PR A [T01	60	66	9.743489	AACACA	1.09863	1.0981
cg0270010	DIP2C	PR A [T01	551	557	9.743489	GTGTGT	1.09863	1.0981
cg0270010	DIP2C	PR A [T01	1613	1619	9.743489	AACACA	1.09863	1.0981
cg0270010	DIP2C	PR A [T01	1777	1783	9.743489	AACACC	1.09863	1.0981
cg0270010	DIP2C	PR A [T01	1936	1942	9.743489	TGGTGT	1.09863	1.0981
cg0270010	DIP2C	PR A [T01	1962	1968	9.743489	CGGTGT	1.09863	1.0981
cg1850382	DIP2C	PR B [T00	587	593	9.743489	AACACC	1.09863	1.0981
cg1850382	DIP2C	PR B [T00	1826	1832	9.743489	AACACA	1.09863	1.0981
cg1850382	DIP2C	PR A [T01	587	593	9.743489	AACACC	1.09863	1.0981
cg1850382	DIP2C	PR A [T01	1826	1832	9.743489	AACACA	1.09863	1.0981
cg1493188	DIP2C	PR B [T00	574	580	9.743489	TTGTGT	1.09863	1.0981
cg1493188	DIP2C	PR B [T00	1064	1070	9.743489	CCGTGT	1.09863	1.0981
cg1493188	DIP2C	PR B [T00	1800	1806	9.743489	AACACC	1.09863	1.0981
cg1493188	DIP2C	PR A [T01	574	580	9.743489	TTGTGT	1.09863	1.0981
cg1493188	DIP2C	PR A [T01	1064	1070	9.743489	CCGTGT	1.09863	1.0981
cg1493188	DIP2C	PR A [T01	1800	1806	9.743489	AACACC	1.09863	1.0981
cg1146814	DIP2C	PR B [T00	139	145	9.743489	AACACA	1.09863	1.0981
cg1146814	DIP2C	PR B [T00	530	536	9.743489	AACACA	1.09863	1.0981
cg1146814	DIP2C	PR B [T00	616	622	9.743489	AACACG	1.09863	1.0981
cg1146814	DIP2C	PR B [T00	651	657	9.743489	AACACA	1.09863	1.0981
cg1146814	DIP2C	PR B [T00	1142	1148	9.743489	GTGTGT	1.09863	1.0981
cg1146814	DIP2C	PR A [T01	139	145	9.743489	AACACA	1.09863	1.0981
cg1146814	DIP2C	PR A [T01	530	536	9.743489	AACACA	1.09863	1.0981
cg1146814	DIP2C	PR A [T01	616	622	9.743489	AACACG	1.09863	1.0981
cg1146814	DIP2C	PR A [T01	651	657	9.743489	AACACA	1.09863	1.0981
cg1146814	DIP2C	PR A [T01	1142	1148	9.743489	GTGTGT	1.09863	1.0981
cg1006492	DIP2C	PR B [T00	697	703	9.743489	AACACC	1.09863	1.0981
cg1006492	DIP2C	PR B [T00	1936	1942	9.743489	AACACA	1.09863	1.0981
cg1006492	DIP2C	PR A [T01	697	703	9.743489	AACACC	1.09863	1.0981
cg1006492	DIP2C	PR A [T01	1936	1942	9.743489	AACACA	1.09863	1.0981
cg0545033	DIP2C	PR B [T00	627	633	9.743489	AACACC	1.09863	1.0981
cg0545033	DIP2C	PR B [T00	1866	1872	9.743489	AACACA	1.09863	1.0981
cg0545033	DIP2C	PR A [T01	627	633	9.743489	AACACC	1.09863	1.0981
cg0545033	DIP2C	PR A [T01	1866	1872	9.743489	AACACA	1.09863	1.0981
cg1850223	DIP2C	c-Myb [T0	1074	1081	9.729271	GAACTG	0.36621	0.34746
cg1850382	DIP2C	c-Myb [T0	816	823	9.729271	ATCAGT	0.36621	0.34746
cg1006492	DIP2C	c-Myb [T0	926	933	9.729271	ATCAGT	0.36621	0.34746
cg0545033	DIP2C	c-Myb [T0	856	863	9.729271	ATCAGT	0.36621	0.34746

cg1850223	DIP2C	LEF-1 [T0	175	182	9.72404	AGACAA	0.21362	0.21229
cg1493188	DIP2C	LEF-1 [T0	1190	1197	9.72404	CTTTGTC	0.21362	0.21229
cg1493188	DIP2C	LEF-1 [T0	1990	1997	9.72404	AGGCAA	0.21362	0.21229
cg0270010	DIP2C	c-Jun [T00	200	206	9.717135	TGACCT	0.73242	0.7366
cg1850223	DIP2C	c-Jun [T00	1537	1543	9.717135	CAGGTC	0.73242	0.7366
cg1850382	DIP2C	c-Jun [T00	1206	1212	9.717135	CAGGTC	0.73242	0.7366
cg1146814	DIP2C	c-Jun [T00	791	797	9.717135	TGACCT	0.73242	0.7366
cg1006492	DIP2C	c-Jun [T00	1316	1322	9.717135	CAGGTC	0.73242	0.7366
cg0545033	DIP2C	c-Jun [T00	1246	1252	9.717135	CAGGTC	0.73242	0.7366
cg0270010	DIP2C	HNF-4alp	163	175	9.675138	CAAAGT	0.01109	0.01049
cg1146814	DIP2C	HNF-4alp	754	766	9.675138	CAAAGT	0.01109	0.01049
cg1850223	DIP2C	RAR-beta	1877	1886	9.641259	CGAGAA	0.21362	0.22369
cg0270010	DIP2C	EBF [T05	473	483	9.625349	TGCCCT	0.06866	0.07687
cg1146814	DIP2C	EBF [T05	1064	1074	9.625349	TGCCCT	0.06866	0.07687
cg1850223	DIP2C	RAR-beta	1928	1937	9.622793	CAGAAA	0.21362	0.22369
cg1850223	DIP2C	NF-AT1 [	785	793	9.557905	GGAAAA	0.16785	0.16528
cg0270010	DIP2C	TFIID [T0	990	996	9.552105	TGTGAA	1.46484	1.37777
cg0270010	DIP2C	TFIID [T0	1392	1398	9.552105	TCCCAA	1.46484	1.37777
cg0270010	DIP2C	TFIID [T0	1476	1482	9.552105	TGTCAA	1.46484	1.37777
cg0270010	DIP2C	TFIID [T0	1760	1766	9.552105	TGGGAA	1.46484	1.37777
cg0270010	DIP2C	Pax-5 [T0	801	807	9.552105	GGGCAA	1.46484	1.61918
cg0270010	DIP2C	Pax-5 [T0	1253	1259	9.552105	GCCGCC	1.46484	1.61918
cg0270010	DIP2C	Pax-5 [T0	1770	1776	9.552105	GGGCGG	1.46484	1.61918
cg0270010	DIP2C	Pax-5 [T0	1830	1836	9.552105	GGGCCA	1.46484	1.61918
cg0270010	DIP2C	Pax-5 [T0	1902	1908	9.552105	GGGCGG	1.46484	1.61918
cg1850223	DIP2C	TFIID [T0	28	34	9.552105	TTTGCC	1.46484	1.37777
cg1850223	DIP2C	TFIID [T0	527	533	9.552105	TTTGTC	1.46484	1.37777
cg1850223	DIP2C	TFIID [T0	802	808	9.552105	TCCGAA	1.46484	1.37777
cg1850223	DIP2C	TFIID [T0	1371	1377	9.552105	TGTGAA	1.46484	1.37777
cg1850382	DIP2C	TFIID [T0	595	601	9.552105	TTTGCC	1.46484	1.37777
cg1850382	DIP2C	TFIID [T0	1453	1459	9.552105	TTTCCC	1.46484	1.37777
cg1850382	DIP2C	TFIID [T0	1649	1655	9.552105	TTCCAA	1.46484	1.37777
cg1850382	DIP2C	TFIID [T0	1872	1878	9.552105	TTTGGG	1.46484	1.37777
cg1850382	DIP2C	Pax-5 [T0	539	545	9.552105	GGGCGC	1.46484	1.61918
cg1493188	DIP2C	TFIID [T0	546	552	9.552105	TTTGGA	1.46484	1.37777
cg1493188	DIP2C	TFIID [T0	934	940	9.552105	TTCCAA	1.46484	1.37777
cg1493188	DIP2C	TFIID [T0	1164	1170	9.552105	TGAGAA	1.46484	1.37777
cg1493188	DIP2C	TFIID [T0	1191	1197	9.552105	TTTGTC	1.46484	1.37777
cg1493188	DIP2C	TFIID [T0	1218	1224	9.552105	TTTGAC	1.46484	1.37777
cg1493188	DIP2C	Pax-5 [T0	1004	1010	9.552105	TCCGCC	1.46484	1.61918
cg1146814	DIP2C	TFIID [T0	1581	1587	9.552105	TGTGAA	1.46484	1.37777
cg1146814	DIP2C	TFIID [T0	1983	1989	9.552105	TCCCAA	1.46484	1.37777
cg1146814	DIP2C	Pax-5 [T0	238	244	9.552105	GGGCGC	1.46484	1.61918
cg1146814	DIP2C	Pax-5 [T0	1392	1398	9.552105	GGGCAA	1.46484	1.61918
cg1146814	DIP2C	Pax-5 [T0	1844	1850	9.552105	GCCGCC	1.46484	1.61918
cg1006492	DIP2C	TFIID [T0	705	711	9.552105	TTTGCC	1.46484	1.37777
cg1006492	DIP2C	TFIID [T0	1563	1569	9.552105	TTTCCC	1.46484	1.37777
cg1006492	DIP2C	TFIID [T0	1759	1765	9.552105	TTCCAA	1.46484	1.37777

cg1006492	DIP2C	TFIID [T0	1982	1988	9.552105	TTTGGG	1.46484	1.37777
cg1006492	DIP2C	Pax-5 [T0(	649	655	9.552105	GGGCGC	1.46484	1.61918
cg0545033	DIP2C	TFIID [T0	635	641	9.552105	TTTGCC	1.46484	1.37777
cg0545033	DIP2C	TFIID [T0	1493	1499	9.552105	TTTCCC	1.46484	1.37777
cg0545033	DIP2C	TFIID [T0	1689	1695	9.552105	TTCCAA	1.46484	1.37777
cg0545033	DIP2C	TFIID [T0	1912	1918	9.552105	TTTGGG	1.46484	1.37777
cg0545033	DIP2C	Pax-5 [T0(	579	585	9.552105	GGGCGC	1.46484	1.61918
cg1493188	DIP2C	NF-1 [T00	1145	1152	9.535536	CCGTCC	0.73242	0.74634
cg1493188	DIP2C	NF-1 [T00	1808	1815	9.513281	CACGCC	0.73242	0.74634
cg0270010	DIP2C	FOXP3 [T	22	27	9.512894	CAGAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	303	308	9.512894	GAGAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	402	407	9.512894	GAGAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	520	525	9.512894	CGCAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	555	560	9.512894	GTTGGG	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	687	692	9.512894	GTTTAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	732	737	9.512894	GGCAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	802	807	9.512894	GGCAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	900	905	9.512894	GTTGGT	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	963	968	9.512894	AATAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	1397	1402	9.512894	AAGAAC	7.32422	7.22156
cg0270010	DIP2C	FOXP3 [T	1508	1513	9.512894	GAGAAC	7.32422	7.22156
cg0270010	DIP2C	TFII-I [T0	165	170	9.512894	AAGTCC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	668	673	9.512894	GTGTCC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	811	816	9.512894	AAGTCC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1130	1135	9.512894	GGAAGG	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1218	1223	9.512894	GGAACG	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1261	1266	9.512894	GGAAAA	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1501	1506	9.512894	GGACAC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1762	1767	9.512894	GGAAAC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1774	1779	9.512894	GGAAAC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1948	1953	9.512894	CCATCC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1955	1960	9.512894	CCATCC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1974	1979	9.512894	CCGTCC	7.32422	7.44385
cg0270010	DIP2C	TFII-I [T0	1982	1987	9.512894	CCGTCC	7.32422	7.44385
cg1850223	DIP2C	FOXP3 [T	36	41	9.512894	GTAAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	195	200	9.512894	GTTGCT	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	308	313	9.512894	AGCAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	492	497	9.512894	GTTCTC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	548	553	9.512894	ATAAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	882	887	9.512894	GTTTAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1017	1022	9.512894	CAGAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1035	1040	9.512894	AGCAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1072	1077	9.512894	CAGAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1314	1319	9.512894	ATAAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1444	1449	9.512894	GAGAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1511	1516	9.512894	CAGAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1560	1565	9.512894	GATAAC	7.32422	7.22156
cg1850223	DIP2C	FOXP3 [T	1878	1883	9.512894	GAGAAC	7.32422	7.22156

cg1850223	DIP2C	FOXP3 [T	1984	1989	9.512894	CAGAAC	7.32422	7.22156
cg1850223	DIP2C	TFII-I [T0	67	72	9.512894	AAGTCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	100	105	9.512894	TTTTCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	187	192	9.512894	GGAAGG	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	378	383	9.512894	GGACAC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	481	486	9.512894	TTATCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	510	515	9.512894	TTTTCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	539	544	9.512894	TTGTCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	614	619	9.512894	GGATAA	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	672	677	9.512894	GGAAAA	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	785	790	9.512894	GGAAAA	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	1059	1064	9.512894	GGAACG	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	1114	1119	9.512894	GGACAC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	1243	1248	9.512894	AATTCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	1383	1388	9.512894	TTTTCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	1559	1564	9.512894	GGATAA	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	1796	1801	9.512894	CGTTCC	7.32422	7.44385
cg1850223	DIP2C	TFII-I [T0	1977	1982	9.512894	TTGTCC	7.32422	7.44385
cg1850382	DIP2C	FOXP3 [T	9	14	9.512894	GTTATC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	55	60	9.512894	ACCAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	86	91	9.512894	AGCAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	171	176	9.512894	GTTGCT	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	306	311	9.512894	GTTTAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	337	342	9.512894	GTTTAT	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	350	355	9.512894	ACCAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	409	414	9.512894	ATAAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	584	589	9.512894	GTAAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	908	913	9.512894	CATAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	946	951	9.512894	CAGAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1108	1113	9.512894	AAGAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1133	1138	9.512894	CATAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1236	1241	9.512894	CGCAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1322	1327	9.512894	GTTATC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1476	1481	9.512894	GTAAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1639	1644	9.512894	CAGAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1760	1765	9.512894	AGCAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1864	1869	9.512894	CCCAAC	7.32422	7.22156
cg1850382	DIP2C	FOXP3 [T	1927	1932	9.512894	GCCAAC	7.32422	7.22156
cg1850382	DIP2C	TFII-I [T0	103	108	9.512894	GGAAAA	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	230	235	9.512894	GGACGG	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	265	270	9.512894	CGTTCC	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	470	475	9.512894	GGAAGG	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	475	480	9.512894	GGAAGG	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	489	494	9.512894	GGAAGG	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	493	498	9.512894	GGACAC	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	551	556	9.512894	CGTTCC	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	560	565	9.512894	GGACAA	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	931	936	9.512894	AAGTCC	7.32422	7.44385

cg1850382	DIP2C	TFII-I [T0	1288	1293	9.512894	GGATAC	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	1368	1373	9.512894	AAGTCC	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	1540	1545	9.512894	GGAAGG	7.32422	7.44385
cg1850382	DIP2C	TFII-I [T0	1684	1689	9.512894	GTGTCC	7.32422	7.44385
cg1493188	DIP2C	FOXP3 [T	631	636	9.512894	GTTTAT	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	641	646	9.512894	GTTATT	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1052	1057	9.512894	CAGAAC	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1582	1587	9.512894	AATAAC	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1656	1661	9.512894	AAGAAC	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1687	1692	9.512894	CAGAAC	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1811	1816	9.512894	GCCAAC	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1820	1825	9.512894	GTTCTT	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1873	1878	9.512894	GTTCTT	7.32422	7.22156
cg1493188	DIP2C	FOXP3 [T	1923	1928	9.512894	GTAAAC	7.32422	7.22156
cg1493188	DIP2C	TFII-I [T0	466	471	9.512894	GTTTCC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	549	554	9.512894	GGAATT	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	932	937	9.512894	GTTTCC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1032	1037	9.512894	CGTTCC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1145	1150	9.512894	CCGTCC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1263	1268	9.512894	CCTTCC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1359	1364	9.512894	AATTCC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1392	1397	9.512894	GGAAGG	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1457	1462	9.512894	GGATAC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1472	1477	9.512894	TTTTCC	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1546	1551	9.512894	GGACAA	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1768	1773	9.512894	GGACGG	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1796	1801	9.512894	GGAAAA	7.32422	7.44385
cg1493188	DIP2C	TFII-I [T0	1915	1920	9.512894	CCTTCC	7.32422	7.44385
cg1146814	DIP2C	FOXP3 [T	136	141	9.512894	GCCAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	145	150	9.512894	GTTGGG	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	305	310	9.512894	GTTATC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	613	618	9.512894	CAGAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	894	899	9.512894	GAGAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	993	998	9.512894	GAGAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1111	1116	9.512894	CGCAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1146	1151	9.512894	GTTGGG	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1278	1283	9.512894	GTTTAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1323	1328	9.512894	GGCAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1393	1398	9.512894	GGCAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1491	1496	9.512894	GTTGGT	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1554	1559	9.512894	AATAAC	7.32422	7.22156
cg1146814	DIP2C	FOXP3 [T	1988	1993	9.512894	AAGAAC	7.32422	7.22156
cg1146814	DIP2C	TFII-I [T0	69	74	9.512894	AATTCC	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	91	96	9.512894	GGAAAA	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	291	296	9.512894	GGATGG	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	312	317	9.512894	CGGTCC	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	333	338	9.512894	GGAAGG	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	464	469	9.512894	GGACCG	7.32422	7.44385

cg1146814	DIP2C	TFII-I [T0	548	553	9.512894	GGAAGG	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	756	761	9.512894	AAGTCC	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	1259	1264	9.512894	GTGTCC	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	1402	1407	9.512894	AAGTCC	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	1721	1726	9.512894	GGAAGG	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	1809	1814	9.512894	GGAACG	7.32422	7.44385
cg1146814	DIP2C	TFII-I [T0	1852	1857	9.512894	GGAAAA	7.32422	7.44385
cg1006492	DIP2C	FOXP3 [T	119	124	9.512894	GTTATC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	165	170	9.512894	ACCAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	196	201	9.512894	AGCAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	281	286	9.512894	GTTGCT	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	416	421	9.512894	GTTTAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	447	452	9.512894	GTTTAT	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	460	465	9.512894	ACCAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	519	524	9.512894	ATAAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	694	699	9.512894	GTAAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1018	1023	9.512894	CATAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1056	1061	9.512894	CAGAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1218	1223	9.512894	AAGAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1243	1248	9.512894	CATAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1346	1351	9.512894	CGCAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1432	1437	9.512894	GTTATC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1586	1591	9.512894	GTAAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1749	1754	9.512894	CAGAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1870	1875	9.512894	AGCAAC	7.32422	7.22156
cg1006492	DIP2C	FOXP3 [T	1974	1979	9.512894	CCCAAC	7.32422	7.22156
cg1006492	DIP2C	TFII-I [T0	213	218	9.512894	GGAAAA	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	340	345	9.512894	GGACGG	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	375	380	9.512894	CGTTCC	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	580	585	9.512894	GGAAGG	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	585	590	9.512894	GGAAGG	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	599	604	9.512894	GGAAGG	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	603	608	9.512894	GGACAC	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	661	666	9.512894	CGTTCC	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	670	675	9.512894	GGACAA	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	1041	1046	9.512894	AAGTCC	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	1398	1403	9.512894	GGATAC	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	1478	1483	9.512894	AAGTCC	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	1650	1655	9.512894	GGAAGG	7.32422	7.44385
cg1006492	DIP2C	TFII-I [T0	1794	1799	9.512894	GTGTCC	7.32422	7.44385
cg0545033	DIP2C	FOXP3 [T	49	54	9.512894	GTTATC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	95	100	9.512894	ACCAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	126	131	9.512894	AGCAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	211	216	9.512894	GTTGCT	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	346	351	9.512894	GTTTAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	377	382	9.512894	GTTTAT	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	390	395	9.512894	ACCAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	449	454	9.512894	ATAAAC	7.32422	7.22156

cg0545033	DIP2C	FOXP3 [T	624	629	9.512894	GTAAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	948	953	9.512894	CATAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	986	991	9.512894	CAGAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1148	1153	9.512894	AAGAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1173	1178	9.512894	CATAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1276	1281	9.512894	CGCAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1362	1367	9.512894	GTTATC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1516	1521	9.512894	GTAAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1679	1684	9.512894	CAGAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1800	1805	9.512894	AGCAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1904	1909	9.512894	CCCAAC	7.32422	7.22156
cg0545033	DIP2C	FOXP3 [T	1967	1972	9.512894	GCCAAC	7.32422	7.22156
cg0545033	DIP2C	TFII-I [T0	143	148	9.512894	GGAAAA	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	270	275	9.512894	GGACGG	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	305	310	9.512894	CGTTCC	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	510	515	9.512894	GGAAGG	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	515	520	9.512894	GGAAGG	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	529	534	9.512894	GGAAGG	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	533	538	9.512894	GGACAC	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	591	596	9.512894	CGTTCC	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	600	605	9.512894	GGACAA	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	971	976	9.512894	AAGTCC	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	1328	1333	9.512894	GGATAC	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	1408	1413	9.512894	AAGTCC	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	1580	1585	9.512894	GGAAGG	7.32422	7.44385
cg0545033	DIP2C	TFII-I [T0	1724	1729	9.512894	GTGTCC	7.32422	7.44385
cg0270010	DIP2C	c-Jun [T00	1439	1445	9.511322	TGACCA	0.73242	0.7366
cg1850382	DIP2C	c-Jun [T00	511	517	9.511322	GTGGTC	0.73242	0.7366
cg1006492	DIP2C	c-Jun [T00	621	627	9.511322	GTGGTC	0.73242	0.7366
cg0545033	DIP2C	c-Jun [T00	551	557	9.511322	GTGGTC	0.73242	0.7366
cg1850382	DIP2C	Ik-1 [T027	847	859	9.497194	AAAGCA	0.02941	0.03137
cg1006492	DIP2C	Ik-1 [T027	957	969	9.497194	AAAGCA	0.02941	0.03137
cg0545033	DIP2C	Ik-1 [T027	887	899	9.497194	AAAGCA	0.02941	0.03137
cg1493188	DIP2C	E2F [T002	1807	1816	9.471338	GCACGC	0.01907	0.02086
cg0270010	DIP2C	TCF-4E [T	161	167	9.453578	TCCAAA	0.48828	0.46934
cg0270010	DIP2C	TCF-4E [T	1571	1577	9.453578	TACAAA	0.48828	0.46934
cg1850223	DIP2C	TCF-4E [T	16	22	9.453578	TCCAAA	0.48828	0.46934
cg1850382	DIP2C	TCF-4E [T	1650	1656	9.453578	TCCAAA	0.48828	0.46934
cg1493188	DIP2C	TCF-4E [T	935	941	9.453578	TCCAAA	0.48828	0.46934
cg1493188	DIP2C	TCF-4E [T	1205	1211	9.453578	CTTTGTA	0.48828	0.46934
cg1493188	DIP2C	TCF-4E [T	1379	1385	9.453578	CTCAAA	0.48828	0.46934
cg1493188	DIP2C	TCF-4E [T	1416	1422	9.453578	CTTTGTA	0.48828	0.46934
cg1146814	DIP2C	TCF-4E [T	124	130	9.453578	GTCAAA	0.48828	0.46934
cg1146814	DIP2C	TCF-4E [T	752	758	9.453578	TCCAAA	0.48828	0.46934
cg1006492	DIP2C	TCF-4E [T	1760	1766	9.453578	TCCAAA	0.48828	0.46934
cg0545033	DIP2C	TCF-4E [T	1690	1696	9.453578	TCCAAA	0.48828	0.46934
cg1850382	DIP2C	c-Jun [T00	611	617	9.442241	TGACGG	0.73242	0.7366
cg1850382	DIP2C	c-Jun [T00	958	964	9.442241	GCCGTC	0.73242	0.7366

cg1146814	DIP2C	c-Jun [T00	363	369	9.442241	GCTGTC	0.73242	0.7366
cg1006492	DIP2C	c-Jun [T00	721	727	9.442241	TGACGG	0.73242	0.7366
cg1006492	DIP2C	c-Jun [T00	1068	1074	9.442241	GCCGTC	0.73242	0.7366
cg0545033	DIP2C	c-Jun [T00	651	657	9.442241	TGACGG	0.73242	0.7366
cg0545033	DIP2C	c-Jun [T00	998	1004	9.442241	GCCGTC	0.73242	0.7366
cg1850223	DIP2C	EBF [T05	385	395	9.441272	CACCCT	0.06866	0.07687
cg0270010	DIP2C	c-Jun [T00	635	641	9.397655	TGACAA	0.73242	0.7366
cg0270010	DIP2C	c-Jun [T00	695	701	9.397655	TGACAA	0.73242	0.7366
cg1850382	DIP2C	c-Jun [T00	1128	1134	9.397655	ATTGTC	0.73242	0.7366
cg1146814	DIP2C	c-Jun [T00	1226	1232	9.397655	TGACAA	0.73242	0.7366
cg1146814	DIP2C	c-Jun [T00	1286	1292	9.397655	TGACAA	0.73242	0.7366
cg1006492	DIP2C	c-Jun [T00	1238	1244	9.397655	ATTGTC	0.73242	0.7366
cg0545033	DIP2C	c-Jun [T00	1168	1174	9.397655	ATTGTC	0.73242	0.7366
cg1850223	DIP2C	NF-AT2 [	506	515	9.386314	TTAATT	0.04578	0.04451
cg0270010	DIP2C	HOXD9 [	963	972	9.356547	AATAAC	0.02289	0.02088
cg0270010	DIP2C	HOXD10	963	972	9.356547	AATAAC	0.02289	0.02088
cg1146814	DIP2C	HOXD9 [	1554	1563	9.356547	AATAAC	0.02289	0.02088
cg1146814	DIP2C	HOXD10	1554	1563	9.356547	AATAAC	0.02289	0.02088
cg0270010	DIP2C	NFI/CTF [	162	169	9.352332	CCAAAG	0.54932	0.55369
cg0270010	DIP2C	NFI/CTF [	523	530	9.352332	AACCTT	0.54932	0.55369
cg1850223	DIP2C	NFI/CTF [	17	24	9.352332	CCAAAG	0.54932	0.55369
cg1850223	DIP2C	NFI/CTF [	873	880	9.352332	AACCTT	0.54932	0.55369
cg1850223	DIP2C	NFI/CTF [	1919	1926	9.352332	CCAAAG	0.54932	0.55369
cg1850382	DIP2C	NFI/CTF [	1651	1658	9.352332	CCAAAG	0.54932	0.55369
cg1493188	DIP2C	NFI/CTF [	936	943	9.352332	CCAAAG	0.54932	0.55369
cg1146814	DIP2C	NFI/CTF [	379	386	9.352332	CCAAAG	0.54932	0.55369
cg1146814	DIP2C	NFI/CTF [	405	412	9.352332	CCAAAG	0.54932	0.55369
cg1146814	DIP2C	NFI/CTF [	753	760	9.352332	CCAAAG	0.54932	0.55369
cg1146814	DIP2C	NFI/CTF [	1114	1121	9.352332	AACCTT	0.54932	0.55369
cg1006492	DIP2C	NFI/CTF [	1761	1768	9.352332	CCAAAG	0.54932	0.55369
cg0545033	DIP2C	NFI/CTF [	1691	1698	9.352332	CCAAAG	0.54932	0.55369
cg0270010	DIP2C	POU2F2 (	1405	1415	9.350233	TGCATT	0.03433	0.03054
cg0270010	DIP2C	AP-1 [T00	310	318	9.3434	TGACTG	0.09155	0.08441
cg1146814	DIP2C	AP-1 [T00	901	909	9.3434	TGACTG	0.09155	0.08441
cg1850382	DIP2C	PEA3 [T0	359	367	9.340643	TGGATG	0.03052	0.0296
cg1006492	DIP2C	PEA3 [T0	469	477	9.340643	TGGATG	0.03052	0.0296
cg0545033	DIP2C	PEA3 [T0	399	407	9.340643	TGGATG	0.03052	0.0296
cg0270010	DIP2C	EBF [T05	1093	1103	9.324368	CCCACA	0.06866	0.07687
cg1146814	DIP2C	EBF [T05	1684	1694	9.324368	CCCACA	0.06866	0.07687
cg1850223	DIP2C	RelA [T00	508	518	9.320377	AATTTT	0.02813	0.02907
cg0270010	DIP2C	LEF-1 [T0	160	167	9.313676	CTCCAA	0.21362	0.21229
cg0270010	DIP2C	LEF-1 [T0	1915	1922	9.313676	CCCCAA	0.21362	0.21229
cg1850223	DIP2C	LEF-1 [T0	15	22	9.313676	CTCCAA	0.21362	0.21229
cg1146814	DIP2C	LEF-1 [T0	751	758	9.313676	CTCCAA	0.21362	0.21229
cg1850223	DIP2C	c-Myb [T0	1257	1264	9.29064	AAACTA	0.36621	0.34746
cg0270010	DIP2C	c-Ets-1 [T	1579	1585	9.276861	GTTCCC	0.36621	0.37402
cg1850382	DIP2C	SRY [T00	1648	1656	9.264664	ATTCCA	0.12207	0.11857
cg1146814	DIP2C	SRY [T00	122	130	9.264664	AGGTCA	0.12207	0.11857

cg1006492	DIP2C	SRY [T00	1758	1766	9.264664	ATTCCA	0.12207	0.11857
cg0545033	DIP2C	SRY [T00	1688	1696	9.264664	ATTCCA	0.12207	0.11857
cg027001	DIP2C	NF-AT1 [	1774	1782	9.225066	GGAAAC	0.22888	0.22581
cg1850382	DIP2C	MEF-2A [	1951	1961	9.220261	TACTAA	0.07343	0.06466
cg1850382	DIP2C	c-Ets-1 [T	1648	1654	9.19359	ATTCCA	0.85449	0.84987
cg1493188	DIP2C	c-Ets-1 [T	547	553	9.19359	TTGGAA	0.85449	0.84987
cg1006492	DIP2C	c-Ets-1 [T	1758	1764	9.19359	ATTCCA	0.85449	0.84987
cg0545033	DIP2C	c-Ets-1 [T	1688	1694	9.19359	ATTCCA	0.85449	0.84987
cg1850382	DIP2C	NF-AT1 [	1054	1062	9.18189	TCGCTT	0.22888	0.22581
cg1493188	DIP2C	NF-AT1 [	1833	1841	9.18189	TCCCTT	0.22888	0.22581
cg1006492	DIP2C	NF-AT1 [	1164	1172	9.18189	TCGCTT	0.22888	0.22581
cg0545033	DIP2C	NF-AT1 [	1094	1102	9.18189	TCGCTT	0.22888	0.22581
cg1146814	DIP2C	PPAR-alp	312	322	9.158357	CGGTCC	0.0515	0.05878
cg1850382	DIP2C	E2F [T002	1096	1105	9.15812	ATTCGC	0.09537	0.09726
cg1006492	DIP2C	E2F [T002	1206	1215	9.15812	ATTCGC	0.09537	0.09726
cg0545033	DIP2C	E2F [T002	1136	1145	9.15812	ATTCGC	0.09537	0.09726
cg027001	DIP2C	c-Ets-1 [T	1098	1104	9.148774	AGGGAA	0.85449	0.84987
cg1146814	DIP2C	c-Ets-1 [T	1689	1695	9.148774	AGGGAA	0.85449	0.84987
cg1850223	DIP2C	c-Myb [T0	1972	1979	9.142015	CTAAGT	0.39673	0.37851
cg1146814	DIP2C	c-Myb [T0	380	387	9.142015	CAAAGT	0.39673	0.37851
cg1850223	DIP2C	HNF-1C [	1321	1329	9.116395	GTTACT	0.12207	0.10938
cg1850223	DIP2C	AP-1 [T00	118	126	9.116043	CATCAG	0.24414	0.23028
cg1006492	DIP2C	AP-1 [T00	25	33	9.116043	CATCAG	0.24414	0.23028
cg1850223	DIP2C	c-Myb [T0	395	402	9.110773	CCAAGT	0.39673	0.37851
cg1493188	DIP2C	LEF-1 [T0	1205	1212	9.099721	CTTTGT	0.54932	0.53171
cg027001	DIP2C	COUP-TF	1141	1153	9.093379	AAGTGA	0.01878	0.01921
cg1850223	DIP2C	COUP-TF	691	703	9.093379	CTCTGA	0.01878	0.01921
cg1146814	DIP2C	COUP-TF	1732	1744	9.093379	AAGTGA	0.01878	0.01921
cg027001	DIP2C	AhR [T01	1183	1193	9.058053	CTCACG	0.03242	0.03333
cg1146814	DIP2C	AhR [T01	1774	1784	9.058053	CTCACG	0.03242	0.03333
cg027001	DIP2C	USF2 [T0	1292	1301	9.056375	CAGGTG	0.1545	0.16206
cg1146814	DIP2C	USF2 [T0	458	467	9.056375	CAGGTG	0.1545	0.16206
cg1146814	DIP2C	USF2 [T0	1883	1892	9.056375	CAGGTG	0.1545	0.16206
cg027001	DIP2C	NFI/CTF [	897	904	9.042931	GCAGTT	0.48828	0.48845
cg1146814	DIP2C	NFI/CTF [	142	149	9.042931	ACAGTT	0.48828	0.48845
cg1146814	DIP2C	NFI/CTF [	1488	1495	9.042931	GCAGTT	0.48828	0.48845
cg1850223	DIP2C	NF-AT1 [	681	689	9.042733	CAAATT	0.22888	0.22581
cg1850223	DIP2C	c-Ets-1 [T	1057	1063	9.020687	GGGGAA	0.85449	0.84987
cg1850223	DIP2C	c-Ets-1 [T	1797	1803	9.020687	GTTCCC	0.85449	0.84987
cg027001	DIP2C	c-Jun [T00	1693	1699	9.013496	TGACAT	0.61035	0.60549
cg1850382	DIP2C	c-Jun [T00	527	533	9.013496	CACGTC	0.61035	0.60549
cg1493188	DIP2C	c-Jun [T00	1230	1236	9.013496	TGACAT	0.61035	0.60549
cg1006492	DIP2C	c-Jun [T00	637	643	9.013496	CACGTC	0.61035	0.60549
cg0545033	DIP2C	c-Jun [T00	567	573	9.013496	CACGTC	0.61035	0.60549
cg027001	DIP2C	LEF-1 [T0	1392	1399	8.973041	TCCCAA	0.54932	0.53171
cg1850382	DIP2C	LEF-1 [T0	1649	1656	8.973041	TTCCAA	0.54932	0.53171
cg1850382	DIP2C	LEF-1 [T0	1871	1878	8.973041	CTTTGG	0.54932	0.53171
cg1493188	DIP2C	LEF-1 [T0	934	941	8.973041	TTCCAA	0.54932	0.53171

cg1146814	DIP2C	LEF-1 [T0	1983	1990	8.973041	TCCCAA	0.54932	0.53171
cg1006492	DIP2C	LEF-1 [T0	1759	1766	8.973041	TTCCAA	0.54932	0.53171
cg1006492	DIP2C	LEF-1 [T0	1981	1988	8.973041	CTTTGGC	0.54932	0.53171
cg0545033	DIP2C	LEF-1 [T0	1689	1696	8.973041	TTCCAA	0.54932	0.53171
cg0545033	DIP2C	LEF-1 [T0	1911	1918	8.973041	CTTTGGC	0.54932	0.53171
cg0270010	DIP2C	GR [T0507	877	883	8.971049	CAAATA	0.61035	0.5928
cg1850223	DIP2C	GR [T0507	18	24	8.971049	CAAAGC	0.61035	0.5928
cg1850223	DIP2C	GR [T0507	831	837	8.971049	CAAAAG	0.61035	0.5928
cg1850382	DIP2C	GR [T0507	1173	1179	8.971049	CAAAAG	0.61035	0.5928
cg1850382	DIP2C	GR [T0507	1652	1658	8.971049	CAAAGC	0.61035	0.5928
cg1493188	DIP2C	GR [T0507	669	675	8.971049	GATTTC	0.61035	0.5928
cg1493188	DIP2C	GR [T0507	1344	1350	8.971049	CAAAGC	0.61035	0.5928
cg1146814	DIP2C	GR [T0507	406	412	8.971049	CAAAGC	0.61035	0.5928
cg1146814	DIP2C	GR [T0507	580	586	8.971049	GCTTTC	0.61035	0.5928
cg1146814	DIP2C	GR [T0507	1468	1474	8.971049	CAAATA	0.61035	0.5928
cg1006492	DIP2C	GR [T0507	1283	1289	8.971049	CAAAAG	0.61035	0.5928
cg1006492	DIP2C	GR [T0507	1762	1768	8.971049	CAAAGC	0.61035	0.5928
cg0545033	DIP2C	GR [T0507	1213	1219	8.971049	CAAAAG	0.61035	0.5928
cg0545033	DIP2C	GR [T0507	1692	1698	8.971049	CAAAGC	0.61035	0.5928
cg1850382	DIP2C	Elk-1 [T00	478	486	8.931691	AGGTGG	0.24414	0.26271
cg1850382	DIP2C	Elk-1 [T00	982	990	8.931691	AGCGGG	0.24414	0.26271
cg1006492	DIP2C	Elk-1 [T00	588	596	8.931691	AGGTGG	0.24414	0.26271
cg1006492	DIP2C	Elk-1 [T00	1092	1100	8.931691	AGCGGG	0.24414	0.26271
cg0545033	DIP2C	Elk-1 [T00	518	526	8.931691	AGGTGG	0.24414	0.26271
cg0545033	DIP2C	Elk-1 [T00	1022	1030	8.931691	AGCGGG	0.24414	0.26271
cg1850382	DIP2C	T3R-beta1	1374	1382	8.924046	TCACCC	0.2594	0.2685
cg1006492	DIP2C	T3R-beta1	1484	1492	8.924046	TCACCC	0.2594	0.2685
cg0545033	DIP2C	T3R-beta1	1414	1422	8.924046	TCACCC	0.2594	0.2685
cg0270010	DIP2C	IRF-1 [T0	1770	1778	8.916359	GGGCGG	0.09155	0.09193
cg1493188	DIP2C	IRF-1 [T0	467	475	8.916359	TTTCCAC	0.09155	0.09193
cg1493188	DIP2C	IRF-1 [T0	1792	1800	8.916359	TTGTGG	0.09155	0.09193
cg0270010	DIP2C	c-Ets-2 [T	915	923	8.912323	TTCCTAA	0.27466	0.27171
cg1850223	DIP2C	c-Ets-2 [T	1119	1127	8.912323	CGTTAGC	0.27466	0.27171
cg1850223	DIP2C	c-Ets-2 [T	1453	1461	8.912323	TTCCTGA	0.27466	0.27171
cg1850223	DIP2C	c-Ets-2 [T	1870	1878	8.912323	TTCCTGC	0.27466	0.27171
cg1850382	DIP2C	c-Ets-2 [T	1059	1067	8.912323	TTCCTAC	0.27466	0.27171
cg1850382	DIP2C	c-Ets-2 [T	1067	1075	8.912323	TTCCTGC	0.27466	0.27171
cg1493188	DIP2C	c-Ets-2 [T	1034	1042	8.912323	TTCCTGA	0.27466	0.27171
cg1146814	DIP2C	c-Ets-2 [T	1506	1514	8.912323	TTCCTAA	0.27466	0.27171
cg1006492	DIP2C	c-Ets-2 [T	1169	1177	8.912323	TTCCTAC	0.27466	0.27171
cg1006492	DIP2C	c-Ets-2 [T	1177	1185	8.912323	TTCCTGC	0.27466	0.27171
cg0545033	DIP2C	c-Ets-2 [T	1099	1107	8.912323	TTCCTAC	0.27466	0.27171
cg0545033	DIP2C	c-Ets-2 [T	1107	1115	8.912323	TTCCTGC	0.27466	0.27171
cg0270010	DIP2C	p53 [T006	536	542	8.912104	AGGGCC	0.12207	0.13824
cg1850223	DIP2C	p53 [T006	1425	1431	8.912104	AGGGCC	0.12207	0.13824
cg1850382	DIP2C	p53 [T006	696	702	8.912104	GGGCCC	0.12207	0.13824
cg1146814	DIP2C	p53 [T006	444	450	8.912104	GGGCCC	0.12207	0.13824
cg1146814	DIP2C	p53 [T006	1127	1133	8.912104	AGGGCC	0.12207	0.13824

cg1006492	DIP2C	p53 [T006	806	812	8.912104	GGGCCC	0.12207	0.13824
cg0545033	DIP2C	p53 [T006	736	742	8.912104	GGGCCC	0.12207	0.13824
cg1146814	DIP2C	c-Ets-1 [T	219	225	8.8926	CGGGAA	0.85449	0.84987
cg1850382	DIP2C	GATA-2 [	209	217	8.888889	GGATAT	0.22888	0.22339
cg1493188	DIP2C	GATA-2 [	1724	1732	8.888889	TCAATA	0.22888	0.22339
cg1006492	DIP2C	GATA-2 [	319	327	8.888889	GGATAT	0.22888	0.22339
cg0545033	DIP2C	GATA-2 [	249	257	8.888889	GGATAT	0.22888	0.22339
cg0270010	DIP2C	ETF [T002	434	444	8.876947	GAGGGG	0.02384	0.02809
cg1146814	DIP2C	ETF [T002	1025	1035	8.876947	GAGGGG	0.02384	0.02809
cg1850382	DIP2C	c-Jun [T00	1670	1676	8.832178	TGACCT	0.61035	0.60549
cg1006492	DIP2C	c-Jun [T00	1780	1786	8.832178	TGACCT	0.61035	0.60549
cg0545033	DIP2C	c-Jun [T00	1710	1716	8.832178	TGACCT	0.61035	0.60549
cg0270010	DIP2C	PR B [T00	706	712	8.827054	AACAGC	0.36621	0.35051
cg0270010	DIP2C	PR A [T01	706	712	8.827054	AACAGC	0.36621	0.35051
cg1850223	DIP2C	PR B [T00	457	463	8.827054	AACAGC	0.36621	0.35051
cg1850223	DIP2C	PR B [T00	1447	1453	8.827054	AACAGA	0.36621	0.35051
cg1850223	DIP2C	PR A [T01	457	463	8.827054	AACAGC	0.36621	0.35051
cg1850223	DIP2C	PR A [T01	1447	1453	8.827054	AACAGA	0.36621	0.35051
cg1146814	DIP2C	PR B [T00	301	307	8.827054	ATCTGT	0.36621	0.35051
cg1146814	DIP2C	PR B [T00	1297	1303	8.827054	AACAGC	0.36621	0.35051
cg1146814	DIP2C	PR A [T01	301	307	8.827054	ATCTGT	0.36621	0.35051
cg1146814	DIP2C	PR A [T01	1297	1303	8.827054	AACAGC	0.36621	0.35051
cg0270010	DIP2C	NFI/CTF [	726	733	8.814757	CCAAGA	0.48828	0.48845
cg1146814	DIP2C	NFI/CTF [	1317	1324	8.814757	CCAAGA	0.48828	0.48845
cg1006492	DIP2C	NFI/CTF [	7	14	8.814757	CCAAAA	0.48828	0.48845
cg1850223	DIP2C	c-Ets-1 [T	1160	1166	8.809329	ATTCCA	0.85449	0.84987
cg1850382	DIP2C	c-Ets-1 [T	1156	1162	8.809329	ATTCCA	0.85449	0.84987
cg1006492	DIP2C	c-Ets-1 [T	1266	1272	8.809329	ATTCCA	0.85449	0.84987
cg0545033	DIP2C	c-Ets-1 [T	1196	1202	8.809329	ATTCCA	0.85449	0.84987
cg1850382	DIP2C	c-Jun [T00	1305	1311	8.807683	TGACGA	0.61035	0.60549
cg1006492	DIP2C	c-Jun [T00	1415	1421	8.807683	TGACGA	0.61035	0.60549
cg0545033	DIP2C	c-Jun [T00	1345	1351	8.807683	TGACGA	0.61035	0.60549
cg1850223	DIP2C	NF-AT2 [	1124	1133	8.794303	GGAAAT	0.05341	0.05145
cg1850382	DIP2C	NF-1 [T00	595	602	8.790071	TTTGCC	0.24414	0.24339
cg1850382	DIP2C	NF-1 [T00	1873	1880	8.790071	TTGGGA	0.24414	0.24339
cg1006492	DIP2C	NF-1 [T00	705	712	8.790071	TTTGCC	0.24414	0.24339
cg1006492	DIP2C	NF-1 [T00	1983	1990	8.790071	TTGGGA	0.24414	0.24339
cg0545033	DIP2C	NF-1 [T00	635	642	8.790071	TTTGCC	0.24414	0.24339
cg0545033	DIP2C	NF-1 [T00	1913	1920	8.790071	TTGGGA	0.24414	0.24339
cg0270010	DIP2C	E2F-1 [T0	516	523	8.76494	GCGGCG	0.27466	0.30178
cg1146814	DIP2C	E2F-1 [T0	1107	1114	8.76494	GCGGCG	0.27466	0.30178
cg0270010	DIP2C	LEF-1 [T0	61	68	8.759086	ACACAA	0.54932	0.53171
cg0270010	DIP2C	LEF-1 [T0	1245	1252	8.759086	ATGCAA	0.54932	0.53171
cg0270010	DIP2C	LEF-1 [T0	1315	1322	8.759086	ACACAA	0.54932	0.53171
cg0270010	DIP2C	LEF-1 [T0	1570	1577	8.759086	TTACAA	0.54932	0.53171
cg0270010	DIP2C	LEF-1 [T0	1616	1623	8.759086	ACACAA	0.54932	0.53171
cg1493188	DIP2C	LEF-1 [T0	1341	1348	8.759086	TCACAA	0.54932	0.53171
cg1146814	DIP2C	LEF-1 [T0	97	104	8.759086	CTTTGC	0.54932	0.53171

cg1146814	DIP2C	LEF-1 [T0	652	659	8.759086	ACACAA	0.54932	0.53171
cg1146814	DIP2C	LEF-1 [T0	1836	1843	8.759086	ATGCAA	0.54932	0.53171
cg1146814	DIP2C	LEF-1 [T0	1906	1913	8.759086	ACACAA	0.54932	0.53171
cg0270010	DIP2C	XBP-1 [T0	320	325	8.75604	ATGAAC	2.92969	2.75329
cg0270010	DIP2C	XBP-1 [T0	1522	1527	8.75604	ATGAAA	2.92969	2.75329
cg0270010	DIP2C	XBP-1 [T0	1821	1826	8.75604	GTTCAT	2.92969	2.75329
cg1850223	DIP2C	XBP-1 [T0	111	116	8.75604	ATGAAC	2.92969	2.75329
cg1850223	DIP2C	XBP-1 [T0	233	238	8.75604	ATGAAC	2.92969	2.75329
cg1850223	DIP2C	XBP-1 [T0	362	367	8.75604	ATGAGC	2.92969	2.75329
cg1850223	DIP2C	XBP-1 [T0	1030	1035	8.75604	ATGAAA	2.92969	2.75329
cg1850223	DIP2C	XBP-1 [T0	1150	1155	8.75604	TTTCAT	2.92969	2.75329
cg1850223	DIP2C	XBP-1 [T0	1474	1479	8.75604	TTTCAT	2.92969	2.75329
cg1850223	DIP2C	XBP-1 [T0	1599	1604	8.75604	ATGATA	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	108	113	8.75604	ATGAGA	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	341	346	8.75604	ATGATC	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	343	348	8.75604	GATCAT	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	656	661	8.75604	ATGAGA	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	672	677	8.75604	ATGAGC	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	920	925	8.75604	ATGAAA	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	1279	1284	8.75604	TCTCAT	2.92969	2.75329
cg1850382	DIP2C	XBP-1 [T0	1494	1499	8.75604	ATGAAA	2.92969	2.75329
cg1493188	DIP2C	XBP-1 [T0	761	766	8.75604	ATGAGC	2.92969	2.75329
cg1493188	DIP2C	XBP-1 [T0	1234	1239	8.75604	ATGAGC	2.92969	2.75329
cg1493188	DIP2C	XBP-1 [T0	1855	1860	8.75604	TTTCAT	2.92969	2.75329
cg1493188	DIP2C	XBP-1 [T0	1961	1966	8.75604	GCTCAT	2.92969	2.75329
cg1146814	DIP2C	XBP-1 [T0	11	16	8.75604	ATGAAA	2.92969	2.75329
cg1146814	DIP2C	XBP-1 [T0	83	88	8.75604	TTTCAT	2.92969	2.75329
cg1146814	DIP2C	XBP-1 [T0	911	916	8.75604	ATGAAC	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	85	90	8.75604	TTTCAT	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	218	223	8.75604	ATGAGA	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	451	456	8.75604	ATGATC	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	453	458	8.75604	GATCAT	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	766	771	8.75604	ATGAGA	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	782	787	8.75604	ATGAGC	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	1030	1035	8.75604	ATGAAA	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	1389	1394	8.75604	TCTCAT	2.92969	2.75329
cg1006492	DIP2C	XBP-1 [T0	1604	1609	8.75604	ATGAAA	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	15	20	8.75604	TTTCAT	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	148	153	8.75604	ATGAGA	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	381	386	8.75604	ATGATC	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	383	388	8.75604	GATCAT	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	696	701	8.75604	ATGAGA	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	712	717	8.75604	ATGAGC	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	960	965	8.75604	ATGAAA	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	1319	1324	8.75604	TCTCAT	2.92969	2.75329
cg0545033	DIP2C	XBP-1 [T0	1534	1539	8.75604	ATGAAA	2.92969	2.75329
cg0270010	DIP2C	c-Myb [T0	1354	1361	8.728118	AAACTT	0.30518	0.28602
cg1146814	DIP2C	c-Myb [T0	1945	1952	8.728118	AAACTT	0.30518	0.28602

cg1850223	DIP2C	STAT1bet	1744	1753	8.695301	ATTTCCA	0.22316	0.2175
cg1850382	DIP2C	STAT1bet	575	584	8.695301	CTTTCCA	0.22316	0.2175
cg1850382	DIP2C	STAT1bet	1057	1066	8.695301	CTTTCCT	0.22316	0.2175
cg1493188	DIP2C	STAT1bet	1670	1679	8.695301	ATTTCCT	0.22316	0.2175
cg1006492	DIP2C	STAT1bet	685	694	8.695301	CTTTCCA	0.22316	0.2175
cg1006492	DIP2C	STAT1bet	1167	1176	8.695301	CTTTCCT	0.22316	0.2175
cg0545033	DIP2C	STAT1bet	615	624	8.695301	CTTTCCA	0.22316	0.2175
cg0545033	DIP2C	STAT1bet	1097	1106	8.695301	CTTTCCT	0.22316	0.2175
cg1850382	DIP2C	RAR-beta	733	742	8.55975	TCAAAA	0.26703	0.27434
cg1006492	DIP2C	RAR-beta	843	852	8.55975	TCAAAA	0.26703	0.27434
cg0545033	DIP2C	RAR-beta	773	782	8.55975	TCAAAA	0.26703	0.27434
cg1493188	DIP2C	NF-AT2 [T	739	748	8.550786	CAGGCT	0.04959	0.04758
cg027001	DIP2C	p53 [T006	1012	1018	8.537081	GGGCTC	0.12207	0.13169
cg1493188	DIP2C	p53 [T006	811	817	8.537081	GGGCTC	0.12207	0.13169
cg1146814	DIP2C	p53 [T006	1603	1609	8.537081	GGGCTC	0.12207	0.13169
cg1850382	DIP2C	NF-AT1 [T	103	111	8.532897	GGAAAA	0.10681	0.10494
cg1006492	DIP2C	NF-AT1 [T	213	221	8.532897	GGAAAA	0.10681	0.10494
cg0545033	DIP2C	NF-AT1 [T	143	151	8.532897	GGAAAA	0.10681	0.10494
cg027001	DIP2C	USF2 [T0	1512	1521	8.532138	ACTGCA	0.103	0.10815
cg027001	DIP2C	USF2 [T0	1718	1727	8.532138	TGTGCA	0.103	0.10815
cg1146814	DIP2C	NF-kappa	219	230	8.518186	CGGGAA	0.01526	0.0164
cg1493188	DIP2C	LEF-1 [T0	1378	1385	8.457856	CCTCAA	0.15259	0.154
cg1146814	DIP2C	EBF [T05	514	524	8.453294	GCTCCA	0.03052	0.03497
cg1850223	DIP2C	c-Myb [T0	1288	1295	8.443873	CAACTG	0.30518	0.28602
cg1850382	DIP2C	AhR:Arnt	1233	1242	8.431005	GCACGC	0.07439	0.08553
cg1006492	DIP2C	AhR:Arnt	1343	1352	8.431005	GCACGC	0.07439	0.08553
cg0545033	DIP2C	AhR:Arnt	1273	1282	8.431005	GCACGC	0.07439	0.08553
cg027001	DIP2C	EBF [T05	1792	1802	8.430724	GTCCCA	0.03052	0.03497
cg1146814	DIP2C	EBF [T05	314	324	8.430724	GTCCCA	0.03052	0.03497
cg1850223	DIP2C	HOXD9 [T	410	419	8.402327	AATATA	0.02289	0.01984
cg1850223	DIP2C	HOXD10 [	410	419	8.402327	AATATA	0.02289	0.01984
cg1850223	DIP2C	NF-kappa	1792	1803	8.393394	GAGACG	0.01526	0.0164
cg1146814	DIP2C	EBF [T05	192	202	8.376595	CGCCCT	0.03052	0.03497
cg1850223	DIP2C	POU2F2 (	1489	1499	8.346865	TGTCTTA	0.0515	0.04751
cg027001	DIP2C	HNF-3alph	1380	1387	8.343064	AATTTA	0.27466	0.23078
cg1850223	DIP2C	HNF-3alph	153	160	8.343064	ATTAAA	0.27466	0.23078
cg1850223	DIP2C	HNF-3alph	1050	1057	8.343064	TTAAAA	0.27466	0.23078
cg1850223	DIP2C	HNF-3alph	1239	1246	8.343064	ATAAAA	0.27466	0.23078
cg1493188	DIP2C	HNF-3alph	680	687	8.343064	CTAAAA	0.27466	0.23078
cg1146814	DIP2C	HNF-3alph	1971	1978	8.343064	AATTTA	0.27466	0.23078
cg1850382	DIP2C	c-Ets-2 [T	161	169	8.339336	TTCCTG	0.13733	0.13927
cg1493188	DIP2C	c-Ets-2 [T	1272	1280	8.339336	CTGCAG	0.13733	0.13927
cg1493188	DIP2C	c-Ets-2 [T	1838	1846	8.339336	TTCCTG	0.13733	0.13927
cg1006492	DIP2C	c-Ets-2 [T	271	279	8.339336	TTCCTG	0.13733	0.13927
cg0545033	DIP2C	c-Ets-2 [T	201	209	8.339336	TTCCTG	0.13733	0.13927
cg027001	DIP2C	PR B [T00	966	972	8.338824	AACAGG	1.09863	1.09384
cg027001	DIP2C	PR B [T00	1874	1880	8.338824	TCCTGTT	1.09863	1.09384
cg027001	DIP2C	PR A [T01	966	972	8.338824	AACAGG	1.09863	1.09384

cg0270010	DIP2C	PR A [T01	1874	1880	8.338824	TCCTGTT	1.09863	1.09384
cg1850223	DIP2C	PR B [T00	247	253	8.338824	AACAGA	1.09863	1.09384
cg1850223	DIP2C	PR B [T00	1662	1668	8.338824	AACAGA	1.09863	1.09384
cg1850223	DIP2C	PR A [T01	247	253	8.338824	AACAGA	1.09863	1.09384
cg1850223	DIP2C	PR A [T01	1662	1668	8.338824	AACAGA	1.09863	1.09384
cg1850382	DIP2C	PR B [T00	602	608	8.338824	AACAGC	1.09863	1.09384
cg1850382	DIP2C	PR B [T00	949	955	8.338824	AACAGA	1.09863	1.09384
cg1850382	DIP2C	PR A [T01	602	608	8.338824	AACAGC	1.09863	1.09384
cg1850382	DIP2C	PR A [T01	949	955	8.338824	AACAGA	1.09863	1.09384
cg1493188	DIP2C	PR B [T00	35	41	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR B [T00	84	90	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR B [T00	280	286	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR B [T00	329	335	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR B [T00	378	384	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR B [T00	1816	1822	8.338824	CTCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR B [T00	1844	1850	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR A [T01	35	41	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR A [T01	84	90	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR A [T01	280	286	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR A [T01	329	335	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR A [T01	378	384	8.338824	CGCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR A [T01	1816	1822	8.338824	CTCTGTT	1.09863	1.09384
cg1493188	DIP2C	PR A [T01	1844	1850	8.338824	CGCTGTT	1.09863	1.09384
cg1146814	DIP2C	PR B [T00	1557	1563	8.338824	AACAGG	1.09863	1.09384
cg1146814	DIP2C	PR A [T01	1557	1563	8.338824	AACAGG	1.09863	1.09384
cg1006492	DIP2C	PR B [T00	712	718	8.338824	AACAGC	1.09863	1.09384
cg1006492	DIP2C	PR B [T00	1059	1065	8.338824	AACAGA	1.09863	1.09384
cg1006492	DIP2C	PR A [T01	712	718	8.338824	AACAGC	1.09863	1.09384
cg1006492	DIP2C	PR A [T01	1059	1065	8.338824	AACAGA	1.09863	1.09384
cg0545033	DIP2C	PR B [T00	642	648	8.338824	AACAGC	1.09863	1.09384
cg0545033	DIP2C	PR B [T00	989	995	8.338824	AACAGA	1.09863	1.09384
cg0545033	DIP2C	PR A [T01	642	648	8.338824	AACAGC	1.09863	1.09384
cg0545033	DIP2C	PR A [T01	989	995	8.338824	AACAGA	1.09863	1.09384
cg1493188	DIP2C	E2F-1 [T0	991	998	8.336446	TCGCCC	0.15259	0.16676
cg1850223	DIP2C	AR [T000	1114	1122	8.330815	GGACAC	0.10681	0.10838
cg1493188	DIP2C	ATF3 [T0	1220	1227	8.313799	TGACAT	0.27466	0.27379
cg0270010	DIP2C	PXR-1:RX	1812	1819	8.304332	TGAACA	0.12207	0.11843
cg0270010	DIP2C	GR-alpha [	74	78	8.281568	CCTTG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	174	178	8.281568	GGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	177	181	8.281568	GGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	326	330	8.281568	CCTCC	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	382	386	8.281568	GGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	457	461	8.281568	CGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	461	465	8.281568	GGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	479	483	8.281568	GAAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	525	529	8.281568	CCTTG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	576	580	8.281568	CCTCC	7.8125	8.20394
cg0270010	DIP2C	GR-alpha [	742	746	8.281568	CCTTC	7.8125	8.20394

cg0270010	DIP2C	GR-alpha |	776	780	8.281568	CCTCC	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	779	783	8.281568	CCTCC	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	936	940	8.281568	GGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1059	1063	8.281568	CCTCG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1131	1135	8.281568	GAAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1549	1553	8.281568	CCTCC	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1586	1590	8.281568	GAAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1602	1606	8.281568	GGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1667	1671	8.281568	CGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1712	1716	8.281568	CCTCC	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1898	1902	8.281568	GGAGG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1945	1949	8.281568	CCTCC	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1959	1963	8.281568	CCTCG	7.8125	8.20394
cg0270010	DIP2C	GR-alpha |	1971	1975	8.281568	CCTCC	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	104	108	8.281568	CCTCC	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	188	192	8.281568	GAAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	227	231	8.281568	GGAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	669	673	8.281568	GAAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	697	701	8.281568	CCTCG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	774	778	8.281568	CAAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	858	862	8.281568	CAAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	875	879	8.281568	CCTTG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1022	1026	8.281568	CCTTC	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1225	1229	8.281568	CCTTG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1302	1306	8.281568	CCTTC	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1586	1590	8.281568	CCTTC	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1610	1614	8.281568	CAAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1622	1626	8.281568	GAAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1645	1649	8.281568	GGAGG	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1656	1660	8.281568	CCTCC	7.8125	8.20394
cg1850223	DIP2C	GR-alpha |	1951	1955	8.281568	CCTCG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	99	103	8.281568	GAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	167	171	8.281568	CCTTG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	179	183	8.281568	CAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	223	227	8.281568	GAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	262	266	8.281568	CCTCG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	434	438	8.281568	GAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	453	457	8.281568	GGAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	459	463	8.281568	GGAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	471	475	8.281568	GAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	476	480	8.281568	GAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	490	494	8.281568	GAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	857	861	8.281568	GGAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	860	864	8.281568	GGAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	899	903	8.281568	CCTCG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	974	978	8.281568	GGAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1041	1045	8.281568	CCTTC	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1142	1146	8.281568	GAAGG	7.8125	8.20394

cg1850382	DIP2C	GR-alpha |	1378	1382	8.281568	CCTCC	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1396	1400	8.281568	CCTCC	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1404	1408	8.281568	CCTCC	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1524	1528	8.281568	CCTTC	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1541	1545	8.281568	GAAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1603	1607	8.281568	CCTCC	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1633	1637	8.281568	CGAGG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1673	1677	8.281568	CCTTG	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1718	1722	8.281568	CCTCC	7.8125	8.20394
cg1850382	DIP2C	GR-alpha |	1876	1880	8.281568	GGAGG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	541	545	8.281568	CAAGG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	977	981	8.281568	CCTTC	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1045	1049	8.281568	CCTCC	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1059	1063	8.281568	CCTCC	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1241	1245	8.281568	CCTTC	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1263	1267	8.281568	CCTTC	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1267	1271	8.281568	CCTTG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1393	1397	8.281568	GAAGG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1398	1402	8.281568	GGAGG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1491	1495	8.281568	CAAGG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1760	1764	8.281568	CGAGG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1790	1794	8.281568	CCTTG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1915	1919	8.281568	CCTTC	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1919	1923	8.281568	CCTTG	7.8125	8.20394
cg1493188	DIP2C	GR-alpha |	1988	1992	8.281568	GGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	43	47	8.281568	CCTTC	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	73	77	8.281568	CCTTC	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	170	174	8.281568	CCTTC	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	211	215	8.281568	CGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	235	239	8.281568	CAAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	258	262	8.281568	GAAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	274	278	8.281568	CGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	295	299	8.281568	GGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	334	338	8.281568	GAAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	389	393	8.281568	GAAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	426	430	8.281568	CCTCG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	549	553	8.281568	GAAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	665	669	8.281568	CCTTG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	765	769	8.281568	GGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	768	772	8.281568	GGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	917	921	8.281568	CCTCC	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	973	977	8.281568	GGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1048	1052	8.281568	CGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1052	1056	8.281568	GGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1070	1074	8.281568	GAAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1116	1120	8.281568	CCTTG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1167	1171	8.281568	CCTCC	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1333	1337	8.281568	CCTTC	7.8125	8.20394

cg1146814	DIP2C	GR-alpha |	1367	1371	8.281568	CCTCC	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1370	1374	8.281568	CCTCC	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1527	1531	8.281568	GGAGG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1650	1654	8.281568	CCTCG	7.8125	8.20394
cg1146814	DIP2C	GR-alpha |	1722	1726	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	71	75	8.281568	CCTTC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	209	213	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	277	281	8.281568	CCTTG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	289	293	8.281568	CAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	333	337	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	372	376	8.281568	CCTCG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	544	548	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	563	567	8.281568	GGAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	569	573	8.281568	GGAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	581	585	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	586	590	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	600	604	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	967	971	8.281568	GGAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	970	974	8.281568	GGAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1009	1013	8.281568	CCTCG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1084	1088	8.281568	GGAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1151	1155	8.281568	CCTTC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1252	1256	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1488	1492	8.281568	CCTCC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1506	1510	8.281568	CCTCC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1514	1518	8.281568	CCTCC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1634	1638	8.281568	CCTTC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1651	1655	8.281568	GAAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1713	1717	8.281568	CCTCC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1743	1747	8.281568	CGAGG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1783	1787	8.281568	CCTTG	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1828	1832	8.281568	CCTCC	7.8125	8.20394
cg1006492	DIP2C	GR-alpha |	1986	1990	8.281568	GGAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	1	5	8.281568	CCTTC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	139	143	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	207	211	8.281568	CCTTG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	219	223	8.281568	CAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	263	267	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	302	306	8.281568	CCTCG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	474	478	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	493	497	8.281568	GGAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	499	503	8.281568	GGAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	511	515	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	516	520	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	530	534	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	897	901	8.281568	GGAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	900	904	8.281568	GGAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha |	939	943	8.281568	CCTCG	7.8125	8.20394

cg0545033	DIP2C	GR-alpha [	1014	1018	8.281568	GGAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1081	1085	8.281568	CCTTC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1182	1186	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1418	1422	8.281568	CCTCC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1436	1440	8.281568	CCTCC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1444	1448	8.281568	CCTCC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1564	1568	8.281568	CCTTC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1581	1585	8.281568	GAAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1643	1647	8.281568	CCTCC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1673	1677	8.281568	CGAGG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1713	1717	8.281568	CCTTG	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1758	1762	8.281568	CCTCC	7.8125	8.20394
cg0545033	DIP2C	GR-alpha [	1916	1920	8.281568	GGAGG	7.8125	8.20394
cg1850382	DIP2C	c-Ets-1 [T(	1597	1603	8.244941	GTGGAA(	0.24414	0.2494
cg1006492	DIP2C	c-Ets-1 [T(	1707	1713	8.244941	GTGGAA(	0.24414	0.2494
cg0545033	DIP2C	c-Ets-1 [T(	1637	1643	8.244941	GTGGAA(	0.24414	0.2494
cg1850223	DIP2C	IRF-1 [T0(	1120	1128	8.242487	GTTAGG.	0.25177	0.2462
cg1850382	DIP2C	IRF-1 [T0(	1058	1066	8.242487	TTTCCTA	0.25177	0.2462
cg1006492	DIP2C	IRF-1 [T0(	1168	1176	8.242487	TTTCCTA	0.25177	0.2462
cg0545033	DIP2C	IRF-1 [T0(	1098	1106	8.242487	TTTCCTA	0.25177	0.2462
cg0270010	DIP2C	c-Jun [T00	1144	1150	8.242207	TGACCT(	0.48828	0.47447
cg1850223	DIP2C	c-Jun [T00	694	700	8.242207	TGACCT(	0.48828	0.47447
cg1850382	DIP2C	c-Jun [T00	1901	1907	8.242207	GAGGTC.	0.48828	0.47447
cg1146814	DIP2C	c-Jun [T00	121	127	8.242207	GAGGTC.	0.48828	0.47447
cg1146814	DIP2C	c-Jun [T00	1735	1741	8.242207	TGACCT(	0.48828	0.47447
cg0545033	DIP2C	c-Jun [T00	1941	1947	8.242207	GAGGTC.	0.48828	0.47447
cg1850382	DIP2C	HNF-1B [	192	200	8.241969	AAATTA.	0.06866	0.0616
cg1006492	DIP2C	HNF-1B [	302	310	8.241969	AAATTA.	0.06866	0.0616
cg0545033	DIP2C	HNF-1B [	232	240	8.241969	AAATTA.	0.06866	0.0616
cg0270010	DIP2C	p53 [T006	111	117	8.208781	GGGGCC	0.48828	0.55336
cg0270010	DIP2C	p53 [T006	441	447	8.208781	GGGCCC	0.48828	0.55336
cg1850223	DIP2C	p53 [T006	1426	1432	8.208781	GGGCCC	0.48828	0.55336
cg1850382	DIP2C	p53 [T006	695	701	8.208781	GGGGCC	0.48828	0.55336
cg1850382	DIP2C	p53 [T006	1001	1007	8.208781	GGGCCC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	1252	1258	8.208781	GGGGCC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	1253	1259	8.208781	GGGCCC	0.48828	0.55336
cg1146814	DIP2C	p53 [T006	443	449	8.208781	GGGGCC	0.48828	0.55336
cg1146814	DIP2C	p53 [T006	520	526	8.208781	GGGGCC	0.48828	0.55336
cg1146814	DIP2C	p53 [T006	521	527	8.208781	GGGCCC	0.48828	0.55336
cg1146814	DIP2C	p53 [T006	702	708	8.208781	GGGGCC	0.48828	0.55336
cg1146814	DIP2C	p53 [T006	1032	1038	8.208781	GGGCCC	0.48828	0.55336
cg1006492	DIP2C	p53 [T006	805	811	8.208781	GGGGCC	0.48828	0.55336
cg1006492	DIP2C	p53 [T006	1111	1117	8.208781	GGGCCC	0.48828	0.55336
cg0545033	DIP2C	p53 [T006	735	741	8.208781	GGGGCC	0.48828	0.55336
cg0545033	DIP2C	p53 [T006	1041	1047	8.208781	GGGCCC	0.48828	0.55336
cg0270010	DIP2C	ENKTF-1	395	402	8.19852	TGGCCG(	0.73242	0.80254
cg1850223	DIP2C	ENKTF-1	1874	1881	8.19852	TGGCGA(	0.73242	0.80254
cg1850382	DIP2C	ENKTF-1	270	277	8.19852	CGCAGC(	0.73242	0.80254

cg1850382	DIP2C	ENKTF-1	1358	1365	8.19852	CCTGGC	0.73242	0.80254
cg1850382	DIP2C	ENKTF-1	1753	1760	8.19852	TGGCGA	0.73242	0.80254
cg1850382	DIP2C	ENKTF-1	1923	1930	8.19852	CCTGGC	0.73242	0.80254
cg1850382	DIP2C	ENKTF-1	1983	1990	8.19852	TGGCGG	0.73242	0.80254
cg1146814	DIP2C	ENKTF-1	986	993	8.19852	TGGCCG	0.73242	0.80254
cg1006492	DIP2C	ENKTF-1	380	387	8.19852	CGCAGC	0.73242	0.80254
cg1006492	DIP2C	ENKTF-1	1468	1475	8.19852	CCTGGC	0.73242	0.80254
cg1006492	DIP2C	ENKTF-1	1863	1870	8.19852	TGGCGA	0.73242	0.80254
cg0545033	DIP2C	ENKTF-1	310	317	8.19852	CGCAGC	0.73242	0.80254
cg0545033	DIP2C	ENKTF-1	1398	1405	8.19852	CCTGGC	0.73242	0.80254
cg0545033	DIP2C	ENKTF-1	1793	1800	8.19852	TGGCGA	0.73242	0.80254
cg0545033	DIP2C	ENKTF-1	1963	1970	8.19852	CCTGGC	0.73242	0.80254
cg1493188	DIP2C	HNF-1C [	1514	1522	8.193285	GTTAGG	0.19836	0.18126
cg1850223	DIP2C	NF-1 [T00	281	288	8.191058	GAGGCC	0.24414	0.24485
cg1850223	DIP2C	NF-1 [T00	1633	1640	8.191058	AAGCCC	0.24414	0.24485
cg1146814	DIP2C	NF-1 [T00	146	153	8.191058	TTGGGC	0.24414	0.24485
cg1006492	DIP2C	NF-1 [T00	3	10	8.191058	GAGCCC	0.24414	0.24485
cg027001	DIP2C	NF-kappa	1128	1138	8.188811	GGGGAA	0.0329	0.03642
cg1146814	DIP2C	NF-kappa	1719	1729	8.188811	GGGGAA	0.0329	0.03642
cg1850382	DIP2C	AhR [T01	1850	1860	8.184723	CTCACG	0.04864	0.05013
cg1006492	DIP2C	AhR [T01	1960	1970	8.184723	CTCACG	0.04864	0.05013
cg0545033	DIP2C	AhR [T01	1890	1900	8.184723	CTCACG	0.04864	0.05013
cg1850223	DIP2C	PXR-1:RX	1468	1475	8.180749	TGAACA	0.12207	0.11255
cg027001	DIP2C	SRY [T00	1615	1623	8.174786	CACACA	0.15259	0.14791
cg1850382	DIP2C	SRY [T00	531	539	8.174786	TCACCA	0.15259	0.14791
cg1146814	DIP2C	SRY [T00	376	384	8.174786	TCACCA	0.15259	0.14791
cg1006492	DIP2C	SRY [T00	641	649	8.174786	TCACCA	0.15259	0.14791
cg0545033	DIP2C	SRY [T00	571	579	8.174786	TCACCA	0.15259	0.14791
cg1146814	DIP2C	p53 [T006	555	561	8.162057	AGCGCC	0.48828	0.55336
cg1493188	DIP2C	IRF-1 [T0	933	941	8.151819	TTTCCA	0.25177	0.2462
cg1493188	DIP2C	NF-AT1 [	1796	1804	8.12076	GGAAAA	0.1297	0.12846
cg027001	DIP2C	c-Ets-1 [T	1235	1241	8.116854	GTTCCA	0.24414	0.2494
cg1850223	DIP2C	c-Ets-1 [T	1178	1184	8.116854	GTTCCA	0.24414	0.2494
cg1850382	DIP2C	c-Ets-1 [T	552	558	8.116854	GTTCCA	0.24414	0.2494
cg1146814	DIP2C	c-Ets-1 [T	1826	1832	8.116854	GTTCCA	0.24414	0.2494
cg1006492	DIP2C	c-Ets-1 [T	662	668	8.116854	GTTCCA	0.24414	0.2494
cg0545033	DIP2C	c-Ets-1 [T	592	598	8.116854	GTTCCA	0.24414	0.2494
cg027001	DIP2C	GR-alpha [	48	52	8.073878	CTAGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	150	154	8.073878	CCAGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	237	241	8.073878	GCAGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	272	276	8.073878	CCTGC	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	288	292	8.073878	CCAGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	331	335	8.073878	CCAGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	342	346	8.073878	CCTGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	503	507	8.073878	GCAGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	508	512	8.073878	CCTGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	534	538	8.073878	CCAGG	7.8125	8.20289
cg027001	DIP2C	GR-alpha [	541	545	8.073878	CCAGG	7.8125	8.20289

cg0270010	DIP2C	GR-alpha	560	564	8.073878	GCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	579	583	8.073878	CCTGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	614	618	8.073878	GCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	904	908	8.073878	GTAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1027	1031	8.073878	GCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1036	1040	8.073878	CCTAC	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1047	1051	8.073878	CCTGC	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1120	1124	8.073878	GCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1154	1158	8.073878	CCTGC	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1215	1219	8.073878	GCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1258	1262	8.073878	CCTGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1453	1457	8.073878	CCTGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1599	1603	8.073878	GCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1707	1711	8.073878	CCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1781	1785	8.073878	CCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1795	1799	8.073878	CCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1846	1850	8.073878	CCAGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1861	1865	8.073878	CCTGG	7.8125	8.20289
cg0270010	DIP2C	GR-alpha	1926	1930	8.073878	CCTGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	220	224	8.073878	CCTAG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	353	357	8.073878	CCTGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	388	392	8.073878	CCTGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	641	645	8.073878	GCAGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	920	924	8.073878	CCAGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	961	965	8.073878	CCTGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1423	1427	8.073878	CCAGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1462	1466	8.073878	CCTGC	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1536	1540	8.073878	GCAGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1556	1560	8.073878	CCAGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1760	1764	8.073878	CCTGC	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1872	1876	8.073878	CCTGG	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1892	1896	8.073878	CCTGC	7.8125	8.20289
cg1850223	DIP2C	GR-alpha	1994	1998	8.073878	CCTGC	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	163	167	8.073878	CCTGC	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	203	207	8.073878	CCTAC	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	227	231	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	240	244	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	415	419	8.073878	CCTGC	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	450	454	8.073878	CCTGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	486	490	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	579	583	8.073878	CCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	620	624	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	700	704	8.073878	CCTGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	740	744	8.073878	CCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	1016	1020	8.073878	CCTGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	1061	1065	8.073878	CCTAG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	1069	1073	8.073878	CCTGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha	1205	1209	8.073878	GCAGG	7.8125	8.20289

cg1850382	DIP2C	GR-alpha |	1268	1272	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1358	1362	8.073878	CCTGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1399	1403	8.073878	CCTAC	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1552	1556	8.073878	CCTGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1592	1596	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1710	1714	8.073878	CCTAC	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1768	1772	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1837	1841	8.073878	CCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1886	1890	8.073878	GCAGG	7.8125	8.20289
cg1850382	DIP2C	GR-alpha |	1923	1927	8.073878	CCTGG	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	791	795	8.073878	CCAGG	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	826	830	8.073878	CCAGG	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	859	863	8.073878	CCTGG	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	1141	1145	8.073878	CCTAC	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	1274	1278	8.073878	GCAGG	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	1373	1377	8.073878	CCTGC	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	1752	1756	8.073878	CCTGG	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	1840	1844	8.073878	CCTGC	7.8125	8.20289
cg1493188	DIP2C	GR-alpha |	1900	1904	8.073878	CCTAC	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	164	168	8.073878	CCTGC	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	317	321	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	339	343	8.073878	CCTGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	416	420	8.073878	CCTGC	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	457	461	8.073878	GCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	471	475	8.073878	CTAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	517	521	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	576	580	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	639	643	8.073878	CTAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	741	745	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	828	832	8.073878	GCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	863	867	8.073878	CCTGC	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	879	883	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	922	926	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	933	937	8.073878	CCTGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1094	1098	8.073878	GCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1099	1103	8.073878	CCTGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1125	1129	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1132	1136	8.073878	CCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1151	1155	8.073878	GCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1170	1174	8.073878	CCTGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1205	1209	8.073878	GCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1495	1499	8.073878	GTAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1618	1622	8.073878	GCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1627	1631	8.073878	CCTAC	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1638	1642	8.073878	CCTGC	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1711	1715	8.073878	GCAGG	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1745	1749	8.073878	CCTGC	7.8125	8.20289
cg1146814	DIP2C	GR-alpha |	1806	1810	8.073878	GCAGG	7.8125	8.20289

cg1146814	DIP2C	GR-alpha |	1849	1853	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	20	24	8.073878	CCTAC	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	58	62	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	92	96	8.073878	CCTAC	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	273	277	8.073878	CCTGC	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	313	317	8.073878	CCTAC	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	337	341	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	350	354	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	525	529	8.073878	CCTGC	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	560	564	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	596	600	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	689	693	8.073878	CCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	730	734	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	810	814	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	850	854	8.073878	CCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1126	1130	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1171	1175	8.073878	CCTAG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1179	1183	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1315	1319	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1378	1382	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1468	1472	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1509	1513	8.073878	CCTAC	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1662	1666	8.073878	CCTGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1702	1706	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1820	1824	8.073878	CCTAC	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1878	1882	8.073878	GCAGG	7.8125	8.20289
cg1006492	DIP2C	GR-alpha |	1947	1951	8.073878	CCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	22	26	8.073878	CCTAC	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	203	207	8.073878	CCTGC	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	243	247	8.073878	CCTAC	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	267	271	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	280	284	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	455	459	8.073878	CCTGC	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	490	494	8.073878	CCTGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	526	530	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	619	623	8.073878	CCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	660	664	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	740	744	8.073878	CCTGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	780	784	8.073878	CCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1056	1060	8.073878	CCTGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1101	1105	8.073878	CCTAG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1109	1113	8.073878	CCTGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1245	1249	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1308	1312	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1398	1402	8.073878	CCTGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1439	1443	8.073878	CCTAC	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1592	1596	8.073878	CCTGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha |	1632	1636	8.073878	GCAGG	7.8125	8.20289

cg0545033	DIP2C	GR-alpha [	1750	1754	8.073878	CCTAC	7.8125	8.20289
cg0545033	DIP2C	GR-alpha [	1808	1812	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha [	1877	1881	8.073878	CCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha [	1926	1930	8.073878	GCAGG	7.8125	8.20289
cg0545033	DIP2C	GR-alpha [	1963	1967	8.073878	CCTGG	7.8125	8.20289
cg0270010	DIP2C	TFIID [T0	261	267	8.014558	TCTGAA	2.19727	1.99811
cg0270010	DIP2C	TFIID [T0	701	707	8.014558	TTACAA	2.19727	1.99811
cg0270010	DIP2C	TFIID [T0	866	872	8.014558	TCACAA	2.19727	1.99811
cg0270010	DIP2C	TFIID [T0	1278	1284	8.014558	TTTCTGA	2.19727	1.99811
cg0270010	DIP2C	TFIID [T0	1409	1415	8.014558	TTAGAA	2.19727	1.99811
cg0270010	DIP2C	TFIID [T0	1490	1496	8.014558	TTTGCA	2.19727	1.99811
cg0270010	DIP2C	TFIID [T0	1570	1576	8.014558	TTACAA	2.19727	1.99811
cg0270010	DIP2C	Pax-5 [T0	111	117	8.014558	GGGGCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	118	124	8.014558	GGGCAG	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	120	126	8.014558	GCAGCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	157	163	8.014558	GGGCTC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	209	215	8.014558	GCAGCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	346	352	8.014558	GGGCAC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	440	446	8.014558	TGGGCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	441	447	8.014558	GGGCCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	471	477	8.014558	GGTGCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	537	543	8.014558	GGGCCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	566	572	8.014558	GCTGCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	595	601	8.014558	GGGCAC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	771	777	8.014558	GCAGCC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	1372	1378	8.014558	GGGCAC	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	1670	1676	8.014558	GGGCTG	2.19727	2.42766
cg0270010	DIP2C	Pax-5 [T0	1856	1862	8.014558	GGGCTC	2.19727	2.42766
cg1850223	DIP2C	TFIID [T0	299	305	8.014558	TTTCAA	2.19727	1.99811
cg1850223	DIP2C	TFIID [T0	451	457	8.014558	TTACAA	2.19727	1.99811
cg1850223	DIP2C	TFIID [T0	1122	1128	8.014558	TAGGAA	2.19727	1.99811
cg1850223	DIP2C	TFIID [T0	1150	1156	8.014558	TTTCATA	2.19727	1.99811
cg1850223	DIP2C	TFIID [T0	1773	1779	8.014558	TCTGAA	2.19727	1.99811
cg1850223	DIP2C	Pax-5 [T0	390	396	8.014558	TGGGCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	391	397	8.014558	GGGCCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	705	711	8.014558	GGGCAC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	768	774	8.014558	TCAGCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	956	962	8.014558	GCAGCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1066	1072	8.014558	GGGCAG	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1293	1299	8.014558	GATGCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1426	1432	8.014558	GGGCCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1632	1638	8.014558	TAAGCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1686	1692	8.014558	GGGCAG	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1714	1720	8.014558	GGAGCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1765	1771	8.014558	TGGGCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1766	1772	8.014558	GGGCCC	2.19727	2.42766
cg1850223	DIP2C	Pax-5 [T0	1832	1838	8.014558	GCAGCC	2.19727	2.42766
cg1850382	DIP2C	TFIID [T0	376	382	8.014558	TTTGAG	2.19727	1.99811

cg1850382	DIP2C	TFIID [T0	515	521	8.014558	TCAGAA	2.19727	1.99811
cg1850382	DIP2C	TFIID [T0	843	849	8.014558	TTTGAA	2.19727	1.99811
cg1850382	DIP2C	TFIID [T0	919	925	8.014558	TATGAA	2.19727	1.99811
cg1850382	DIP2C	TFIID [T0	1058	1064	8.014558	TTTCCTA	2.19727	1.99811
cg1850382	DIP2C	TFIID [T0	1334	1340	8.014558	TTTCAG	2.19727	1.99811
cg1850382	DIP2C	TFIID [T0	1469	1475	8.014558	TTTCAG	2.19727	1.99811
cg1850382	DIP2C	Pax-5 [T0	41	47	8.014558	GGGCCG	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	68	74	8.014558	GCAGCC	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	182	188	8.014558	GGGCTT	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	257	263	8.014558	GGAGCC	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	695	701	8.014558	GGGGCC	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	1001	1007	8.014558	GGGCCC	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	1036	1042	8.014558	TGTGCC	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	1636	1642	8.014558	GGGCAG	2.19727	2.42766
cg1850382	DIP2C	Pax-5 [T0	1987	1993	8.014558	GGGCAC	2.19727	2.42766
cg1493188	DIP2C	TFIID [T0	664	670	8.014558	TTTCTG	2.19727	1.99811
cg1493188	DIP2C	TFIID [T0	677	683	8.014558	TTTCTA	2.19727	1.99811
cg1493188	DIP2C	TFIID [T0	727	733	8.014558	TCAGAA	2.19727	1.99811
cg1493188	DIP2C	TFIID [T0	933	939	8.014558	TTTCCA	2.19727	1.99811
cg1493188	DIP2C	TFIID [T0	1341	1347	8.014558	TCACAA	2.19727	1.99811
cg1493188	DIP2C	TFIID [T0	1473	1479	8.014558	TTTCCA	2.19727	1.99811
cg1493188	DIP2C	TFIID [T0	1576	1582	8.014558	TTGCAA	2.19727	1.99811
cg1493188	DIP2C	TFIID [T0	1671	1677	8.014558	TTTCCTA	2.19727	1.99811
cg1493188	DIP2C	Pax-5 [T0	15	21	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	64	70	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	113	119	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	211	217	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	260	266	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	309	315	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	358	364	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	407	413	8.014558	GGGCTC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	862	868	8.014558	GGGCTT	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	1235	1241	8.014558	TGAGCC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	1252	1258	8.014558	GGGGCC	2.19727	2.42766
cg1493188	DIP2C	Pax-5 [T0	1253	1259	8.014558	GGGCCC	2.19727	2.42766
cg1146814	DIP2C	TFIID [T0	98	104	8.014558	TTTGCA	2.19727	1.99811
cg1146814	DIP2C	TFIID [T0	99	105	8.014558	TTGCAA	2.19727	1.99811
cg1146814	DIP2C	TFIID [T0	852	858	8.014558	TCTGAA	2.19727	1.99811
cg1146814	DIP2C	TFIID [T0	1292	1298	8.014558	TTACAA	2.19727	1.99811
cg1146814	DIP2C	TFIID [T0	1457	1463	8.014558	TCACAA	2.19727	1.99811
cg1146814	DIP2C	TFIID [T0	1869	1875	8.014558	TTTCTG	2.19727	1.99811
cg1146814	DIP2C	Pax-5 [T0	197	203	8.014558	TGAGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	242	248	8.014558	GCAGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	275	281	8.014558	GAGGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	343	349	8.014558	GGGCTC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	443	449	8.014558	GGGGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	476	482	8.014558	GGAGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	520	526	8.014558	GGGGCC	2.19727	2.42766

cg1146814	DIP2C	Pax-5 [T0	521	527	8.014558	GGGCCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	702	708	8.014558	GGGGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	709	715	8.014558	GGGCAG	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	711	717	8.014558	GCAGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	748	754	8.014558	GGGCTC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	800	806	8.014558	GCAGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	937	943	8.014558	GGGCAC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1031	1037	8.014558	TGGGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1032	1038	8.014558	GGGCCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1062	1068	8.014558	GGTGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1128	1134	8.014558	GGGCCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1157	1163	8.014558	GCTGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1186	1192	8.014558	GGGCAC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1362	1368	8.014558	GCAGCC	2.19727	2.42766
cg1146814	DIP2C	Pax-5 [T0	1963	1969	8.014558	GGGCAC	2.19727	2.42766
cg1006492	DIP2C	TFIID [T0	85	91	8.014558	TTTCATA	2.19727	1.99811
cg1006492	DIP2C	TFIID [T0	486	492	8.014558	TTTGAG	2.19727	1.99811
cg1006492	DIP2C	TFIID [T0	625	631	8.014558	TCAGAA	2.19727	1.99811
cg1006492	DIP2C	TFIID [T0	953	959	8.014558	TTTGAA	2.19727	1.99811
cg1006492	DIP2C	TFIID [T0	1029	1035	8.014558	TATGAA	2.19727	1.99811
cg1006492	DIP2C	TFIID [T0	1168	1174	8.014558	TTTCCTA	2.19727	1.99811
cg1006492	DIP2C	TFIID [T0	1444	1450	8.014558	TTTCAG	2.19727	1.99811
cg1006492	DIP2C	TFIID [T0	1579	1585	8.014558	TTTCAG	2.19727	1.99811
cg1006492	DIP2C	Pax-5 [T0	2	8	8.014558	GGAGCC	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	151	157	8.014558	GGGCCG	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	178	184	8.014558	GCAGCC	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	292	298	8.014558	GGGCTT	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	367	373	8.014558	GGAGCC	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	805	811	8.014558	GGGGCC	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	1111	1117	8.014558	GGGCCC	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	1146	1152	8.014558	TGTGCC	2.19727	2.42766
cg1006492	DIP2C	Pax-5 [T0	1746	1752	8.014558	GGGCAG	2.19727	2.42766
cg0545033	DIP2C	TFIID [T0	15	21	8.014558	TTTCATA	2.19727	1.99811
cg0545033	DIP2C	TFIID [T0	416	422	8.014558	TTTGAG	2.19727	1.99811
cg0545033	DIP2C	TFIID [T0	555	561	8.014558	TCAGAA	2.19727	1.99811
cg0545033	DIP2C	TFIID [T0	883	889	8.014558	TTTGAA	2.19727	1.99811
cg0545033	DIP2C	TFIID [T0	959	965	8.014558	TATGAA	2.19727	1.99811
cg0545033	DIP2C	TFIID [T0	1098	1104	8.014558	TTTCCTA	2.19727	1.99811
cg0545033	DIP2C	TFIID [T0	1374	1380	8.014558	TTTCAG	2.19727	1.99811
cg0545033	DIP2C	TFIID [T0	1509	1515	8.014558	TTTCAG	2.19727	1.99811
cg0545033	DIP2C	Pax-5 [T0	81	87	8.014558	GGGCCG	2.19727	2.42766
cg0545033	DIP2C	Pax-5 [T0	108	114	8.014558	GCAGCC	2.19727	2.42766
cg0545033	DIP2C	Pax-5 [T0	222	228	8.014558	GGGCTT	2.19727	2.42766
cg0545033	DIP2C	Pax-5 [T0	297	303	8.014558	GGAGCC	2.19727	2.42766
cg0545033	DIP2C	Pax-5 [T0	735	741	8.014558	GGGGCC	2.19727	2.42766
cg0545033	DIP2C	Pax-5 [T0	1041	1047	8.014558	GGGCCC	2.19727	2.42766
cg0545033	DIP2C	Pax-5 [T0	1076	1082	8.014558	TGTGCC	2.19727	2.42766
cg0545033	DIP2C	Pax-5 [T0	1676	1682	8.014558	GGGCAG	2.19727	2.42766

cg1493188	DIP2C	USF2 [T0	1367	1376	8.007902	AGCACA	0.01717	0.01801
cg1850382	DIP2C	c-Myb [T0	196	203	8.005241	TAACTC	0.21362	0.20997
cg1006492	DIP2C	c-Myb [T0	306	313	8.005241	TAACTC	0.21362	0.20997
cg0545033	DIP2C	c-Myb [T0	236	243	8.005241	TAACTC	0.21362	0.20997
cg1493188	DIP2C	MEF-2A [	697	707	7.982343	AAAGAA	0.04005	0.03447
cg1850382	DIP2C	RAR-alpha	1386	1398	7.963622	ACCCAC	0.01627	0.01726
cg1006492	DIP2C	RAR-alpha	1496	1508	7.963622	ACCCAC	0.01627	0.01726
cg0545033	DIP2C	RAR-alpha	1426	1438	7.963622	ACCCAC	0.01627	0.01726
cg0270010	DIP2C	EBF [T05	147	157	7.960895	TCTCCA	0.04196	0.04563
cg1146814	DIP2C	EBF [T05	738	748	7.960895	TCTCCA	0.04196	0.04563
cg0270010	DIP2C	ETF [T002	774	784	7.870358	GCCCTC	0.07153	0.08737
cg0270010	DIP2C	ETF [T002	1895	1905	7.870358	GTGGGA	0.07153	0.08737
cg1850223	DIP2C	ATF-1 [T0	77	87	7.870358	TAATGA	0.07153	0.07126
cg1850223	DIP2C	ETF [T002	1300	1310	7.870358	GCCCTT	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	8	18	7.870358	GGGTGC	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	57	67	7.870358	GGGTGC	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	106	116	7.870358	GGGTGC	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	204	214	7.870358	GGGTGC	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	253	263	7.870358	GGGTGC	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	302	312	7.870358	GGGTGC	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	351	361	7.870358	GGGTGC	0.07153	0.08737
cg1493188	DIP2C	ETF [T002	400	410	7.870358	GGGTGC	0.07153	0.08737
cg1146814	DIP2C	ETF [T002	1365	1375	7.870358	GCCCTC	0.07153	0.08737
cg1850382	DIP2C	HNF-1C [	646	654	7.864676	CTGAGT	0.19836	0.18126
cg1006492	DIP2C	HNF-1C [	756	764	7.864676	CTGAGT	0.19836	0.18126
cg0545033	DIP2C	HNF-1C [	686	694	7.864676	CTGAGT	0.19836	0.18126
cg0270010	DIP2C	NF-kappa	1297	1307	7.856943	GGGGAG	0.0329	0.03642
cg1146814	DIP2C	NF-kappa	1888	1898	7.856943	GGGGAG	0.0329	0.03642
cg1850382	DIP2C	p53 [T006	1727	1733	7.853573	GGGCCA	0.48828	0.55336
cg1006492	DIP2C	p53 [T006	1837	1843	7.853573	GGGCCA	0.48828	0.55336
cg0545033	DIP2C	p53 [T006	1767	1773	7.853573	GGGCCA	0.48828	0.55336
cg1850223	DIP2C	c-Ets-2 [T	1188	1196	7.84116	TTCCTG	0.32043	0.30792
cg1493188	DIP2C	c-Ets-2 [T	1118	1126	7.84116	TTCCTG	0.32043	0.30792
cg0270010	DIP2C	E2F-1 [T0	677	684	7.839654	GCGGGT	0.30518	0.32869
cg1146814	DIP2C	E2F-1 [T0	1268	1275	7.839654	GCGGGT	0.30518	0.32869
cg0270010	DIP2C	p53 [T006	157	163	7.833758	GGGCTC	0.48828	0.55336
cg0270010	DIP2C	p53 [T006	1856	1862	7.833758	GGGCTC	0.48828	0.55336
cg1850223	DIP2C	p53 [T006	1714	1720	7.833758	GGAGCC	0.48828	0.55336
cg1850382	DIP2C	p53 [T006	257	263	7.833758	GGAGCC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	15	21	7.833758	GGGCTC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	64	70	7.833758	GGGCTC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	113	119	7.833758	GGGCTC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	211	217	7.833758	GGGCTC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	260	266	7.833758	GGGCTC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	309	315	7.833758	GGGCTC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	358	364	7.833758	GGGCTC	0.48828	0.55336
cg1493188	DIP2C	p53 [T006	407	413	7.833758	GGGCTC	0.48828	0.55336
cg1146814	DIP2C	p53 [T006	343	349	7.833758	GGGCTC	0.48828	0.55336

cg1146814	DIP2C	p53 [T006	476	482	7.833758	GGAGCC	0.48828	0.55336
cg1146814	DIP2C	p53 [T006	748	754	7.833758	GGGCTC	0.48828	0.55336
cg1006492	DIP2C	p53 [T006	2	8	7.833758	GGAGCC	0.48828	0.55336
cg1006492	DIP2C	p53 [T006	367	373	7.833758	GGAGCC	0.48828	0.55336
cg0545033	DIP2C	p53 [T006	297	303	7.833758	GGAGCC	0.48828	0.55336
cg0270010	DIP2C	NF-kappa	1732	1742	7.826592	GGGGAC	0.0329	0.03642
cg1850223	DIP2C	IRF-1 [T0	1187	1195	7.82345	TTTCCT	0.25177	0.2462
cg1850382	DIP2C	IRF-1 [T0	160	168	7.82345	TTTCCT	0.25177	0.2462
cg1006492	DIP2C	IRF-1 [T0	270	278	7.82345	TTTCCT	0.25177	0.2462
cg0545033	DIP2C	IRF-1 [T0	200	208	7.82345	TTTCCT	0.25177	0.2462
cg0270010	DIP2C	RXR-alph	649	655	7.815913	GCCACC	0.24414	0.26389
cg1850382	DIP2C	RXR-alph	1697	1703	7.815913	GCCACC	0.24414	0.26389
cg1146814	DIP2C	RXR-alph	159	165	7.815913	GCCACC	0.24414	0.26389
cg1146814	DIP2C	RXR-alph	1240	1246	7.815913	GCCACC	0.24414	0.26389
cg1006492	DIP2C	RXR-alph	1807	1813	7.815913	GCCACC	0.24414	0.26389
cg0545033	DIP2C	RXR-alph	1737	1743	7.815913	GCCACC	0.24414	0.26389
cg1850382	DIP2C	T3R-beta1	788	796	7.813363	TCACCC	0.27466	0.28753
cg1006492	DIP2C	T3R-beta1	898	906	7.813363	TCACCC	0.27466	0.28753
cg0545033	DIP2C	T3R-beta1	828	836	7.813363	TCACCC	0.27466	0.28753
cg1493188	DIP2C	NF-AT2 [	1494	1503	7.779688	GGAAAT	0.08965	0.08482
cg1493188	DIP2C	GATA-2 [	1293	1301	7.777778	TGATAC	0.30518	0.29346
cg1850382	DIP2C	NF-AT1 [	1449	1457	7.744746	CAGCTT	0.19836	0.19379
cg1006492	DIP2C	NF-AT1 [	1559	1567	7.744746	CAGCTT	0.19836	0.19379
cg0545033	DIP2C	NF-AT1 [	1489	1497	7.744746	CAGCTT	0.19836	0.19379
cg1850382	DIP2C	c-Myb [T0	1410	1417	7.739476	CTCAGT	0.42725	0.40917
cg1006492	DIP2C	c-Myb [T0	1520	1527	7.739476	CTCAGT	0.42725	0.40917
cg0545033	DIP2C	c-Myb [T0	1450	1457	7.739476	CTCAGT	0.42725	0.40917
cg0270010	DIP2C	IRF-1 [T0	1257	1265	7.732782	CCCTGG	0.14496	0.14723
cg0270010	DIP2C	IRF-1 [T0	1452	1460	7.732782	CCCTGG	0.14496	0.14723
cg1850382	DIP2C	IRF-1 [T0	576	584	7.732782	TTTCCA	0.14496	0.14723
cg1146814	DIP2C	IRF-1 [T0	1848	1856	7.732782	CCCTGG	0.14496	0.14723
cg1006492	DIP2C	IRF-1 [T0	686	694	7.732782	TTTCCA	0.14496	0.14723
cg0545033	DIP2C	IRF-1 [T0	616	624	7.732782	TTTCCA	0.14496	0.14723
cg1146814	DIP2C	LEF-1 [T0	123	130	7.719635	GGTCAA	0.21362	0.21504
cg0270010	DIP2C	c-Jun [T00	1736	1742	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	45	51	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	94	100	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	143	149	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	192	198	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	241	247	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	290	296	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	339	345	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	388	394	7.686747	ACAGTC	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	636	642	7.686747	TGACTG	0.48828	0.48672
cg1493188	DIP2C	c-Jun [T00	1158	1164	7.686747	TGACTG	0.48828	0.48672
cg1146814	DIP2C	c-Jun [T00	57	63	7.686747	ACAGTC	0.48828	0.48672
cg1850223	DIP2C	STAT5A [	883	895	7.681787	TTTACA	0.00894	0.00812
cg1493188	DIP2C	c-Ets-1 [T	1360	1366	7.642098	ATTCCG	0.48828	0.48642

cg0270010	DIP2C	p53 [T006	71	77	7.641867	GGGCCT	0.73242	0.79826
cg0270010	DIP2C	p53 [T006	480	486	7.641867	AAGGCC	0.73242	0.79826
cg1146814	DIP2C	p53 [T006	662	668	7.641867	GGGCCT	0.73242	0.79826
cg1146814	DIP2C	p53 [T006	1071	1077	7.641867	AAGGCC	0.73242	0.79826
cg1493188	DIP2C	ELF-1 [T0	1114	1126	7.634825	TCACTTC	0.00846	0.00821
cg1850223	DIP2C	AR [T0004	1974	1982	7.623968	AAGTTG	0.25177	0.2544
cg1850382	DIP2C	AR [T0004	560	568	7.623968	GGACAA	0.25177	0.2544
cg1006492	DIP2C	AR [T0004	670	678	7.623968	GGACAA	0.25177	0.2544
cg0545033	DIP2C	AR [T0004	600	608	7.623968	GGACAA	0.25177	0.2544
cg0270010	DIP2C	NFI/CTF [	1466	1473	7.587343	CCAAAT	0.36621	0.36269
cg1850382	DIP2C	NFI/CTF [	1680	1687	7.587343	CCAAGT	0.36621	0.36269
cg1493188	DIP2C	NFI/CTF [	1451	1458	7.587343	ACACTT	0.36621	0.36269
cg1006492	DIP2C	NFI/CTF [	1790	1797	7.587343	CCAAGT	0.36621	0.36269
cg0545033	DIP2C	NFI/CTF [	1720	1727	7.587343	CCAAGT	0.36621	0.36269
cg1850223	DIP2C	NF-AT1 [	672	680	7.574801	GGAAAA	0.19836	0.19379
cg0270010	DIP2C	NF-kappa	414	424	7.565255	GGGGAG	0.04435	0.04858
cg1146814	DIP2C	NF-kappa	1005	1015	7.565255	GGGGAG	0.04435	0.04858
cg0270010	DIP2C	c-Myb [T0	1339	1346	7.545286	AAACTG	0.42725	0.40917
cg1146814	DIP2C	c-Myb [T0	1930	1937	7.545286	AAACTG	0.42725	0.40917
cg1850382	DIP2C	c-Jun [T00	46	52	7.538568	GATGTC	0.48828	0.48672
cg1006492	DIP2C	c-Jun [T00	156	162	7.538568	GATGTC	0.48828	0.48672
cg0545033	DIP2C	c-Jun [T00	86	92	7.538568	GATGTC	0.48828	0.48672
cg0270010	DIP2C	GR [T050	704	710	7.527031	CAAACA	1.83105	1.71535
cg0270010	DIP2C	GR [T050	1479	1485	7.527031	CAAAAG	1.83105	1.71535
cg0270010	DIP2C	GR [T050	1619	1625	7.527031	CAAAGC	1.83105	1.71535
cg0270010	DIP2C	GR [T050	1652	1658	7.527031	CAAAAG	1.83105	1.71535
cg1850223	DIP2C	GR [T050	25	31	7.527031	TCTTTTG	1.83105	1.71535
cg1850223	DIP2C	GR [T050	143	149	7.527031	ATATTTC	1.83105	1.71535
cg1850223	DIP2C	GR [T050	408	414	7.527031	CAAATA	1.83105	1.71535
cg1850223	DIP2C	GR [T050	1278	1284	7.527031	CAAATA	1.83105	1.71535
cg1850223	DIP2C	GR [T050	1660	1666	7.527031	CAAACA	1.83105	1.71535
cg1850382	DIP2C	GR [T050	373	379	7.527031	TCTTTTG	1.83105	1.71535
cg1850382	DIP2C	GR [T050	563	569	7.527031	CAAAAT	1.83105	1.71535
cg1850382	DIP2C	GR [T050	600	606	7.527031	CAAACA	1.83105	1.71535
cg1850382	DIP2C	GR [T050	1660	1666	7.527031	CAAATA	1.83105	1.71535
cg1493188	DIP2C	GR [T050	906	912	7.527031	AATTTC	1.83105	1.71535
cg1493188	DIP2C	GR [T050	1170	1176	7.527031	ATGTTTC	1.83105	1.71535
cg1493188	DIP2C	GR [T050	1414	1420	7.527031	TGCTTTC	1.83105	1.71535
cg1493188	DIP2C	GR [T050	1579	1585	7.527031	CAAAAT	1.83105	1.71535
cg1493188	DIP2C	GR [T050	1613	1619	7.527031	AATTTC	1.83105	1.71535
cg1493188	DIP2C	GR [T050	1939	1945	7.527031	CATTTC	1.83105	1.71535
cg1146814	DIP2C	GR [T050	102	108	7.527031	CAAATA	1.83105	1.71535
cg1146814	DIP2C	GR [T050	357	363	7.527031	AGCTTTC	1.83105	1.71535
cg1146814	DIP2C	GR [T050	1295	1301	7.527031	CAAACA	1.83105	1.71535
cg1006492	DIP2C	GR [T050	8	14	7.527031	CAAAAG	1.83105	1.71535
cg1006492	DIP2C	GR [T050	101	107	7.527031	CAAAGC	1.83105	1.71535
cg1006492	DIP2C	GR [T050	483	489	7.527031	TCTTTTG	1.83105	1.71535
cg1006492	DIP2C	GR [T050	673	679	7.527031	CAAAAT	1.83105	1.71535

cg1006492	DIP2C	GR [T050	710	716	7.527031	CAAACA	1.83105	1.71535
cg1006492	DIP2C	GR [T050	1770	1776	7.527031	CAAATA	1.83105	1.71535
cg0545033	DIP2C	GR [T050	31	37	7.527031	CAAAGC	1.83105	1.71535
cg0545033	DIP2C	GR [T050	413	419	7.527031	TCTTTTG	1.83105	1.71535
cg0545033	DIP2C	GR [T050	603	609	7.527031	CAAAAT	1.83105	1.71535
cg0545033	DIP2C	GR [T050	640	646	7.527031	CAAACA	1.83105	1.71535
cg0545033	DIP2C	GR [T050	1700	1706	7.527031	CAAATA	1.83105	1.71535
cg1850223	DIP2C	RAR-beta	1104	1113	7.496706	TGGGTT	0.24414	0.25121
cg1850223	DIP2C	RAR-beta	1966	1975	7.496706	TGGGTT	0.24414	0.25121
cg1493188	DIP2C	c-Jun [T00	1502	1508	7.491008	TGACCG	0.48828	0.48672
cg1850223	DIP2C	p53 [T006	1594	1600	7.47855	GGGCTA	0.73242	0.79826
cg0270010	DIP2C	RAR-beta	401	410	7.47824	GGAGAA	0.24414	0.25121
cg1146814	DIP2C	RAR-beta	992	1001	7.47824	GGAGAA	0.24414	0.25121
cg1493188	DIP2C	RAR-beta:	15	26	7.477995	GGGCTC	0.02861	0.03163
cg1493188	DIP2C	RAR-beta:	64	75	7.477995	GGGCTC	0.02861	0.03163
cg1493188	DIP2C	RAR-beta:	211	222	7.477995	GGGCTC	0.02861	0.03163
cg1493188	DIP2C	RAR-beta:	358	369	7.477995	GGGCTC	0.02861	0.03163
cg1493188	DIP2C	IRF-1 [T0	1837	1845	7.477948	TTTCCT	0.14496	0.14723
cg1850382	DIP2C	C/EBPalph	1220	1226	7.465744	TTCAAT	0.48828	0.45033
cg1850382	DIP2C	C/EBPalph	1255	1261	7.465744	TTCAAT	0.48828	0.45033
cg1850382	DIP2C	C/EBPalph	1490	1496	7.465744	TTCAAT	0.48828	0.45033
cg1493188	DIP2C	C/EBPalph	710	716	7.465744	TTCAAT	0.48828	0.45033
cg1006492	DIP2C	C/EBPalph	1330	1336	7.465744	TTCAAT	0.48828	0.45033
cg1006492	DIP2C	C/EBPalph	1365	1371	7.465744	TTCAAT	0.48828	0.45033
cg1006492	DIP2C	C/EBPalph	1600	1606	7.465744	TTCAAT	0.48828	0.45033
cg0545033	DIP2C	C/EBPalph	1260	1266	7.465744	TTCAAT	0.48828	0.45033
cg0545033	DIP2C	C/EBPalph	1295	1301	7.465744	TTCAAT	0.48828	0.45033
cg0545033	DIP2C	C/EBPalph	1530	1536	7.465744	TTCAAT	0.48828	0.45033
cg0270010	DIP2C	MAZ [T00	1893	1905	7.461929	GGGTGG	0.00641	0.00703
cg1850382	DIP2C	p53 [T006	539	545	7.458735	GGGCGC	0.73242	0.79826
cg1006492	DIP2C	p53 [T006	649	655	7.458735	GGGCGC	0.73242	0.79826
cg0545033	DIP2C	p53 [T006	579	585	7.458735	GGGCGC	0.73242	0.79826
cg0270010	DIP2C	AR [T000	1787	1795	7.429939	AGCCTG	0.25177	0.2544
cg0270010	DIP2C	PEA3 [T0	1953	1961	7.421728	CCCCAT	0.34332	0.35389
cg1850382	DIP2C	LEF-1 [T0	34	41	7.396545	GCACAA	0.21362	0.21504
cg1493188	DIP2C	LEF-1 [T0	1416	1423	7.396545	CTTTGTA	0.21362	0.21504
cg1006492	DIP2C	LEF-1 [T0	98	105	7.396545	GCACAA	0.21362	0.21504
cg1006492	DIP2C	LEF-1 [T0	144	151	7.396545	GCACAA	0.21362	0.21504
cg0545033	DIP2C	LEF-1 [T0	28	35	7.396545	GCACAA	0.21362	0.21504
cg0545033	DIP2C	LEF-1 [T0	74	81	7.396545	GCACAA	0.21362	0.21504
cg1850382	DIP2C	C/EBPalph	127	133	7.396431	AATTGT	0.48828	0.45033
cg1006492	DIP2C	C/EBPalph	237	243	7.396431	AATTGT	0.48828	0.45033
cg0545033	DIP2C	C/EBPalph	167	173	7.396431	AATTGT	0.48828	0.45033
cg1850223	DIP2C	IRF-1 [T0	781	789	7.387351	GCGGGG	0.14496	0.14723
cg1146814	DIP2C	PPAR-alph	338	348	7.370536	GCCTGG	0.04482	0.04884
cg1850382	DIP2C	PXR-1:RX	1167	1174	7.362674	CACGTT	0.24414	0.24326
cg1493188	DIP2C	PXR-1:RX	1539	1546	7.362674	TGAACA	0.24414	0.24326
cg1006492	DIP2C	PXR-1:RX	1277	1284	7.362674	CACGTT	0.24414	0.24326

cg0545033	DIP2C	PXR-1:RX	1207	1214	7.362674	CACGTT	0.24414	0.24326
cg1850382	DIP2C	NF-kappa	1543	1553	7.353256	AGGTGG	0.04435	0.04858
cg1006492	DIP2C	NF-kappa	1653	1663	7.353256	AGGTGG	0.04435	0.04858
cg0545033	DIP2C	NF-kappa	1583	1593	7.353256	AGGTGG	0.04435	0.04858
cg027001	DIP2C	E2F-1 [T0	1904	1911	7.336545	GCGGCA	0.45776	0.49661
cg1850223	DIP2C	E2F-1 [T0	936	943	7.336545	GCTGCC	0.45776	0.49661
cg1850223	DIP2C	IRF-1 [T0	685	693	7.299819	TTTCCA	0.14496	0.14723
cg027001	DIP2C	c-Ets-2 [T	1213	1221	7.268173	AAGCAG	0.09155	0.08977
cg1850382	DIP2C	c-Ets-2 [T	484	492	7.268173	AAGCAG	0.09155	0.08977
cg1146814	DIP2C	c-Ets-2 [T	1804	1812	7.268173	AAGCAG	0.09155	0.08977
cg1006492	DIP2C	c-Ets-2 [T	594	602	7.268173	AAGCAG	0.09155	0.08977
cg0545033	DIP2C	c-Ets-2 [T	524	532	7.268173	AAGCAG	0.09155	0.08977
cg1850382	DIP2C	p53 [T006	445	451	7.266844	AAAGCC	0.73242	0.79826
cg1850382	DIP2C	p53 [T006	1175	1181	7.266844	AAAGCC	0.73242	0.79826
cg1006492	DIP2C	p53 [T006	555	561	7.266844	AAAGCC	0.73242	0.79826
cg1006492	DIP2C	p53 [T006	1285	1291	7.266844	AAAGCC	0.73242	0.79826
cg0545033	DIP2C	p53 [T006	485	491	7.266844	AAAGCC	0.73242	0.79826
cg0545033	DIP2C	p53 [T006	1215	1221	7.266844	AAAGCC	0.73242	0.79826
cg1850382	DIP2C	PU.1 [T02	1577	1589	7.265417	TGACTT	0.01001	0.0098
cg1006492	DIP2C	PU.1 [T02	1687	1699	7.265417	TGACTT	0.01001	0.0098
cg0545033	DIP2C	PU.1 [T02	1617	1629	7.265417	TGACTT	0.01001	0.0098
cg1850382	DIP2C	HNF-1C [	191	199	7.229698	AAAATT	0.08392	0.07499
cg1006492	DIP2C	HNF-1C [	301	309	7.229698	AAAATT	0.08392	0.07499
cg0545033	DIP2C	HNF-1C [	231	239	7.229698	AAAATT	0.08392	0.07499
cg1850223	DIP2C	AR [T000	378	386	7.215567	GGACAC	0.23651	0.23986
cg027001	DIP2C	c-Ets-1 [T	1760	1766	7.199436	TGGGAA	0.73242	0.73732
cg1850382	DIP2C	c-Ets-1 [T	1453	1459	7.199436	TTTCCC	0.73242	0.73732
cg1006492	DIP2C	c-Ets-1 [T	1563	1569	7.199436	TTTCCC	0.73242	0.73732
cg0545033	DIP2C	c-Ets-1 [T	1493	1499	7.199436	TTTCCC	0.73242	0.73732
cg027001	DIP2C	GCF [T00	764	772	7.186486	CCTCTG	0.45776	0.50397
cg027001	DIP2C	GCF [T00	1190	1198	7.186486	ACACTG	0.45776	0.50397
cg1850223	DIP2C	GCF [T00	1895	1903	7.186486	GCGCAG	0.45776	0.50397
cg1850382	DIP2C	GCF [T00	29	37	7.186486	GCGCAG	0.45776	0.50397
cg1146814	DIP2C	GCF [T00	1355	1363	7.186486	CCTCTG	0.45776	0.50397
cg1146814	DIP2C	GCF [T00	1781	1789	7.186486	ACACTG	0.45776	0.50397
cg1006492	DIP2C	GCF [T00	139	147	7.186486	GCGCAG	0.45776	0.50397
cg0545033	DIP2C	GCF [T00	69	77	7.186486	GCGCAG	0.45776	0.50397
cg027001	DIP2C	c-Jun [T00	678	684	7.178905	CGGGTC	0.73242	0.73062
cg1146814	DIP2C	c-Jun [T00	1269	1275	7.178905	CGGGTC	0.73242	0.73062
cg027001	DIP2C	SRY [T00	60	68	7.175614	AACACA	0.30518	0.29547
cg027001	DIP2C	SRY [T00	1314	1322	7.175614	GACACA	0.30518	0.29547
cg1850223	DIP2C	SRY [T00	174	182	7.175614	GAGACA	0.30518	0.29547
cg1850223	DIP2C	SRY [T00	1671	1679	7.175614	AAACCA	0.30518	0.29547
cg1850223	DIP2C	SRY [T00	1916	1924	7.175614	GCACCA	0.30518	0.29547
cg1493188	DIP2C	SRY [T00	1340	1348	7.175614	CTCACA	0.30518	0.29547
cg1146814	DIP2C	SRY [T00	359	367	7.175614	CTTTGC	0.30518	0.29547
cg1146814	DIP2C	SRY [T00	651	659	7.175614	AACACA	0.30518	0.29547
cg1146814	DIP2C	SRY [T00	1905	1913	7.175614	GACACA	0.30518	0.29547

cg1006492	DIP2C	SRY [T00	97	105	7.175614	TGCACA	0.30518	0.29547
cg0545033	DIP2C	SRY [T00	27	35	7.175614	TGCACA	0.30518	0.29547
cg0270010	DIP2C	XBP-1 [T0	256	261	7.172312	ACTCAT	2.92969	2.7512
cg0270010	DIP2C	XBP-1 [T0	743	748	7.172312	CTTCAT	2.92969	2.7512
cg0270010	DIP2C	XBP-1 [T0	1368	1373	7.172312	ATGAGG	2.92969	2.7512
cg0270010	DIP2C	XBP-1 [T0	1432	1437	7.172312	ATGAGG	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	41	46	7.172312	CTTCAT	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	183	188	7.172312	ATGAGG	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	622	627	7.172312	ATGATT	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	814	819	7.172312	ATGAAG	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	901	906	7.172312	CATCAT	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	1214	1219	7.172312	ACTCAT	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	1218	1223	7.172312	ATGATT	2.92969	2.7512
cg1850223	DIP2C	XBP-1 [T0	1436	1441	7.172312	ATGAAG	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	18	23	7.172312	ATTCAT	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	22	27	7.172312	ATGAGT	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	1042	1047	7.172312	CTTCAT	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	1247	1252	7.172312	ATGATG	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	1262	1267	7.172312	CATCAT	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	1441	1446	7.172312	ATGAAG	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	1731	1736	7.172312	CATCAT	2.92969	2.7512
cg1850382	DIP2C	XBP-1 [T0	1807	1812	7.172312	ATTCAT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	599	604	7.172312	ATGATT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	757	762	7.172312	ACTCAT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	926	931	7.172312	ATGAGT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	1109	1114	7.172312	ATGAGT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	1177	1182	7.172312	ATGATG	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	1309	1314	7.172312	CATCAT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	1598	1603	7.172312	ATGATT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	1718	1723	7.172312	ATTCAT	2.92969	2.7512
cg1493188	DIP2C	XBP-1 [T0	1823	1828	7.172312	CTTCAT	2.92969	2.7512
cg1146814	DIP2C	XBP-1 [T0	131	136	7.172312	ATGAAG	2.92969	2.7512
cg1146814	DIP2C	XBP-1 [T0	847	852	7.172312	ACTCAT	2.92969	2.7512
cg1146814	DIP2C	XBP-1 [T0	1334	1339	7.172312	CTTCAT	2.92969	2.7512
cg1146814	DIP2C	XBP-1 [T0	1959	1964	7.172312	ATGAGG	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	128	133	7.172312	ATTCAT	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	132	137	7.172312	ATGAGT	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	1152	1157	7.172312	CTTCAT	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	1357	1362	7.172312	ATGATG	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	1372	1377	7.172312	CATCAT	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	1551	1556	7.172312	ATGAAG	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	1841	1846	7.172312	CATCAT	2.92969	2.7512
cg1006492	DIP2C	XBP-1 [T0	1917	1922	7.172312	ATTCAT	2.92969	2.7512
cg0545033	DIP2C	XBP-1 [T0	58	63	7.172312	ATTCAT	2.92969	2.7512
cg0545033	DIP2C	XBP-1 [T0	62	67	7.172312	ATGAGT	2.92969	2.7512
cg0545033	DIP2C	XBP-1 [T0	1082	1087	7.172312	CTTCAT	2.92969	2.7512
cg0545033	DIP2C	XBP-1 [T0	1287	1292	7.172312	ATGATG	2.92969	2.7512
cg0545033	DIP2C	XBP-1 [T0	1302	1307	7.172312	CATCAT	2.92969	2.7512

cg0545033	DIP2C	XBP-1 [T	1481	1486	7.172312	ATGAAG	2.92969	2.7512
cg0545033	DIP2C	XBP-1 [T	1771	1776	7.172312	CATCAT	2.92969	2.7512
cg0545033	DIP2C	XBP-1 [T	1847	1852	7.172312	ATTCAT	2.92969	2.7512
cg027001	DIP2C	p53 [T006	440	446	7.153797	TGGGCC	1.09863	1.22478
cg027001	DIP2C	p53 [T006	537	543	7.153797	GGGCCC	1.09863	1.22478
cg1850223	DIP2C	p53 [T006	390	396	7.153797	TGGGCC	1.09863	1.22478
cg1850223	DIP2C	p53 [T006	391	397	7.153797	GGGCCC	1.09863	1.22478
cg1850223	DIP2C	p53 [T006	1765	1771	7.153797	TGGGCC	1.09863	1.22478
cg1850223	DIP2C	p53 [T006	1766	1772	7.153797	GGGCCC	1.09863	1.22478
cg1146814	DIP2C	p53 [T006	1031	1037	7.153797	TGGGCC	1.09863	1.22478
cg1146814	DIP2C	p53 [T006	1128	1134	7.153797	GGGCCC	1.09863	1.22478
cg1850382	DIP2C	Ik-1 [T027	1863	1875	7.122895	TCCCAA	0.01064	0.01145
cg1493188	DIP2C	Ik-1 [T027	1975	1987	7.122895	TCCCAG	0.01064	0.01145
cg1006492	DIP2C	Ik-1 [T027	1973	1985	7.122895	TCCCAA	0.01064	0.01145
cg0545033	DIP2C	Ik-1 [T027	1903	1915	7.122895	TCCCAA	0.01064	0.01145
cg1850223	DIP2C	c-Jun [T00	5	11	7.096776	GCAGTC	0.73242	0.73062
cg1493188	DIP2C	c-Jun [T00	439	445	7.096776	GCAGTC	0.73242	0.73062
cg1493188	DIP2C	c-Jun [T00	1038	1044	7.096776	TGACTG	0.73242	0.73062
cg027001	DIP2C	NF-AT1 [	1261	1269	7.095752	GGAAAA	0.15259	0.14325
cg1850223	DIP2C	NF-AT1 [	97	105	7.095752	TTGTTTT	0.15259	0.14325
cg1850223	DIP2C	NF-AT1 [	507	515	7.095752	TAATTT	0.15259	0.14325
cg1850223	DIP2C	NF-AT1 [	1380	1388	7.095752	TTATTT	0.15259	0.14325
cg1493188	DIP2C	NF-AT1 [	1469	1477	7.095752	CTATTT	0.15259	0.14325
cg1146814	DIP2C	NF-AT1 [	1852	1860	7.095752	GGAAAA	0.15259	0.14325
cg1850382	DIP2C	c-Ets-1 [T	101	107	7.071349	AGGGAA	0.73242	0.73732
cg1006492	DIP2C	c-Ets-1 [T	211	217	7.071349	AGGGAA	0.73242	0.73732
cg0545033	DIP2C	c-Ets-1 [T	141	147	7.071349	AGGGAA	0.73242	0.73732
cg1850223	DIP2C	c-Jun [T00	148	154	7.052189	TGACTA	0.73242	0.73062
cg1850382	DIP2C	c-Jun [T00	403	409	7.052189	ATAGTC	0.73242	0.73062
cg1006492	DIP2C	c-Jun [T00	513	519	7.052189	ATAGTC	0.73242	0.73062
cg0545033	DIP2C	c-Jun [T00	443	449	7.052189	ATAGTC	0.73242	0.73062
cg1850382	DIP2C	C/EBPalp	717	723	7.00174	GCCAAT	0.73242	0.68282
cg1006492	DIP2C	C/EBPalp	827	833	7.00174	GCCAAT	0.73242	0.68282
cg0545033	DIP2C	C/EBPalp	757	763	7.00174	GCCAAT	0.73242	0.68282
cg027001	DIP2C	HNF-3alp	888	895	7.000129	TAAAAA	0.82397	0.71909
cg1850223	DIP2C	HNF-3alp	1381	1388	7.000129	TATTTC	0.82397	0.71909
cg1850223	DIP2C	HNF-3alp	1578	1585	7.000129	TAAAAA	0.82397	0.71909
cg1850382	DIP2C	HNF-3alp	1963	1970	7.000129	AAAAAA	0.82397	0.71909
cg1493188	DIP2C	HNF-3alp	568	575	7.000129	AATTTT	0.82397	0.71909
cg1493188	DIP2C	HNF-3alp	700	707	7.000129	GAAAAA	0.82397	0.71909
cg1493188	DIP2C	HNF-3alp	720	727	7.000129	AGAAAA	0.82397	0.71909
cg1493188	DIP2C	HNF-3alp	1124	1131	7.000129	AAAAAA	0.82397	0.71909
cg1493188	DIP2C	HNF-3alp	1470	1477	7.000129	TATTTC	0.82397	0.71909
cg1493188	DIP2C	HNF-3alp	1578	1585	7.000129	GCAAAA	0.82397	0.71909
cg1146814	DIP2C	HNF-3alp	100	107	7.000129	TGCAAA	0.82397	0.71909
cg1146814	DIP2C	HNF-3alp	1479	1486	7.000129	TAAAAA	0.82397	0.71909
cg1006492	DIP2C	HNF-3alp	82	89	7.000129	CATTTC	0.82397	0.71909
cg0545033	DIP2C	HNF-3alp	12	19	7.000129	CATTTC	0.82397	0.71909

cg1850223	DIP2C	GCF [T00	1955	1963	6.987525	GCGCTG	0.45776	0.50397
cg1493188	DIP2C	GCF [T00	1843	1851	6.987525	GCGCTG	0.45776	0.50397
cg0270010	DIP2C	EBF [T05	1049	1059	6.983657	TGCCCT	0.03052	0.03432
cg1146814	DIP2C	EBF [T05	1640	1650	6.983657	TGCCCT	0.03052	0.03432
cg0270010	DIP2C	AR [T000	1866	1874	6.974607	GGACAG	0.23651	0.23986
cg1493188	DIP2C	AR [T000	1827	1835	6.974607	ATTCTG	0.23651	0.23986
cg0270010	DIP2C	E2F-1 [T0	781	788	6.967231	TCCCCC	0.30518	0.33862
cg1850382	DIP2C	E2F-1 [T0	62	69	6.967231	TACCCC	0.30518	0.33862
cg1146814	DIP2C	E2F-1 [T0	1372	1379	6.967231	TCCCCC	0.30518	0.33862
cg1006492	DIP2C	E2F-1 [T0	172	179	6.967231	TACCCC	0.30518	0.33862
cg0545033	DIP2C	E2F-1 [T0	102	109	6.967231	TACCCC	0.30518	0.33862
cg1850223	DIP2C	c-Ets-1 [T	243	249	6.949623	TCGGAA	0.73242	0.73732
cg1850382	DIP2C	c-Ets-1 [T	901	907	6.949623	TCGGAA	0.73242	0.73732
cg1006492	DIP2C	c-Ets-1 [T	1011	1017	6.949623	TCGGAA	0.73242	0.73732
cg0545033	DIP2C	c-Ets-1 [T	941	947	6.949623	TCGGAA	0.73242	0.73732
cg1850223	DIP2C	NF-1 [T00	1427	1434	6.948522	GGCCCC	0.48828	0.50205
cg1493188	DIP2C	NF-1 [T00	1943	1950	6.948522	TTGGGG	0.48828	0.50205
cg1146814	DIP2C	NF-1 [T00	522	529	6.948522	GGCCCC	0.48828	0.50205
cg1850223	DIP2C	c-Ets-1 [T	511	517	6.943262	TTTCCCC	0.73242	0.73732
cg1850223	DIP2C	c-Ets-1 [T	783	789	6.943262	GGGGAA	0.73242	0.73732
cg1850223	DIP2C	c-Ets-1 [T	1384	1390	6.943262	TTTCCCC	0.73242	0.73732
cg1006492	DIP2C	c-Ets-1 [T	76	82	6.943262	TTTCCCC	0.73242	0.73732
cg0545033	DIP2C	c-Ets-1 [T	6	12	6.943262	TTTCCCC	0.73242	0.73732
cg0270010	DIP2C	ENKTF-1	81	88	6.942764	TGGCTT	1.46484	1.56616
cg0270010	DIP2C	ENKTF-1	645	652	6.942764	CCATGC	1.46484	1.56616
cg0270010	DIP2C	ENKTF-1	1056	1063	6.942764	TGGCCT	1.46484	1.56616
cg1850223	DIP2C	ENKTF-1	355	362	6.942764	TGGCGT	1.46484	1.56616
cg1850223	DIP2C	ENKTF-1	634	641	6.942764	TGGCCA	1.46484	1.56616
cg1850223	DIP2C	ENKTF-1	729	736	6.942764	TGGCTA	1.46484	1.56616
cg1850223	DIP2C	ENKTF-1	1477	1484	6.942764	CATTGC	1.46484	1.56616
cg1850223	DIP2C	ENKTF-1	1737	1744	6.942764	CCGTGC	1.46484	1.56616
cg1850382	DIP2C	ENKTF-1	539	546	6.942764	GGGCGC	1.46484	1.56616
cg1850382	DIP2C	ENKTF-1	713	720	6.942764	CTCAGC	1.46484	1.56616
cg1850382	DIP2C	ENKTF-1	995	1002	6.942764	TGGCTC	1.46484	1.56616
cg1850382	DIP2C	ENKTF-1	1096	1103	6.942764	ATTCGC	1.46484	1.56616
cg1850382	DIP2C	ENKTF-1	1360	1367	6.942764	TGGCCA	1.46484	1.56616
cg1850382	DIP2C	ENKTF-1	1832	1839	6.942764	CACAGC	1.46484	1.56616
cg1493188	DIP2C	ENKTF-1	556	563	6.942764	TGGCAG	1.46484	1.56616
cg1493188	DIP2C	ENKTF-1	1807	1814	6.942764	GCACGC	1.46484	1.56616
cg1146814	DIP2C	ENKTF-1	155	162	6.942764	AACCGC	1.46484	1.56616
cg1146814	DIP2C	ENKTF-1	501	508	6.942764	CACAGC	1.46484	1.56616
cg1146814	DIP2C	ENKTF-1	672	679	6.942764	TGGCTT	1.46484	1.56616
cg1146814	DIP2C	ENKTF-1	1236	1243	6.942764	CCATGC	1.46484	1.56616
cg1146814	DIP2C	ENKTF-1	1647	1654	6.942764	TGGCCT	1.46484	1.56616
cg1006492	DIP2C	ENKTF-1	649	656	6.942764	GGGCGC	1.46484	1.56616
cg1006492	DIP2C	ENKTF-1	823	830	6.942764	CTCAGC	1.46484	1.56616
cg1006492	DIP2C	ENKTF-1	1105	1112	6.942764	TGGCTC	1.46484	1.56616
cg1006492	DIP2C	ENKTF-1	1206	1213	6.942764	ATTCGC	1.46484	1.56616

cg1006492	DIP2C	ENKTF-1	1470	1477	6.942764	TGGCCA	1.46484	1.56616
cg1006492	DIP2C	ENKTF-1	1942	1949	6.942764	CACAGC	1.46484	1.56616
cg0545033	DIP2C	ENKTF-1	579	586	6.942764	GGGCGC	1.46484	1.56616
cg0545033	DIP2C	ENKTF-1	753	760	6.942764	CTCAGC	1.46484	1.56616
cg0545033	DIP2C	ENKTF-1	1035	1042	6.942764	TGGCTC	1.46484	1.56616
cg0545033	DIP2C	ENKTF-1	1136	1143	6.942764	ATTCGC	1.46484	1.56616
cg0545033	DIP2C	ENKTF-1	1400	1407	6.942764	TGGCCA	1.46484	1.56616
cg0545033	DIP2C	ENKTF-1	1872	1879	6.942764	CACAGC	1.46484	1.56616
cg1146814	DIP2C	p53 [T006	275	281	6.938545	GAGGCC	1.09863	1.22478
cg1850223	DIP2C	AhR:Arnt	1843	1852	6.928166	CCACGC	0.0515	0.0599
cg027001	DIP2C	VDR [T00	317	325	6.925682	CACATG	0.42725	0.41
cg1850223	DIP2C	VDR [T00	1464	1472	6.925682	TGCCTG	0.42725	0.41
cg1850382	DIP2C	VDR [T00	768	776	6.925682	GTTCAG	0.42725	0.41
cg1850382	DIP2C	VDR [T00	1379	1387	6.925682	CTCCTG	0.42725	0.41
cg1493188	DIP2C	VDR [T00	1535	1543	6.925682	AAACTG	0.42725	0.41
cg1146814	DIP2C	VDR [T00	908	916	6.925682	CACATG	0.42725	0.41
cg1006492	DIP2C	VDR [T00	878	886	6.925682	GTTCAG	0.42725	0.41
cg1006492	DIP2C	VDR [T00	1489	1497	6.925682	CTCCTG	0.42725	0.41
cg0545033	DIP2C	VDR [T00	808	816	6.925682	GTTCAG	0.42725	0.41
cg0545033	DIP2C	VDR [T00	1419	1427	6.925682	CTCCTG	0.42725	0.41
cg1146814	DIP2C	EBF [T05	200	210	6.8994	GCCCCT	0.03052	0.03432
cg1493188	DIP2C	IRF-1 [T0	1473	1481	6.880783	TTTCCA	0.1297	0.12685
cg1850382	DIP2C	EBF [T05	447	457	6.872118	AGCCCT	0.03052	0.03432
cg1006492	DIP2C	EBF [T05	557	567	6.872118	AGCCCT	0.03052	0.03432
cg0545033	DIP2C	EBF [T05	487	497	6.872118	AGCCCT	0.03052	0.03432
cg027001	DIP2C	C/EBPalp	1530	1536	6.85549	TTCAAT	0.73242	0.68282
cg1850223	DIP2C	C/EBPalp	1203	1209	6.85549	TTCAAT	0.73242	0.68282
cg1850382	DIP2C	C/EBPalp	363	369	6.85549	TGCAAT	0.73242	0.68282
cg1006492	DIP2C	C/EBPalp	473	479	6.85549	TGCAAT	0.73242	0.68282
cg0545033	DIP2C	C/EBPalp	403	409	6.85549	TGCAAT	0.73242	0.68282
cg1850382	DIP2C	E2F-1 [T0	265	272	6.839754	CGTTCC	0.30518	0.33862
cg1006492	DIP2C	E2F-1 [T0	375	382	6.839754	CGTTCC	0.30518	0.33862
cg0545033	DIP2C	E2F-1 [T0	305	312	6.839754	CGTTCC	0.30518	0.33862
cg1850223	DIP2C	PEA3 [T0	1754	1762	6.824411	ATGCAT	0.22888	0.22744
cg027001	DIP2C	c-Jun [T00	1417	1423	6.787369	TGACAG	0.73242	0.73062
cg1850223	DIP2C	c-Jun [T00	718	724	6.787369	TCTGTC	0.73242	0.73062
cg1493188	DIP2C	c-Jun [T00	1635	1641	6.787369	TGACAG	0.73242	0.73062
cg1146814	DIP2C	c-Jun [T00	372	378	6.787369	TCTGTC	0.73242	0.73062
cg1850223	DIP2C	C/EBPalp	161	167	6.786177	TACAAT	0.73242	0.68282
cg1493188	DIP2C	C/EBPalp	1475	1481	6.786177	TCCAAT	0.73242	0.68282
cg027001	DIP2C	NFI/CTF [	81	88	6.786076	TGGCTT	0.73242	0.74795
cg1850223	DIP2C	NFI/CTF [	285	292	6.786076	CCAAGC	0.73242	0.74795
cg1850223	DIP2C	NFI/CTF [	637	644	6.786076	CCAAGC	0.73242	0.74795
cg1850223	DIP2C	NFI/CTF [	1231	1238	6.786076	CCAAGC	0.73242	0.74795
cg1850223	DIP2C	NFI/CTF [	1659	1666	6.786076	CCAAAC	0.73242	0.74795
cg1850382	DIP2C	NFI/CTF [	599	606	6.786076	CCAAAC	0.73242	0.74795
cg1146814	DIP2C	NFI/CTF [	672	679	6.786076	TGGCTT	0.73242	0.74795
cg1006492	DIP2C	NFI/CTF [	709	716	6.786076	CCAAAC	0.73242	0.74795

cg0545033	DIP2C	NFI/CTF [	639	646	6.786076	CCAAAC	0.73242	0.74795
cg0270010	DIP2C	RXR-alpha	1940	1946	6.785809	GTTACC	0.36621	0.38841
cg0270010	DIP2C	RXR-alpha	1966	1972	6.785809	GTTACC	0.36621	0.38841
cg0270010	DIP2C	RXR-alpha	1993	1999	6.785809	GTTACC	0.36621	0.38841
cg1493188	DIP2C	p53 [T006	1235	1241	6.778774	TGAGCC	1.09863	1.22478
cg1146814	DIP2C	p53 [T006	197	203	6.778774	TGAGCC	1.09863	1.22478
cg1850223	DIP2C	EBF [T05	1588	1598	6.76967	TTCTCAC	0.03052	0.03432
cg1493188	DIP2C	AR [T000	1546	1554	6.760234	GGACAA	0.23651	0.23986
cg0270010	DIP2C	ATF3 [T01	1473	1480	6.744803	TTGTGTC	0.27466	0.26471
cg1850223	DIP2C	ATF3 [T01	355	362	6.744803	TGGCGTC	0.27466	0.26471
cg1146814	DIP2C	TCF-4 [T0	122	131	6.735684	AGGTCA	0.04959	0.04686
cg1493188	DIP2C	POU2F2 (	1920	1930	6.735173	CTTGTA	0.04292	0.03779
cg1850223	DIP2C	Elk-1 [T00	1808	1816	6.732355	CTTCCGC	0.06104	0.06731
cg1146814	DIP2C	AR [T000	22	30	6.723093	GGACAG	0.19836	0.20813
cg0270010	DIP2C	NF-1 [T00	556	563	6.722386	TTGGGC	0.24414	0.2565
cg1850223	DIP2C	NF-1 [T00	633	640	6.722386	CTGGCC	0.24414	0.2565
cg1850223	DIP2C	NF-1 [T00	1227	1234	6.722386	TTGCCC	0.24414	0.2565
cg1850382	DIP2C	NF-1 [T00	1359	1366	6.722386	CTGGCC	0.24414	0.2565
cg1850382	DIP2C	NF-1 [T00	1924	1931	6.722386	CTGGCC	0.24414	0.2565
cg1146814	DIP2C	NF-1 [T00	1147	1154	6.722386	TTGGGC	0.24414	0.2565
cg1006492	DIP2C	NF-1 [T00	1469	1476	6.722386	CTGGCC	0.24414	0.2565
cg0545033	DIP2C	NF-1 [T00	1399	1406	6.722386	CTGGCC	0.24414	0.2565
cg0545033	DIP2C	NF-1 [T00	1964	1971	6.722386	CTGGCC	0.24414	0.2565
cg1850382	DIP2C	GATA-3 [	502	513	6.717073	CAAGAT	0.01049	0.01022
cg1006492	DIP2C	GATA-3 [	612	623	6.717073	CAAGAT	0.01049	0.01022
cg0545033	DIP2C	GATA-3 [	542	553	6.717073	CAAGAT	0.01049	0.01022
cg1850382	DIP2C	T3R-beta1	1931	1939	6.702681	ACATGG	0.21362	0.2251
cg0545033	DIP2C	T3R-beta1	1971	1979	6.702681	ACATGG	0.21362	0.2251
cg1850223	DIP2C	AhR:Arnt	368	377	6.698963	GCAAGC	0.01717	0.01925
cg1850382	DIP2C	c-Ets-1 [T	266	272	6.693449	GTTCCGC	0.48828	0.48842
cg1006492	DIP2C	c-Ets-1 [T	376	382	6.693449	GTTCCGC	0.48828	0.48842
cg0545033	DIP2C	c-Ets-1 [T	306	312	6.693449	GTTCCGC	0.48828	0.48842
cg1850223	DIP2C	T3R-beta1	1524	1532	6.683388	TCACCC	0.21362	0.2251
cg0270010	DIP2C	PXR-1:RX	1611	1618	6.668182	TGAACA	0.24414	0.23169
cg1850223	DIP2C	PXR-1:RX	112	119	6.668182	TGAACA	0.24414	0.23169
cg1850223	DIP2C	PXR-1:RX	234	241	6.668182	TGAACA	0.24414	0.23169
cg1850223	DIP2C	c-Jun [T00	608	614	6.668031	TGACTTC	0.61035	0.6179
cg1850223	DIP2C	GATA-2 [	1495	1503	6.666667	AGATAT	0.24414	0.2357
cg1850223	DIP2C	GATA-2 [	1923	1931	6.666667	AGATAC	0.24414	0.2357
cg1850223	DIP2C	T3R-beta1	124	132	6.664094	TCACCC	0.21362	0.2251
cg1493188	DIP2C	c-Fos [T00	1111	1120	6.660217	GAGTCA	0.04578	0.04485
cg1850382	DIP2C	IRF-1 [T0	1453	1461	6.622811	TTTCCCA	0.19073	0.1875
cg1006492	DIP2C	IRF-1 [T0	1563	1571	6.622811	TTTCCCA	0.19073	0.1875
cg0545033	DIP2C	IRF-1 [T0	1493	1501	6.622811	TTTCCCA	0.19073	0.1875
cg0270010	DIP2C	FOXP3 [T	1352	1357	6.581441	TAAAAC	0.97656	0.904
cg0270010	DIP2C	TFII-I [T0	93	98	6.581441	CACTCC	0.97656	0.9991
cg1850223	DIP2C	FOXP3 [T	423	428	6.581441	TTCAAC	0.97656	0.904
cg1850223	DIP2C	FOXP3 [T	762	767	6.581441	TAAAAC	0.97656	0.904

cg1850223	DIP2C	TFII-I [T0	13	18	6.581441	ATCTCC	0.97656	0.9991
cg1850223	DIP2C	TFII-I [T0	992	997	6.581441	CACTCC	0.97656	0.9991
cg1850223	DIP2C	TFII-I [T0	1400	1405	6.581441	GGAGTG	0.97656	0.9991
cg1850223	DIP2C	TFII-I [T0	1503	1508	6.581441	ATCTCC	0.97656	0.9991
cg1850223	DIP2C	TFII-I [T0	1839	1844	6.581441	CACTCC	0.97656	0.9991
cg1493188	DIP2C	FOXP3 [T	516	521	6.581441	TTCAAC	0.97656	0.904
cg1493188	DIP2C	FOXP3 [T	1934	1939	6.581441	TAAAAC	0.97656	0.904
cg1493188	DIP2C	TFII-I [T0	1702	1707	6.581441	CACTCC	0.97656	0.9991
cg1493188	DIP2C	TFII-I [T0	1859	1864	6.581441	ATCTCC	0.97656	0.9991
cg1146814	DIP2C	FOXP3 [T	1943	1948	6.581441	TAAAAC	0.97656	0.904
cg1146814	DIP2C	TFII-I [T0	684	689	6.581441	CACTCC	0.97656	0.9991
cg1493188	DIP2C	AR [T000	794	802	6.568287	GGCATG	0.19836	0.20813
cg1850382	DIP2C	RXR-alpha	494	500	6.563693	GACACC	0.24414	0.25119
cg1493188	DIP2C	RXR-alpha	457	463	6.563693	GACACC	0.24414	0.25119
cg1006492	DIP2C	RXR-alpha	604	610	6.563693	GACACC	0.24414	0.25119
cg0545033	DIP2C	RXR-alpha	534	540	6.563693	GACACC	0.24414	0.25119
cg0270010	DIP2C	p53 [T006	120	126	6.563521	GCAGCC	0.48828	0.54643
cg0270010	DIP2C	p53 [T006	209	215	6.563521	GCAGCC	0.48828	0.54643
cg0270010	DIP2C	p53 [T006	771	777	6.563521	GCAGCC	0.48828	0.54643
cg1850223	DIP2C	p53 [T006	956	962	6.563521	GCAGCC	0.48828	0.54643
cg1850223	DIP2C	p53 [T006	1832	1838	6.563521	GCAGCC	0.48828	0.54643
cg1850382	DIP2C	p53 [T006	68	74	6.563521	GCAGCC	0.48828	0.54643
cg1493188	DIP2C	p53 [T006	862	868	6.563521	GGGCTT	0.48828	0.54643
cg1146814	DIP2C	p53 [T006	242	248	6.563521	GCAGCC	0.48828	0.54643
cg1146814	DIP2C	p53 [T006	711	717	6.563521	GCAGCC	0.48828	0.54643
cg1146814	DIP2C	p53 [T006	800	806	6.563521	GCAGCC	0.48828	0.54643
cg1146814	DIP2C	p53 [T006	1362	1368	6.563521	GCAGCC	0.48828	0.54643
cg1006492	DIP2C	p53 [T006	178	184	6.563521	GCAGCC	0.48828	0.54643
cg0545033	DIP2C	p53 [T006	108	114	6.563521	GCAGCC	0.48828	0.54643
cg0270010	DIP2C	PPAR-alph	1851	1861	6.51544	CTCTGG	0.03719	0.04058
cg1850382	DIP2C	AR [T000	493	501	6.50872	GGACAC	0.19836	0.20813
cg1006492	DIP2C	AR [T000	603	611	6.50872	GGACAC	0.19836	0.20813
cg0545033	DIP2C	AR [T000	533	541	6.50872	GGACAC	0.19836	0.20813
cg1850223	DIP2C	IRF-1 [T0	1745	1753	6.497844	TTTCCAC	0.19073	0.1875
cg0270010	DIP2C	XBP-1 [T0	647	652	6.478682	ATGCCA	0.97656	0.99906
cg1850223	DIP2C	XBP-1 [T0	92	97	6.478682	TGGCAT	0.97656	0.99906
cg1850223	DIP2C	XBP-1 [T0	1294	1299	6.478682	ATGCCC	0.97656	0.99906
cg1850382	DIP2C	XBP-1 [T0	567	572	6.478682	ATGCCC	0.97656	0.99906
cg1493188	DIP2C	XBP-1 [T0	1306	1311	6.478682	TGGCAT	0.97656	0.99906
cg1493188	DIP2C	XBP-1 [T0	1318	1323	6.478682	TGGCAT	0.97656	0.99906
cg1146814	DIP2C	XBP-1 [T0	1238	1243	6.478682	ATGCCA	0.97656	0.99906
cg1006492	DIP2C	XBP-1 [T0	677	682	6.478682	ATGCCC	0.97656	0.99906
cg0545033	DIP2C	XBP-1 [T0	607	612	6.478682	ATGCCC	0.97656	0.99906
cg1850382	DIP2C	c-Jun [T00	1799	1805	6.475265	TGACAC	0.61035	0.6179
cg1493188	DIP2C	c-Jun [T00	1737	1743	6.475265	CGTGTC	0.61035	0.6179
cg1006492	DIP2C	c-Jun [T00	1909	1915	6.475265	TGACAC	0.61035	0.6179
cg0545033	DIP2C	c-Jun [T00	1839	1845	6.475265	TGACAC	0.61035	0.6179
cg0270010	DIP2C	c-Jun [T00	1282	1288	6.462218	TGACTA	0.61035	0.6179

cg1146814	DIP2C	c-Jun [T00	1873	1879	6.462218	TGACTA(	0.61035	0.6179
cg1850223	DIP2C	C/EBPalph	1477	1483	6.460799	CATTGC(	0.48828	0.47407
cg1146814	DIP2C	c-Myb [T0	141	148	6.454077	CACAGT	0.30518	0.30272
cg1850223	DIP2C	RAR-beta	1936	1945	6.452127	CACGAA	0.18311	0.1857
cg1850382	DIP2C	RBP-Jkapp	1452	1463	6.448184	CTTTCCC	0.01311	0.01274
cg1006492	DIP2C	RBP-Jkapp	1562	1573	6.448184	CTTTCCC	0.01311	0.01274
cg0545033	DIP2C	RBP-Jkapp	1492	1503	6.448184	CTTTCCC	0.01311	0.01274
cg1850382	DIP2C	NF-kappaI	1890	1900	6.433492	GGGGAT	0.03052	0.03409
cg0545033	DIP2C	NF-kappaI	1930	1940	6.433492	GGGGAT	0.03052	0.03409
cg1493188	DIP2C	TCF-4 [T0	1377	1386	6.425494	CCCTCA	0.04959	0.04686
cg1493188	DIP2C	c-Ets-1 [T	933	939	6.423689	TTTCCA	0.48828	0.48842
cg1493188	DIP2C	c-Ets-1 [T	1473	1479	6.423689	TTTCCA	0.48828	0.48842
cg0270010	DIP2C	c-Myb [T0	1764	1771	6.422836	AAACTG	0.30518	0.30272
cg1850382	DIP2C	RAR-beta	1936	1945	6.415195	GTGAAA	0.18311	0.1857
cg0545033	DIP2C	RAR-beta	1976	1985	6.415195	GTGAAA	0.18311	0.1857
cg1146814	DIP2C	p53 [T006	238	244	6.403751	GGGCGC	0.48828	0.54643
cg0270010	DIP2C	AR [T000	429	437	6.400417	GGACAG	0.19836	0.20813
cg1146814	DIP2C	AR [T000	1020	1028	6.400417	GGACAG	0.19836	0.20813
cg0270010	DIP2C	p53 [T006	1089	1095	6.400205	GTCGCC(	0.48828	0.54643
cg1146814	DIP2C	p53 [T006	1680	1686	6.400205	GTCGCC(	0.48828	0.54643
cg0270010	DIP2C	C/EBPalph	696	702	6.391486	GACAAT	0.48828	0.47407
cg1850223	DIP2C	C/EBPalph	89	95	6.391486	AATTGG(	0.48828	0.47407
cg1493188	DIP2C	C/EBPalph	1641	1647	6.391486	AATTGT(	0.48828	0.47407
cg1146814	DIP2C	C/EBPalph	1287	1293	6.391486	GACAAT	0.48828	0.47407
cg1850223	DIP2C	TCF-4E [T	1673	1679	6.302385	ACCAAA	0.61035	0.59686
cg1850223	DIP2C	TCF-4E [T	1918	1924	6.302385	ACCAAA	0.61035	0.59686
cg1850382	DIP2C	TCF-4E [T	533	539	6.302385	ACCAAA	0.61035	0.59686
cg1493188	DIP2C	TCF-4E [T	1991	1997	6.302385	GGCAAA	0.61035	0.59686
cg1146814	DIP2C	TCF-4E [T	378	384	6.302385	ACCAAA	0.61035	0.59686
cg1146814	DIP2C	TCF-4E [T	404	410	6.302385	ACCAAA	0.61035	0.59686
cg1006492	DIP2C	TCF-4E [T	643	649	6.302385	ACCAAA	0.61035	0.59686
cg0545033	DIP2C	TCF-4E [T	573	579	6.302385	ACCAAA	0.61035	0.59686
cg1850382	DIP2C	c-Jun [T00	1392	1398	6.293948	TGACCC	0.61035	0.6179
cg1006492	DIP2C	c-Jun [T00	1502	1508	6.293948	TGACCC	0.61035	0.6179
cg0545033	DIP2C	c-Jun [T00	1432	1438	6.293948	TGACCC	0.61035	0.6179
cg0270010	DIP2C	GR-alpha [	205	209	6.263098	TGAGG	3.90625	3.89624
cg0270010	DIP2C	GR-alpha [	672	676	6.263098	CCTCA	3.90625	3.89624
cg0270010	DIP2C	GR-alpha [	1182	1186	6.263098	CCTCA	3.90625	3.89624
cg0270010	DIP2C	GR-alpha [	1369	1373	6.263098	TGAGG	3.90625	3.89624
cg0270010	DIP2C	GR-alpha [	1433	1437	6.263098	TGAGG	3.90625	3.89624
cg1850223	DIP2C	GR-alpha [	184	188	6.263098	TGAGG	3.90625	3.89624
cg1850223	DIP2C	GR-alpha [	414	418	6.263098	TAAGG	3.90625	3.89624
cg1850223	DIP2C	GR-alpha [	914	918	6.263098	TGAGG	3.90625	3.89624
cg1850223	DIP2C	GR-alpha [	1247	1251	6.263098	CCTTA	3.90625	3.89624
cg1850223	DIP2C	GR-alpha [	1508	1512	6.263098	CCTCA	3.90625	3.89624
cg1850223	DIP2C	GR-alpha [	1981	1985	6.263098	CCTCA	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	323	327	6.263098	CCTTA	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	747	751	6.263098	CCTCA	3.90625	3.89624

cg1850382	DIP2C	GR-alpha [	941	945	6.263098	TGAGG	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	1372	1376	6.263098	CCTCA	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	1432	1436	6.263098	TGAGG	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	1516	1520	6.263098	CCTCA	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	1583	1587	6.263098	CCTCA	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	1882	1886	6.263098	TGAGG	3.90625	3.89624
cg1850382	DIP2C	GR-alpha [	1900	1904	6.263098	TGAGG	3.90625	3.89624
cg1493188	DIP2C	GR-alpha [	747	751	6.263098	CCTTA	3.90625	3.89624
cg1493188	DIP2C	GR-alpha [	1378	1382	6.263098	CCTCA	3.90625	3.89624
cg1493188	DIP2C	GR-alpha [	1765	1769	6.263098	TAAGG	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	3	7	6.263098	TGAGG	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	448	452	6.263098	CCTCA	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	545	549	6.263098	TGAGG	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	589	593	6.263098	CCTCA	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	796	800	6.263098	TGAGG	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	1263	1267	6.263098	CCTCA	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	1773	1777	6.263098	CCTCA	3.90625	3.89624
cg1146814	DIP2C	GR-alpha [	1960	1964	6.263098	TGAGG	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	433	437	6.263098	CCTTA	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	857	861	6.263098	CCTCA	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	1051	1055	6.263098	TGAGG	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	1482	1486	6.263098	CCTCA	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	1542	1546	6.263098	TGAGG	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	1626	1630	6.263098	CCTCA	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	1693	1697	6.263098	CCTCA	3.90625	3.89624
cg1006492	DIP2C	GR-alpha [	1992	1996	6.263098	TGAGG	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	363	367	6.263098	CCTTA	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	787	791	6.263098	CCTCA	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	981	985	6.263098	TGAGG	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	1412	1416	6.263098	CCTCA	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	1472	1476	6.263098	TGAGG	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	1556	1560	6.263098	CCTCA	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	1623	1627	6.263098	CCTCA	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	1922	1926	6.263098	TGAGG	3.90625	3.89624
cg0545033	DIP2C	GR-alpha [	1940	1944	6.263098	TGAGG	3.90625	3.89624
cg0270010	DIP2C	c-Myb [T0	1510	1517	6.259888	GAACTG	0.30518	0.30272
cg1850382	DIP2C	c-Myb [T0	764	771	6.259888	TGCAGT	0.30518	0.30272
cg1006492	DIP2C	c-Myb [T0	874	881	6.259888	TGCAGT	0.30518	0.30272
cg0545033	DIP2C	c-Myb [T0	804	811	6.259888	TGCAGT	0.30518	0.30272
cg1850382	DIP2C	NF-AT1 [	572	580	6.253078	CGTCTT	0.03815	0.03735
cg1006492	DIP2C	NF-AT1 [	682	690	6.253078	CGTCTT	0.03815	0.03735
cg0545033	DIP2C	NF-AT1 [	612	620	6.253078	CGTCTT	0.03815	0.03735
cg1850223	DIP2C	C/EBPalph	1573	1579	6.245236	TGCAAT	0.97656	0.91422
cg1850382	DIP2C	C/EBPalph	212	218	6.245236	TATTGA	0.97656	0.91422
cg1493188	DIP2C	C/EBPalph	1723	1729	6.245236	TTCAAT	0.97656	0.91422
cg1006492	DIP2C	C/EBPalph	322	328	6.245236	TATTGA	0.97656	0.91422
cg0545033	DIP2C	C/EBPalph	252	258	6.245236	TATTGA	0.97656	0.91422
cg1850223	DIP2C	IRF-1 [T0	101	109	6.24301	TTTCCTC	0.16785	0.16217

cg1146814	DIP2C	PEA3 [T0	8	16	6.227095	TGGATG	0.03815	0.03662
cg1493188	DIP2C	HNF-1B [	640	648	6.211503	TGTTATT	0.09918	0.08736
cg0270010	DIP2C	p53 [T006	1253	1259	6.188498	GCCGCC	0.61035	0.68483
cg0270010	DIP2C	p53 [T006	1902	1908	6.188498	GGGCGG	0.61035	0.68483
cg1146814	DIP2C	p53 [T006	1844	1850	6.188498	GCCGCC	0.61035	0.68483
cg1850223	DIP2C	RelA [T00	1794	1804	6.181091	GACGTT	0.01097	0.01155
cg1850382	DIP2C	SRY [T00	33	41	6.176442	AGCACA	0.15259	0.14742
cg1493188	DIP2C	SRY [T00	1190	1198	6.176442	CTTTGTC	0.15259	0.14742
cg1146814	DIP2C	SRY [T00	402	410	6.176442	GGACCA	0.15259	0.14742
cg1006492	DIP2C	SRY [T00	143	151	6.176442	AGCACA	0.15259	0.14742
cg0545033	DIP2C	SRY [T00	73	81	6.176442	AGCACA	0.15259	0.14742
cg1850223	DIP2C	c-Ets-1 [T	685	691	6.167515	TTTCCAC	0.36621	0.36174
cg1850223	DIP2C	c-Ets-1 [T	1745	1751	6.167515	TTTCCAC	0.36621	0.36174
cg1493188	DIP2C	c-Ets-1 [T	467	473	6.167515	TTTCCAC	0.36621	0.36174
cg1493188	DIP2C	c-Ets-1 [T	1794	1800	6.167515	GTGGAA	0.36621	0.36174
cg1850223	DIP2C	c-Jun [T00	527	533	6.152811	TTTGTCA	0.36621	0.34478
cg1493188	DIP2C	c-Jun [T00	1191	1197	6.152811	TTTGTCA	0.36621	0.34478
cg1850382	DIP2C	c-Myb [T0	387	394	6.12608	GCAAGT	0.21362	0.2053
cg1006492	DIP2C	c-Myb [T0	497	504	6.12608	GCAAGT	0.21362	0.2053
cg0545033	DIP2C	c-Myb [T0	427	434	6.12608	GCAAGT	0.21362	0.2053
cg1850382	DIP2C	RXR-alph	1399	1405	6.119461	CCTACC	0.73242	0.78318
cg1006492	DIP2C	RXR-alph	1509	1515	6.119461	CCTACC	0.73242	0.78318
cg0545033	DIP2C	RXR-alph	1439	1445	6.119461	CCTACC	0.73242	0.78318
cg0270010	DIP2C	GCF [T00	769	777	6.116216	GCGCAG	0.64087	0.72542
cg1850223	DIP2C	GCF [T00	954	962	6.116216	GCGCAG	0.64087	0.72542
cg1146814	DIP2C	GCF [T00	240	248	6.116216	GCGCAG	0.64087	0.72542
cg1146814	DIP2C	GCF [T00	1360	1368	6.116216	GCGCAG	0.64087	0.72542
cg0270010	DIP2C	AR [T000	1134	1142	6.110872	GGACAG	0.24414	0.25115
cg1146814	DIP2C	AR [T000	1725	1733	6.110872	GGACAG	0.24414	0.25115
cg0270010	DIP2C	c-Fos [T00	821	830	6.103724	ACAGTG	0.09155	0.09198
cg1850382	DIP2C	c-Fos [T00	868	877	6.103724	ACAGTG	0.09155	0.09198
cg1146814	DIP2C	c-Fos [T00	1412	1421	6.103724	ACAGTG	0.09155	0.09198
cg1006492	DIP2C	c-Fos [T00	978	987	6.103724	ACAGTG	0.09155	0.09198
cg0545033	DIP2C	c-Fos [T00	908	917	6.103724	ACAGTG	0.09155	0.09198
cg0270010	DIP2C	p53 [T006	1830	1836	6.095267	GGGCCA	0.61035	0.68483
cg0270010	DIP2C	GR-alpha [	203	207	6.055408	CCTGA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	216	220	6.055408	CCTGA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	308	312	6.055408	CCTGA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	476	480	6.055408	CCTGA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	621	625	6.055408	CCTGA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	654	658	6.055408	CCTGA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	798	802	6.055408	TCAGG	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	886	890	6.055408	CCTAA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	917	921	6.055408	CCTAA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	1309	1313	6.055408	CCTAA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	1335	1339	6.055408	CCTGA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	1377	1381	6.055408	CCTAA	3.90625	3.89835
cg0270010	DIP2C	GR-alpha [	1518	1522	6.055408	CCTGA	3.90625	3.89835

cg0270010	DIP2C	GR-alpha |	1740	1744	6.055408	TCAGG	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	107	111	6.055408	CCTAA	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	202	206	6.055408	CCTGA	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	516	520	6.055408	CCTAA	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	592	596	6.055408	TTAGG	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	912	916	6.055408	CCTGA	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1110	1114	6.055408	TCAGG	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1121	1125	6.055408	TTAGG	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1190	1194	6.055408	CCTGA	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1455	1459	6.055408	CCTGA	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1466	1470	6.055408	CCTGA	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1591	1595	6.055408	TCAGG	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1698	1702	6.055408	TCAGG	3.90625	3.89835
cg1850223	DIP2C	GR-alpha |	1732	1736	6.055408	TCAGG	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	770	774	6.055408	TCAGG	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	971	975	6.055408	TCAGG	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1006	1010	6.055408	CCTAA	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1285	1289	6.055408	TCAGG	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1381	1385	6.055408	CCTGA	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1518	1522	6.055408	TCAGG	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1531	1535	6.055408	TTAGG	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1688	1692	6.055408	CCTGA	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1738	1742	6.055408	TTAGG	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1898	1902	6.055408	CCTGA	3.90625	3.89835
cg1850382	DIP2C	GR-alpha |	1905	1909	6.055408	TCAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	534	538	6.055408	TTAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	618	622	6.055408	TCAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	738	742	6.055408	TCAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	752	756	6.055408	TTAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	894	898	6.055408	TCAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	1036	1040	6.055408	CCTGA	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	1120	1124	6.055408	CCTGA	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	1356	1360	6.055408	CCTAA	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	1515	1519	6.055408	TTAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	1741	1745	6.055408	TCAGG	3.90625	3.89835
cg1493188	DIP2C	GR-alpha |	1985	1989	6.055408	TTAGG	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	195	199	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	203	207	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	248	252	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	543	547	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	794	798	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	807	811	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	899	903	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	1067	1071	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	1212	1216	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	1245	1249	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	1389	1393	6.055408	TCAGG	3.90625	3.89835
cg1146814	DIP2C	GR-alpha |	1477	1481	6.055408	CCTAA	3.90625	3.89835

cg1146814	DIP2C	GR-alpha [	1508	1512	6.055408	CCTAA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha [	1900	1904	6.055408	CCTAA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha [	1926	1930	6.055408	CCTGA	3.90625	3.89835
cg1146814	DIP2C	GR-alpha [	1968	1972	6.055408	CCTAA	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	880	884	6.055408	TCAGG	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1081	1085	6.055408	TCAGG	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1116	1120	6.055408	CCTAA	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1395	1399	6.055408	TCAGG	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1491	1495	6.055408	CCTGA	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1628	1632	6.055408	TCAGG	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1641	1645	6.055408	TTAGG	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1798	1802	6.055408	CCTGA	3.90625	3.89835
cg1006492	DIP2C	GR-alpha [	1848	1852	6.055408	TTAGG	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	810	814	6.055408	TCAGG	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1011	1015	6.055408	TCAGG	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1046	1050	6.055408	CCTAA	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1325	1329	6.055408	TCAGG	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1421	1425	6.055408	CCTGA	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1558	1562	6.055408	TCAGG	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1571	1575	6.055408	TTAGG	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1728	1732	6.055408	CCTGA	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1778	1782	6.055408	TTAGG	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1938	1942	6.055408	CCTGA	3.90625	3.89835
cg0545033	DIP2C	GR-alpha [	1945	1949	6.055408	TCAGG	3.90625	3.89835
cg1850382	DIP2C	c-Myb [T0	1422	1429	6.04018	AAACTG	0.21362	0.2053
cg1006492	DIP2C	c-Myb [T0	1532	1539	6.04018	AAACTG	0.21362	0.2053
cg0545033	DIP2C	c-Myb [T0	1462	1469	6.04018	AAACTG	0.21362	0.2053
cg0270010	DIP2C	c-Ets-1 [T	1259	1265	6.039428	CTGGAA	0.36621	0.36174
cg0270010	DIP2C	c-Ets-1 [T	1454	1460	6.039428	CTGGAA	0.36621	0.36174
cg1850382	DIP2C	c-Ets-1 [T	576	582	6.039428	TTTCCA	0.36621	0.36174
cg1146814	DIP2C	c-Ets-1 [T	89	95	6.039428	CTGGAA	0.36621	0.36174
cg1146814	DIP2C	c-Ets-1 [T	1850	1856	6.039428	CTGGAA	0.36621	0.36174
cg1006492	DIP2C	c-Ets-1 [T	686	692	6.039428	TTTCCA	0.36621	0.36174
cg0545033	DIP2C	c-Ets-1 [T	616	622	6.039428	TTTCCA	0.36621	0.36174
cg1850223	DIP2C	C/EBPalph	95	101	5.996794	CATTGT	0.97656	0.91422
cg0270010	DIP2C	RXR-alpha	347	353	5.937582	GGCACC	0.73242	0.78318
cg1850223	DIP2C	RXR-alpha	123	129	5.937582	GTCACC	0.73242	0.78318
cg1850223	DIP2C	RXR-alpha	706	712	5.937582	GGCACC	0.73242	0.78318
cg1850382	DIP2C	RXR-alpha	1627	1633	5.937582	GGGTGC	0.73242	0.78318
cg1146814	DIP2C	RXR-alpha	938	944	5.937582	GGCACC	0.73242	0.78318
cg1006492	DIP2C	RXR-alpha	1737	1743	5.937582	GGGTGC	0.73242	0.78318
cg0545033	DIP2C	RXR-alpha	1667	1673	5.937582	GGGTGC	0.73242	0.78318
cg0270010	DIP2C	GCF [T00	514	522	5.917256	CGGCGG	0.64087	0.72542
cg1493188	DIP2C	GCF [T00	34	42	5.917256	GCGCTG	0.64087	0.72542
cg1493188	DIP2C	GCF [T00	83	91	5.917256	GCGCTG	0.64087	0.72542
cg1493188	DIP2C	GCF [T00	279	287	5.917256	GCGCTG	0.64087	0.72542
cg1493188	DIP2C	GCF [T00	328	336	5.917256	GCGCTG	0.64087	0.72542
cg1493188	DIP2C	GCF [T00	377	385	5.917256	GCGCTG	0.64087	0.72542

cg1493188	DIP2C	GCF [T00	1707	1715	5.917256	CCACGG	0.64087	0.72542
cg1146814	DIP2C	GCF [T00	551	559	5.917256	AGGCAG	0.64087	0.72542
cg1146814	DIP2C	GCF [T00	1105	1113	5.917256	CGGCGG	0.64087	0.72542
cg1146814	DIP2C	AhR [T01	449	459	5.89925	CTCACG	0.0248	0.02643
cg1850223	DIP2C	HOXD9 [T	291	300	5.898575	AATAAG	0.05722	0.04686
cg1850223	DIP2C	HOXD10 [	291	300	5.898575	AATAAG	0.05722	0.04686
cg1850382	DIP2C	p53 [T006	41	47	5.883561	GGGCCG	0.61035	0.68483
cg1006492	DIP2C	p53 [T006	151	157	5.883561	GGGCCG	0.61035	0.68483
cg0545033	DIP2C	p53 [T006	81	87	5.883561	GGGCCG	0.61035	0.68483
cg027001	DIP2C	STAT4 [T	1130	1135	5.882353	GGAAGG	0.48828	0.51201
cg1850223	DIP2C	STAT4 [T	187	192	5.882353	GGAAGG	0.48828	0.51201
cg1850382	DIP2C	STAT4 [T	470	475	5.882353	GGAAGG	0.48828	0.51201
cg1850382	DIP2C	STAT4 [T	475	480	5.882353	GGAAGG	0.48828	0.51201
cg1850382	DIP2C	STAT4 [T	489	494	5.882353	GGAAGG	0.48828	0.51201
cg1850382	DIP2C	STAT4 [T	1540	1545	5.882353	GGAAGG	0.48828	0.51201
cg1493188	DIP2C	STAT4 [T	1263	1268	5.882353	CCTTCC	0.48828	0.51201
cg1493188	DIP2C	STAT4 [T	1392	1397	5.882353	GGAAGG	0.48828	0.51201
cg1493188	DIP2C	STAT4 [T	1915	1920	5.882353	CCTTCC	0.48828	0.51201
cg1146814	DIP2C	STAT4 [T	333	338	5.882353	GGAAGG	0.48828	0.51201
cg1146814	DIP2C	STAT4 [T	548	553	5.882353	GGAAGG	0.48828	0.51201
cg1146814	DIP2C	STAT4 [T	1721	1726	5.882353	GGAAGG	0.48828	0.51201
cg1006492	DIP2C	STAT4 [T	580	585	5.882353	GGAAGG	0.48828	0.51201
cg1006492	DIP2C	STAT4 [T	585	590	5.882353	GGAAGG	0.48828	0.51201
cg1006492	DIP2C	STAT4 [T	599	604	5.882353	GGAAGG	0.48828	0.51201
cg1006492	DIP2C	STAT4 [T	1650	1655	5.882353	GGAAGG	0.48828	0.51201
cg0545033	DIP2C	STAT4 [T	510	515	5.882353	GGAAGG	0.48828	0.51201
cg0545033	DIP2C	STAT4 [T	515	520	5.882353	GGAAGG	0.48828	0.51201
cg0545033	DIP2C	STAT4 [T	529	534	5.882353	GGAAGG	0.48828	0.51201
cg0545033	DIP2C	STAT4 [T	1580	1585	5.882353	GGAAGG	0.48828	0.51201
cg027001	DIP2C	E2F-1 [T0	1772	1779	5.846171	GCGGAA	0.18311	0.19383
cg1850223	DIP2C	c-Ets-1 [T	740	746	5.814485	CTTCCC	0.36621	0.36174
cg1493188	DIP2C	c-Ets-1 [T	1390	1396	5.814485	TGGGAA	0.36621	0.36174
cg027001	DIP2C	STAT1bet	1452	1461	5.796867	CCCTGG	0.1545	0.14881
cg1850223	DIP2C	STAT1bet	1186	1195	5.796867	ATTTCCT	0.1545	0.14881
cg1850382	DIP2C	c-Jun [T00	1330	1336	5.783074	TGACTT	0.36621	0.34478
cg1006492	DIP2C	c-Jun [T00	1440	1446	5.783074	TGACTT	0.36621	0.34478
cg0545033	DIP2C	c-Jun [T00	1370	1376	5.783074	TGACTT	0.36621	0.34478
cg1850223	DIP2C	C/EBPalp	537	543	5.781231	TATTGT	0.97656	0.91422
cg1850382	DIP2C	C/EBPalp	1127	1133	5.781231	TATTGT	0.97656	0.91422
cg1006492	DIP2C	C/EBPalp	1237	1243	5.781231	TATTGT	0.97656	0.91422
cg0545033	DIP2C	C/EBPalp	1167	1173	5.781231	TATTGT	0.97656	0.91422
cg1493188	DIP2C	PU.1 [T02	1114	1126	5.775822	TCACTT	0.00432	0.00425
cg1006492	DIP2C	NF-AT1 [	72	80	5.77403	CTTCTTT	0.06866	0.06621
cg0545033	DIP2C	NF-AT1 [	2	10	5.77403	CTTCTTT	0.06866	0.06621
cg027001	DIP2C	VDR [T00	1607	1615	5.771401	TCTGTG	0.42725	0.41266
cg027001	DIP2C	VDR [T00	1821	1829	5.771401	GTTCAT	0.42725	0.41266
cg1850223	DIP2C	VDR [T00	108	116	5.771401	CTAATG	0.42725	0.41266
cg1850223	DIP2C	VDR [T00	340	348	5.771401	GTTCAC	0.42725	0.41266

cg1850382	DIP2C	VDR [T00	1170	1178	5.771401	GTTCAA	0.42725	0.41266
cg1006492	DIP2C	VDR [T00	1280	1288	5.771401	GTTCAA	0.42725	0.41266
cg0545033	DIP2C	VDR [T00	1210	1218	5.771401	GTTCAA	0.42725	0.41266
cg1850223	DIP2C	IRF-1 [T0	511	519	5.770812	TTTCCC	0.16785	0.16217
cg0270010	DIP2C	AR [T000	1501	1509	5.754178	GGACAC	0.24414	0.25115
cg0270010	DIP2C	PXR-1:RX	1818	1825	5.726524	GTGGTT	0.06104	0.06086
cg1850382	DIP2C	RXR-alph	587	593	5.715466	AACACC	0.61035	0.65415
cg1006492	DIP2C	RXR-alph	697	703	5.715466	AACACC	0.61035	0.65415
cg0545033	DIP2C	RXR-alph	627	633	5.715466	AACACC	0.61035	0.65415
cg1850223	DIP2C	HNF-1C [	433	441	5.695506	GTATTT	0.07629	0.06785
cg0270010	DIP2C	ENKTF-1	276	283	5.687009	CTGAGC	0.73242	0.76357
cg0270010	DIP2C	ENKTF-1	830	837	5.687009	CAGAGC	0.73242	0.76357
cg0270010	DIP2C	ENKTF-1	1069	1076	5.687009	CTGTGC	0.73242	0.76357
cg0270010	DIP2C	ENKTF-1	1167	1174	5.687009	CTAAGC	0.73242	0.76357
cg0270010	DIP2C	ENKTF-1	1803	1810	5.687009	CAGAGC	0.73242	0.76357
cg0270010	DIP2C	ENKTF-1	1828	1835	5.687009	CTGGGC	0.73242	0.76357
cg1850223	DIP2C	ENKTF-1	92	99	5.687009	TGGCAT	0.73242	0.76357
cg1850382	DIP2C	ENKTF-1	1652	1659	5.687009	CAAAGC	0.73242	0.76357
cg1850382	DIP2C	ENKTF-1	1725	1732	5.687009	CTGGGC	0.73242	0.76357
cg1493188	DIP2C	ENKTF-1	1324	1331	5.687009	CTGTGC	0.73242	0.76357
cg1493188	DIP2C	ENKTF-1	1344	1351	5.687009	CAAAGC	0.73242	0.76357
cg1493188	DIP2C	ENKTF-1	1584	1591	5.687009	TAACGC	0.73242	0.76357
cg1146814	DIP2C	ENKTF-1	867	874	5.687009	CTGAGC	0.73242	0.76357
cg1146814	DIP2C	ENKTF-1	1421	1428	5.687009	CAGAGC	0.73242	0.76357
cg1146814	DIP2C	ENKTF-1	1660	1667	5.687009	CTGTGC	0.73242	0.76357
cg1146814	DIP2C	ENKTF-1	1758	1765	5.687009	CTAAGC	0.73242	0.76357
cg1006492	DIP2C	ENKTF-1	1762	1769	5.687009	CAAAGC	0.73242	0.76357
cg1006492	DIP2C	ENKTF-1	1835	1842	5.687009	CTGGGC	0.73242	0.76357
cg0545033	DIP2C	ENKTF-1	1692	1699	5.687009	CAAAGC	0.73242	0.76357
cg0545033	DIP2C	ENKTF-1	1765	1772	5.687009	CTGGGC	0.73242	0.76357
cg1850382	DIP2C	c-Ets-1 [T	473	479	5.686398	AGGGAA	0.36621	0.38732
cg1006492	DIP2C	c-Ets-1 [T	583	589	5.686398	AGGGAA	0.36621	0.38732
cg0545033	DIP2C	c-Ets-1 [T	513	519	5.686398	AGGGAA	0.36621	0.38732
cg1146814	DIP2C	IRF-1 [T0	87	95	5.65977	ATCTGG	0.22888	0.21959
cg1493188	DIP2C	USF1 [T0	1735	1744	5.632041	CACGTG	0.04578	0.04717
cg1146814	DIP2C	NF-1 [T00	401	408	5.626299	GGGACC	0.24414	0.25051
cg1493188	DIP2C	c-Ets-2 [T	1672	1680	5.624023	TTCCTAT	0.01526	0.01376
cg1493188	DIP2C	AhR:Arnt	1807	1816	5.620669	GCACGC	0.0515	0.05997
cg1850223	DIP2C	HNF-1A [	1542	1549	5.610392	CACTTA	0.24414	0.23087
cg0270010	DIP2C	AR [T000	665	673	5.597291	GCCGTG	0.05341	0.05856
cg1146814	DIP2C	AR [T000	1256	1264	5.597291	GCCGTG	0.05341	0.05856
cg0270010	DIP2C	c-Jun [T00	1674	1680	5.590308	TGACAC	0.48828	0.49294
cg1493188	DIP2C	c-Jun [T00	1522	1528	5.587335	TAGGTC	0.48828	0.49294
cg1850223	DIP2C	NF-kappa	1793	1803	5.583518	AGACGT	0.02384	0.02626
cg1850223	DIP2C	AP-2alpha	603	608	5.568965	GCCTAT	0.48828	0.48642
cg1850382	DIP2C	AP-2alpha	1025	1030	5.568965	GCCTAT	0.48828	0.48642
cg1493188	DIP2C	AP-2alpha	1224	1229	5.568965	ATAGGC	0.48828	0.48642
cg1006492	DIP2C	AP-2alpha	1135	1140	5.568965	GCCTAT	0.48828	0.48642

cg0545033	DIP2C	AP-2alpha	1065	1070	5.568965	GCCTAT	0.48828	0.48642
cg027001	DIP2C	NFI/CTF [	1833	1840	5.558661	CCAATC	0.54932	0.55504
cg1493188	DIP2C	NFI/CTF [	543	550	5.558661	AGGTTT	0.54932	0.55504
cg027001	DIP2C	c-Ets-1 [T	1128	1134	5.558311	GGGGAA	0.36621	0.38732
cg1850223	DIP2C	c-Ets-1 [T	966	972	5.558311	CTTCCC	0.36621	0.38732
cg1146814	DIP2C	c-Ets-1 [T	331	337	5.558311	GGGGAA	0.36621	0.38732
cg1146814	DIP2C	c-Ets-1 [T	1719	1725	5.558311	GGGGAA	0.36621	0.38732
cg027001	DIP2C	c-Myb [T0	1264	1271	5.55549	AAACTG	0.09155	0.08971
cg1146814	DIP2C	c-Myb [T0	1855	1862	5.55549	AAACTG	0.09155	0.08971
cg027001	DIP2C	TFIID [T0	885	891	5.544826	TCCTAA	0.73242	0.65314
cg027001	DIP2C	TFIID [T0	916	922	5.544826	TCCTAA	0.73242	0.65314
cg1850223	DIP2C	TFIID [T0	61	67	5.544826	TTTAAC	0.73242	0.65314
cg1850223	DIP2C	TFIID [T0	429	435	5.544826	TTTAGT	0.73242	0.65314
cg1850223	DIP2C	TFIID [T0	759	765	5.544826	TGATAA	0.73242	0.65314
cg1850223	DIP2C	TFIID [T0	1208	1214	5.544826	TTTATC	0.73242	0.65314
cg1850223	DIP2C	Pax-5 [T0	1594	1600	5.544826	GGGCTA	0.73242	0.79
cg1850382	DIP2C	TFIID [T0	307	313	5.544826	TTTACC	0.73242	0.65314
cg1850382	DIP2C	TFIID [T0	821	827	5.544826	TTCTAA	0.73242	0.65314
cg1850382	DIP2C	TFIID [T0	1737	1743	5.544826	TTTAGG	0.73242	0.65314
cg1850382	DIP2C	TFIID [T0	1951	1957	5.544826	TACTAA	0.73242	0.65314
cg1850382	DIP2C	Pax-5 [T0	1727	1733	5.544826	GGGCCA	0.73242	0.79
cg1493188	DIP2C	TFIID [T0	678	684	5.544826	TTCTAA	0.73242	0.65314
cg1493188	DIP2C	TFIID [T0	1102	1108	5.544826	TACTAA	0.73242	0.65314
cg1493188	DIP2C	TFIID [T0	1984	1990	5.544826	TTTAGG	0.73242	0.65314
cg1146814	DIP2C	TFIID [T0	1476	1482	5.544826	TCCTAA	0.73242	0.65314
cg1146814	DIP2C	TFIID [T0	1507	1513	5.544826	TCCTAA	0.73242	0.65314
cg1146814	DIP2C	Pax-5 [T0	555	561	5.544826	AGCGCC	0.73242	0.79
cg1006492	DIP2C	TFIID [T0	417	423	5.544826	TTTACC	0.73242	0.65314
cg1006492	DIP2C	TFIID [T0	931	937	5.544826	TTCTAA	0.73242	0.65314
cg1006492	DIP2C	TFIID [T0	1847	1853	5.544826	TTTAGG	0.73242	0.65314
cg1006492	DIP2C	Pax-5 [T0	1837	1843	5.544826	GGGCCA	0.73242	0.79
cg0545033	DIP2C	TFIID [T0	347	353	5.544826	TTTACC	0.73242	0.65314
cg0545033	DIP2C	TFIID [T0	861	867	5.544826	TTCTAA	0.73242	0.65314
cg0545033	DIP2C	TFIID [T0	1777	1783	5.544826	TTTAGG	0.73242	0.65314
cg0545033	DIP2C	TFIID [T0	1991	1997	5.544826	TACTAA	0.73242	0.65314
cg0545033	DIP2C	Pax-5 [T0	1767	1773	5.544826	GGGCCA	0.73242	0.79
cg1493188	DIP2C	NF-AT1 [	463	472	5.512555	CCCGTT	0.05913	0.05666
cg1493188	DIP2C	NF-AT1 [	929	938	5.512555	AGTGTT	0.05913	0.05666
cg027001	DIP2C	p53 [T006	1670	1676	5.508538	GGGCTG	0.61035	0.65765
cg1850223	DIP2C	p53 [T006	768	774	5.508538	TCAGCC	0.61035	0.65765
cg1850223	DIP2C	p53 [T006	1632	1638	5.508538	TAAGCC	0.61035	0.65765
cg1850382	DIP2C	p53 [T006	182	188	5.508538	GGGCTT	0.61035	0.65765
cg1006492	DIP2C	p53 [T006	292	298	5.508538	GGGCTT	0.61035	0.65765
cg0545033	DIP2C	p53 [T006	222	228	5.508538	GGGCTT	0.61035	0.65765
cg1850223	DIP2C	E2F-1 [T0	781	788	5.476857	GCGGGG	0.03052	0.03364
cg1146814	DIP2C	E2F-1 [T0	329	336	5.476857	GCGGGG	0.03052	0.03364
cg1850382	DIP2C	HNF-1A [	1148	1155	5.466509	CTCTTA	0.24414	0.23087
cg1006492	DIP2C	HNF-1A [	1258	1265	5.466509	CTCTTA	0.24414	0.23087

cg0545033	DIP2C	HNF-1A [	1188	1195	5.466509	CTCTTA	0.24414	0.23087
cg1850223	DIP2C	C/EBPalp	253	259	5.455853	ATCAAT	0.73242	0.68229
cg1493188	DIP2C	C/EBPalp	1411	1417	5.455853	CATTGC	0.73242	0.68229
cg0270010	DIP2C	c-Ets-1 [T	791	797	5.430224	CTTCCC	0.36621	0.38732
cg1850223	DIP2C	c-Ets-1 [T	1910	1916	5.430224	CGGGAA	0.36621	0.38732
cg1850382	DIP2C	c-Ets-1 [T	468	474	5.430224	CGGGAA	0.36621	0.38732
cg1850382	DIP2C	c-Ets-1 [T	984	990	5.430224	CGGGAA	0.36621	0.38732
cg1146814	DIP2C	c-Ets-1 [T	1382	1388	5.430224	CTTCCC	0.36621	0.38732
cg1006492	DIP2C	c-Ets-1 [T	578	584	5.430224	CGGGAA	0.36621	0.38732
cg1006492	DIP2C	c-Ets-1 [T	1094	1100	5.430224	CGGGAA	0.36621	0.38732
cg0545033	DIP2C	c-Ets-1 [T	508	514	5.430224	CGGGAA	0.36621	0.38732
cg0545033	DIP2C	c-Ets-1 [T	1024	1030	5.430224	CGGGAA	0.36621	0.38732
cg0270010	DIP2C	p53 [T006	112	118	5.39549	GGGCCC	0.61035	0.65765
cg1850382	DIP2C	p53 [T006	1000	1006	5.39549	CGGGCC	0.61035	0.65765
cg1146814	DIP2C	p53 [T006	703	709	5.39549	GGGCCC	0.61035	0.65765
cg1006492	DIP2C	p53 [T006	1110	1116	5.39549	CGGGCC	0.61035	0.65765
cg0545033	DIP2C	p53 [T006	1040	1046	5.39549	CGGGCC	0.61035	0.65765
cg1850382	DIP2C	C/EBPalp	310	316	5.38654	ACCAAT	0.73242	0.68229
cg1006492	DIP2C	C/EBPalp	420	426	5.38654	ACCAAT	0.73242	0.68229
cg0545033	DIP2C	C/EBPalp	350	356	5.38654	ACCAAT	0.73242	0.68229
cg1850223	DIP2C	NF-1 [T00	769	776	5.377909	CAGCCC	0.24414	0.25051
cg1850382	DIP2C	NF-1 [T00	69	76	5.377909	CAGCCC	0.24414	0.25051
cg1146814	DIP2C	NF-1 [T00	230	237	5.377909	CAGCCC	0.24414	0.25051
cg1006492	DIP2C	NF-1 [T00	179	186	5.377909	CAGCCC	0.24414	0.25051
cg0545033	DIP2C	NF-1 [T00	109	116	5.377909	CAGCCC	0.24414	0.25051
cg1493188	DIP2C	RAR-beta	628	637	5.370617	TGGGTT	0.15259	0.15813
cg1850223	DIP2C	NF-AT1 [	1124	1132	5.354841	GGAAAT	0.03815	0.03643
cg0270010	DIP2C	IRF-1 [T0	1758	1766	5.351774	GATGGG	0.22888	0.21959
cg1850223	DIP2C	MEF-2A [	135	145	5.321562	ACCTAT	0.02003	0.01733
cg1850382	DIP2C	MEF-2A [	1655	1665	5.321562	AGCCAC	0.02003	0.01733
cg1006492	DIP2C	MEF-2A [	1765	1775	5.321562	AGCCAC	0.02003	0.01733
cg0545033	DIP2C	MEF-2A [	1695	1705	5.321562	AGCCAC	0.02003	0.01733
cg0270010	DIP2C	PPAR-alp	1765	1775	5.285833	AACTGG	0.03529	0.03856
cg0270010	DIP2C	RXR-alph	437	443	5.271235	GGGTGG	0.61035	0.65415
cg0270010	DIP2C	RXR-alph	1893	1899	5.271235	GGGTGG	0.61035	0.65415
cg1850382	DIP2C	RXR-alph	87	93	5.271235	GCAACC	0.61035	0.65415
cg1850382	DIP2C	RXR-alph	288	294	5.271235	TCTACC	0.61035	0.65415
cg1850382	DIP2C	RXR-alph	835	841	5.271235	ACGACC	0.61035	0.65415
cg1493188	DIP2C	RXR-alph	621	627	5.271235	GGGTAG	0.61035	0.65415
cg1493188	DIP2C	RXR-alph	1258	1264	5.271235	CCCACC	0.61035	0.65415
cg1146814	DIP2C	RXR-alph	1028	1034	5.271235	GGGTGG	0.61035	0.65415
cg1006492	DIP2C	RXR-alph	53	59	5.271235	TCTACC	0.61035	0.65415
cg1006492	DIP2C	RXR-alph	197	203	5.271235	GCAACC	0.61035	0.65415
cg1006492	DIP2C	RXR-alph	398	404	5.271235	TCTACC	0.61035	0.65415
cg1006492	DIP2C	RXR-alph	945	951	5.271235	ACGACC	0.61035	0.65415
cg0545033	DIP2C	RXR-alph	127	133	5.271235	GCAACC	0.61035	0.65415
cg0545033	DIP2C	RXR-alph	328	334	5.271235	TCTACC	0.61035	0.65415
cg0545033	DIP2C	RXR-alph	875	881	5.271235	ACGACC	0.61035	0.65415

cg1850382	DIP2C	ETF [T002	1629	1639	5.246906	GTGCCG	0.02861	0.03569
cg1146814	DIP2C	ETF [T002	278	288	5.246906	GCCCCC	0.02861	0.03569
cg1006492	DIP2C	ETF [T002	1739	1749	5.246906	GTGCCG	0.02861	0.03569
cg0545033	DIP2C	ETF [T002	1669	1679	5.246906	GTGCCG	0.02861	0.03569
cg1493188	DIP2C	C/EBPalph	1632	1638	5.240291	TATTGA	0.97656	0.90302
cg1493188	DIP2C	C/EBPalph	1663	1669	5.240291	TATTGC	0.97656	0.90302
cg1850223	DIP2C	POU2F2 (	256	266	5.23012	AATGTA	0.02432	0.02134
cg1850223	DIP2C	POU2F2 (	846	856	5.23012	ACTATA	0.02432	0.02134
cg1850382	DIP2C	GR [T050	74	80	5.207533	CAAAAC	0.24414	0.24013
cg1850382	DIP2C	GR [T050	734	740	5.207533	CAAAAC	0.24414	0.24013
cg1850382	DIP2C	GR [T050	1705	1711	5.207533	CAAAAC	0.24414	0.24013
cg1493188	DIP2C	GR [T050	937	943	5.207533	CAAAGA	0.24414	0.24013
cg1006492	DIP2C	GR [T050	184	190	5.207533	CAAAAC	0.24414	0.24013
cg1006492	DIP2C	GR [T050	844	850	5.207533	CAAAAC	0.24414	0.24013
cg1006492	DIP2C	GR [T050	1815	1821	5.207533	CAAAAC	0.24414	0.24013
cg0545033	DIP2C	GR [T050	114	120	5.207533	CAAAAC	0.24414	0.24013
cg0545033	DIP2C	GR [T050	774	780	5.207533	CAAAAC	0.24414	0.24013
cg0545033	DIP2C	GR [T050	1745	1751	5.207533	CAAAAC	0.24414	0.24013
cg027001	DIP2C	c-Jun [T00	88	94	5.193102	GAAGTC	0.61035	0.60573
cg027001	DIP2C	c-Jun [T00	1880	1886	5.193102	TGACTT	0.61035	0.60573
cg1850382	DIP2C	c-Jun [T00	1577	1583	5.193102	TGACTT	0.61035	0.60573
cg1146814	DIP2C	c-Jun [T00	679	685	5.193102	GAAGTC	0.61035	0.60573
cg1006492	DIP2C	c-Jun [T00	1687	1693	5.193102	TGACTT	0.61035	0.60573
cg0545033	DIP2C	c-Jun [T00	1617	1623	5.193102	TGACTT	0.61035	0.60573
cg1493188	DIP2C	c-Ets-2 [T	1265	1273	5.162974	TTCCTT	0.13733	0.13279
cg027001	DIP2C	p53 [T006	1770	1776	5.133514	GGGCGG	0.48828	0.53921
cg1493188	DIP2C	p53 [T006	1004	1010	5.133514	TCCGCC	0.48828	0.53921
cg1850382	DIP2C	EBF [T05	697	707	5.130966	GGCCCT	0.02289	0.02569
cg1006492	DIP2C	EBF [T05	807	817	5.130966	GGCCCT	0.02289	0.02569
cg0545033	DIP2C	EBF [T05	737	747	5.130966	GGCCCT	0.02289	0.02569
cg027001	DIP2C	AP-2alpha	42	47	5.100982	GCCTTT	0.97656	0.97517
cg027001	DIP2C	AP-2alpha	994	999	5.100982	AAAGGC	0.97656	0.97517
cg027001	DIP2C	AP-2alpha	1019	1024	5.100982	GCCTTT	0.97656	0.97517
cg027001	DIP2C	AP-2alpha	1249	1254	5.100982	AAAGGC	0.97656	0.97517
cg027001	DIP2C	AP-2alpha	1919	1924	5.100982	AAAGGC	0.97656	0.97517
cg1850223	DIP2C	AP-2alpha	788	793	5.100982	AAAGGC	0.97656	0.97517
cg1850223	DIP2C	AP-2alpha	1727	1732	5.100982	GCCTTT	0.97656	0.97517
cg1850382	DIP2C	AP-2alpha	638	643	5.100982	AAAGGC	0.97656	0.97517
cg1146814	DIP2C	AP-2alpha	633	638	5.100982	GCCTTT	0.97656	0.97517
cg1146814	DIP2C	AP-2alpha	1585	1590	5.100982	AAAGGC	0.97656	0.97517
cg1146814	DIP2C	AP-2alpha	1610	1615	5.100982	GCCTTT	0.97656	0.97517
cg1146814	DIP2C	AP-2alpha	1840	1845	5.100982	AAAGGC	0.97656	0.97517
cg1006492	DIP2C	AP-2alpha	748	753	5.100982	AAAGGC	0.97656	0.97517
cg0545033	DIP2C	AP-2alpha	678	683	5.100982	AAAGGC	0.97656	0.97517
cg1850223	DIP2C	RXR-alpha	1523	1529	5.089356	ATCACC	0.48828	0.51407
cg027001	DIP2C	USF2 [T0	615	624	5.052423	CAGGTG	0.103	0.10797
cg1146814	DIP2C	USF2 [T0	1206	1215	5.052423	CAGGTG	0.103	0.10797
cg027001	DIP2C	GR-beta [	879	883	5.042296	AATAC	3.90625	3.7093

cg0270010	DIP2C	GR-beta [T	1835	1839	5.042296	AATCC	3.90625	3.7093
cg0270010	DIP2C	GR-beta [T	1872	1876	5.042296	AATCC	3.90625	3.7093
cg1850223	DIP2C	GR-beta [T	164	168	5.042296	AATAC	3.90625	3.7093
cg1850223	DIP2C	GR-beta [T	433	437	5.042296	GTATT	3.90625	3.7093
cg1850382	DIP2C	GR-beta [T	882	886	5.042296	AATCC	3.90625	3.7093
cg1850382	DIP2C	GR-beta [T	1805	1809	5.042296	GTATT	3.90625	3.7093
cg1850382	DIP2C	GR-beta [T	1861	1865	5.042296	AATCC	3.90625	3.7093
cg1850382	DIP2C	GR-beta [T	1958	1962	5.042296	AATAC	3.90625	3.7093
cg1493188	DIP2C	GR-beta [T	660	664	5.042296	GTATT	3.90625	3.7093
cg1493188	DIP2C	GR-beta [T	1478	1482	5.042296	AATAC	3.90625	3.7093
cg1493188	DIP2C	GR-beta [T	1606	1610	5.042296	AATAC	3.90625	3.7093
cg1493188	DIP2C	GR-beta [T	1683	1687	5.042296	AATAC	3.90625	3.7093
cg1493188	DIP2C	GR-beta [T	1886	1890	5.042296	GTATT	3.90625	3.7093
cg1493188	DIP2C	GR-beta [T	1973	1977	5.042296	AATCC	3.90625	3.7093
cg1146814	DIP2C	GR-beta [T	1470	1474	5.042296	AATAC	3.90625	3.7093
cg1006492	DIP2C	GR-beta [T	992	996	5.042296	AATCC	3.90625	3.7093
cg1006492	DIP2C	GR-beta [T	1915	1919	5.042296	GTATT	3.90625	3.7093
cg1006492	DIP2C	GR-beta [T	1971	1975	5.042296	AATCC	3.90625	3.7093
cg0545033	DIP2C	GR-beta [T	922	926	5.042296	AATCC	3.90625	3.7093
cg0545033	DIP2C	GR-beta [T	1845	1849	5.042296	GTATT	3.90625	3.7093
cg0545033	DIP2C	GR-beta [T	1901	1905	5.042296	AATCC	3.90625	3.7093
cg0270010	DIP2C	c-Ets-1 [T0	85	91	5.038739	TTGGAA	0.48828	0.48026
cg1493188	DIP2C	c-Ets-1 [T0	1462	1468	5.038739	CTTCCAA	0.48828	0.48026
cg1146814	DIP2C	c-Ets-1 [T0	676	682	5.038739	TTGGAA	0.48828	0.48026
cg1493188	DIP2C	HOXD9 [T	637	646	5.035116	GACTGTT	0.00763	0.00669
cg1493188	DIP2C	HOXD10 [	637	646	5.035116	GACTGTT	0.00763	0.00669
cg0270010	DIP2C	PXR-1:RX	321	328	5.032032	TGAACC	0.12207	0.11843
cg1146814	DIP2C	PXR-1:RX	912	919	5.032032	TGAACC	0.12207	0.11843
cg0270010	DIP2C	C/EBPalph	1199	1205	5.024728	TTCAAT	0.97656	0.90302
cg1493188	DIP2C	C/EBPalph	1574	1580	5.024728	GATTGCA	0.97656	0.90302
cg1146814	DIP2C	C/EBPalph	1790	1796	5.024728	TTCAAT	0.97656	0.90302
cg1850382	DIP2C	NFI/CTF [	534	541	5.021086	CCAAAG	0.24414	0.25666
cg1006492	DIP2C	NFI/CTF [	644	651	5.021086	CCAAAG	0.24414	0.25666
cg0545033	DIP2C	NFI/CTF [	574	581	5.021086	CCAAAG	0.24414	0.25666
cg1146814	DIP2C	p53 [T006	148	154	5.020467	GGGCTC	0.48828	0.53921
cg1850223	DIP2C	c-Jun [T00	356	362	5.000337	GGCGTCA	0.61035	0.60573
cg1850223	DIP2C	c-Jun [T00	1457	1463	5.000337	TGACGC	0.61035	0.60573
cg1146814	DIP2C	NF-AT2 [T	91	100	4.979362	GGAAAA	0.03815	0.03519
cg1850223	DIP2C	IRF-1 [T0	1384	1392	4.968836	TTTCCCC	0.1297	0.12724
cg1006492	DIP2C	IRF-1 [T0	76	84	4.968836	TTTCCCC	0.1297	0.12724
cg0545033	DIP2C	IRF-1 [T0	6	14	4.968836	TTTCCCC	0.1297	0.12724
cg1850223	DIP2C	IRF-1 [T0	668	676	4.963725	CGAAGG	0.1297	0.12724
cg0270010	DIP2C	PXR-1:RX	1272	1279	4.90845	TGAACCT	0.12207	0.11843
cg1146814	DIP2C	PXR-1:RX	1863	1870	4.90845	TGAACCT	0.12207	0.11843
cg1850223	DIP2C	XBP-1 [T0	945	950	4.894955	ATGCCG	0.97656	0.99839
cg1850223	DIP2C	XBP-1 [T0	1583	1588	4.894955	ATGCCT	0.97656	0.99839
cg1493188	DIP2C	XBP-1 [T0	793	798	4.894955	AGGCAT	0.97656	0.99839
cg1493188	DIP2C	XBP-1 [T0	1138	1143	4.894955	ATGCCT	0.97656	0.99839

cg1493188	DIP2C	XBP-1 [T	1965	1970	4.894955	ATGCCT	0.97656	0.99839
cg027001	DIP2C	AP-2alpha	1308	1313	4.890408	GCCTAA	0.97656	0.97517
cg1850382	DIP2C	AP-2alpha	1531	1536	4.890408	TTAGGC	0.97656	0.97517
cg1146814	DIP2C	AP-2alpha	1899	1904	4.890408	GCCTAA	0.97656	0.97517
cg1006492	DIP2C	AP-2alpha	1641	1646	4.890408	TTAGGC	0.97656	0.97517
cg0545033	DIP2C	AP-2alpha	1571	1576	4.890408	TTAGGC	0.97656	0.97517
cg1850223	DIP2C	c-Jun [T00	80	86	4.883696	TGACGT	0.61035	0.60573
cg1493188	DIP2C	c-Jun [T00	1220	1226	4.883696	TGACAT	0.61035	0.60573
cg1146814	DIP2C	NF-1 [T00	321	328	4.880836	GGTCCC	0.24414	0.24345
cg027001	DIP2C	RXR-alph	1743	1749	4.86724	GGGTCT	0.48828	0.51407
cg1850382	DIP2C	RXR-alph	60	66	4.86724	CATACC	0.48828	0.51407
cg1006492	DIP2C	RXR-alph	170	176	4.86724	CATACC	0.48828	0.51407
cg0545033	DIP2C	RXR-alph	100	106	4.86724	CATACC	0.48828	0.51407
cg1850223	DIP2C	NF-Y [T0	1428	1435	4.867193	GCCCCA	0.36621	0.35921
cg1850382	DIP2C	HNF-3alp	189	196	4.842999	TTAAAA	0.09155	0.07438
cg1493188	DIP2C	HNF-3alp	525	532	4.842999	TTTAAA	0.09155	0.07438
cg1493188	DIP2C	HNF-3alp	1887	1894	4.842999	TATTTA	0.09155	0.07438
cg1006492	DIP2C	HNF-3alp	299	306	4.842999	TTAAAA	0.09155	0.07438
cg0545033	DIP2C	HNF-3alp	229	236	4.842999	TTAAAA	0.09155	0.07438
cg1850382	DIP2C	p53 [T006	330	336	4.786849	GGGCAC	0.48828	0.53921
cg1006492	DIP2C	p53 [T006	440	446	4.786849	GGGCAC	0.48828	0.53921
cg0545033	DIP2C	p53 [T006	370	376	4.786849	GGGCAC	0.48828	0.53921
cg1493188	DIP2C	MAZ [T00	1042	1054	4.784243	TGCCCT	0.00611	0.00711
cg1850382	DIP2C	c-Ets-1 [T	480	486	4.782565	GTGGAA	0.48828	0.48026
cg1146814	DIP2C	c-Ets-1 [T	34	40	4.782565	CTTCCA	0.48828	0.48026
cg1006492	DIP2C	c-Ets-1 [T	590	596	4.782565	GTGGAA	0.48828	0.48026
cg0545033	DIP2C	c-Ets-1 [T	520	526	4.782565	GTGGAA	0.48828	0.48026
cg027001	DIP2C	FOXP3 [T	358	363	4.756447	GAAAAC	2.92969	2.82
cg027001	DIP2C	FOXP3 [T	640	645	4.756447	ATCAAC	2.92969	2.82
cg027001	DIP2C	FOXP3 [T	870	875	4.756447	AAAAAC	2.92969	2.82
cg027001	DIP2C	FOXP3 [T	1262	1267	4.756447	GAAAAC	2.92969	2.82
cg027001	DIP2C	FOXP3 [T	1488	1493	4.756447	GTTTTG	2.92969	2.82
cg027001	DIP2C	FOXP3 [T	1878	1883	4.756447	GTTGAC	2.92969	2.82
cg027001	DIP2C	TFII-I [T0	1456	1461	4.756447	GGAAAT	2.92969	2.89715
cg027001	DIP2C	TFII-I [T0	1834	1839	4.756447	CAATCC	2.92969	2.89715
cg1850223	DIP2C	FOXP3 [T	99	104	4.756447	GTTTTC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	263	268	4.756447	CTCAAC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	454	459	4.756447	CAAAAC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	477	482	4.756447	GTTTTT	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	1095	1100	4.756447	CTCAAC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	1255	1260	4.756447	AAAAAC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	1286	1291	4.756447	ATCAAC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	1605	1610	4.756447	CTCAAC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	1669	1674	4.756447	AAAAAC	2.92969	2.82
cg1850223	DIP2C	FOXP3 [T	1679	1684	4.756447	GAAAAC	2.92969	2.82
cg1850223	DIP2C	TFII-I [T0	684	689	4.756447	ATTTCC	2.92969	2.89715
cg1850223	DIP2C	TFII-I [T0	1124	1129	4.756447	GGAAAT	2.92969	2.89715
cg1850223	DIP2C	TFII-I [T0	1186	1191	4.756447	ATTTCC	2.92969	2.89715

cg1850223	DIP2C	TFII-I [T0	1744	1749	4.756447	ATTTCC	2.92969	2.89715
cg1850382	DIP2C	FOXP3 [T	74	79	4.756447	CAAAAC	2.92969	2.82
cg1850382	DIP2C	FOXP3 [T	391	396	4.756447	GTTTTT	2.92969	2.82
cg1850382	DIP2C	FOXP3 [T	734	739	4.756447	CAAAAC	2.92969	2.82
cg1850382	DIP2C	FOXP3 [T	1217	1222	4.756447	GTTTTC	2.92969	2.82
cg1850382	DIP2C	FOXP3 [T	1252	1257	4.756447	GTTTTC	2.92969	2.82
cg1850382	DIP2C	FOXP3 [T	1465	1470	4.756447	GTTTTT	2.92969	2.82
cg1850382	DIP2C	FOXP3 [T	1705	1710	4.756447	CAAAAC	2.92969	2.82
cg1850382	DIP2C	TFII-I [T0	209	214	4.756447	GGATAT	2.92969	2.89715
cg1850382	DIP2C	TFII-I [T0	687	692	4.756447	GGACTG	2.92969	2.89715
cg1850382	DIP2C	TFII-I [T0	1155	1160	4.756447	CATTCC	2.92969	2.89715
cg1850382	DIP2C	TFII-I [T0	1160	1165	4.756447	CAGTCC	2.92969	2.89715
cg1850382	DIP2C	TFII-I [T0	1647	1652	4.756447	CATTCC	2.92969	2.89715
cg1493188	DIP2C	FOXP3 [T	578	583	4.756447	GTTTTT	2.92969	2.82
cg1493188	DIP2C	FOXP3 [T	675	680	4.756447	GTTTTC	2.92969	2.82
cg1493188	DIP2C	FOXP3 [T	898	903	4.756447	GTTTTT	2.92969	2.82
cg1493188	DIP2C	FOXP3 [T	1533	1538	4.756447	GAAAAC	2.92969	2.82
cg1493188	DIP2C	FOXP3 [T	1697	1702	4.756447	CTCAAC	2.92969	2.82
cg1493188	DIP2C	FOXP3 [T	1797	1802	4.756447	GAAAAC	2.92969	2.82
cg1493188	DIP2C	FOXP3 [T	1848	1853	4.756447	GTTTTT	2.92969	2.82
cg1493188	DIP2C	FOXP3 [T	1867	1872	4.756447	GTTTTG	2.92969	2.82
cg1493188	DIP2C	TFII-I [T0	797	802	4.756447	ATGTCC	2.92969	2.89715
cg1493188	DIP2C	TFII-I [T0	1494	1499	4.756447	GGAAAT	2.92969	2.89715
cg1493188	DIP2C	TFII-I [T0	1670	1675	4.756447	ATTTCC	2.92969	2.89715
cg1493188	DIP2C	TFII-I [T0	1727	1732	4.756447	ATATCC	2.92969	2.89715
cg1146814	DIP2C	FOXP3 [T	81	86	4.756447	GTTTTC	2.92969	2.82
cg1146814	DIP2C	FOXP3 [T	92	97	4.756447	GAAAAC	2.92969	2.82
cg1146814	DIP2C	FOXP3 [T	384	389	4.756447	GTTGAG	2.92969	2.82
cg1146814	DIP2C	FOXP3 [T	527	532	4.756447	CAAAAC	2.92969	2.82
cg1146814	DIP2C	FOXP3 [T	949	954	4.756447	GAAAAC	2.92969	2.82
cg1146814	DIP2C	FOXP3 [T	1231	1236	4.756447	ATCAAC	2.92969	2.82
cg1146814	DIP2C	FOXP3 [T	1461	1466	4.756447	AAAAAC	2.92969	2.82
cg1146814	DIP2C	FOXP3 [T	1853	1858	4.756447	GAAAAC	2.92969	2.82
cg1146814	DIP2C	TFII-I [T0	392	397	4.756447	GGACTG	2.92969	2.89715
cg1006492	DIP2C	FOXP3 [T	184	189	4.756447	CAAAAC	2.92969	2.82
cg1006492	DIP2C	FOXP3 [T	501	506	4.756447	GTTTTT	2.92969	2.82
cg1006492	DIP2C	FOXP3 [T	844	849	4.756447	CAAAAC	2.92969	2.82
cg1006492	DIP2C	FOXP3 [T	1327	1332	4.756447	GTTTTC	2.92969	2.82
cg1006492	DIP2C	FOXP3 [T	1362	1367	4.756447	GTTTTC	2.92969	2.82
cg1006492	DIP2C	FOXP3 [T	1575	1580	4.756447	GTTTTT	2.92969	2.82
cg1006492	DIP2C	FOXP3 [T	1815	1820	4.756447	CAAAAC	2.92969	2.82
cg1006492	DIP2C	TFII-I [T0	319	324	4.756447	GGATAT	2.92969	2.89715
cg1006492	DIP2C	TFII-I [T0	797	802	4.756447	GGACTG	2.92969	2.89715
cg1006492	DIP2C	TFII-I [T0	1265	1270	4.756447	CATTCC	2.92969	2.89715
cg1006492	DIP2C	TFII-I [T0	1270	1275	4.756447	CAGTCC	2.92969	2.89715
cg1006492	DIP2C	TFII-I [T0	1757	1762	4.756447	CATTCC	2.92969	2.89715
cg0545033	DIP2C	FOXP3 [T	114	119	4.756447	CAAAAC	2.92969	2.82
cg0545033	DIP2C	FOXP3 [T	431	436	4.756447	GTTTTT	2.92969	2.82

cg0545033	DIP2C	FOXP3 [T	774	779	4.756447	CAAAAC	2.92969	2.82
cg0545033	DIP2C	FOXP3 [T	1257	1262	4.756447	GTTTTC	2.92969	2.82
cg0545033	DIP2C	FOXP3 [T	1292	1297	4.756447	GTTTTC	2.92969	2.82
cg0545033	DIP2C	FOXP3 [T	1505	1510	4.756447	GTTTTT	2.92969	2.82
cg0545033	DIP2C	FOXP3 [T	1745	1750	4.756447	CAAAAC	2.92969	2.82
cg0545033	DIP2C	TFII-I [T0	249	254	4.756447	GGATAT	2.92969	2.89715
cg0545033	DIP2C	TFII-I [T0	727	732	4.756447	GGACTG	2.92969	2.89715
cg0545033	DIP2C	TFII-I [T0	1195	1200	4.756447	CATTCC	2.92969	2.89715
cg0545033	DIP2C	TFII-I [T0	1200	1205	4.756447	CAGTCC	2.92969	2.89715
cg0545033	DIP2C	TFII-I [T0	1687	1692	4.756447	CATTCC	2.92969	2.89715
cg1850382	DIP2C	c-Ets-1 [T	1538	1544	4.654478	CTGGAA	0.85449	0.8381
cg1006492	DIP2C	c-Ets-1 [T	1648	1654	4.654478	CTGGAA	0.85449	0.8381
cg0545033	DIP2C	c-Ets-1 [T	1578	1584	4.654478	CTGGAA	0.85449	0.8381
cg0270010	DIP2C	VDR [T00	709	717	4.617121	AGCTTG	0.37384	0.36855
cg0270010	DIP2C	VDR [T00	1268	1276	4.617121	TGCGTG	0.37384	0.36855
cg1850223	DIP2C	VDR [T00	230	238	4.617121	GGGATG	0.37384	0.36855
cg1146814	DIP2C	VDR [T00	1300	1308	4.617121	AGCTTG	0.37384	0.36855
cg1146814	DIP2C	VDR [T00	1859	1867	4.617121	TGCGTG	0.37384	0.36855
cg0270010	DIP2C	c-Ets-1 [T	1772	1778	4.616023	GCGGAA	0.85449	0.8381
cg1850223	DIP2C	c-Ets-2 [T	667	675	4.589988	GCGAAG	0.06866	0.06805
cg0270010	DIP2C	C/EBPalph	636	642	4.560723	GACAAT	0.24414	0.24373
cg0270010	DIP2C	C/EBPalph	1832	1838	4.560723	GCCAAT	0.24414	0.24373
cg1146814	DIP2C	C/EBPalph	1227	1233	4.560723	GACAAT	0.24414	0.24373
cg1146814	DIP2C	COUP-TF	118	130	4.54669	CAAGAG	0.00358	0.00369
cg0270010	DIP2C	c-Ets-1 [T	914	920	4.539113	ATTCCT	0.85449	0.8381
cg1146814	DIP2C	c-Ets-1 [T	1505	1511	4.539113	ATTCCT	0.85449	0.8381
cg0270010	DIP2C	USF2 [T0	1920	1929	4.528187	AAGGCA	0.06866	0.07203
cg1850382	DIP2C	USF2 [T0	1010	1019	4.528187	ACGGCA	0.06866	0.07203
cg1850382	DIP2C	USF2 [T0	1892	1901	4.528187	GGATCA	0.06866	0.07203
cg1850382	DIP2C	USF2 [T0	1986	1995	4.528187	CGGGCA	0.06866	0.07203
cg1006492	DIP2C	USF2 [T0	1120	1129	4.528187	ACGGCA	0.06866	0.07203
cg0545033	DIP2C	USF2 [T0	1050	1059	4.528187	ACGGCA	0.06866	0.07203
cg0545033	DIP2C	USF2 [T0	1932	1941	4.528187	GGATCA	0.06866	0.07203
cg0270010	DIP2C	T3R-beta1	1463	1471	4.481316	TCACCA	0.27466	0.27245
cg1850223	DIP2C	NF-AT2 [	1182	1191	4.460114	CAGAAT	0.04196	0.03925
cg1493188	DIP2C	GATA-2 [	1077	1085	4.444445	ACTCTA	0.24414	0.23857
cg0270010	DIP2C	c-Jun [T00	310	316	4.441904	TGACTG	0.12207	0.11843
cg1850223	DIP2C	c-Jun [T00	120	126	4.441904	TCAGTC	0.12207	0.11843
cg1146814	DIP2C	c-Jun [T00	901	907	4.441904	TGACTG	0.12207	0.11843
cg1006492	DIP2C	c-Jun [T00	27	33	4.441904	TCAGTC	0.12207	0.11843
cg1850223	DIP2C	ATF-2 [T0	79	88	4.430002	ATGACG	0.03815	0.03703
cg1850382	DIP2C	RXR-alph	1595	1601	4.423008	GGGTGG	0.24414	0.25781
cg1006492	DIP2C	RXR-alph	1705	1711	4.423008	GGGTGG	0.24414	0.25781
cg0545033	DIP2C	RXR-alph	1635	1641	4.423008	GGGTGG	0.24414	0.25781
cg0270010	DIP2C	STAT4 [T	367	372	4.411765	GGAAGC	1.95312	1.99838
cg0270010	DIP2C	STAT4 [T	790	795	4.411765	GCTTCC	1.95312	1.99838
cg0270010	DIP2C	STAT4 [T	1218	1223	4.411765	GGAACG	1.95312	1.99838
cg1850223	DIP2C	STAT4 [T	739	744	4.411765	GCTTCC	1.95312	1.99838

cg1850223	DIP2C	STAT4 [T	965	970	4.411765	GCTTCC	1.95312	1.99838
cg1850223	DIP2C	STAT4 [T	1059	1064	4.411765	GGAACG	1.95312	1.99838
cg1850223	DIP2C	STAT4 [T	1613	1618	4.411765	GGAAGC	1.95312	1.99838
cg1850223	DIP2C	STAT4 [T	1648	1653	4.411765	GGAAGC	1.95312	1.99838
cg1850223	DIP2C	STAT4 [T	1796	1801	4.411765	CGTTCC	1.95312	1.99838
cg1850223	DIP2C	STAT4 [T	1868	1873	4.411765	TCTTCC	1.95312	1.99838
cg1850223	DIP2C	STAT4 [T	1912	1917	4.411765	GGAAGC	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	265	270	4.411765	CGTTCC	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	437	442	4.411765	GGAAGA	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	482	487	4.411765	GGAAGC	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	551	556	4.411765	CGTTCC	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	863	868	4.411765	GGAAGA	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	986	991	4.411765	GGAAGC	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	1065	1070	4.411765	GCTTCC	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	1155	1160	4.411765	CATTCC	1.95312	1.99838
cg1850382	DIP2C	STAT4 [T	1647	1652	4.411765	CATTCC	1.95312	1.99838
cg1493188	DIP2C	STAT4 [T	1032	1037	4.411765	CGTTCC	1.95312	1.99838
cg1146814	DIP2C	STAT4 [T	33	38	4.411765	GCTTCC	1.95312	1.99838
cg1146814	DIP2C	STAT4 [T	958	963	4.411765	GGAAGC	1.95312	1.99838
cg1146814	DIP2C	STAT4 [T	1381	1386	4.411765	GCTTCC	1.95312	1.99838
cg1146814	DIP2C	STAT4 [T	1809	1814	4.411765	GGAACG	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	375	380	4.411765	CGTTCC	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	547	552	4.411765	GGAAGA	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	592	597	4.411765	GGAAGC	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	661	666	4.411765	CGTTCC	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	973	978	4.411765	GGAAGA	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	1096	1101	4.411765	GGAAGC	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	1175	1180	4.411765	GCTTCC	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	1265	1270	4.411765	CATTCC	1.95312	1.99838
cg1006492	DIP2C	STAT4 [T	1757	1762	4.411765	CATTCC	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	305	310	4.411765	CGTTCC	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	477	482	4.411765	GGAAGA	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	522	527	4.411765	GGAAGC	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	591	596	4.411765	CGTTCC	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	903	908	4.411765	GGAAGA	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	1026	1031	4.411765	GGAAGC	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	1105	1110	4.411765	GCTTCC	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	1195	1200	4.411765	CATTCC	1.95312	1.99838
cg0545033	DIP2C	STAT4 [T	1687	1692	4.411765	CATTCC	1.95312	1.99838
cg1850223	DIP2C	c-Ets-1 [T	1244	1250	4.411026	ATTCCT	0.85449	0.8381
cg1146814	DIP2C	c-Ets-1 [T	70	76	4.411026	ATTCCT	0.85449	0.8381
cg1850223	DIP2C	NF-AT1 [	1183	1191	4.396744	AGAATT	0.06866	0.06549
cg1493188	DIP2C	NF-AT1 [	1494	1502	4.396744	GGAAAT	0.06866	0.06549
cg027001	DIP2C	PEA3 [T0	130	138	4.30818	TGGATG	0.13733	0.13607
cg1146814	DIP2C	PEA3 [T0	570	578	4.30818	CCACAT	0.13733	0.13607
cg1146814	DIP2C	PEA3 [T0	721	729	4.30818	TGGATG	0.13733	0.13607
cg1850382	DIP2C	RAR-beta	1381	1390	4.307573	CCTGAA	0.14496	0.14853
cg1006492	DIP2C	RAR-beta	1491	1500	4.307573	CCTGAA	0.14496	0.14853

cg0545033	DIP2C	RAR-beta	1421	1430	4.307573	CCTGAA	0.14496	0.14853
cg0270010	DIP2C	RAR-beta	319	328	4.289108	CATGAA	0.14496	0.14853
cg1850382	DIP2C	RAR-beta	408	417	4.289108	CATAAA	0.14496	0.14853
cg1146814	DIP2C	RAR-beta	910	919	4.289108	CATGAA	0.14496	0.14853
cg1006492	DIP2C	RAR-beta	518	527	4.289108	CATAAA	0.14496	0.14853
cg0545033	DIP2C	RAR-beta	448	457	4.289108	CATAAA	0.14496	0.14853
cg1850382	DIP2C	CREB [T0	525	533	4.261795	ACCACG	0.04578	0.0464
cg1006492	DIP2C	CREB [T0	635	643	4.261795	ACCACG	0.04578	0.0464
cg0545033	DIP2C	CREB [T0	565	573	4.261795	ACCACG	0.04578	0.0464
cg0270010	DIP2C	RXR-alpha	679	685	4.24113	GGGTCA	0.97656	1.02803
cg1850223	DIP2C	RXR-alpha	1629	1635	4.24113	GGGTAA	0.97656	1.02803
cg1146814	DIP2C	RXR-alpha	186	192	4.24113	GGGACC	0.97656	1.02803
cg1146814	DIP2C	RXR-alpha	320	326	4.24113	GGGTCC	0.97656	1.02803
cg1146814	DIP2C	RXR-alpha	1270	1276	4.24113	GGGTCA	0.97656	1.02803
cg1850223	DIP2C	C/EBPalph	288	294	4.235345	AGCAAT	0.48828	0.46347
cg1850223	DIP2C	C/EBPalph	1498	1504	4.235345	TATTGAT	0.48828	0.46347
cg0270010	DIP2C	Sp1 [T007	1251	1260	4.222204	AGGCCG	0.08965	0.10391
cg1146814	DIP2C	Sp1 [T007	1842	1851	4.222204	AGGCCG	0.08965	0.10391
cg1493188	DIP2C	AP-2alpha	1140	1145	4.211849	GCCTAC	0.97656	1.02535
cg1493188	DIP2C	IRF-1 [T0	1671	1679	4.207433	TTTCCTA	0.1297	0.12468
cg0270010	DIP2C	GR-beta [T	639	643	4.201913	AATCA	7.8125	7.23274
cg0270010	DIP2C	GR-beta [T	864	868	4.201913	AATCA	7.8125	7.23274
cg0270010	DIP2C	GR-beta [T	912	916	4.201913	CGATT	7.8125	7.23274
cg0270010	DIP2C	GR-beta [T	963	967	4.201913	AATAA	7.8125	7.23274
cg0270010	DIP2C	GR-beta [T	1202	1206	4.201913	AATCA	7.8125	7.23274
cg0270010	DIP2C	GR-beta [T	1231	1235	4.201913	AATAG	7.8125	7.23274
cg0270010	DIP2C	GR-beta [T	1537	1541	4.201913	AATCA	7.8125	7.23274
cg0270010	DIP2C	GR-beta [T	1566	1570	4.201913	CTATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	151	155	4.201913	CTATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	252	256	4.201913	AATCA	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	291	295	4.201913	AATAA	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	448	452	4.201913	TTATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	469	473	4.201913	TGATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	536	540	4.201913	CTATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	623	627	4.201913	TGATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	1127	1131	4.201913	AATCG	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	1219	1223	4.201913	TGATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	1238	1242	4.201913	AATAA	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	1280	1284	4.201913	AATAA	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	1380	1384	4.201913	TTATT	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	1522	1526	4.201913	AATCA	7.8125	7.23274
cg1850223	DIP2C	GR-beta [T	1576	1580	4.201913	AATAA	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	186	190	4.201913	TTATT	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	402	406	4.201913	AATAG	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	680	684	4.201913	AATAA	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	798	802	4.201913	AATCA	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	804	808	4.201913	TGATT	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	815	819	4.201913	AATCA	7.8125	7.23274

cg1850382	DIP2C	GR-beta [T	1094	1098	4.201913	TTATT	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	1119	1123	4.201913	AATCA	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	1126	1130	4.201913	CTATT	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	1481	1485	4.201913	CTATT	7.8125	7.23274
cg1850382	DIP2C	GR-beta [T	1499	1503	4.201913	AATAA	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	583	587	4.201913	TGATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	600	604	4.201913	TGATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	610	614	4.201913	TGATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	642	646	4.201913	TTATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	668	672	4.201913	TGATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	704	708	4.201913	AATAA	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	749	753	4.201913	TTATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	1469	1473	4.201913	CTATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	1582	1586	4.201913	AATAA	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	1599	1603	4.201913	TGATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	1618	1622	4.201913	TGATT	7.8125	7.23274
cg1493188	DIP2C	GR-beta [T	1675	1679	4.201913	CTATT	7.8125	7.23274
cg1146814	DIP2C	GR-beta [T	498	502	4.201913	AATCA	7.8125	7.23274
cg1146814	DIP2C	GR-beta [T	1230	1234	4.201913	AATCA	7.8125	7.23274
cg1146814	DIP2C	GR-beta [T	1455	1459	4.201913	AATCA	7.8125	7.23274
cg1146814	DIP2C	GR-beta [T	1503	1507	4.201913	CGATT	7.8125	7.23274
cg1146814	DIP2C	GR-beta [T	1554	1558	4.201913	AATAA	7.8125	7.23274
cg1146814	DIP2C	GR-beta [T	1793	1797	4.201913	AATCA	7.8125	7.23274
cg1146814	DIP2C	GR-beta [T	1822	1826	4.201913	AATAG	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	296	300	4.201913	TTATT	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	512	516	4.201913	AATAG	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	790	794	4.201913	AATAA	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	908	912	4.201913	AATCA	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	914	918	4.201913	TGATT	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	925	929	4.201913	AATCA	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	1204	1208	4.201913	TTATT	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	1229	1233	4.201913	AATCA	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	1236	1240	4.201913	CTATT	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	1591	1595	4.201913	CTATT	7.8125	7.23274
cg1006492	DIP2C	GR-beta [T	1609	1613	4.201913	AATAA	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	226	230	4.201913	TTATT	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	442	446	4.201913	AATAG	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	720	724	4.201913	AATAA	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	838	842	4.201913	AATCA	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	844	848	4.201913	TGATT	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	855	859	4.201913	AATCA	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	1134	1138	4.201913	TTATT	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	1159	1163	4.201913	AATCA	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	1166	1170	4.201913	CTATT	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	1521	1525	4.201913	CTATT	7.8125	7.23274
cg0545033	DIP2C	GR-beta [T	1539	1543	4.201913	AATAA	7.8125	7.23274
cg1493188	DIP2C	NF-Y [T0	1473	1480	4.186615	TTTCCA	0.18311	0.17499
cg1850223	DIP2C	c-Ets-1 [T	1452	1458	4.154851	ATTCCT	0.24414	0.23719

cg1850382	DIP2C	NF-AT1 [	572	581	4.134416	CGTCTT	0.08392	0.07965
cg1006492	DIP2C	NF-AT1 [	682	691	4.134416	CGTCTT	0.08392	0.07965
cg0545033	DIP2C	NF-AT1 [	612	621	4.134416	CGTCTT	0.08392	0.07965
cg1850382	DIP2C	p53 [T006	1031	1037	4.125254	GGGCCT	0.73242	0.82434
cg1493188	DIP2C	p53 [T006	1742	1748	4.125254	CAGGCC	0.73242	0.82434
cg1006492	DIP2C	p53 [T006	1141	1147	4.125254	GGGCCT	0.73242	0.82434
cg0545033	DIP2C	p53 [T006	1071	1077	4.125254	GGGCCT	0.73242	0.82434
cg1850223	DIP2C	c-Ets-2 [T	1245	1253	4.091811	TTCCTTA	0.16022	0.15061
cg1850223	DIP2C	c-Ets-2 [T	1608	1616	4.091811	AACAAG	0.16022	0.15061
cg1493188	DIP2C	c-Ets-2 [T	745	753	4.091811	TTCCTTA	0.16022	0.15061
cg1493188	DIP2C	c-Ets-2 [T	1489	1497	4.091811	GACAAG	0.16022	0.15061
cg0270010	DIP2C	SRY [T00	1569	1577	4.087393	TTTACA	0.12207	0.11312
cg1493188	DIP2C	SRY [T00	1205	1213	4.087393	CTTTGT	0.12207	0.11312
cg1493188	DIP2C	SRY [T00	1416	1424	4.087393	CTTTGT	0.12207	0.11312
cg0270010	DIP2C	p53 [T006	346	352	4.083527	GGGCAC	0.73242	0.82434
cg0270010	DIP2C	p53 [T006	471	477	4.083527	GGTGCC	0.73242	0.82434
cg0270010	DIP2C	p53 [T006	595	601	4.083527	GGGCAC	0.73242	0.82434
cg0270010	DIP2C	p53 [T006	1372	1378	4.083527	GGGCAC	0.73242	0.82434
cg1850223	DIP2C	p53 [T006	705	711	4.083527	GGGCAC	0.73242	0.82434
cg1850382	DIP2C	p53 [T006	1987	1993	4.083527	GGGCAC	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	937	943	4.083527	GGGCAC	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	1062	1068	4.083527	GGTGCC	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	1186	1192	4.083527	GGGCAC	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	1963	1969	4.083527	GGGCAC	0.73242	0.82434
cg1850223	DIP2C	C/EBPalp	530	536	4.019783	GTCAAT	0.48828	0.46347
cg1850223	DIP2C	RXR-alph	559	565	4.019014	GGGTAT	0.97656	1.02803
cg1850223	DIP2C	RXR-alph	1105	1111	4.019014	GGGTTT	0.97656	1.02803
cg1850223	DIP2C	RXR-alph	1930	1936	4.019014	GAAACC	0.97656	1.02803
cg1850382	DIP2C	RXR-alph	1938	1944	4.019014	GAAACC	0.97656	1.02803
cg1850382	DIP2C	RXR-alph	1975	1981	4.019014	GGGTGT	0.97656	1.02803
cg0545033	DIP2C	RXR-alph	1978	1984	4.019014	GAAACC	0.97656	1.02803
cg1493188	DIP2C	STAT1bet	1490	1499	4.01053	ACAAGG	0.03433	0.03308
cg0270010	DIP2C	TFIID [T0	1349	1355	4.007279	TTATAA	1.09863	0.94722
cg0270010	DIP2C	TFIID [T0	1362	1368	4.007279	TTTTAA	1.09863	0.94722
cg0270010	DIP2C	TFIID [T0	1569	1575	4.007279	TTTACA	1.09863	0.94722
cg0270010	DIP2C	Pax-5 [T0	71	77	4.007279	GGGCCT	1.09863	1.18533
cg0270010	DIP2C	Pax-5 [T0	480	486	4.007279	AAGGCC	1.09863	1.18533
cg0270010	DIP2C	Pax-5 [T0	536	542	4.007279	AGGGCC	1.09863	1.18533
cg0270010	DIP2C	Pax-5 [T0	895	901	4.007279	GGGCAG	1.09863	1.18533
cg0270010	DIP2C	Pax-5 [T0	1012	1018	4.007279	GGGCTC	1.09863	1.18533
cg1850223	DIP2C	TFIID [T0	152	158	4.007279	TATTAA	1.09863	0.94722
cg1850223	DIP2C	TFIID [T0	400	406	4.007279	TTTAAG	1.09863	0.94722
cg1850223	DIP2C	TFIID [T0	564	570	4.007279	TATTAA	1.09863	0.94722
cg1850223	DIP2C	TFIID [T0	1048	1054	4.007279	TTTTAA	1.09863	0.94722
cg1850223	DIP2C	TFIID [T0	1237	1243	4.007279	TAATAA	1.09863	0.94722
cg1850223	DIP2C	Pax-5 [T0	1425	1431	4.007279	AGGGCC	1.09863	1.18533
cg1850382	DIP2C	TFIID [T0	0	6	4.007279	TAGTAA	1.09863	0.94722
cg1850382	DIP2C	TFIID [T0	129	135	4.007279	TTGTAA	1.09863	0.94722

cg1850382	DIP2C	TFIID [T0	187	193	4.007279	TATTAA	1.09863	0.94722
cg1850382	DIP2C	TFIID [T0	338	344	4.007279	TTTATGA	1.09863	0.94722
cg1850382	DIP2C	TFIID [T0	407	413	4.007279	TCATAA	1.09863	0.94722
cg1850382	DIP2C	TFIID [T0	634	640	4.007279	TTTTAAA	1.09863	0.94722
cg1850382	DIP2C	Pax-5 [T0	330	336	4.007279	GGGCAC	1.09863	1.18533
cg1850382	DIP2C	Pax-5 [T0	445	451	4.007279	AAAGCC	1.09863	1.18533
cg1850382	DIP2C	Pax-5 [T0	566	572	4.007279	AATGCC	1.09863	1.18533
cg1850382	DIP2C	Pax-5 [T0	696	702	4.007279	GGGCCC	1.09863	1.18533
cg1850382	DIP2C	Pax-5 [T0	1175	1181	4.007279	AAAGCC	1.09863	1.18533
cg1493188	DIP2C	TFIID [T0	632	638	4.007279	TTTATGA	1.09863	0.94722
cg1493188	DIP2C	TFIID [T0	645	651	4.007279	TTTATAA	1.09863	0.94722
cg1493188	DIP2C	TFIID [T0	692	698	4.007279	TTTATAA	1.09863	0.94722
cg1493188	DIP2C	TFIID [T0	693	699	4.007279	TTATAA	1.09863	0.94722
cg1493188	DIP2C	TFIID [T0	1100	1106	4.007279	TTTACTA	1.09863	0.94722
cg1493188	DIP2C	TFIID [T0	1210	1216	4.007279	TAGTAA	1.09863	0.94722
cg1493188	DIP2C	TFIID [T0	1921	1927	4.007279	TTGTAA	1.09863	0.94722
cg1493188	DIP2C	TFIID [T0	1931	1937	4.007279	TCTTAA	1.09863	0.94722
cg1493188	DIP2C	Pax-5 [T0	811	817	4.007279	GGGCTC	1.09863	1.18533
cg1493188	DIP2C	Pax-5 [T0	1040	1046	4.007279	ACTGCC	1.09863	1.18533
cg1146814	DIP2C	TFIID [T0	1940	1946	4.007279	TTATAA	1.09863	0.94722
cg1146814	DIP2C	TFIID [T0	1953	1959	4.007279	TTTTAAA	1.09863	0.94722
cg1146814	DIP2C	Pax-5 [T0	224	230	4.007279	ACTGCC	1.09863	1.18533
cg1146814	DIP2C	Pax-5 [T0	444	450	4.007279	GGGCCC	1.09863	1.18533
cg1146814	DIP2C	Pax-5 [T0	662	668	4.007279	GGGCCT	1.09863	1.18533
cg1146814	DIP2C	Pax-5 [T0	1071	1077	4.007279	AAGGCC	1.09863	1.18533
cg1146814	DIP2C	Pax-5 [T0	1127	1133	4.007279	AGGGCC	1.09863	1.18533
cg1146814	DIP2C	Pax-5 [T0	1486	1492	4.007279	GGGCAG	1.09863	1.18533
cg1146814	DIP2C	Pax-5 [T0	1603	1609	4.007279	GGGCTC	1.09863	1.18533
cg1006492	DIP2C	TFIID [T0	110	116	4.007279	TAGTAA	1.09863	0.94722
cg1006492	DIP2C	TFIID [T0	239	245	4.007279	TTGTAA	1.09863	0.94722
cg1006492	DIP2C	TFIID [T0	297	303	4.007279	TATTAA	1.09863	0.94722
cg1006492	DIP2C	TFIID [T0	448	454	4.007279	TTTATGA	1.09863	0.94722
cg1006492	DIP2C	TFIID [T0	517	523	4.007279	TCATAA	1.09863	0.94722
cg1006492	DIP2C	TFIID [T0	744	750	4.007279	TTTTAAA	1.09863	0.94722
cg1006492	DIP2C	Pax-5 [T0	440	446	4.007279	GGGCAC	1.09863	1.18533
cg1006492	DIP2C	Pax-5 [T0	555	561	4.007279	AAAGCC	1.09863	1.18533
cg1006492	DIP2C	Pax-5 [T0	676	682	4.007279	AATGCC	1.09863	1.18533
cg1006492	DIP2C	Pax-5 [T0	806	812	4.007279	GGGCCC	1.09863	1.18533
cg1006492	DIP2C	Pax-5 [T0	1285	1291	4.007279	AAAGCC	1.09863	1.18533
cg0545033	DIP2C	TFIID [T0	40	46	4.007279	TAGTAA	1.09863	0.94722
cg0545033	DIP2C	TFIID [T0	169	175	4.007279	TTGTAA	1.09863	0.94722
cg0545033	DIP2C	TFIID [T0	227	233	4.007279	TATTAA	1.09863	0.94722
cg0545033	DIP2C	TFIID [T0	378	384	4.007279	TTTATGA	1.09863	0.94722
cg0545033	DIP2C	TFIID [T0	447	453	4.007279	TCATAA	1.09863	0.94722
cg0545033	DIP2C	TFIID [T0	674	680	4.007279	TTTTAAA	1.09863	0.94722
cg0545033	DIP2C	Pax-5 [T0	370	376	4.007279	GGGCAC	1.09863	1.18533
cg0545033	DIP2C	Pax-5 [T0	485	491	4.007279	AAAGCC	1.09863	1.18533
cg0545033	DIP2C	Pax-5 [T0	606	612	4.007279	AATGCC	1.09863	1.18533

cg0545033	DIP2C	Pax-5 [T0	736	742	4.007279	GGGCCC	1.09863	1.18533
cg0545033	DIP2C	Pax-5 [T0	1215	1221	4.007279	AAAGCC	1.09863	1.18533
cg0270010	DIP2C	USF2 [T0	336	345	4.003951	AGCTCA	0.01144	0.01199
cg1146814	DIP2C	USF2 [T0	927	936	4.003951	AGCTCA	0.01144	0.01199
cg0270010	DIP2C	MAZ [T00	323	335	3.973255	AACCCT	0.00587	0.00674
cg1146814	DIP2C	MAZ [T00	914	926	3.973255	AACCCT	0.00587	0.00674
cg0270010	DIP2C	AP-2alpha	73	78	3.970052	GCCTTG	0.97656	1.02535
cg1850382	DIP2C	AP-2alpha	166	171	3.970052	GCCTTG	0.97656	1.02535
cg1493188	DIP2C	AP-2alpha	1789	1794	3.970052	GCCTTG	0.97656	1.02535
cg1146814	DIP2C	AP-2alpha	664	669	3.970052	GCCTTG	0.97656	1.02535
cg1006492	DIP2C	AP-2alpha	276	281	3.970052	GCCTTG	0.97656	1.02535
cg0545033	DIP2C	AP-2alpha	206	211	3.970052	GCCTTG	0.97656	1.02535
cg1146814	DIP2C	NF-kappa	331	341	3.96663	GGGGAA	0.01097	0.01194
cg0270010	DIP2C	p53 [T006	947	953	3.961937	GGGCTA	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	1538	1544	3.961937	GGGCTA	0.73242	0.82434
cg0270010	DIP2C	PPAR-alp	341	351	3.872523	ACCTGG	0.02575	0.0279
cg0270010	DIP2C	PPAR-alp	1496	1506	3.872523	AGCTGG	0.02575	0.0279
cg0270010	DIP2C	PPAR-alp	1790	1800	3.872523	CTGTCC	0.02575	0.0279
cg1146814	DIP2C	PPAR-alp	932	942	3.872523	ACCTGG	0.02575	0.0279
cg0270010	DIP2C	Sp1 [T007	1769	1778	3.861329	GGGGCG	0.08965	0.10391
cg1850223	DIP2C	AR [T000	536	544	3.814754	CTATTG	0.06866	0.06981
cg1850382	DIP2C	AR [T000	1681	1689	3.814754	CAAGTG	0.06866	0.06981
cg1006492	DIP2C	AR [T000	1791	1799	3.814754	CAAGTG	0.06866	0.06981
cg0545033	DIP2C	AR [T000	1721	1729	3.814754	CAAGTG	0.06866	0.06981
cg0270010	DIP2C	NFI/CTF [	1917	1924	3.793671	CCAAAG	0.18311	0.19063
cg1850223	DIP2C	NFI/CTF [	773	780	3.793671	CCAAGG	0.18311	0.19063
cg1146814	DIP2C	NFI/CTF [	234	241	3.793671	CCAAGG	0.18311	0.19063
cg1850223	DIP2C	ATF [T00	76	87	3.791339	ATAATG	0.00858	0.00843
cg1493188	DIP2C	E2F-1 [T0	846	853	3.784875	TCTGCC	0.15259	0.15999
cg0270010	DIP2C	GR [T050	1395	1401	3.763516	CAAAGA	0.73242	0.6946
cg0270010	DIP2C	GR [T050	1487	1493	3.763516	CGTTTT	0.73242	0.6946
cg1850223	DIP2C	GR [T050	178	184	3.763516	CAAAGA	0.73242	0.6946
cg1850223	DIP2C	GR [T050	454	460	3.763516	CAAAAC	0.73242	0.6946
cg1850223	DIP2C	GR [T050	1675	1681	3.763516	CAAAGA	0.73242	0.6946
cg1850223	DIP2C	GR [T050	1920	1926	3.763516	CAAAGA	0.73242	0.6946
cg1850382	DIP2C	GR [T050	1748	1754	3.763516	CTCTTT	0.73242	0.6946
cg1493188	DIP2C	GR [T050	1203	1209	3.763516	TTCTTTG	0.73242	0.6946
cg1493188	DIP2C	GR [T050	1381	1387	3.763516	CAAAGA	0.73242	0.6946
cg1493188	DIP2C	GR [T050	1866	1872	3.763516	TGTTTT	0.73242	0.6946
cg1146814	DIP2C	GR [T050	126	132	3.763516	CAAAGA	0.73242	0.6946
cg1146814	DIP2C	GR [T050	527	533	3.763516	CAAAAC	0.73242	0.6946
cg1146814	DIP2C	GR [T050	1986	1992	3.763516	CAAAGA	0.73242	0.6946
cg1006492	DIP2C	GR [T050	1858	1864	3.763516	CTCTTT	0.73242	0.6946
cg0545033	DIP2C	GR [T050	1788	1794	3.763516	CTCTTT	0.73242	0.6946
cg1850382	DIP2C	E2F [T002	1751	1760	3.762198	TTTGGC	0.04578	0.04554
cg1006492	DIP2C	E2F [T002	1861	1870	3.762198	TTTGGC	0.04578	0.04554
cg0545033	DIP2C	E2F [T002	1791	1800	3.762198	TTTGGC	0.04578	0.04554
cg0270010	DIP2C	p53 [T006	101	107	3.750231	CCAGCC	0.73242	0.82434

cg0270010	DIP2C	p53 [T006	571	577	3.750231	CCAGCC	0.73242	0.82434
cg0270010	DIP2C	p53 [T006	737	743	3.750231	CAAGCC	0.73242	0.82434
cg1850382	DIP2C	p53 [T006	703	709	3.750231	GGGCTG	0.73242	0.82434
cg1850382	DIP2C	p53 [T006	1620	1626	3.750231	GGGCTG	0.73242	0.82434
cg1493188	DIP2C	p53 [T006	1946	1952	3.750231	GGGCTG	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	229	235	3.750231	CCAGCC	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	692	698	3.750231	CCAGCC	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	1162	1168	3.750231	CCAGCC	0.73242	0.82434
cg1146814	DIP2C	p53 [T006	1328	1334	3.750231	CAAGCC	0.73242	0.82434
cg1006492	DIP2C	p53 [T006	813	819	3.750231	GGGCTG	0.73242	0.82434
cg1006492	DIP2C	p53 [T006	1730	1736	3.750231	GGGCTG	0.73242	0.82434
cg0545033	DIP2C	p53 [T006	743	749	3.750231	GGGCTG	0.73242	0.82434
cg0545033	DIP2C	p53 [T006	1660	1666	3.750231	GGGCTG	0.73242	0.82434
cg0270010	DIP2C	AP-2alpha	479	484	3.743866	GAAGGC	0.48828	0.5124
cg1850223	DIP2C	AP-2alpha	188	193	3.743866	GAAGGC	0.48828	0.5124
cg1850223	DIP2C	AP-2alpha	1585	1590	3.743866	GCCTTC	0.48828	0.5124
cg1850223	DIP2C	AP-2alpha	1622	1627	3.743866	GAAGGC	0.48828	0.5124
cg1850382	DIP2C	AP-2alpha	223	228	3.743866	GAAGGC	0.48828	0.5124
cg1493188	DIP2C	AP-2alpha	976	981	3.743866	GCCTTC	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	42	47	3.743866	GCCTTC	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	334	339	3.743866	GAAGGC	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	549	554	3.743866	GAAGGC	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	1070	1075	3.743866	GAAGGC	0.48828	0.5124
cg1006492	DIP2C	AP-2alpha	333	338	3.743866	GAAGGC	0.48828	0.5124
cg0545033	DIP2C	AP-2alpha	263	268	3.743866	GAAGGC	0.48828	0.5124
cg1850223	DIP2C	c-Ets-1 [T	1043	1049	3.71855	GTTCCTT	0.61035	0.61936
cg1006492	DIP2C	c-Ets-1 [T	68	74	3.71855	GTTCCTT	0.61035	0.61936
cg0270010	DIP2C	Sp1 [T007	1901	1910	3.623596	GGGGCG	0.07439	0.08783
cg1850382	DIP2C	c-Ets-1 [T	744	750	3.590463	GTTCCTC	0.61035	0.61936
cg1006492	DIP2C	c-Ets-1 [T	854	860	3.590463	GTTCCTC	0.61035	0.61936
cg0545033	DIP2C	c-Ets-1 [T	784	790	3.590463	GTTCCTC	0.61035	0.61936
cg1493188	DIP2C	p53 [T006	990	996	3.586914	CTCGCC	0.73242	0.80362
cg1850223	DIP2C	RXR-alpha	923	929	3.574782	GGGTCG	1.09863	1.1653
cg1493188	DIP2C	NF-AT2 [T	928	937	3.571424	GAGTGT	0.03433	0.03138
cg1850382	DIP2C	E2F-1 [T0	983	990	3.55167	GCGGGA	0.15259	0.16507
cg1006492	DIP2C	E2F-1 [T0	1093	1100	3.55167	GCGGGA	0.15259	0.16507
cg0545033	DIP2C	E2F-1 [T0	1023	1030	3.55167	GCGGGA	0.15259	0.16507
cg1493188	DIP2C	Sp1 [T007	1002	1011	3.54287	ACTCCG	0.07439	0.08783
cg1850382	DIP2C	c-Ets-2 [T	432	440	3.518824	CAGAAG	0.18311	0.18314
cg1146814	DIP2C	c-Ets-2 [T	71	79	3.518824	TTCCTTC	0.18311	0.18314
cg1006492	DIP2C	c-Ets-2 [T	69	77	3.518824	TTCCTTC	0.18311	0.18314
cg1006492	DIP2C	c-Ets-2 [T	542	550	3.518824	CAGAAG	0.18311	0.18314
cg0545033	DIP2C	c-Ets-2 [T	472	480	3.518824	CAGAAG	0.18311	0.18314
cg0270010	DIP2C	p53 [T006	895	901	3.516613	GGGCAG	0.73242	0.80362
cg1850382	DIP2C	p53 [T006	566	572	3.516613	AATGCC	0.73242	0.80362
cg1493188	DIP2C	p53 [T006	1040	1046	3.516613	ACTGCC	0.73242	0.80362
cg1146814	DIP2C	p53 [T006	224	230	3.516613	ACTGCC	0.73242	0.80362
cg1146814	DIP2C	p53 [T006	1486	1492	3.516613	GGGCAG	0.73242	0.80362

cg1006492	DIP2C	p53 [T006	676	682	3.516613	AATGCC	0.73242	0.80362
cg0545033	DIP2C	p53 [T006	606	612	3.516613	AATGCC	0.73242	0.80362
cg0270010	DIP2C	HNF-3alph	1567	1574	3.500065	TATTTAC	0.27466	0.23175
cg1850223	DIP2C	HNF-3alph	85	92	3.500065	TAAAAA	0.27466	0.23175
cg1850223	DIP2C	HNF-3alph	138	145	3.500065	TATAAA	0.27466	0.23175
cg1493188	DIP2C	HNF-3alph	643	650	3.500065	TATTTAT	0.27466	0.23175
cg1493188	DIP2C	HNF-3alph	661	668	3.500065	TATTTTC	0.27466	0.23175
cg1493188	DIP2C	HNF-3alph	1613	1620	3.500065	AATTTTC	0.27466	0.23175
cg1146814	DIP2C	HNF-3alph	65	72	3.500065	TAAAAA	0.27466	0.23175
cg1146814	DIP2C	HNF-3alph	108	115	3.500065	TATTTAC	0.27466	0.23175
cg1850223	DIP2C	c-Ets-1 [T	800	806	3.487246	CTTCCG	0.61035	0.61936
cg0270010	DIP2C	c-Ets-1 [T	1216	1222	3.462376	CAGGAA	0.61035	0.61936
cg1493188	DIP2C	c-Ets-1 [T	1033	1039	3.462376	GTTCCTC	0.61035	0.61936
cg1493188	DIP2C	c-Ets-1 [T	1275	1281	3.462376	CAGGAA	0.61035	0.61936
cg1146814	DIP2C	c-Ets-1 [T	1807	1813	3.462376	CAGGAA	0.61035	0.61936
cg1850223	DIP2C	NF-AT1 [	1741	1750	3.445347	GCCATT	0.07629	0.07204
cg1493188	DIP2C	NF-AT1 [	1795	1804	3.445347	TGGAAA	0.07629	0.07204
cg1850382	DIP2C	PXR-1:RX	1383	1390	3.395883	TGAACC	0.12207	0.11883
cg1006492	DIP2C	PXR-1:RX	1493	1500	3.395883	TGAACC	0.12207	0.11883
cg0545033	DIP2C	PXR-1:RX	1423	1430	3.395883	TGAACC	0.12207	0.11883
cg1850223	DIP2C	RXR-alpha	383	389	3.392904	CGCACC	1.09863	1.1653
cg1850223	DIP2C	RXR-alpha	777	783	3.392904	GGGTGC	1.09863	1.1653
cg1850382	DIP2C	RXR-alpha	582	588	3.392904	GGGTAA	1.09863	1.1653
cg1850382	DIP2C	RXR-alpha	787	793	3.392904	CTCACC	1.09863	1.1653
cg1850382	DIP2C	RXR-alpha	1373	1379	3.392904	CTCACC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	8	14	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	57	63	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	106	112	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	155	161	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	204	210	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	253	259	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	302	308	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	351	357	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	400	406	3.392904	GGGTGC	1.09863	1.1653
cg1493188	DIP2C	RXR-alpha	1591	1597	3.392904	ATGACC	1.09863	1.1653
cg1006492	DIP2C	RXR-alpha	692	698	3.392904	GGGTAA	1.09863	1.1653
cg1006492	DIP2C	RXR-alpha	897	903	3.392904	CTCACC	1.09863	1.1653
cg1006492	DIP2C	RXR-alpha	1483	1489	3.392904	CTCACC	1.09863	1.1653
cg0545033	DIP2C	RXR-alpha	622	628	3.392904	GGGTAA	1.09863	1.1653
cg0545033	DIP2C	RXR-alpha	827	833	3.392904	CTCACC	1.09863	1.1653
cg0545033	DIP2C	RXR-alpha	1413	1419	3.392904	CTCACC	1.09863	1.1653
cg1850223	DIP2C	Elk-1 [T00	183	191	3.381796	ATGAGG	0.04578	0.04517
cg1493188	DIP2C	Elk-1 [T00	1117	1125	3.381796	CTTCCTC	0.04578	0.04517
cg1146814	DIP2C	Elk-1 [T00	544	552	3.381796	CTGAGG	0.04578	0.04517
cg0270010	DIP2C	p53 [T006	153	159	3.375208	GGGCGG	0.73242	0.80362
cg1850223	DIP2C	p53 [T006	1297	1303	3.375208	CCCGCC	0.73242	0.80362
cg1493188	DIP2C	p53 [T006	1747	1753	3.375208	CCCGCC	0.73242	0.80362
cg1493188	DIP2C	p53 [T006	1951	1957	3.375208	GGGCGT	0.73242	0.80362

cg1146814	DIP2C	p53 [T006	190	196	3.375208	CCCGCC	0.73242	0.80362
cg1146814	DIP2C	p53 [T006	744	750	3.375208	GGGCGG	0.73242	0.80362
cg1850382	DIP2C	T3R-beta1	704	712	3.370634	GGCTGG	0.27466	0.27326
cg1493188	DIP2C	T3R-beta1	1334	1342	3.370634	TCACCT	0.27466	0.27326
cg1006492	DIP2C	T3R-beta1	814	822	3.370634	GGCTGG	0.27466	0.27326
cg0545033	DIP2C	T3R-beta1	744	752	3.370634	GGCTGG	0.27466	0.27326
cg027001	DIP2C	GR-beta [	232	236	3.361531	AATAT	3.90625	3.51525
cg027001	DIP2C	GR-beta [	625	629	3.361531	ATATT	3.90625	3.51525
cg027001	DIP2C	GR-beta [	1346	1350	3.361531	ATATT	3.90625	3.51525
cg027001	DIP2C	GR-beta [	1526	1530	3.361531	AATAT	3.90625	3.51525
cg027001	DIP2C	GR-beta [	1527	1531	3.361531	ATATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	142	146	3.361531	AATAT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	143	147	3.361531	ATATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	157	161	3.361531	AATAT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	410	414	3.361531	AATAT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	533	537	3.361531	AATCT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	563	567	3.361531	ATATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	1142	1146	3.361531	AATCT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	1158	1162	3.361531	AGATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	1165	1169	3.361531	AGATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	1367	1371	3.361531	AATCT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	1433	1437	3.361531	AATAT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	1450	1454	3.361531	AGATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	1497	1501	3.361531	ATATT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	134	138	3.361531	AATCT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	211	215	3.361531	ATATT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	440	444	3.361531	AGATT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	917	921	3.361531	AATAT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	1297	1301	3.361531	AATAT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	1662	1666	3.361531	AATAT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	529	533	3.361531	AATAT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	530	534	3.361531	ATATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	684	688	3.361531	AATAT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	685	689	3.361531	ATATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	914	918	3.361531	AGATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1384	1388	3.361531	AGATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1573	1577	3.361531	AGATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1631	1635	3.361531	ATATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1662	1666	3.361531	ATATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1726	1730	3.361531	AATAT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	50	54	3.361531	AGATT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	104	108	3.361531	AATAT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	107	111	3.361531	ATATT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	823	827	3.361531	AATAT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	1216	1220	3.361531	ATATT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	1937	1941	3.361531	ATATT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [	244	248	3.361531	AATCT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [	321	325	3.361531	ATATT	3.90625	3.51525

cg1006492	DIP2C	GR-beta [	550	554	3.361531	AGATT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [	1027	1031	3.361531	AATAT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [	1407	1411	3.361531	AATAT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [	1772	1776	3.361531	AATAT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	174	178	3.361531	AATCT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	251	255	3.361531	ATATT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	480	484	3.361531	AGATT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	957	961	3.361531	AATAT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	1337	1341	3.361531	AATAT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	1702	1706	3.361531	AATAT	3.90625	3.51525
cg027001	DIP2C	c-Ets-1 [T	365	371	3.359159	ACGGAA	0.61035	0.61936
cg1146814	DIP2C	c-Ets-1 [T	956	962	3.359159	ACGGAA	0.61035	0.61936
cg1493188	DIP2C	T3R-beta1	888	896	3.351341	TCACCA	0.27466	0.27326
cg027001	DIP2C	GATA-2 [	745	753	3.333333	TCATTA	0.30518	0.29349
cg1146814	DIP2C	GATA-2 [	1336	1344	3.333333	TCATTA	0.30518	0.29349
cg027001	DIP2C	T3R-beta1	339	347	3.332047	TCACCT	0.27466	0.27326
cg1146814	DIP2C	T3R-beta1	930	938	3.332047	TCACCT	0.27466	0.27326
cg1850223	DIP2C	HNF-1B [	434	442	3.302045	TATTTA	0.04578	0.04011
cg027001	DIP2C	PR B [T00	1468	1474	3.29756	AAATGT	0.24414	0.21408
cg027001	DIP2C	PR A [T01	1468	1474	3.29756	AAATGT	0.24414	0.21408
cg1850223	DIP2C	PR B [T00	581	587	3.29756	AAATGT	0.24414	0.21408
cg1850223	DIP2C	PR B [T00	1470	1476	3.29756	AACATT	0.24414	0.21408
cg1850223	DIP2C	PR A [T01	581	587	3.29756	AAATGT	0.24414	0.21408
cg1850223	DIP2C	PR A [T01	1470	1476	3.29756	AACATT	0.24414	0.21408
cg1493188	DIP2C	PR B [T00	732	738	3.29756	AACATT	0.24414	0.21408
cg1493188	DIP2C	PR B [T00	1168	1174	3.29756	AAATGT	0.24414	0.21408
cg1493188	DIP2C	PR B [T00	1937	1943	3.29756	AACATT	0.24414	0.21408
cg1493188	DIP2C	PR A [T01	732	738	3.29756	AACATT	0.24414	0.21408
cg1493188	DIP2C	PR A [T01	1168	1174	3.29756	AAATGT	0.24414	0.21408
cg1493188	DIP2C	PR A [T01	1937	1943	3.29756	AACATT	0.24414	0.21408
cg1850382	DIP2C	c-Ets-2 [T	745	753	3.2883	TTCCTC	0.18311	0.18314
cg1850382	DIP2C	c-Ets-2 [T	1581	1589	3.2883	TTCCTC	0.18311	0.18314
cg1146814	DIP2C	c-Ets-2 [T	543	551	3.2883	CCTGAG	0.18311	0.18314
cg1006492	DIP2C	c-Ets-2 [T	855	863	3.2883	TTCCTC	0.18311	0.18314
cg1006492	DIP2C	c-Ets-2 [T	1691	1699	3.2883	TTCCTC	0.18311	0.18314
cg0545033	DIP2C	c-Ets-2 [T	785	793	3.2883	TTCCTC	0.18311	0.18314
cg0545033	DIP2C	c-Ets-2 [T	1621	1629	3.2883	TTCCTC	0.18311	0.18314
cg1850223	DIP2C	NF-Y [T0	90	97	3.263282	ATTGGC	0.48828	0.48427
cg1850382	DIP2C	Elk-1 [T00	1580	1588	3.247448	CTTCCT	0.07629	0.07518
cg1006492	DIP2C	Elk-1 [T00	1690	1698	3.247448	CTTCCT	0.07629	0.07518
cg0545033	DIP2C	Elk-1 [T00	1620	1628	3.247448	CTTCCT	0.07629	0.07518
cg027001	DIP2C	AP-2alpha	7	12	3.229049	AGAGGC	0.48828	0.5124
cg027001	DIP2C	AP-2alpha	729	734	3.229049	AGAGGC	0.48828	0.5124
cg027001	DIP2C	AP-2alpha	763	768	3.229049	GCCTCT	0.48828	0.5124
cg027001	DIP2C	AP-2alpha	1005	1010	3.229049	AGAGGC	0.48828	0.5124
cg1850223	DIP2C	AP-2alpha	22	27	3.229049	GCCTCT	0.48828	0.5124
cg1850223	DIP2C	AP-2alpha	280	285	3.229049	AGAGGC	0.48828	0.5124
cg1850223	DIP2C	AP-2alpha	754	759	3.229049	GCCTCT	0.48828	0.5124

cg1850382	DIP2C	AP-2alpha	111	116	3.229049	AGAGGC	0.48828	0.5124
cg1850382	DIP2C	AP-2alpha	251	256	3.229049	AGAGGC	0.48828	0.5124
cg1493188	DIP2C	AP-2alpha	958	963	3.229049	GCCTCT	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	16	21	3.229049	AGAGGC	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	598	603	3.229049	AGAGGC	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	1320	1325	3.229049	AGAGGC	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	1354	1359	3.229049	GCCTCT	0.48828	0.5124
cg1146814	DIP2C	AP-2alpha	1596	1601	3.229049	AGAGGC	0.48828	0.5124
cg1006492	DIP2C	AP-2alpha	48	53	3.229049	GCCTCT	0.48828	0.5124
cg1006492	DIP2C	AP-2alpha	221	226	3.229049	AGAGGC	0.48828	0.5124
cg1006492	DIP2C	AP-2alpha	361	366	3.229049	AGAGGC	0.48828	0.5124
cg0545033	DIP2C	AP-2alpha	151	156	3.229049	AGAGGC	0.48828	0.5124
cg0545033	DIP2C	AP-2alpha	291	296	3.229049	AGAGGC	0.48828	0.5124
cg1850223	DIP2C	RAR-beta	596	605	3.226064	GGGGTT	0.12207	0.12558
cg1850382	DIP2C	RAR-beta	303	312	3.226064	CGGGTT	0.12207	0.12558
cg1850382	DIP2C	RAR-beta	1049	1058	3.226064	TGGGTT	0.12207	0.12558
cg1006492	DIP2C	RAR-beta	413	422	3.226064	CGGGTT	0.12207	0.12558
cg1006492	DIP2C	RAR-beta	1159	1168	3.226064	TGGGTT	0.12207	0.12558
cg0545033	DIP2C	RAR-beta	343	352	3.226064	CGGGTT	0.12207	0.12558
cg0545033	DIP2C	RAR-beta	1089	1098	3.226064	TGGGTT	0.12207	0.12558
cg1850382	DIP2C	ATF-2 [T0	525	534	3.201112	ACCACG	0.06104	0.06208
cg1006492	DIP2C	ATF-2 [T0	635	644	3.201112	ACCACG	0.06104	0.06208
cg0545033	DIP2C	ATF-2 [T0	565	574	3.201112	ACCACG	0.06104	0.06208
cg0270010	DIP2C	RXR-alph	51	57	3.170788	GGGTGT	0.24414	0.24551
cg1850382	DIP2C	RXR-alph	735	741	3.170788	AAAACC	0.24414	0.24551
cg1146814	DIP2C	RXR-alph	642	648	3.170788	GGGTGT	0.24414	0.24551
cg1006492	DIP2C	RXR-alph	845	851	3.170788	AAAACC	0.24414	0.24551
cg0545033	DIP2C	RXR-alph	775	781	3.170788	AAAACC	0.24414	0.24551
cg0270010	DIP2C	c-Fos [T00	250	259	3.154982	TGGCTG	0.06104	0.06233
cg1146814	DIP2C	c-Fos [T00	841	850	3.154982	TGGCTG	0.06104	0.06233
cg0270010	DIP2C	TCF-4E [	1246	1252	3.151193	TGCAAA	0.24414	0.23169
cg1146814	DIP2C	TCF-4E [	97	103	3.151193	CTTTGC	0.24414	0.23169
cg1146814	DIP2C	TCF-4E [	1837	1843	3.151193	TGCAAA	0.24414	0.23169
cg1850223	DIP2C	Elk-1 [T00	1609	1617	3.121991	ACAAGG	0.07629	0.07518
cg1493188	DIP2C	Elk-1 [T00	1916	1924	3.121991	CTTCCTT	0.07629	0.07518
cg0270010	DIP2C	POU2F2 (	656	666	3.116744	TGAATT	0.02575	0.02261
cg1146814	DIP2C	POU2F2 (	1247	1257	3.116744	TGAATT	0.02575	0.02261
cg1850223	DIP2C	c-Ets-1 [T	1808	1814	3.102985	CTTCCG	0.24414	0.26272
cg1493188	DIP2C	NF-AT1 [	740	748	3.098758	AGGCTT	0.03052	0.0304
cg1850382	DIP2C	c-Fos [T00	706	715	3.081206	CTGGTG	0.06104	0.06233
cg1006492	DIP2C	c-Fos [T00	816	825	3.081206	CTGGTG	0.06104	0.06233
cg0545033	DIP2C	c-Fos [T00	746	755	3.081206	CTGGTG	0.06104	0.06233
cg0270010	DIP2C	TFIID [T0	1489	1495	3.075094	TTTTGC	0.12207	0.11309
cg1493188	DIP2C	TFIID [T0	908	914	3.075094	TTTTGC	0.12207	0.11309
cg1493188	DIP2C	TFIID [T0	1577	1583	3.075094	TGCAAA	0.12207	0.11309
cg1493188	DIP2C	Pax-5 [T0	990	996	3.075094	CTCGCC	0.12207	0.13819
cg1493188	DIP2C	NF-AT1 [	929	937	3.075022	AGTGTT	0.03052	0.0304
cg1493188	DIP2C	c-Jun [T00	1592	1598	3.049104	TGACCC	0.24414	0.2435

cg1850382	DIP2C	p53 [T006	1036	1042	3.028543	TGTGCC	0.48828	0.53227
cg1006492	DIP2C	p53 [T006	1146	1152	3.028543	TGTGCC	0.48828	0.53227
cg0545033	DIP2C	p53 [T006	1076	1082	3.028543	TGTGCC	0.48828	0.53227
cg0270010	DIP2C	p53 [T006	801	807	3.024997	GGGCAA	0.48828	0.53227
cg1146814	DIP2C	p53 [T006	1392	1398	3.024997	GGGCAA	0.48828	0.53227
cg1493188	DIP2C	c-Ets-2 [T	1917	1925	3.020647	TTCCTTC	0.06104	0.05567
cg1493188	DIP2C	Elk-1 [T00	1264	1272	2.987643	CTTCCTT	0.07629	0.07518
cg1850382	DIP2C	C/EBPalph	1211	1217	2.981957	CACAAT	0.48828	0.47526
cg1006492	DIP2C	C/EBPalph	1321	1327	2.981957	CACAAT	0.48828	0.47526
cg0545033	DIP2C	C/EBPalph	1251	1257	2.981957	CACAAT	0.48828	0.47526
cg0270010	DIP2C	STAT4 [T	87	92	2.941176	GGAAGT	2.92969	2.92382
cg0270010	DIP2C	STAT4 [T	913	918	2.941176	GATTCC	2.92969	2.92382
cg0270010	DIP2C	STAT4 [T	1100	1105	2.941176	GGAACA	2.92969	2.92382
cg0270010	DIP2C	STAT4 [T	1578	1583	2.941176	TGTTCC	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	245	250	2.941176	GGAACA	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	799	804	2.941176	ACTTCC	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	1042	1047	2.941176	TGTTCC	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	1159	1164	2.941176	GATTCC	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	1177	1182	2.941176	GGTTCC	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	1220	1225	2.941176	GATTCC	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	1451	1456	2.941176	GATTCC	2.92969	2.92382
cg1850223	DIP2C	STAT4 [T	1807	1812	2.941176	ACTTCC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	159	164	2.941176	CTTTCC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	575	580	2.941176	CTTTCC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	743	748	2.941176	GGTTCC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	903	908	2.941176	GGAACC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	1057	1062	2.941176	CTTTCC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	1452	1457	2.941176	CTTTCC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	1579	1584	2.941176	ACTTCC	2.92969	2.92382
cg1850382	DIP2C	STAT4 [T	1599	1604	2.941176	GGAACC	2.92969	2.92382
cg1493188	DIP2C	STAT4 [T	743	748	2.941176	CTTTCC	2.92969	2.92382
cg1493188	DIP2C	STAT4 [T	1116	1121	2.941176	ACTTCC	2.92969	2.92382
cg1493188	DIP2C	STAT4 [T	1277	1282	2.941176	GGAACA	2.92969	2.92382
cg1493188	DIP2C	STAT4 [T	1461	1466	2.941176	ACTTCC	2.92969	2.92382
cg1493188	DIP2C	STAT4 [T	1836	1841	2.941176	CTTTCC	2.92969	2.92382
cg1146814	DIP2C	STAT4 [T	678	683	2.941176	GGAAGT	2.92969	2.92382
cg1146814	DIP2C	STAT4 [T	1504	1509	2.941176	GATTCC	2.92969	2.92382
cg1146814	DIP2C	STAT4 [T	1691	1696	2.941176	GGAACA	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	67	72	2.941176	TGTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	75	80	2.941176	CTTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	269	274	2.941176	CTTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	685	690	2.941176	CTTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	853	858	2.941176	GGTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	1013	1018	2.941176	GGAACC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	1167	1172	2.941176	CTTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	1562	1567	2.941176	CTTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	1689	1694	2.941176	ACTTCC	2.92969	2.92382
cg1006492	DIP2C	STAT4 [T	1709	1714	2.941176	GGAACC	2.92969	2.92382

cg0545033	DIP2C	STAT4 [T	5	10	2.941176	CTTTCC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	199	204	2.941176	CTTTCC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	615	620	2.941176	CTTTCC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	783	788	2.941176	GGTTCC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	943	948	2.941176	GGAACC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	1097	1102	2.941176	CTTTCC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	1492	1497	2.941176	CTTTCC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	1619	1624	2.941176	ACTTCC	2.92969	2.92382
cg0545033	DIP2C	STAT4 [T	1639	1644	2.941176	GGAACC	2.92969	2.92382
cg1493188	DIP2C	IRF-1 [T0	744	752	2.890712	TTTCCTT	0.07629	0.07093
cg1493188	DIP2C	IRF-1 [T0	1490	1498	2.890712	ACAAGG	0.07629	0.07093
cg0270010	DIP2C	p53 [T006	118	124	2.813291	GGGCAG	0.48828	0.53227
cg0270010	DIP2C	p53 [T006	566	572	2.813291	GCTGCC	0.48828	0.53227
cg1850223	DIP2C	p53 [T006	1066	1072	2.813291	GGGCAG	0.48828	0.53227
cg1850223	DIP2C	p53 [T006	1293	1299	2.813291	GATGCC	0.48828	0.53227
cg1146814	DIP2C	p53 [T006	709	715	2.813291	GGGCAG	0.48828	0.53227
cg1146814	DIP2C	p53 [T006	1157	1163	2.813291	GCTGCC	0.48828	0.53227
cg1850223	DIP2C	NF-1 [T00	391	398	2.813149	GGGCCC	0.24414	0.2566
cg1850223	DIP2C	PR B [T00	95	101	2.80933	CATTGT	0.73242	0.66711
cg1850223	DIP2C	PR B [T00	1195	1201	2.80933	AACATT	0.73242	0.66711
cg1850223	DIP2C	PR A [T01	95	101	2.80933	CATTGT	0.73242	0.66711
cg1850223	DIP2C	PR A [T01	1195	1201	2.80933	AACATT	0.73242	0.66711
cg1850382	DIP2C	PR B [T00	1111	1117	2.80933	AACATT	0.73242	0.66711
cg1850382	DIP2C	PR B [T00	1153	1159	2.80933	AACATT	0.73242	0.66711
cg1850382	DIP2C	PR B [T00	1213	1219	2.80933	CAATGT	0.73242	0.66711
cg1850382	DIP2C	PR A [T01	1111	1117	2.80933	AACATT	0.73242	0.66711
cg1850382	DIP2C	PR A [T01	1153	1159	2.80933	AACATT	0.73242	0.66711
cg1850382	DIP2C	PR A [T01	1213	1219	2.80933	CAATGT	0.73242	0.66711
cg1006492	DIP2C	PR B [T00	1221	1227	2.80933	AACATT	0.73242	0.66711
cg1006492	DIP2C	PR B [T00	1263	1269	2.80933	AACATT	0.73242	0.66711
cg1006492	DIP2C	PR B [T00	1323	1329	2.80933	CAATGT	0.73242	0.66711
cg1006492	DIP2C	PR A [T01	1221	1227	2.80933	AACATT	0.73242	0.66711
cg1006492	DIP2C	PR A [T01	1263	1269	2.80933	AACATT	0.73242	0.66711
cg1006492	DIP2C	PR A [T01	1323	1329	2.80933	CAATGT	0.73242	0.66711
cg0545033	DIP2C	PR B [T00	1151	1157	2.80933	AACATT	0.73242	0.66711
cg0545033	DIP2C	PR B [T00	1193	1199	2.80933	AACATT	0.73242	0.66711
cg0545033	DIP2C	PR B [T00	1253	1259	2.80933	CAATGT	0.73242	0.66711
cg0545033	DIP2C	PR A [T01	1151	1157	2.80933	AACATT	0.73242	0.66711
cg0545033	DIP2C	PR A [T01	1193	1199	2.80933	AACATT	0.73242	0.66711
cg0545033	DIP2C	PR A [T01	1253	1259	2.80933	CAATGT	0.73242	0.66711
cg0270010	DIP2C	TBP [T007	1346	1355	2.807313	ATATTA	0.12207	0.10444
cg1850223	DIP2C	TBP [T007	543	552	2.807313	CCCATA	0.12207	0.10444
cg1493188	DIP2C	TBP [T007	690	699	2.807313	CTTTTAT	0.12207	0.10444
cg1493188	DIP2C	TBP [T007	692	701	2.807313	TTTATA	0.12207	0.10444
cg1146814	DIP2C	TBP [T007	1937	1946	2.807313	ATATTA	0.12207	0.10444
cg1493188	DIP2C	NF-AT1 [	1469	1478	2.756277	CTATTTT	0.05913	0.05541
cg1146814	DIP2C	NF-AT1 [	90	99	2.756277	TGGAAA	0.05913	0.05541
cg1850382	DIP2C	CTF [T001	715	726	2.746279	CAGCCA	0.0062	0.0062

cg1006492	DIP2C	CTF [T001	825	836	2.746279	CAGCCA	0.0062	0.0062
cg0545033	DIP2C	CTF [T001	755	766	2.746279	CAGCCA	0.0062	0.0062
cg1850382	DIP2C	AR [T000	1422	1430	2.733525	AAACTG	0.11444	0.11078
cg1006492	DIP2C	AR [T000	1532	1540	2.733525	AAACTG	0.11444	0.11078
cg0545033	DIP2C	AR [T000	1462	1470	2.733525	AAACTG	0.11444	0.11078
cg1850223	DIP2C	CREB [T0	80	88	2.702696	TGACGT	0.06104	0.05921
cg1850382	DIP2C	PXR-1:RX	765	772	2.577808	GCAGTT	0.12207	0.11843
cg1006492	DIP2C	PXR-1:RX	875	882	2.577808	GCAGTT	0.12207	0.11843
cg0545033	DIP2C	PXR-1:RX	805	812	2.577808	GCAGTT	0.12207	0.11843
cg1850223	DIP2C	LEF-1 [T0	1917	1924	2.558995	CACCAA	0.09155	0.09076
cg1850382	DIP2C	LEF-1 [T0	532	539	2.558995	CACCAA	0.09155	0.09076
cg1146814	DIP2C	LEF-1 [T0	377	384	2.558995	CACCAA	0.09155	0.09076
cg1006492	DIP2C	LEF-1 [T0	642	649	2.558995	CACCAA	0.09155	0.09076
cg0545033	DIP2C	LEF-1 [T0	572	579	2.558995	CACCAA	0.09155	0.09076
cg027001	DIP2C	AP-2alpha	205	210	2.550491	TGAGGC	0.48828	0.51216
cg027001	DIP2C	AP-2alpha	1181	1186	2.550491	GCCTCA	0.48828	0.51216
cg027001	DIP2C	AP-2alpha	1433	1438	2.550491	TGAGGC	0.48828	0.51216
cg1850382	DIP2C	AP-2alpha	941	946	2.550491	TGAGGC	0.48828	0.51216
cg1850382	DIP2C	AP-2alpha	1432	1437	2.550491	TGAGGC	0.48828	0.51216
cg1850382	DIP2C	AP-2alpha	1882	1887	2.550491	TGAGGC	0.48828	0.51216
cg1146814	DIP2C	AP-2alpha	588	593	2.550491	GCCTCA	0.48828	0.51216
cg1146814	DIP2C	AP-2alpha	796	801	2.550491	TGAGGC	0.48828	0.51216
cg1146814	DIP2C	AP-2alpha	1772	1777	2.550491	GCCTCA	0.48828	0.51216
cg1006492	DIP2C	AP-2alpha	1051	1056	2.550491	TGAGGC	0.48828	0.51216
cg1006492	DIP2C	AP-2alpha	1542	1547	2.550491	TGAGGC	0.48828	0.51216
cg1006492	DIP2C	AP-2alpha	1992	1997	2.550491	TGAGGC	0.48828	0.51216
cg0545033	DIP2C	AP-2alpha	981	986	2.550491	TGAGGC	0.48828	0.51216
cg0545033	DIP2C	AP-2alpha	1472	1477	2.550491	TGAGGC	0.48828	0.51216
cg0545033	DIP2C	AP-2alpha	1922	1927	2.550491	TGAGGC	0.48828	0.51216
cg027001	DIP2C	RXR-alph	403	409	2.544678	AGAACC	0.85449	0.89683
cg027001	DIP2C	RXR-alph	490	496	2.544678	TGCACC	0.85449	0.89683
cg027001	DIP2C	RXR-alph	1798	1804	2.544678	GGGTGC	0.85449	0.89683
cg1850223	DIP2C	RXR-alph	1879	1885	2.544678	AGAACC	0.85449	0.89683
cg1850223	DIP2C	RXR-alph	1967	1973	2.544678	GGGTTC	0.85449	0.89683
cg1146814	DIP2C	RXR-alph	179	185	2.544678	TGCACC	0.85449	0.89683
cg1146814	DIP2C	RXR-alph	994	1000	2.544678	AGAACC	0.85449	0.89683
cg1146814	DIP2C	RXR-alph	1081	1087	2.544678	TGCACC	0.85449	0.89683
cg1850223	DIP2C	PXR-1:RX	337	344	2.454225	GTAGTT	0.12207	0.11843
cg1850382	DIP2C	C/EBPalp	144	150	2.441016	CTCAAT	0.48828	0.47439
cg1850382	DIP2C	C/EBPalp	1437	1443	2.441016	CTCAAT	0.48828	0.47439
cg1006492	DIP2C	C/EBPalp	254	260	2.441016	CTCAAT	0.48828	0.47439
cg1006492	DIP2C	C/EBPalp	1547	1553	2.441016	CTCAAT	0.48828	0.47439
cg0545033	DIP2C	C/EBPalp	184	190	2.441016	CTCAAT	0.48828	0.47439
cg0545033	DIP2C	C/EBPalp	1477	1483	2.441016	CTCAAT	0.48828	0.47439
cg1850382	DIP2C	IRF-1 [T0	99	107	2.418514	GAAGGG	0.02289	0.02196
cg1006492	DIP2C	IRF-1 [T0	209	217	2.418514	GAAGGG	0.02289	0.02196
cg0545033	DIP2C	IRF-1 [T0	139	147	2.418514	GAAGGG	0.02289	0.02196
cg1493188	DIP2C	HNF-1C [	641	649	2.372238	GTTATT	0.04578	0.04064

cg1493188	DIP2C	C/EBPalp	605	611	2.371703	AATTGT	0.48828	0.47439
cg1850382	DIP2C	NF-Y [T0	715	722	2.355069	CAGCCA	0.21362	0.20842
cg1006492	DIP2C	NF-Y [T0	825	832	2.355069	CAGCCA	0.21362	0.20842
cg0545033	DIP2C	NF-Y [T0	755	762	2.355069	CAGCCA	0.21362	0.20842
cg027001	DIP2C	c-Jun [T00	314	320	2.345465	TGACAC	0.48828	0.48077
cg027001	DIP2C	c-Jun [T00	1474	1480	2.345465	TGTGTC	0.48828	0.48077
cg1146814	DIP2C	c-Jun [T00	905	911	2.345465	TGACAC	0.48828	0.48077
cg1146814	DIP2C	LEF-1 [T0	359	366	2.345041	CTTTGCT	0.09155	0.09076
cg1850223	DIP2C	GCF [T00	1890	1898	2.339499	AGCCTG	0.06104	0.06908
cg1493188	DIP2C	GCF [T00	1838	1846	2.339499	TTCCTGC	0.06104	0.06908
cg027001	DIP2C	VDR [T00	1808	1816	2.308561	CCAGTG	0.10681	0.1091
cg1493188	DIP2C	T3R-beta1	1397	1405	2.259951	GGGAGG	0.03052	0.03203
cg1850382	DIP2C	T3R-beta1	348	356	2.240658	TCACCA	0.15259	0.15303
cg1006492	DIP2C	T3R-beta1	458	466	2.240658	TCACCA	0.15259	0.15303
cg0545033	DIP2C	T3R-beta1	388	396	2.240658	TCACCA	0.15259	0.15303
cg1850382	DIP2C	GATA-2 [	504	512	2.222222	AGATAG	0.22888	0.21978
cg1006492	DIP2C	GATA-2 [	614	622	2.222222	AGATAG	0.22888	0.21978
cg0545033	DIP2C	GATA-2 [	544	552	2.222222	AGATAG	0.22888	0.21978
cg1850382	DIP2C	T3R-beta1	531	539	2.221365	TCACCA	0.15259	0.15303
cg1850382	DIP2C	T3R-beta1	1895	1903	2.221365	TCACCT	0.15259	0.15303
cg1146814	DIP2C	T3R-beta1	376	384	2.221365	TCACCA	0.15259	0.15303
cg1006492	DIP2C	T3R-beta1	641	649	2.221365	TCACCA	0.15259	0.15303
cg0545033	DIP2C	T3R-beta1	571	579	2.221365	TCACCA	0.15259	0.15303
cg0545033	DIP2C	T3R-beta1	1935	1943	2.221365	TCACCT	0.15259	0.15303
cg1850223	DIP2C	LEF-1 [T0	1672	1679	2.21836	AACCAA	0.18311	0.17215
cg1850223	DIP2C	c-Ets-2 [T	182	190	2.217136	GATGAG	0.16785	0.16456
cg1850223	DIP2C	GATA-1 [	482	487	2.176375	TATCCA	3.90625	3.79558
cg1850223	DIP2C	GATA-1 [	613	618	2.176375	TGGATA	3.90625	3.79558
cg1850223	DIP2C	GATA-1 [	1558	1563	2.176375	AGGATA	3.90625	3.79558
cg1850382	DIP2C	GATA-1 [	208	213	2.176375	TGGATA	3.90625	3.79558
cg1850382	DIP2C	GATA-1 [	1287	1292	2.176375	AGGATA	3.90625	3.79558
cg1493188	DIP2C	GATA-1 [	1081	1086	2.176375	TATCCT	3.90625	3.79558
cg1493188	DIP2C	GATA-1 [	1456	1461	2.176375	TGGATA	3.90625	3.79558
cg1493188	DIP2C	GATA-1 [	1728	1733	2.176375	TATCCA	3.90625	3.79558
cg1006492	DIP2C	GATA-1 [	318	323	2.176375	TGGATA	3.90625	3.79558
cg1006492	DIP2C	GATA-1 [	1397	1402	2.176375	AGGATA	3.90625	3.79558
cg0545033	DIP2C	GATA-1 [	248	253	2.176375	TGGATA	3.90625	3.79558
cg0545033	DIP2C	GATA-1 [	1327	1332	2.176375	AGGATA	3.90625	3.79558
cg1850223	DIP2C	Elk-1 [T00	1869	1877	2.164966	CTTCCTC	0.05341	0.05461
cg1850382	DIP2C	Elk-1 [T00	1066	1074	2.164966	CTTCCTC	0.05341	0.05461
cg1006492	DIP2C	Elk-1 [T00	1176	1184	2.164966	CTTCCTC	0.05341	0.05461
cg0545033	DIP2C	Elk-1 [T00	1106	1114	2.164966	CTTCCTC	0.05341	0.05461
cg1493188	DIP2C	USF1 [T0	1731	1740	2.121976	CCACCA	0.03624	0.03891
cg027001	DIP2C	AP-2alpha	1058	1063	2.098119	GCCTCG	0.97656	1.07805
cg1850382	DIP2C	AP-2alpha	898	903	2.098119	GCCTCG	0.97656	1.07805
cg1146814	DIP2C	AP-2alpha	274	279	2.098119	CGAGGC	0.97656	1.07805
cg1146814	DIP2C	AP-2alpha	1649	1654	2.098119	GCCTCG	0.97656	1.07805
cg1006492	DIP2C	AP-2alpha	1008	1013	2.098119	GCCTCG	0.97656	1.07805

cg0545033	DIP2C	AP-2alpha	938	943	2.098119	GCCTCG	0.97656	1.07805
cg0270010	DIP2C	NF-1 [T00	722	729	2.067686	TGTCCCA	0.12207	0.12476
cg1850382	DIP2C	NF-1 [T00	395	402	2.067686	TTGGCAC	0.12207	0.12476
cg1850382	DIP2C	NF-1 [T00	1676	1683	2.067686	TGTGCCA	0.12207	0.12476
cg1146814	DIP2C	NF-1 [T00	1313	1320	2.067686	TGTCCCA	0.12207	0.12476
cg1006492	DIP2C	NF-1 [T00	505	512	2.067686	TTGGCAC	0.12207	0.12476
cg1006492	DIP2C	NF-1 [T00	1786	1793	2.067686	TGTGCCA	0.12207	0.12476
cg0545033	DIP2C	NF-1 [T00	435	442	2.067686	TTGGCAC	0.12207	0.12476
cg0545033	DIP2C	NF-1 [T00	1716	1723	2.067686	TGTGCCA	0.12207	0.12476
cg0270010	DIP2C	Sp1 [T007	152	161	2.067619	AGGGCG	0.03624	0.04341
cg1850223	DIP2C	Sp1 [T007	1295	1304	2.067619	TGCCCGC	0.03624	0.04341
cg1146814	DIP2C	Sp1 [T007	743	752	2.067619	AGGGCG	0.03624	0.04341
cg0270010	DIP2C	NF-AT1 [T	1260	1269	2.067208	TGGAAA	0.03815	0.03545
cg1146814	DIP2C	NF-AT1 [T	1851	1860	2.067208	TGGAAA	0.03815	0.03545
cg1146814	DIP2C	Sp1 [T007	188	197	2.043035	GACCCGC	0.03624	0.04341
cg1850382	DIP2C	PPAR-alph	1723	1733	2.028114	CACTGGC	0.00668	0.00699
cg1006492	DIP2C	PPAR-alph	1833	1843	2.028114	CACTGGC	0.00668	0.00699
cg0545033	DIP2C	PPAR-alph	1763	1773	2.028114	CACTGGC	0.00668	0.00699
cg1493188	DIP2C	GATA-1 [	1518	1523	2.001358	GGGATA	3.90625	3.79558
cg1146814	DIP2C	NF-AT1 [T	91	99	1.970716	GGAAAA	0.06866	0.0623
cg0270010	DIP2C	PR B [T00	1575	1581	1.892895	AAGTGTT	0.12207	0.1127
cg0270010	DIP2C	PR A [T01	1575	1581	1.892895	AAGTGTT	0.12207	0.1127
cg1850382	DIP2C	PR B [T00	1867	1873	1.892895	AACACTT	0.12207	0.1127
cg1850382	DIP2C	PR A [T01	1867	1873	1.892895	AACACTT	0.12207	0.1127
cg1006492	DIP2C	PR B [T00	1977	1983	1.892895	AACACTT	0.12207	0.1127
cg1006492	DIP2C	PR A [T01	1977	1983	1.892895	AACACTT	0.12207	0.1127
cg0545033	DIP2C	PR B [T00	1907	1913	1.892895	AACACTT	0.12207	0.1127
cg0545033	DIP2C	PR A [T01	1907	1913	1.892895	AACACTT	0.12207	0.1127
cg1850223	DIP2C	c-Ets-2 [T	1044	1052	1.874674	TTCCTTT	0.16785	0.16456
cg0270010	DIP2C	AP-2alpha	177	182	1.871933	GGAGGC	0.97656	1.07805
cg0270010	DIP2C	AP-2alpha	461	466	1.871933	GGAGGC	0.97656	1.07805
cg0270010	DIP2C	AP-2alpha	936	941	1.871933	GGAGGC	0.97656	1.07805
cg0270010	DIP2C	AP-2alpha	1711	1716	1.871933	GCCTCC	0.97656	1.07805
cg1850382	DIP2C	AP-2alpha	459	464	1.871933	GGAGGC	0.97656	1.07805
cg1850382	DIP2C	AP-2alpha	974	979	1.871933	GGAGGC	0.97656	1.07805
cg1850382	DIP2C	AP-2alpha	1876	1881	1.871933	GGAGGC	0.97656	1.07805
cg1493188	DIP2C	AP-2alpha	1058	1063	1.871933	GCCTCC	0.97656	1.07805
cg1493188	DIP2C	AP-2alpha	1988	1993	1.871933	GGAGGC	0.97656	1.07805
cg1146814	DIP2C	AP-2alpha	768	773	1.871933	GGAGGC	0.97656	1.07805
cg1146814	DIP2C	AP-2alpha	1052	1057	1.871933	GGAGGC	0.97656	1.07805
cg1146814	DIP2C	AP-2alpha	1527	1532	1.871933	GGAGGC	0.97656	1.07805
cg1006492	DIP2C	AP-2alpha	569	574	1.871933	GGAGGC	0.97656	1.07805
cg1006492	DIP2C	AP-2alpha	1084	1089	1.871933	GGAGGC	0.97656	1.07805
cg1006492	DIP2C	AP-2alpha	1986	1991	1.871933	GGAGGC	0.97656	1.07805
cg0545033	DIP2C	AP-2alpha	499	504	1.871933	GGAGGC	0.97656	1.07805
cg0545033	DIP2C	AP-2alpha	1014	1019	1.871933	GGAGGC	0.97656	1.07805
cg0545033	DIP2C	AP-2alpha	1916	1921	1.871933	GGAGGC	0.97656	1.07805
cg1850223	DIP2C	TBP [T007	134	143	1.871542	AACCTAT	0.18311	0.15671

cg1850223	DIP2C	TBP [T007	844	853	1.871542	AGACTA	0.18311	0.15671
cg1493188	DIP2C	TBP [T007	645	654	1.871542	TTTATAA	0.18311	0.15671
cg0270010	DIP2C	PPAR-alpl	1826	1836	1.869153	TACTGG(	0.00668	0.00699
cg1850223	DIP2C	C/EBPalpl	1145	1151	1.830762	CTCAAT	0.48828	0.46352
cg1850382	DIP2C	C/EBPalpl	14	20	1.830762	CTCAAT	0.48828	0.46352
cg1006492	DIP2C	C/EBPalpl	124	130	1.830762	CTCAAT	0.48828	0.46352
cg0545033	DIP2C	C/EBPalpl	54	60	1.830762	CTCAAT	0.48828	0.46352
cg0270010	DIP2C	TFII-I [T0	146	151	1.824994	CTCTCC	0.48828	0.51201
cg0270010	DIP2C	TFII-I [T0	300	305	1.824994	GGAGAG	0.48828	0.51201
cg1850223	DIP2C	TFII-I [T0	278	283	1.824994	GGAGAG	0.48828	0.51201
cg1850223	DIP2C	TFII-I [T0	1701	1706	1.824994	GGAGAG	0.48828	0.51201
cg1850382	DIP2C	FOXP3 [T	122	127	1.824994	GTTGTA	0.48828	0.46414
cg1850382	DIP2C	FOXP3 [T	782	787	1.824994	TACAAC	0.48828	0.46414
cg1850382	DIP2C	FOXP3 [T	1416	1421	1.824994	TACAAC	0.48828	0.46414
cg1850382	DIP2C	TFII-I [T0	773	778	1.824994	GGAGAG	0.48828	0.51201
cg1493188	DIP2C	TFII-I [T0	820	825	1.824994	GGAGAG	0.48828	0.51201
cg1146814	DIP2C	TFII-I [T0	737	742	1.824994	CTCTCC	0.48828	0.51201
cg1146814	DIP2C	TFII-I [T0	891	896	1.824994	GGAGAG	0.48828	0.51201
cg1006492	DIP2C	FOXP3 [T	232	237	1.824994	GTTGTA	0.48828	0.46414
cg1006492	DIP2C	FOXP3 [T	892	897	1.824994	TACAAC	0.48828	0.46414
cg1006492	DIP2C	FOXP3 [T	1526	1531	1.824994	TACAAC	0.48828	0.46414
cg1006492	DIP2C	TFII-I [T0	40	45	1.824994	CTCTCC	0.48828	0.51201
cg1006492	DIP2C	TFII-I [T0	883	888	1.824994	GGAGAG	0.48828	0.51201
cg0545033	DIP2C	FOXP3 [T	162	167	1.824994	GTTGTA	0.48828	0.46414
cg0545033	DIP2C	FOXP3 [T	822	827	1.824994	TACAAC	0.48828	0.46414
cg0545033	DIP2C	FOXP3 [T	1456	1461	1.824994	TACAAC	0.48828	0.46414
cg0545033	DIP2C	TFII-I [T0	813	818	1.824994	GGAGAG	0.48828	0.51201
cg1850223	DIP2C	c-Ets-1 [T(	1122	1128	1.769212	TAGGAA	0.12207	0.11281
cg1850382	DIP2C	c-Ets-1 [T(	1058	1064	1.769212	TTTCCTA	0.12207	0.11281
cg1493188	DIP2C	c-Ets-1 [T(	1671	1677	1.769212	TTTCCTA	0.12207	0.11281
cg1006492	DIP2C	c-Ets-1 [T(	1168	1174	1.769212	TTTCCTA	0.12207	0.11281
cg0545033	DIP2C	c-Ets-1 [T(	1098	1104	1.769212	TTTCCTA	0.12207	0.11281
cg1850223	DIP2C	C/EBPalpl	1430	1436	1.761449	CCCAAT	0.48828	0.46352
cg1850382	DIP2C	C/EBPalpl	399	405	1.761449	CACAAT	0.48828	0.46352
cg1006492	DIP2C	C/EBPalpl	509	515	1.761449	CACAAT	0.48828	0.46352
cg0545033	DIP2C	C/EBPalpl	439	445	1.761449	CACAAT	0.48828	0.46352
cg1850223	DIP2C	p53 [T006	1686	1692	1.758307	GGGCAG	0.36621	0.38097
cg1850382	DIP2C	p53 [T006	1636	1642	1.758307	GGGCAG	0.36621	0.38097
cg1006492	DIP2C	p53 [T006	1746	1752	1.758307	GGGCAG	0.36621	0.38097
cg0545033	DIP2C	p53 [T006	1676	1682	1.758307	GGGCAG	0.36621	0.38097
cg0270010	DIP2C	NF-Y [T0(	1830	1837	1.749852	GGGCCA	0.18311	0.17671
cg1006492	DIP2C	AR [T000	61	69	1.727468	GGACAG	0.09155	0.09239
cg1850223	DIP2C	RXR-alpha	1851	1857	1.696452	GGGTCC(	0.48828	0.52093
cg1850382	DIP2C	RXR-alpha	1391	1397	1.696452	CTGACC(	0.48828	0.52093
cg1493188	DIP2C	RXR-alpha	163	169	1.696452	GGGTCC(	0.48828	0.52093
cg1006492	DIP2C	RXR-alpha	1501	1507	1.696452	CTGACC(	0.48828	0.52093
cg0545033	DIP2C	RXR-alpha	1431	1437	1.696452	CTGACC(	0.48828	0.52093
cg0270010	DIP2C	GR-beta [T	657	661	1.680765	GAATT	3.90625	3.70067

cg0270010	DIP2C	GR-beta [T	1244	1248	1.680765	AATGC	3.90625	3.70067
cg0270010	DIP2C	GR-beta [T	1406	1410	1.680765	GCATT	3.90625	3.70067
cg1850223	DIP2C	GR-beta [T	58	62	1.680765	GCATT	3.90625	3.70067
cg1850223	DIP2C	GR-beta [T	94	98	1.680765	GCATT	3.90625	3.70067
cg1850223	DIP2C	GR-beta [T	1184	1188	1.680765	GAATT	3.90625	3.70067
cg1850223	DIP2C	GR-beta [T	1243	1247	1.680765	AATTC	3.90625	3.70067
cg1850223	DIP2C	GR-beta [T	1582	1586	1.680765	AATGC	3.90625	3.70067
cg1850382	DIP2C	GR-beta [T	17	21	1.680765	AATTC	3.90625	3.70067
cg1850382	DIP2C	GR-beta [T	566	570	1.680765	AATGC	3.90625	3.70067
cg1850382	DIP2C	GR-beta [T	1090	1094	1.680765	GCATT	3.90625	3.70067
cg1850382	DIP2C	GR-beta [T	1223	1227	1.680765	AATGC	3.90625	3.70067
cg1850382	DIP2C	GR-beta [T	1258	1262	1.680765	AATGC	3.90625	3.70067
cg1850382	DIP2C	GR-beta [T	1612	1616	1.680765	AATGC	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	550	554	1.680765	GAATT	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	551	555	1.680765	AATTC	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	708	712	1.680765	AATTC	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	724	728	1.680765	AATTC	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	1359	1363	1.680765	AATTC	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	1410	1414	1.680765	GCATT	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	1497	1501	1.680765	AATGC	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	1553	1557	1.680765	AATGC	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	1612	1616	1.680765	GAATT	3.90625	3.70067
cg1493188	DIP2C	GR-beta [T	1640	1644	1.680765	GAATT	3.90625	3.70067
cg1146814	DIP2C	GR-beta [T	69	73	1.680765	AATTC	3.90625	3.70067
cg1146814	DIP2C	GR-beta [T	1248	1252	1.680765	GAATT	3.90625	3.70067
cg1146814	DIP2C	GR-beta [T	1835	1839	1.680765	AATGC	3.90625	3.70067
cg1006492	DIP2C	GR-beta [T	127	131	1.680765	AATTC	3.90625	3.70067
cg1006492	DIP2C	GR-beta [T	676	680	1.680765	AATGC	3.90625	3.70067
cg1006492	DIP2C	GR-beta [T	1200	1204	1.680765	GCATT	3.90625	3.70067
cg1006492	DIP2C	GR-beta [T	1333	1337	1.680765	AATGC	3.90625	3.70067
cg1006492	DIP2C	GR-beta [T	1368	1372	1.680765	AATGC	3.90625	3.70067
cg1006492	DIP2C	GR-beta [T	1722	1726	1.680765	AATGC	3.90625	3.70067
cg0545033	DIP2C	GR-beta [T	57	61	1.680765	AATTC	3.90625	3.70067
cg0545033	DIP2C	GR-beta [T	606	610	1.680765	AATGC	3.90625	3.70067
cg0545033	DIP2C	GR-beta [T	1130	1134	1.680765	GCATT	3.90625	3.70067
cg0545033	DIP2C	GR-beta [T	1263	1267	1.680765	AATGC	3.90625	3.70067
cg0545033	DIP2C	GR-beta [T	1298	1302	1.680765	AATGC	3.90625	3.70067
cg0545033	DIP2C	GR-beta [T	1652	1656	1.680765	AATGC	3.90625	3.70067
cg1850223	DIP2C	c-Ets-2 [T(	1643	1651	1.64415	AAGGAG	0.04578	0.04602
cg1850382	DIP2C	c-Ets-2 [T(	858	866	1.64415	GAGGAG	0.04578	0.04602
cg1006492	DIP2C	c-Ets-2 [T(	968	976	1.64415	GAGGAG	0.04578	0.04602
cg0545033	DIP2C	c-Ets-2 [T(	898	906	1.64415	GAGGAG	0.04578	0.04602
cg1850223	DIP2C	c-Ets-1 [T(	670	676	1.641124	AAGGAA	0.36621	0.35197
cg1493188	DIP2C	c-Ets-1 [T(	744	750	1.641124	TTTCCTT	0.36621	0.35197
cg1493188	DIP2C	c-Ets-1 [T(	1492	1498	1.641124	AAGGAA	0.36621	0.35197
cg0270010	DIP2C	C/EBPbeta	85	88	1.639871	TTGG	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	162	165	1.639871	CCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	298	301	1.639871	TTGG	15.625	15.23827

cg0270010	DIP2C	C/EBPbeta	527	530	1.639871	TTGG	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	556	559	1.639871	TTGG	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	726	729	1.639871	CCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	901	904	1.639871	TTGG	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1394	1397	1.639871	CCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1466	1469	1.639871	CCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1833	1836	1.639871	CCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1917	1920	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	17	20	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	91	94	1.639871	TTGG	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	285	288	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	395	398	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	485	488	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	612	615	1.639871	TTGG	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	637	640	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	773	776	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	857	860	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	877	880	1.639871	TTGG	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1139	1142	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1231	1234	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1431	1434	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1637	1640	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1659	1662	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1674	1677	1.639871	CCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1919	1922	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	56	59	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	73	76	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	311	314	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	351	354	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	395	398	1.639871	TTGG	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	534	537	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	599	602	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	718	721	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	885	888	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1101	1104	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1363	1366	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1606	1609	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1651	1654	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1680	1683	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1704	1707	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1752	1755	1.639871	TTGG	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1865	1868	1.639871	CCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1873	1876	1.639871	TTGG	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1928	1931	1.639871	CCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	547	550	1.639871	TTGG	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	936	939	1.639871	CCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1149	1152	1.639871	CCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1455	1458	1.639871	TTGG	15.625	15.23827

cg1493188	DIP2C	C/EBPbeta	1465	1468	1.639871	CCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1476	1479	1.639871	CCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1570	1573	1.639871	CCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1812	1815	1.639871	CCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1870	1873	1.639871	TTGG	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1943	1946	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	30	33	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	137	140	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	146	149	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	234	237	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	325	328	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	379	382	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	405	408	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	526	529	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	676	679	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	753	756	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	889	892	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1118	1121	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1147	1150	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1317	1320	1.639871	CCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1492	1495	1.639871	TTGG	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1985	1988	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	7	10	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	166	169	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	183	186	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	421	424	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	461	464	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	505	508	1.639871	TTGG	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	644	647	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	709	712	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	828	831	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	995	998	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1211	1214	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1473	1476	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1716	1719	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1761	1764	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1790	1793	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1814	1817	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1862	1865	1.639871	TTGG	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1975	1978	1.639871	CCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1983	1986	1.639871	TTGG	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	96	99	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	113	116	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	351	354	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	391	394	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	435	438	1.639871	TTGG	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	574	577	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	639	642	1.639871	CCAA	15.625	15.23827

cg0545033	DIP2C	C/EBPbeta	758	761	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	925	928	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1141	1144	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1403	1406	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1646	1649	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1691	1694	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1720	1723	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1744	1747	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1792	1795	1.639871	TTGG	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1905	1908	1.639871	CCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1913	1916	1.639871	TTGG	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1968	1971	1.639871	CCAA	15.625	15.23827
cg027001	DIP2C	AR [T000	1734	1742	1.618276	GGACAG	0.09155	0.09239
cg027001	DIP2C	XBP-1 [T	634	639	1.583727	ATGACA	0.97656	0.94995
cg027001	DIP2C	XBP-1 [T	818	823	1.583727	ATGACA	0.97656	0.94995
cg027001	DIP2C	XBP-1 [T	1692	1697	1.583727	ATGACA	0.97656	0.94995
cg1850382	DIP2C	XBP-1 [T	1130	1135	1.583727	TGTCAT	0.97656	0.94995
cg1493188	DIP2C	XBP-1 [T	1193	1198	1.583727	TGTCAT	0.97656	0.94995
cg1493188	DIP2C	XBP-1 [T	1591	1596	1.583727	ATGACC	0.97656	0.94995
cg1493188	DIP2C	XBP-1 [T	1627	1632	1.583727	GGTCAT	0.97656	0.94995
cg1146814	DIP2C	XBP-1 [T	1225	1230	1.583727	ATGACA	0.97656	0.94995
cg1146814	DIP2C	XBP-1 [T	1409	1414	1.583727	ATGACA	0.97656	0.94995
cg1006492	DIP2C	XBP-1 [T	1240	1245	1.583727	TGTCAT	0.97656	0.94995
cg0545033	DIP2C	XBP-1 [T	1170	1175	1.583727	TGTCAT	0.97656	0.94995
cg027001	DIP2C	TFIID [T0	1260	1266	1.537547	TGGAAA	0.73242	0.65627
cg027001	DIP2C	Pax-5 [T0	153	159	1.537547	GGGCGG	0.73242	0.83087
cg027001	DIP2C	Pax-5 [T0	947	953	1.537547	GGGCTA	0.73242	0.83087
cg1850223	DIP2C	TFIID [T0	300	306	1.537547	TTCAAA	0.73242	0.65627
cg1850223	DIP2C	TFIID [T0	452	458	1.537547	TACAAA	0.73242	0.65627
cg1850223	DIP2C	TFIID [T0	484	490	1.537547	TCCAAA	0.73242	0.65627
cg1850223	DIP2C	Pax-5 [T0	1226	1232	1.537547	CTTGCC	0.73242	0.83087
cg1850223	DIP2C	Pax-5 [T0	1297	1303	1.537547	CCCGCC	0.73242	0.83087
cg1850382	DIP2C	TFIID [T0	1171	1177	1.537547	TTCAAA	0.73242	0.65627
cg1850382	DIP2C	TFIID [T0	1467	1473	1.537547	TTTTTCA	0.73242	0.65627
cg1850382	DIP2C	TFIID [T0	1690	1696	1.537547	TGAAAA	0.73242	0.65627
cg1850382	DIP2C	TFIID [T0	1960	1966	1.537547	TACAAA	0.73242	0.65627
cg1493188	DIP2C	TFIID [T0	513	519	1.537547	TTTTTCA	0.73242	0.65627
cg1493188	DIP2C	TFIID [T0	588	594	1.537547	TTTTACA	0.73242	0.65627
cg1493188	DIP2C	TFIID [T0	1122	1128	1.537547	TGAAAA	0.73242	0.65627
cg1493188	DIP2C	TFIID [T0	1472	1478	1.537547	TTTTCCA	0.73242	0.65627
cg1493188	DIP2C	TFIID [T0	1795	1801	1.537547	TGGAAA	0.73242	0.65627
cg1493188	DIP2C	TFIID [T0	1878	1884	1.537547	TTTTTCA	0.73242	0.65627
cg1493188	DIP2C	Pax-5 [T0	1747	1753	1.537547	CCCGCC	0.73242	0.83087
cg1493188	DIP2C	Pax-5 [T0	1951	1957	1.537547	GGGCGT	0.73242	0.83087
cg1146814	DIP2C	TFIID [T0	90	96	1.537547	TGGAAA	0.73242	0.65627
cg1146814	DIP2C	TFIID [T0	1851	1857	1.537547	TGGAAA	0.73242	0.65627
cg1146814	DIP2C	Pax-5 [T0	190	196	1.537547	CCCGCC	0.73242	0.83087
cg1146814	DIP2C	Pax-5 [T0	744	750	1.537547	GGGCGG	0.73242	0.83087

cg1146814	DIP2C	Pax-5 [T0	1538	1544	1.537547	GGGCTA	0.73242	0.83087
cg1006492	DIP2C	TFIID [T0	1281	1287	1.537547	TTCAAA	0.73242	0.65627
cg1006492	DIP2C	TFIID [T0	1577	1583	1.537547	TTTTTCA	0.73242	0.65627
cg1006492	DIP2C	TFIID [T0	1800	1806	1.537547	TGAAAA	0.73242	0.65627
cg0545033	DIP2C	TFIID [T0	1211	1217	1.537547	TTCAAA	0.73242	0.65627
cg0545033	DIP2C	TFIID [T0	1507	1513	1.537547	TTTTTCA	0.73242	0.65627
cg0545033	DIP2C	TFIID [T0	1730	1736	1.537547	TGAAAA	0.73242	0.65627
cg1850382	DIP2C	NF-Y [T0	308	315	1.51343	TTACCA	0.18311	0.17671
cg1006492	DIP2C	NF-Y [T0	418	425	1.51343	TTACCA	0.18311	0.17671
cg0545033	DIP2C	NF-Y [T0	348	355	1.51343	TTACCA	0.18311	0.17671
cg1850223	DIP2C	c-Ets-1 [T	101	107	1.513038	TTTCCTC	0.36621	0.35197
cg1850223	DIP2C	RXR-alph	597	603	1.474336	GGGTTT	0.48828	0.52093
cg027001	DIP2C	STAT4 [T	1234	1239	1.470588	AGTTCC	1.95312	1.90161
cg027001	DIP2C	STAT4 [T	1261	1266	1.470588	GGAAAA	1.95312	1.90161
cg027001	DIP2C	STAT4 [T	1762	1767	1.470588	GGAAAC	1.95312	1.90161
cg027001	DIP2C	STAT4 [T	1774	1779	1.470588	GGAAAC	1.95312	1.90161
cg1850223	DIP2C	STAT4 [T	100	105	1.470588	TTTTCC	1.95312	1.90161
cg1850223	DIP2C	STAT4 [T	510	515	1.470588	TTTTCC	1.95312	1.90161
cg1850223	DIP2C	STAT4 [T	672	677	1.470588	GGAAAA	1.95312	1.90161
cg1850223	DIP2C	STAT4 [T	785	790	1.470588	GGAAAA	1.95312	1.90161
cg1850223	DIP2C	STAT4 [T	1243	1248	1.470588	AATTCC	1.95312	1.90161
cg1850223	DIP2C	STAT4 [T	1383	1388	1.470588	TTTTCC	1.95312	1.90161
cg1850382	DIP2C	STAT4 [T	103	108	1.470588	GGAAAA	1.95312	1.90161
cg1493188	DIP2C	STAT4 [T	466	471	1.470588	GTTTCC	1.95312	1.90161
cg1493188	DIP2C	STAT4 [T	549	554	1.470588	GGAATT	1.95312	1.90161
cg1493188	DIP2C	STAT4 [T	932	937	1.470588	GTTTCC	1.95312	1.90161
cg1493188	DIP2C	STAT4 [T	1359	1364	1.470588	AATTCC	1.95312	1.90161
cg1493188	DIP2C	STAT4 [T	1472	1477	1.470588	TTTTCC	1.95312	1.90161
cg1493188	DIP2C	STAT4 [T	1796	1801	1.470588	GGAAAA	1.95312	1.90161
cg1146814	DIP2C	STAT4 [T	69	74	1.470588	AATTCC	1.95312	1.90161
cg1146814	DIP2C	STAT4 [T	91	96	1.470588	GGAAAA	1.95312	1.90161
cg1146814	DIP2C	STAT4 [T	221	226	1.470588	GGAACT	1.95312	1.90161
cg1146814	DIP2C	STAT4 [T	1825	1830	1.470588	AGTTCC	1.95312	1.90161
cg1146814	DIP2C	STAT4 [T	1852	1857	1.470588	GGAAAA	1.95312	1.90161
cg1006492	DIP2C	STAT4 [T	213	218	1.470588	GGAAAA	1.95312	1.90161
cg0545033	DIP2C	STAT4 [T	143	148	1.470588	GGAAAA	1.95312	1.90161
cg1850382	DIP2C	NFI/CTF [	885	892	1.455588	CCAACC	0.06104	0.06595
cg1006492	DIP2C	NFI/CTF [	995	1002	1.455588	CCAACC	0.06104	0.06595
cg0545033	DIP2C	NFI/CTF [	925	932	1.455588	CCAACC	0.06104	0.06595
cg027001	DIP2C	GR [T050	869	875	1.444018	CAAAAA	0.12207	0.11476
cg1850223	DIP2C	GR [T050	1668	1674	1.444018	CAAAAA	0.12207	0.11476
cg1850382	DIP2C	GR [T050	391	397	1.444018	GTTTTT	0.12207	0.11476
cg1493188	DIP2C	GR [T050	578	584	1.444018	GTTTTT	0.12207	0.11476
cg1146814	DIP2C	GR [T050	1460	1466	1.444018	CAAAAA	0.12207	0.11476
cg1006492	DIP2C	GR [T050	501	507	1.444018	GTTTTT	0.12207	0.11476
cg0545033	DIP2C	GR [T050	431	437	1.444018	GTTTTT	0.12207	0.11476
cg027001	DIP2C	PR B [T00	926	932	1.404665	AACACT	0.36621	0.35143
cg027001	DIP2C	PR B [T00	1102	1108	1.404665	AACACT	0.36621	0.35143

cg0270010	DIP2C	PR B [T00	1400	1406	1.404665	AACACT	0.36621	0.35143
cg0270010	DIP2C	PR A [T01	926	932	1.404665	AACACT	0.36621	0.35143
cg0270010	DIP2C	PR A [T01	1102	1108	1.404665	AACACT	0.36621	0.35143
cg0270010	DIP2C	PR A [T01	1400	1406	1.404665	AACACT	0.36621	0.35143
cg1493188	DIP2C	PR B [T00	130	136	1.404665	CAGTGT	0.36621	0.35143
cg1493188	DIP2C	PR B [T00	928	934	1.404665	GAGTGT	0.36621	0.35143
cg1493188	DIP2C	PR B [T00	1279	1285	1.404665	AACACT	0.36621	0.35143
cg1493188	DIP2C	PR B [T00	1700	1706	1.404665	AACACT	0.36621	0.35143
cg1493188	DIP2C	PR A [T01	130	136	1.404665	CAGTGT	0.36621	0.35143
cg1493188	DIP2C	PR A [T01	928	934	1.404665	GAGTGT	0.36621	0.35143
cg1493188	DIP2C	PR A [T01	1279	1285	1.404665	AACACT	0.36621	0.35143
cg1493188	DIP2C	PR A [T01	1700	1706	1.404665	AACACT	0.36621	0.35143
cg1146814	DIP2C	PR B [T00	1517	1523	1.404665	AACACT	0.36621	0.35143
cg1146814	DIP2C	PR B [T00	1693	1699	1.404665	AACACT	0.36621	0.35143
cg1146814	DIP2C	PR B [T00	1991	1997	1.404665	AACACT	0.36621	0.35143
cg1146814	DIP2C	PR A [T01	1517	1523	1.404665	AACACT	0.36621	0.35143
cg1146814	DIP2C	PR A [T01	1693	1699	1.404665	AACACT	0.36621	0.35143
cg1146814	DIP2C	PR A [T01	1991	1997	1.404665	AACACT	0.36621	0.35143
cg1006492	DIP2C	PR B [T00	64	70	1.404665	CAGTGT	0.36621	0.35143
cg1006492	DIP2C	PR A [T01	64	70	1.404665	CAGTGT	0.36621	0.35143
cg1850223	DIP2C	c-Ets-1 [T	1187	1193	1.384951	TTTCCTC	0.36621	0.35197
cg1850382	DIP2C	c-Ets-1 [T	160	166	1.384951	TTTCCTC	0.36621	0.35197
cg1493188	DIP2C	c-Ets-1 [T	1837	1843	1.384951	TTTCCTC	0.36621	0.35197
cg1006492	DIP2C	c-Ets-1 [T	270	276	1.384951	TTTCCTC	0.36621	0.35197
cg0545033	DIP2C	c-Ets-1 [T	200	206	1.384951	TTTCCTC	0.36621	0.35197
cg1850223	DIP2C	NF-AT1 [	681	690	1.378139	CAAATT	0.01907	0.01758
cg0270010	DIP2C	C/EBPbeta	4	7	1.366559	TCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	76	79	1.366559	TTGA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	641	644	1.366559	TCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	712	715	1.366559	TTGA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	876	879	1.366559	TCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1200	1203	1.366559	TCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1478	1481	1.366559	TCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1531	1534	1.366559	TCAA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1543	1546	1.366559	TTGA	15.625	15.23827
cg0270010	DIP2C	C/EBPbeta	1879	1882	1.366559	TTGA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	147	150	1.366559	TTGA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	254	257	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	264	267	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	301	304	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	407	410	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	424	427	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	468	471	1.366559	TTGA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	531	534	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	830	833	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1096	1099	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1146	1149	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1204	1207	1.366559	TCAA	15.625	15.23827

cg1850223	DIP2C	C/EBPbeta	1287	1290	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1500	1503	1.366559	TTGA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1520	1523	1.366559	TCAA	15.625	15.23827
cg1850223	DIP2C	C/EBPbeta	1606	1609	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	15	18	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	145	148	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	178	181	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	214	217	1.366559	TTGA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	377	380	1.366559	TTGA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	733	736	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	844	847	1.366559	TTGA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1080	1083	1.366559	TTGA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1116	1119	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1121	1124	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1172	1175	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1221	1224	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1256	1259	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1312	1315	1.366559	TTGA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1438	1441	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1491	1494	1.366559	TCAA	15.625	15.23827
cg1850382	DIP2C	C/EBPbeta	1798	1801	1.366559	TTGA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	496	499	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	517	520	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	582	585	1.366559	TTGA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	595	598	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	711	714	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1174	1177	1.366559	TTGA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1219	1222	1.366559	TTGA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1244	1247	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1380	1383	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1526	1529	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1617	1620	1.366559	TTGA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1634	1637	1.366559	TTGA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1698	1701	1.366559	TCAA	15.625	15.23827
cg1493188	DIP2C	C/EBPbeta	1724	1727	1.366559	TCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	125	128	1.366559	TCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	385	388	1.366559	TTGA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	493	496	1.366559	TCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	595	598	1.366559	TCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	667	670	1.366559	TTGA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1232	1235	1.366559	TCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1303	1306	1.366559	TTGA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1467	1470	1.366559	TCAA	15.625	15.23827
cg1146814	DIP2C	C/EBPbeta	1791	1794	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	125	128	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	255	258	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	288	291	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	324	327	1.366559	TTGA	15.625	15.23827

cg1006492	DIP2C	C/EBPbeta	487	490	1.366559	TTGA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	843	846	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	954	957	1.366559	TTGA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1190	1193	1.366559	TTGA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1226	1229	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1231	1234	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1282	1285	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1331	1334	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1366	1369	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1422	1425	1.366559	TTGA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1548	1551	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1601	1604	1.366559	TCAA	15.625	15.23827
cg1006492	DIP2C	C/EBPbeta	1908	1911	1.366559	TTGA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	55	58	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	185	188	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	218	221	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	254	257	1.366559	TTGA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	417	420	1.366559	TTGA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	773	776	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	884	887	1.366559	TTGA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1120	1123	1.366559	TTGA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1156	1159	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1161	1164	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1212	1215	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1261	1264	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1296	1299	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1352	1355	1.366559	TTGA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1478	1481	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1531	1534	1.366559	TCAA	15.625	15.23827
cg0545033	DIP2C	C/EBPbeta	1838	1841	1.366559	TTGA	15.625	15.23827
cg0270010	DIP2C	AP-2alpha	967	972	1.357116	ACAGGC	0.48828	0.51319
cg0270010	DIP2C	AP-2alpha	1067	1072	1.357116	GCCTGT	0.48828	0.51319
cg0270010	DIP2C	AP-2alpha	1788	1793	1.357116	GCCTGT	0.48828	0.51319
cg1850223	DIP2C	AP-2alpha	333	338	1.357116	GCCTGT	0.48828	0.51319
cg1850382	DIP2C	AP-2alpha	1033	1038	1.357116	GCCTGT	0.48828	0.51319
cg1850382	DIP2C	AP-2alpha	1568	1573	1.357116	ACAGGC	0.48828	0.51319
cg1850382	DIP2C	AP-2alpha	1855	1860	1.357116	GCCTGT	0.48828	0.51319
cg1493188	DIP2C	AP-2alpha	951	956	1.357116	GCCTGT	0.48828	0.51319
cg1493188	DIP2C	AP-2alpha	1967	1972	1.357116	GCCTGT	0.48828	0.51319
cg1146814	DIP2C	AP-2alpha	1558	1563	1.357116	ACAGGC	0.48828	0.51319
cg1146814	DIP2C	AP-2alpha	1658	1663	1.357116	GCCTGT	0.48828	0.51319
cg1006492	DIP2C	AP-2alpha	1143	1148	1.357116	GCCTGT	0.48828	0.51319
cg1006492	DIP2C	AP-2alpha	1678	1683	1.357116	ACAGGC	0.48828	0.51319
cg1006492	DIP2C	AP-2alpha	1965	1970	1.357116	GCCTGT	0.48828	0.51319
cg0545033	DIP2C	AP-2alpha	1073	1078	1.357116	GCCTGT	0.48828	0.51319
cg0545033	DIP2C	AP-2alpha	1608	1613	1.357116	ACAGGC	0.48828	0.51319
cg0545033	DIP2C	AP-2alpha	1895	1900	1.357116	GCCTGT	0.48828	0.51319
cg1146814	DIP2C	c-Myb [T0	222	229	1.285398	GAACTG	0.06104	0.06236

cg1146814	DIP2C	NFI/CTF [	325	332	1.227415	CCAAGC	0.18311	0.19134
cg1146814	DIP2C	T3R-beta1	367	375	1.110682	TCACCT	0.07629	0.07886
cg1493188	DIP2C	GCF [T00	29	37	1.070269	GACCGG	0.18311	0.21473
cg1493188	DIP2C	GCF [T00	78	86	1.070269	GACCGG	0.18311	0.21473
cg1493188	DIP2C	GCF [T00	274	282	1.070269	GACCGG	0.18311	0.21473
cg1493188	DIP2C	GCF [T00	323	331	1.070269	GACCGG	0.18311	0.21473
cg1493188	DIP2C	GCF [T00	372	380	1.070269	GACCGG	0.18311	0.21473
cg1850223	DIP2C	GATA-1 [	1599	1604	1.038567	ATGATA	1.95312	1.80234
cg1850382	DIP2C	GATA-1 [	1312	1317	1.038567	TTGATA	1.95312	1.80234
cg1006492	DIP2C	GATA-1 [	1422	1427	1.038567	TTGATA	1.95312	1.80234
cg0545033	DIP2C	GATA-1 [	1352	1357	1.038567	TTGATA	1.95312	1.80234
cg1850382	DIP2C	Elk-1 [T00	433	441	0.957025	AGAAGG	0.03052	0.03046
cg1006492	DIP2C	Elk-1 [T00	543	551	0.957025	AGAAGG	0.03052	0.03046
cg0545033	DIP2C	Elk-1 [T00	473	481	0.957025	AGAAGG	0.03052	0.03046
cg1850223	DIP2C	HOXD9 [	1238	1247	0.954221	AATAAA	0.01526	0.01263
cg1850223	DIP2C	HOXD9 [	1576	1585	0.954221	AATAAA	0.01526	0.01263
cg1850223	DIP2C	HOXD10 [	1238	1247	0.954221	AATAAA	0.01526	0.01263
cg1850223	DIP2C	HOXD10 [	1576	1585	0.954221	AATAAA	0.01526	0.01263
cg1850223	DIP2C	HNF-1A [	59	66	0.925521	CATTTA	0.48828	0.45029
cg0270010	DIP2C	AR [T000	718	726	0.863734	TCACTG	0.03815	0.03934
cg0270010	DIP2C	AR [T000	1748	1756	0.863734	TCACTG	0.03815	0.03934
cg1146814	DIP2C	AR [T000	1309	1317	0.863734	TCACTG	0.03815	0.03934
cg0270010	DIP2C	GATA-1 [	749	754	0.863549	TATCAC	1.95312	1.80234
cg1850223	DIP2C	GATA-1 [	1210	1215	0.863549	TATCAC	1.95312	1.80234
cg1493188	DIP2C	GATA-1 [	886	891	0.863549	TATCAC	1.95312	1.80234
cg1493188	DIP2C	GATA-1 [	1292	1297	0.863549	GTGATA	1.95312	1.80234
cg1146814	DIP2C	GATA-1 [	1340	1345	0.863549	TATCAC	1.95312	1.80234
cg1146814	DIP2C	LEF-1 [T0	403	410	0.85582	GACCAA	0.03052	0.03064
cg1850223	DIP2C	RXR-alph	215	221	0.848226	TGGACC	0.48828	0.51313
cg1850223	DIP2C	RXR-alph	1938	1944	0.848226	CGAACC	0.48828	0.51313
cg1850382	DIP2C	RXR-alph	1050	1056	0.848226	GGGTTC	0.48828	0.51313
cg1006492	DIP2C	RXR-alph	1160	1166	0.848226	GGGTTC	0.48828	0.51313
cg0545033	DIP2C	RXR-alph	1090	1096	0.848226	GGGTTC	0.48828	0.51313
cg0270010	DIP2C	GR-beta [	603	607	0.840383	TCATT	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	658	662	0.840383	AATTA	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	698	702	0.840383	CAATT	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	699	703	0.840383	AATTA	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	745	749	0.840383	TCATT	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	892	896	0.840383	AATGG	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	921	925	0.840383	AATTA	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	1367	1371	0.840383	AATGA	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	1379	1383	0.840383	TAATT	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	1532	1536	0.840383	CAATT	7.8125	7.2174
cg0270010	DIP2C	GR-beta [	1533	1537	0.840383	AATTA	7.8125	7.2174
cg1850223	DIP2C	GR-beta [	43	47	0.840383	TCATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [	71	75	0.840383	CCATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [	78	82	0.840383	AATGA	7.8125	7.2174
cg1850223	DIP2C	GR-beta [	89	93	0.840383	AATTG	7.8125	7.2174

cg1850223	DIP2C	GR-beta [T	110	114	0.840383	AATGA	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	498	502	0.840383	TAATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	499	503	0.840383	AATTA	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	504	508	0.840383	AATTA	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	507	511	0.840383	TAATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	556	560	0.840383	AATGG	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	588	592	0.840383	TAATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	892	896	0.840383	AATGG	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1054	1058	0.840383	AATGG	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1147	1151	0.840383	CAATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1205	1209	0.840383	CAATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1389	1393	0.840383	CCATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1476	1480	0.840383	TCATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1567	1571	0.840383	TAATT	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1568	1572	0.840383	AATTA	7.8125	7.2174
cg1850223	DIP2C	GR-beta [T	1742	1746	0.840383	CCATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	16	20	0.840383	CAATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	107	111	0.840383	AATGA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	126	130	0.840383	TAATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	127	131	0.840383	AATTG	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	193	197	0.840383	AATTA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	312	316	0.840383	CAATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	313	317	0.840383	AATTA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	357	361	0.840383	AATGG	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	365	369	0.840383	CAATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	366	370	0.840383	AATTA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	592	596	0.840383	CCATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	671	675	0.840383	AATGA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	683	687	0.840383	AATGG	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	840	844	0.840383	CCATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	1246	1250	0.840383	AATGA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	1281	1285	0.840383	TCATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	1440	1444	0.840383	AATGA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	1493	1497	0.840383	AATGA	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	1646	1650	0.840383	CCATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	1733	1737	0.840383	TCATT	7.8125	7.2174
cg1850382	DIP2C	GR-beta [T	1967	1971	0.840383	AATTA	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	567	571	0.840383	TAATT	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	598	602	0.840383	AATGA	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	604	608	0.840383	TAATT	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	605	609	0.840383	AATTG	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	905	909	0.840383	TAATT	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	925	929	0.840383	AATGA	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	1108	1112	0.840383	AATGA	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	1128	1132	0.840383	AATTA	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	1358	1362	0.840383	TAATT	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	1431	1435	0.840383	TAATT	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	1641	1645	0.840383	AATTG	7.8125	7.2174

cg1493188	DIP2C	GR-beta [T	1668	1672	0.840383	CCATT	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	1720	1724	0.840383	TCATT	7.8125	7.2174
cg1493188	DIP2C	GR-beta [T	1825	1829	0.840383	TCATT	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	61	65	0.840383	TCATT	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1194	1198	0.840383	TCATT	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1249	1253	0.840383	AATTA	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1289	1293	0.840383	CAATT	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1290	1294	0.840383	AATTA	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1336	1340	0.840383	TCATT	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1483	1487	0.840383	AATGG	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1512	1516	0.840383	AATTA	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1958	1962	0.840383	AATGA	7.8125	7.2174
cg1146814	DIP2C	GR-beta [T	1970	1974	0.840383	TAATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	81	85	0.840383	CCATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	126	130	0.840383	CAATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	217	221	0.840383	AATGA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	236	240	0.840383	TAATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	237	241	0.840383	AATTG	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	303	307	0.840383	AATTA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	422	426	0.840383	CAATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	423	427	0.840383	AATTA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	467	471	0.840383	AATGG	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	475	479	0.840383	CAATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	476	480	0.840383	AATTA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	702	706	0.840383	CCATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	781	785	0.840383	AATGA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	793	797	0.840383	AATGG	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	950	954	0.840383	CCATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	1356	1360	0.840383	AATGA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	1391	1395	0.840383	TCATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	1550	1554	0.840383	AATGA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	1603	1607	0.840383	AATGA	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	1756	1760	0.840383	CCATT	7.8125	7.2174
cg1006492	DIP2C	GR-beta [T	1843	1847	0.840383	TCATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	11	15	0.840383	CCATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	56	60	0.840383	CAATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	147	151	0.840383	AATGA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	166	170	0.840383	TAATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	167	171	0.840383	AATTG	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	233	237	0.840383	AATTA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	352	356	0.840383	CAATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	353	357	0.840383	AATTA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	397	401	0.840383	AATGG	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	405	409	0.840383	CAATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	406	410	0.840383	AATTA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	632	636	0.840383	CCATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	711	715	0.840383	AATGA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	723	727	0.840383	AATGG	7.8125	7.2174

cg0545033	DIP2C	GR-beta [T	880	884	0.840383	CCATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	1286	1290	0.840383	AATGA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	1321	1325	0.840383	TCATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	1480	1484	0.840383	AATGA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	1533	1537	0.840383	AATGA	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	1686	1690	0.840383	CCATT	7.8125	7.2174
cg0545033	DIP2C	GR-beta [T	1773	1777	0.840383	TCATT	7.8125	7.2174
cg1493188	DIP2C	Sp1 [T007	1745	1754	0.813764	GCCCCG	0.01335	0.01658
cg027001	DIP2C	GATA-1 [	622	627	0.758539	CTGATA	1.95312	1.80234
cg1850223	DIP2C	GATA-1 [	758	763	0.758539	CTGATA	1.95312	1.80234
cg1850382	DIP2C	GATA-1 [	1187	1192	0.758539	TATCAG	1.95312	1.80234
cg1146814	DIP2C	GATA-1 [	1213	1218	0.758539	CTGATA	1.95312	1.80234
cg1006492	DIP2C	GATA-1 [	1297	1302	0.758539	TATCAG	1.95312	1.80234
cg0545033	DIP2C	GATA-1 [	1227	1232	0.758539	TATCAG	1.95312	1.80234
cg027001	DIP2C	NF-AT1 [T	1455	1464	0.689069	TGGAAA	0.00763	0.00694
cg027001	DIP2C	AP-2alpha	620	625	0.678558	GCCTGA	0.48828	0.51196
cg1850223	DIP2C	AP-2alpha	911	916	0.678558	GCCTGA	0.48828	0.51196
cg1850223	DIP2C	AP-2alpha	1465	1470	0.678558	GCCTGA	0.48828	0.51196
cg1850223	DIP2C	AP-2alpha	1732	1737	0.678558	TCAGGC	0.48828	0.51196
cg1493188	DIP2C	AP-2alpha	738	743	0.678558	TCAGGC	0.48828	0.51196
cg1493188	DIP2C	AP-2alpha	1741	1746	0.678558	TCAGGC	0.48828	0.51196
cg1146814	DIP2C	AP-2alpha	542	547	0.678558	GCCTGA	0.48828	0.51196
cg1146814	DIP2C	AP-2alpha	1211	1216	0.678558	GCCTGA	0.48828	0.51196
cg1850382	DIP2C	RXR-alph	304	310	0.62611	GGGTTT	0.12207	0.11915
cg1850382	DIP2C	RXR-alph	410	416	0.62611	TAAACC	0.12207	0.11915
cg1493188	DIP2C	RXR-alph	629	635	0.62611	GGGTTT	0.12207	0.11915
cg1006492	DIP2C	RXR-alph	414	420	0.62611	GGGTTT	0.12207	0.11915
cg1006492	DIP2C	RXR-alph	520	526	0.62611	TAAACC	0.12207	0.11915
cg0545033	DIP2C	RXR-alph	344	350	0.62611	GGGTTT	0.12207	0.11915
cg0545033	DIP2C	RXR-alph	450	456	0.62611	TAAACC	0.12207	0.11915
cg027001	DIP2C	PEA3 [T0	880	888	0.597316	ATACAT	0.04578	0.04362
cg1146814	DIP2C	PEA3 [T0	1471	1479	0.597316	ATACAT	0.04578	0.04362
cg1850223	DIP2C	c-Ets-2 [T	102	110	0.572986	TTCCTC	0.00763	0.0074
cg1850382	DIP2C	HIF-1 [T0	1764	1772	0.543748	ACGTGC	0.04578	0.04961
cg1006492	DIP2C	HIF-1 [T0	1874	1882	0.543748	ACGTGC	0.04578	0.04961
cg0545033	DIP2C	HIF-1 [T0	1804	1812	0.543748	ACGTGC	0.04578	0.04961
cg1850382	DIP2C	AP-1 [T00	872	880	0.489074	TGACTC	0.09155	0.08806
cg1006492	DIP2C	AP-1 [T00	982	990	0.489074	TGACTC	0.09155	0.08806
cg0545033	DIP2C	AP-1 [T00	912	920	0.489074	TGACTC	0.09155	0.08806
cg1850223	DIP2C	PR B [T00	1317	1323	0.48823	AACTGT	0.12207	0.11255
cg1850223	DIP2C	PR A [T01	1317	1323	0.48823	AACTGT	0.12207	0.11255
cg027001	DIP2C	AP-1 [T00	825	833	0.436196	TGACTC	0.09155	0.08806
cg1146814	DIP2C	AP-1 [T00	1416	1424	0.436196	TGACTC	0.09155	0.08806
cg1493188	DIP2C	AP-1 [T00	1108	1116	0.348957	AATGAG	0.09155	0.08806
cg1850223	DIP2C	GATA-1 [	1494	1499	0.280028	TAGATA	0.97656	0.8795
cg1850223	DIP2C	GATA-1 [	1922	1927	0.280028	AAGATA	0.97656	0.8795
cg1850382	DIP2C	GATA-1 [	503	508	0.280028	AAGATA	0.97656	0.8795
cg1493188	DIP2C	GATA-1 [	1131	1136	0.280028	TATCTA	0.97656	0.8795

cg1493188	DIP2C	GATA-1 [	1892	1897	0.280028	TATCTT	0.97656	0.8795
cg1006492	DIP2C	GATA-1 [	613	618	0.280028	AAGATA	0.97656	0.8795
cg0545033	DIP2C	GATA-1 [	543	548	0.280028	AAGATA	0.97656	0.8795
cg1850223	DIP2C	c-Ets-1 [T	1611	1617	0.256174	AAGGAA	0.24414	0.23743
cg1850382	DIP2C	c-Ets-1 [T	435	441	0.256174	AAGGAA	0.24414	0.23743
cg1493188	DIP2C	c-Ets-1 [T	1264	1270	0.256174	CTTCCTT	0.24414	0.23743
cg1493188	DIP2C	c-Ets-1 [T	1916	1922	0.256174	CTTCCTT	0.24414	0.23743
cg1006492	DIP2C	c-Ets-1 [T	545	551	0.256174	AAGGAA	0.24414	0.23743
cg0545033	DIP2C	c-Ets-1 [T	475	481	0.256174	AAGGAA	0.24414	0.23743
cg0270010	DIP2C	AP-2alpha	507	512	0.226186	GCCTGG	0.97656	1.07867
cg0270010	DIP2C	AP-2alpha	1707	1712	0.226186	CCAGGC	0.97656	1.07867
cg0270010	DIP2C	AP-2alpha	1846	1851	0.226186	CCAGGC	0.97656	1.07867
cg1850223	DIP2C	AP-2alpha	352	357	0.226186	GCCTGG	0.97656	1.07867
cg1850382	DIP2C	AP-2alpha	1837	1842	0.226186	CCAGGC	0.97656	1.07867
cg1850382	DIP2C	AP-2alpha	1922	1927	0.226186	GCCTGG	0.97656	1.07867
cg1493188	DIP2C	AP-2alpha	791	796	0.226186	CCAGGC	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	338	343	0.226186	GCCTGG	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	576	581	0.226186	CCAGGC	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	1098	1103	0.226186	GCCTGG	0.97656	1.07867
cg1006492	DIP2C	AP-2alpha	1947	1952	0.226186	CCAGGC	0.97656	1.07867
cg0545033	DIP2C	AP-2alpha	1877	1882	0.226186	CCAGGC	0.97656	1.07867
cg0545033	DIP2C	AP-2alpha	1962	1967	0.226186	GCCTGG	0.97656	1.07867
cg1850223	DIP2C	p53 [T006	1226	1232	0.211706	CTTGCCC	0.36621	0.40082
cg0270010	DIP2C	GR-alpha [	7	11	0.207689	AGAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	43	47	0.207689	CCTTT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	126	130	0.207689	CCTCT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	265	269	0.207689	AAAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	433	437	0.207689	AGAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	729	733	0.207689	AGAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	764	768	0.207689	CCTCT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	994	998	0.207689	AAAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1005	1009	0.207689	AGAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1020	1024	0.207689	CCTTT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1147	1151	0.207689	CCTCT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1249	1253	0.207689	AAAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1276	1280	0.207689	CCTTT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1319	1323	0.207689	AAAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1919	1923	0.207689	AAAGG	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	23	27	0.207689	CCTCT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	280	284	0.207689	AGAGG	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	755	759	0.207689	CCTCT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	788	792	0.207689	AAAGG	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	971	975	0.207689	CCTCT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	1046	1050	0.207689	CCTTT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	1485	1489	0.207689	CCTCT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	1642	1646	0.207689	AAAGG	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	1728	1732	0.207689	CCTTT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	1777	1781	0.207689	AAAGG	7.8125	7.79817

cg1850382	DIP2C	GR-alpha |	38	42	0.207689	AAAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	111	115	0.207689	AGAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	251	255	0.207689	AGAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	327	331	0.207689	AAAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	536	540	0.207689	AAAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	557	561	0.207689	AGAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	638	642	0.207689	AAAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	760	764	0.207689	CCTCT	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	1407	1411	0.207689	CCTCT	7.8125	7.79817
cg1850382	DIP2C	GR-alpha |	1747	1751	0.207689	CCTCT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	836	840	0.207689	AGAGG	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	959	963	0.207689	CCTCT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	1009	1013	0.207689	CCTTT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	1084	1088	0.207689	CCTCT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	1337	1341	0.207689	CCTCT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	1508	1512	0.207689	AAAGG	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	1835	1839	0.207689	CCTTT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha |	1994	1998	0.207689	AAAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	16	20	0.207689	AGAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	120	124	0.207689	AGAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	370	374	0.207689	CCTCT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	598	602	0.207689	AGAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	634	638	0.207689	CCTTT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	717	721	0.207689	CCTCT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	856	860	0.207689	AAAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1024	1028	0.207689	AGAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1320	1324	0.207689	AGAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1355	1359	0.207689	CCTCT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1585	1589	0.207689	AAAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1596	1600	0.207689	AGAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1611	1615	0.207689	CCTTT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1738	1742	0.207689	CCTCT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1840	1844	0.207689	AAAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1867	1871	0.207689	CCTTT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha |	1910	1914	0.207689	AAAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	49	53	0.207689	CCTCT	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	148	152	0.207689	AAAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	221	225	0.207689	AGAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	361	365	0.207689	AGAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	437	441	0.207689	AAAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	646	650	0.207689	AAAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	667	671	0.207689	AGAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	748	752	0.207689	AAAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	870	874	0.207689	CCTCT	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	1517	1521	0.207689	CCTCT	7.8125	7.79817
cg1006492	DIP2C	GR-alpha |	1857	1861	0.207689	CCTCT	7.8125	7.79817
cg0545033	DIP2C	GR-alpha |	78	82	0.207689	AAAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha |	151	155	0.207689	AGAGG	7.8125	7.79817

cg0545033	DIP2C	GR-alpha [	291	295	0.207689	AGAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	367	371	0.207689	AAAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	576	580	0.207689	AAAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	597	601	0.207689	AGAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	678	682	0.207689	AAAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	800	804	0.207689	CCTCT	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	1447	1451	0.207689	CCTCT	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	1787	1791	0.207689	CCTCT	7.8125	7.79817
cg1850223	DIP2C	HNF-1A [	434	441	0.143882	TATTTA	0.24414	0.20853
cg1850382	DIP2C	HNF-1A [	192	199	0.143882	AAATTA	0.24414	0.20853
cg1006492	DIP2C	HNF-1A [	302	309	0.143882	AAATTA	0.24414	0.20853
cg0545033	DIP2C	HNF-1A [	232	239	0.143882	AAATTA	0.24414	0.20853
cg1850223	DIP2C	Elk-1 [T00	1644	1652	0.134348	AGGAGG	0.06104	0.06399
cg1850382	DIP2C	Elk-1 [T00	485	493	0.134348	AGCAGG	0.06104	0.06399
cg1850382	DIP2C	Elk-1 [T00	859	867	0.134348	AGGAGG	0.06104	0.06399
cg1006492	DIP2C	Elk-1 [T00	595	603	0.134348	AGCAGG	0.06104	0.06399
cg1006492	DIP2C	Elk-1 [T00	969	977	0.134348	AGGAGG	0.06104	0.06399
cg0545033	DIP2C	Elk-1 [T00	525	533	0.134348	AGCAGG	0.06104	0.06399
cg0545033	DIP2C	Elk-1 [T00	899	907	0.134348	AGGAGG	0.06104	0.06399
cg1850223	DIP2C	c-Ets-1 [T	185	191	0.128087	GAGGAA	0.24414	0.24982
cg1850223	DIP2C	c-Ets-1 [T	1646	1652	0.128087	GAGGAA	0.24414	0.24982
cg1850382	DIP2C	c-Ets-1 [T	861	867	0.128087	GAGGAA	0.24414	0.24982
cg1850382	DIP2C	c-Ets-1 [T	1580	1586	0.128087	CTTCCTC	0.24414	0.24982
cg1146814	DIP2C	c-Ets-1 [T	546	552	0.128087	GAGGAA	0.24414	0.24982
cg1006492	DIP2C	c-Ets-1 [T	971	977	0.128087	GAGGAA	0.24414	0.24982
cg1006492	DIP2C	c-Ets-1 [T	1690	1696	0.128087	CTTCCTC	0.24414	0.24982
cg0545033	DIP2C	c-Ets-1 [T	901	907	0.128087	GAGGAA	0.24414	0.24982
cg0545033	DIP2C	c-Ets-1 [T	1620	1626	0.128087	CTTCCTC	0.24414	0.24982
cg0270010	DIP2C	PXR-1:RX	713	720	0.123583	TGAACT	0.12207	0.11255
cg1146814	DIP2C	PXR-1:RX	1304	1311	0.123583	TGAACT	0.12207	0.11255
cg1850223	DIP2C	GATA-1 [	1092	1097	0.105011	TATCTC	0.97656	0.92541
cg1850382	DIP2C	GATA-1 [	11	16	0.105011	TATCTC	0.97656	0.92541
cg1493188	DIP2C	GATA-1 [	614	619	0.105011	TATCTC	0.97656	0.92541
cg1146814	DIP2C	GATA-1 [	307	312	0.105011	TATCTC	0.97656	0.92541
cg1006492	DIP2C	GATA-1 [	121	126	0.105011	TATCTC	0.97656	0.92541
cg0545033	DIP2C	GATA-1 [	51	56	0.105011	TATCTC	0.97656	0.92541
cg0270010	DIP2C	GR-beta [T	920	924	0	AAATT	3.90625	3.51525
cg0270010	DIP2C	GR-beta [T	1380	1384	0	AATTT	3.90625	3.51525
cg0270010	DIP2C	GR-beta [T	1458	1462	0	AAATT	3.90625	3.51525
cg0270010	DIP2C	GR-beta [T	1459	1463	0	AATTT	3.90625	3.51525
cg0270010	DIP2C	GR-beta [T	1469	1473	0	AATGT	3.90625	3.51525
cg0270010	DIP2C	XBP-1 [T	601	606	0	CGTCAT	0.97656	0.94838
cg0270010	DIP2C	TFIID [T0	606	612	0	TTTTAG	1.09863	0.95175
cg0270010	DIP2C	TFIID [T0	1350	1356	0	TATAAA	1.09863	0.95175
cg0270010	DIP2C	TFIID [T0	1382	1388	0	TTTAAA	1.09863	0.95175
cg0270010	DIP2C	AP-1 [T00	254	262	0	TGACTC	0.03052	0.03037
cg0270010	DIP2C	c-Jun [T00	254	260	0	TGACTC	0.12207	0.11843
cg0270010	DIP2C	c-Jun [T00	825	831	0	TGACTC	0.12207	0.11843

cg0270010	DIP2C	GR-alpha [	967	971	0	ACAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	988	992	0	CCTGT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1052	1056	0	CCTGT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1068	1072	0	CCTGT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1096	1100	0	ACAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1291	1295	0	ACAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1444	1448	0	ACAGG	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1724	1728	0	CCTGT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1789	1793	0	CCTGT	7.8125	7.79817
cg0270010	DIP2C	GR-alpha [	1875	1879	0	CCTGT	7.8125	7.79817
cg0270010	DIP2C	FOXP3 [T	1472	1477	0	GTTGTG	1.46484	1.44953
cg0270010	DIP2C	PR B [T00	683	689	0	CACTGT	0.36621	0.35051
cg0270010	DIP2C	PR B [T00	928	934	0	CACTGT	0.36621	0.35051
cg0270010	DIP2C	PR B [T00	1814	1820	0	AACAGT	0.36621	0.35051
cg0270010	DIP2C	PR A [T01	683	689	0	CACTGT	0.36621	0.35051
cg0270010	DIP2C	PR A [T01	928	934	0	CACTGT	0.36621	0.35051
cg0270010	DIP2C	PR A [T01	1814	1820	0	AACAGT	0.36621	0.35051
cg0270010	DIP2C	C/EBPbeta	63	66	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	194	197	0	TTGC	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	220	223	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	452	455	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	521	524	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	637	640	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	697	700	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	703	706	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	733	736	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	736	739	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	759	762	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	803	806	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	868	871	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1247	1250	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1317	1320	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1473	1476	0	TTGT	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1491	1494	0	TTGC	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1493	1496	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1572	1575	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1618	1621	0	ACAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1623	1626	0	GCAA	15.625	15.26275
cg0270010	DIP2C	C/EBPbeta	1651	1654	0	ACAA	15.625	15.26275
cg0270010	DIP2C	NF-1 [T00	1829	1836	0	TGGGCC	0.12207	0.13147
cg0270010	DIP2C	YY1 [T00	593	596	0	ATGG	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	645	648	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	816	819	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	893	896	0	ATGG	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	1172	1175	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	1430	1433	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	1639	1642	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	1641	1644	0	ATGG	7.8125	7.79459

cg0270010	DIP2C	YY1 [T00	1715	1718	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	1759	1762	0	ATGG	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	1948	1951	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	YY1 [T00	1955	1958	0	CCAT	7.8125	7.79459
cg0270010	DIP2C	TFII-I [T0	429	434	0	GGACAG	1.46484	1.48598
cg0270010	DIP2C	TFII-I [T0	721	726	0	CTGTCC	1.46484	1.48598
cg0270010	DIP2C	TFII-I [T0	1134	1139	0	GGACAG	1.46484	1.48598
cg0270010	DIP2C	TFII-I [T0	1734	1739	0	GGACAG	1.46484	1.48598
cg0270010	DIP2C	TFII-I [T0	1751	1756	0	CTGTCC	1.46484	1.48598
cg0270010	DIP2C	TFII-I [T0	1790	1795	0	CTGTCC	1.46484	1.48598
cg0270010	DIP2C	TFII-I [T0	1866	1871	0	GGACAG	1.46484	1.48598
cg0270010	DIP2C	STAT4 [T	1456	1461	0	GGAAAT	0.48828	0.46235
cg0270010	DIP2C	c-Myb [T0	896	903	0	GGCAGT	0.03052	0.03205
cg0270010	DIP2C	ER-alpha [	200	204	0	TGACC	1.95312	1.99744
cg0270010	DIP2C	ER-alpha [	680	684	0	GGTCA	1.95312	1.99744
cg0270010	DIP2C	ER-alpha [	1084	1088	0	TGACC	1.95312	1.99744
cg0270010	DIP2C	ER-alpha [	1144	1148	0	TGACC	1.95312	1.99744
cg0270010	DIP2C	ER-alpha [	1439	1443	0	TGACC	1.95312	1.99744
cg0270010	DIP2C	RXR-alpha	321	327	0	TGAACC	0.24414	0.24342
cg0270010	DIP2C	NFI/CTF [	294	301	0	ACGCTT	0.18311	0.191
cg0270010	DIP2C	Pax-5 [T0	101	107	0	CCAGCC	1.09863	1.24633
cg0270010	DIP2C	Pax-5 [T0	112	118	0	GGGCCC	1.09863	1.24633
cg0270010	DIP2C	Pax-5 [T0	558	564	0	GGGCAG	1.09863	1.24633
cg0270010	DIP2C	Pax-5 [T0	571	577	0	CCAGCC	1.09863	1.24633
cg0270010	DIP2C	Pax-5 [T0	737	743	0	CAAGCC	1.09863	1.24633
cg0270010	DIP2C	Pax-5 [T0	1047	1053	0	CCTGCC	1.09863	1.24633
cg0270010	DIP2C	p53 [T006	558	564	0	GGGCAG	0.36621	0.40082
cg0270010	DIP2C	p53 [T006	1047	1053	0	CCTGCC	0.36621	0.40082
cg0270010	DIP2C	AP-2alpha	237	242	0	GCAGGC	0.97656	1.07867
cg0270010	DIP2C	AP-2alpha	503	508	0	GCAGGC	0.97656	1.07867
cg0270010	DIP2C	AP-2alpha	1027	1032	0	GCAGGC	0.97656	1.07867
cg0270010	DIP2C	AP-2alpha	1046	1051	0	GCCTGC	0.97656	1.07867
cg0270010	DIP2C	AP-2alpha	1120	1125	0	GCAGGC	0.97656	1.07867
cg0270010	DIP2C	AP-2alpha	1153	1158	0	GCCTGC	0.97656	1.07867
cg0270010	DIP2C	IRF-2 [T0	1141	1146	0	AAGTGA	0.48828	0.46235
cg0270010	DIP2C	IRF-2 [T0	1414	1419	0	AAGTGA	0.48828	0.46235
cg0270010	DIP2C	IRF-2 [T0	1539	1544	0	TCACTT	0.48828	0.46235
cg0270010	DIP2C	IRF-2 [T0	1593	1598	0	AAGTGA	0.48828	0.46235
cg0270010	DIP2C	HNF-1A [	625	632	0	ATATTA	0.24414	0.20853
cg1850223	DIP2C	GR-beta [	88	92	0	AAATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	239	243	0	ACATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	256	260	0	AATGT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	503	507	0	AAATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	508	512	0	AATTT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	524	528	0	ACATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	582	586	0	AATGT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	589	593	0	AATTT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [	682	686	0	AAATT	3.90625	3.51525

cg1850223	DIP2C	GR-beta [T	683	687	0	AATTT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [T	1148	1152	0	AATTT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [T	1185	1189	0	AATTT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [T	1196	1200	0	ACATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [T	1206	1210	0	AATTT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [T	1242	1246	0	AAATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [T	1471	1475	0	ACATT	3.90625	3.51525
cg1850223	DIP2C	GR-beta [T	1530	1534	0	ACATT	3.90625	3.51525
cg1850223	DIP2C	XBP-1 [T	79	84	0	ATGACG	0.97656	0.94838
cg1850223	DIP2C	XBP-1 [T	358	363	0	CGTCAT	0.97656	0.94838
cg1850223	DIP2C	XBP-1 [T	607	612	0	ATGACT	0.97656	0.94838
cg1850223	DIP2C	TFIID [T0	301	307	0	TCAAAA	1.09863	0.95175
cg1850223	DIP2C	TFIID [T0	1049	1055	0	TTTAAA	1.09863	0.95175
cg1850223	DIP2C	TFIID [T0	1392	1398	0	TTTTAGA	1.09863	0.95175
cg1850223	DIP2C	GR-alpha [	136	140	0	CCTAT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	170	174	0	ATAGG	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	334	338	0	CCTGT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	604	608	0	CCTAT	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	1174	1178	0	ACAGG	7.8125	7.79817
cg1850223	DIP2C	GR-alpha [	1817	1821	0	CCTGT	7.8125	7.79817
cg1850223	DIP2C	FOXP3 [T	1273	1278	0	CACAAC	1.46484	1.44953
cg1850223	DIP2C	FOXP3 [T	1976	1981	0	GTTGTC	1.46484	1.44953
cg1850223	DIP2C	C/EBPbeta	29	32	0	TTGC	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	54	57	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	65	68	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	97	100	0	TTGT	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	132	135	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	162	165	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	177	180	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	196	199	0	TTGC	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	289	292	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	309	312	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	368	371	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	453	456	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	528	531	0	TTGT	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	539	542	0	TTGT	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	579	582	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	601	604	0	TTGC	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	680	683	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	871	874	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1036	1039	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1227	1230	0	TTGC	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1274	1277	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1277	1280	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1330	1333	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1418	1421	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1479	1482	0	TTGC	15.625	15.26275
cg1850223	DIP2C	C/EBPbeta	1534	1537	0	TTGC	15.625	15.26275

cg1850223	DIP2C	C/EBPbet	1574	1577	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbet	1609	1612	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbet	1667	1670	0	ACAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbet	1788	1791	0	TTGC	15.625	15.26275
cg1850223	DIP2C	C/EBPbet	1863	1866	0	GCAA	15.625	15.26275
cg1850223	DIP2C	C/EBPbet	1977	1980	0	TTGT	15.625	15.26275
cg1850223	DIP2C	YY1 [T00	32	35	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	71	74	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	128	131	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	168	171	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	225	228	0	ATGG	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	544	547	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	557	560	0	ATGG	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	657	660	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	734	737	0	ATGG	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	793	796	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	893	896	0	ATGG	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	1055	1058	0	ATGG	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	1263	1266	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	1389	1392	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	1398	1401	0	ATGG	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	1742	1745	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	YY1 [T00	1770	1773	0	CCAT	7.8125	7.79459
cg1850223	DIP2C	C/EBPalp	1519	1525	0	CTCAAT	0.24414	0.24342
cg1850223	DIP2C	STAT4 [T	684	689	0	ATTTCC	0.48828	0.46235
cg1850223	DIP2C	STAT4 [T	1124	1129	0	GGAAAT	0.48828	0.46235
cg1850223	DIP2C	STAT4 [T	1186	1191	0	ATTTCC	0.48828	0.46235
cg1850223	DIP2C	STAT4 [T	1744	1749	0	ATTTCC	0.48828	0.46235
cg1850223	DIP2C	c-Ets-1 [T	1869	1875	0	CTTCCT	0.24414	0.24982
cg1850223	DIP2C	c-Myb [T0	191	198	0	GGCAGT	0.03052	0.03205
cg1850223	DIP2C	ER-alpha [	694	698	0	TGACC	1.95312	1.99744
cg1850223	DIP2C	ER-alpha [	895	899	0	GGTCA	1.95312	1.99744
cg1850223	DIP2C	ER-alpha [	989	993	0	GGTCA	1.95312	1.99744
cg1850223	DIP2C	ER-alpha [	1539	1543	0	GGTCA	1.95312	1.99744
cg1850223	DIP2C	GR [T050	302	308	0	CAAAAA	0.36621	0.33174
cg1850223	DIP2C	GR [T050	486	492	0	CAAAAA	0.36621	0.33174
cg1850223	DIP2C	AP-2alpha	1461	1466	0	GCCTGC	0.97656	1.07867
cg1850223	DIP2C	AP-2alpha	1891	1896	0	GCCTGC	0.97656	1.07867
cg1850223	DIP2C	ATF3 [T0	80	87	0	TGACGT	0.03052	0.02884
cg1850223	DIP2C	IRF-2 [T0	1541	1546	0	TCACTT	0.48828	0.46235
cg1850382	DIP2C	GR-beta [	147	151	0	AATGT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	192	196	0	AAATT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	720	724	0	AATGT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	1076	1080	0	AAATT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	1077	1081	0	AATTT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	1112	1116	0	ACATT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	1154	1158	0	ACATT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [	1214	1218	0	AATGT	3.90625	3.51525

cg1850382	DIP2C	GR-beta [T	1502	1506	0	AATGT	3.90625	3.51525
cg1850382	DIP2C	GR-beta [T	1966	1970	0	AAATT	3.90625	3.51525
cg1850382	DIP2C	XBP-1 [T0	405	410	0	AGTCAT	0.97656	0.94838
cg1850382	DIP2C	XBP-1 [T0	960	965	0	CGTCAT	0.97656	0.94838
cg1850382	DIP2C	TFIID [T0	632	638	0	TTTTTTA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	633	639	0	TTTTTAA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	807	813	0	TTAAAA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	808	814	0	TAAAAA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	822	828	0	TCTAAA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	824	830	0	TAAAAA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	1218	1224	0	TTTTCAA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	1253	1259	0	TTTTCAA	1.09863	0.95175
cg1850382	DIP2C	TFIID [T0	1488	1494	0	TTTTCAA	1.09863	0.95175
cg1850382	DIP2C	AP-1 [T00	710	718	0	TGACTC	0.03052	0.03037
cg1850382	DIP2C	c-Jun [T00	710	716	0	TGACTC	0.12207	0.11843
cg1850382	DIP2C	c-Jun [T00	872	878	0	TGACTC	0.12207	0.11843
cg1850382	DIP2C	GR-alpha [	1026	1030	0	CCTAT	7.8125	7.79817
cg1850382	DIP2C	GR-alpha [	1034	1038	0	CCTGT	7.8125	7.79817
cg1850382	DIP2C	GR-alpha [	1568	1572	0	ACAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha [	1617	1621	0	ACAGG	7.8125	7.79817
cg1850382	DIP2C	GR-alpha [	1856	1860	0	CCTGT	7.8125	7.79817
cg1850382	DIP2C	GR-alpha [	1992	1996	0	CCTGT	7.8125	7.79817
cg1850382	DIP2C	FOXP3 [T	139	144	0	CACAAC	1.46484	1.44953
cg1850382	DIP2C	FOXP3 [T	235	240	0	GTTGTG	1.46484	1.44953
cg1850382	DIP2C	FOXP3 [T	1348	1353	0	AACAAC	1.46484	1.44953
cg1850382	DIP2C	PR B [T00	333	339	0	CACTGT	0.36621	0.35051
cg1850382	DIP2C	PR B [T00	1820	1826	0	AACAGT	0.36621	0.35051
cg1850382	DIP2C	PR A [T01	333	339	0	CACTGT	0.36621	0.35051
cg1850382	DIP2C	PR A [T01	1820	1826	0	AACAGT	0.36621	0.35051
cg1850382	DIP2C	HNF-3alpl	1495	1502	0	TGAAAA	0.09155	0.07727
cg1850382	DIP2C	HNF-3alpl	1954	1961	0	TAAAAA	0.09155	0.07727
cg1850382	DIP2C	C/EBPbeta	36	39	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	87	90	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	123	126	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	129	132	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	140	143	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	169	172	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	172	175	0	TTGC	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	236	239	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	354	357	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	364	367	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	387	390	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	400	403	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	501	504	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	562	565	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	596	599	0	TTGC	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	616	619	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	628	631	0	TTGC	15.625	15.26275

cg1850382	DIP2C	C/EBPbeta	665	668	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	783	786	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	893	896	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	912	915	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	929	932	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1129	1132	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1212	1215	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1231	1234	0	TTGC	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1237	1240	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1349	1352	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1417	1420	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1420	1423	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1463	1466	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1659	1662	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1675	1678	0	TTGT	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1713	1716	0	ACAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1761	1764	0	GCAA	15.625	15.26275
cg1850382	DIP2C	C/EBPbeta	1961	1964	0	ACAA	15.625	15.26275
cg1850382	DIP2C	YY1 [T00	358	361	0	ATGG	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	420	423	0	ATGG	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	544	547	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	592	595	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	684	687	0	ATGG	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	793	796	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	840	843	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	907	910	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	964	967	0	ATGG	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	1029	1032	0	ATGG	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	1276	1279	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	1646	1649	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	1730	1733	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	1784	1787	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	1933	1936	0	ATGG	7.8125	7.79459
cg1850382	DIP2C	YY1 [T00	1944	1947	0	CCAT	7.8125	7.79459
cg1850382	DIP2C	TFII-I [T0	159	164	0	CTTTCC	1.46484	1.48598
cg1850382	DIP2C	TFII-I [T0	575	580	0	CTTTCC	1.46484	1.48598
cg1850382	DIP2C	TFII-I [T0	1057	1062	0	CTTTCC	1.46484	1.48598
cg1850382	DIP2C	TFII-I [T0	1425	1430	0	CTGTCC	1.46484	1.48598
cg1850382	DIP2C	TFII-I [T0	1452	1457	0	CTTTCC	1.46484	1.48598
cg1850382	DIP2C	c-Ets-1 [T	487	493	0	CAGGAA	0.24414	0.24982
cg1850382	DIP2C	c-Ets-1 [T	1066	1072	0	CTTCCTC	0.24414	0.24982
cg1850382	DIP2C	ER-alpha [	513	517	0	GGTCA	1.95312	1.99744
cg1850382	DIP2C	ER-alpha [	1208	1212	0	GGTCA	1.95312	1.99744
cg1850382	DIP2C	ER-alpha [	1392	1396	0	TGACC	1.95312	1.99744
cg1850382	DIP2C	ER-alpha [	1555	1559	0	GGTCA	1.95312	1.99744
cg1850382	DIP2C	ER-alpha [	1670	1674	0	TGACC	1.95312	1.99744
cg1850382	DIP2C	ER-alpha [	1903	1907	0	GGTCA	1.95312	1.99744
cg1850382	DIP2C	RXR-alpha	1383	1389	0	TGAACC	0.24414	0.24342

cg1850382	DIP2C	GR [T050	1962	1968	0	CAAAAA	0.36621	0.33174
cg1850382	DIP2C	GATA-1 [	1299	1304	0	TATCTG	0.97656	0.92541
cg1850382	DIP2C	GATA-1 [	1324	1329	0	TATCTG	0.97656	0.92541
cg1850382	DIP2C	GATA-1 [	1337	1342	0	CAGATA	0.97656	0.92541
cg1850382	DIP2C	GATA-1 [	1664	1669	0	TATCTG	0.97656	0.92541
cg1850382	DIP2C	Pax-5 [T0	703	709	0	GGGCTG	1.09863	1.24633
cg1850382	DIP2C	Pax-5 [T0	1000	1006	0	CGGGCC	1.09863	1.24633
cg1850382	DIP2C	Pax-5 [T0	1031	1037	0	GGGCCT	1.09863	1.24633
cg1850382	DIP2C	Pax-5 [T0	1620	1626	0	GGGCTG	1.09863	1.24633
cg1850382	DIP2C	AP-2alpha	240	245	0	GCAGGC	0.97656	1.07867
cg1850382	DIP2C	AP-2alpha	1768	1773	0	GCAGGC	0.97656	1.07867
cg1493188	DIP2C	GR-beta [	510	514	0	ACATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	568	572	0	AATTT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	707	711	0	AAATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	713	717	0	AATGT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	723	727	0	AAATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	733	737	0	ACATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	779	783	0	ACATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	785	789	0	AATGT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	906	910	0	AATTT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1127	1131	0	AAATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1169	1173	0	AATGT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1215	1219	0	AAATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1216	1220	0	AATTT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1426	1430	0	AAATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1427	1431	0	AATTT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1432	1436	0	AATTT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1613	1617	0	AATTT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1716	1720	0	ACATT	3.90625	3.51525
cg1493188	DIP2C	GR-beta [	1938	1942	0	ACATT	3.90625	3.51525
cg1493188	DIP2C	XBP-1 [T	635	640	0	ATGACT	0.97656	0.94838
cg1493188	DIP2C	TFIID [T0	514	520	0	TTTTCAA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	579	585	0	TTTTTGA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	586	592	0	TTTTTTA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	676	682	0	TTTTCTA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	679	685	0	TCTAAA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	691	697	0	TTTTATA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	719	725	0	TAGAAA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	900	906	0	TTTTTTA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	901	907	0	TTTTTAA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	920	926	0	TAGAAA	1.09863	0.95175
cg1493188	DIP2C	TFIID [T0	1531	1537	0	TAGAAA	1.09863	0.95175
cg1493188	DIP2C	c-Jun [T00	1110	1116	0	TGAGTC	0.12207	0.11843
cg1493188	DIP2C	GR-alpha [	801	805	0	CCTGT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha [	952	956	0	CCTGT	7.8125	7.79817
cg1493188	DIP2C	GR-alpha [	1224	1228	0	ATAGG	7.8125	7.79817
cg1493188	DIP2C	GR-alpha [	1521	1525	0	ATAGG	7.8125	7.79817
cg1493188	DIP2C	GR-alpha [	1674	1678	0	CCTAT	7.8125	7.79817

cg1493188	DIP2C	GR-alpha [	1968	1972	0	CCTGT	7.8125	7.79817
cg1493188	DIP2C	FOXP3 [T	134	139	0	GTTGTT	1.46484	1.44953
cg1493188	DIP2C	FOXP3 [T	183	188	0	GTTGTT	1.46484	1.44953
cg1493188	DIP2C	FOXP3 [T	232	237	0	GTTGTT	1.46484	1.44953
cg1493188	DIP2C	FOXP3 [T	428	433	0	GTTGTT	1.46484	1.44953
cg1493188	DIP2C	PR B [T00	44	50	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	93	99	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	142	148	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	191	197	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	240	246	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	289	295	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	338	344	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	387	393	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR B [T00	637	643	0	GACTGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	44	50	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	93	99	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	142	148	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	191	197	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	240	246	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	289	295	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	338	344	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	387	393	0	AACAGT	0.36621	0.35051
cg1493188	DIP2C	PR A [T01	637	643	0	GACTGT	0.36621	0.35051
cg1493188	DIP2C	C/EBPbeta	135	138	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	184	187	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	233	236	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	429	432	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	540	543	0	ACAA	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	574	577	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	607	610	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	673	676	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	879	882	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	910	913	0	TTGC	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1185	1188	0	ACAA	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1192	1195	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1207	1210	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1269	1272	0	TTGC	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1343	1346	0	ACAA	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1413	1416	0	TTGC	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1418	1421	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1490	1493	0	ACAA	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1548	1551	0	ACAA	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1576	1579	0	TTGC	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1578	1581	0	GCAA	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1643	1646	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1654	1657	0	ACAA	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1665	1668	0	TTGC	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1792	1795	0	TTGT	15.625	15.26275

cg1493188	DIP2C	C/EBPbeta	1921	1924	0	TTGT	15.625	15.26275
cg1493188	DIP2C	C/EBPbeta	1992	1995	0	GCAA	15.625	15.26275
cg1493188	DIP2C	YY1 [T00	627	630	0	ATGG	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	818	821	0	ATGG	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	891	894	0	CCAT	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1180	1183	0	ATGG	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1317	1320	0	ATGG	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1544	1547	0	ATGG	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1589	1592	0	CCAT	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1596	1599	0	CCAT	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1668	1671	0	CCAT	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1863	1866	0	CCAT	7.8125	7.79459
cg1493188	DIP2C	YY1 [T00	1928	1931	0	CCAT	7.8125	7.79459
cg1493188	DIP2C	TFII-I [T0	743	748	0	CTTTCC	1.46484	1.48598
cg1493188	DIP2C	TFII-I [T0	1080	1085	0	CTATCC	1.46484	1.48598
cg1493188	DIP2C	TFII-I [T0	1519	1524	0	GGATAG	1.46484	1.48598
cg1493188	DIP2C	TFII-I [T0	1830	1835	0	CTGTCC	1.46484	1.48598
cg1493188	DIP2C	TFII-I [T0	1836	1841	0	CTTTCC	1.46484	1.48598
cg1493188	DIP2C	STAT4 [T	1494	1499	0	GGAAAT	0.48828	0.46235
cg1493188	DIP2C	STAT4 [T	1670	1675	0	ATTTCC	0.48828	0.46235
cg1493188	DIP2C	c-Ets-1 [T	1117	1123	0	CTTCCTC	0.24414	0.24982
cg1493188	DIP2C	ER-alpha [	1502	1506	0	TGACC	1.95312	1.99744
cg1493188	DIP2C	ER-alpha [	1524	1528	0	GGTCA	1.95312	1.99744
cg1493188	DIP2C	ER-alpha [	1592	1596	0	TGACC	1.95312	1.99744
cg1493188	DIP2C	ER-alpha [	1627	1631	0	GGTCA	1.95312	1.99744
cg1493188	DIP2C	GR [T050	570	576	0	TTTTTTG	0.36621	0.33174
cg1493188	DIP2C	GR [T050	1549	1555	0	CAAAAA	0.36621	0.33174
cg1493188	DIP2C	c-Myc [T0	1735	1740	0	CACGTG	0.48828	0.51196
cg1493188	DIP2C	Pax-5 [T0	1373	1379	0	CCTGCC	1.09863	1.24633
cg1493188	DIP2C	Pax-5 [T0	1742	1748	0	CAGGCC	1.09863	1.24633
cg1493188	DIP2C	Pax-5 [T0	1946	1952	0	GGGCTG	1.09863	1.24633
cg1493188	DIP2C	p53 [T006	1373	1379	0	CCTGCC	0.36621	0.40082
cg1493188	DIP2C	IRF-2 [T0	1114	1119	0	TCACTT	0.48828	0.46235
cg1146814	DIP2C	GR-beta [	68	72	0	AAATT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	1511	1515	0	AAATT	3.90625	3.51525
cg1146814	DIP2C	GR-beta [	1971	1975	0	AATTT	3.90625	3.51525
cg1146814	DIP2C	XBP-1 [T	59	64	0	AGTCAT	0.97656	0.94838
cg1146814	DIP2C	XBP-1 [T	1192	1197	0	CGTCAT	0.97656	0.94838
cg1146814	DIP2C	TFIID [T0	64	70	0	TTAAAA	1.09863	0.95175
cg1146814	DIP2C	TFIID [T0	493	499	0	TCAAAA	1.09863	0.95175
cg1146814	DIP2C	TFIID [T0	1197	1203	0	TTTTAGA	1.09863	0.95175
cg1146814	DIP2C	TFIID [T0	1941	1947	0	TATAAA	1.09863	0.95175
cg1146814	DIP2C	TFIID [T0	1973	1979	0	TTTAAA	1.09863	0.95175
cg1146814	DIP2C	AP-1 [T00	845	853	0	TGACTC	0.03052	0.03037
cg1146814	DIP2C	c-Jun [T00	845	851	0	TGACTC	0.12207	0.11843
cg1146814	DIP2C	c-Jun [T00	1416	1422	0	TGACTC	0.12207	0.11843
cg1146814	DIP2C	GR-alpha [	1558	1562	0	ACAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha [	1579	1583	0	CCTGT	7.8125	7.79817

cg1146814	DIP2C	GR-alpha [	1643	1647	0	CCTGT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha [	1659	1663	0	CCTGT	7.8125	7.79817
cg1146814	DIP2C	GR-alpha [	1687	1691	0	ACAGG	7.8125	7.79817
cg1146814	DIP2C	GR-alpha [	1882	1886	0	ACAGG	7.8125	7.79817
cg1146814	DIP2C	PR B [T00	1274	1280	0	CACTGT	0.36621	0.35051
cg1146814	DIP2C	PR B [T00	1519	1525	0	CACTGT	0.36621	0.35051
cg1146814	DIP2C	PR A [T01	1274	1280	0	CACTGT	0.36621	0.35051
cg1146814	DIP2C	PR A [T01	1519	1525	0	CACTGT	0.36621	0.35051
cg1146814	DIP2C	C/EBPbeta	99	102	0	TTGC	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	101	104	0	GCAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	117	120	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	361	364	0	TTGC	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	508	511	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	533	536	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	584	587	0	TTGT	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	654	657	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	785	788	0	TTGC	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	811	814	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1043	1046	0	GCAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1112	1115	0	GCAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1228	1231	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1288	1291	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1294	1297	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1324	1327	0	GCAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1327	1330	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1350	1353	0	GCAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1394	1397	0	GCAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1459	1462	0	ACAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1838	1841	0	GCAA	15.625	15.26275
cg1146814	DIP2C	C/EBPbeta	1908	1911	0	ACAA	15.625	15.26275
cg1146814	DIP2C	YY1 [T00	289	292	0	ATGG	7.8125	7.79459
cg1146814	DIP2C	YY1 [T00	293	296	0	ATGG	7.8125	7.79459
cg1146814	DIP2C	YY1 [T00	441	444	0	ATGG	7.8125	7.79459
cg1146814	DIP2C	YY1 [T00	1184	1187	0	ATGG	7.8125	7.79459
cg1146814	DIP2C	YY1 [T00	1236	1239	0	CCAT	7.8125	7.79459
cg1146814	DIP2C	YY1 [T00	1407	1410	0	CCAT	7.8125	7.79459
cg1146814	DIP2C	YY1 [T00	1484	1487	0	ATGG	7.8125	7.79459
cg1146814	DIP2C	YY1 [T00	1763	1766	0	CCAT	7.8125	7.79459
cg1146814	DIP2C	TFII-I [T0	22	27	0	GGACAG	1.46484	1.48598
cg1146814	DIP2C	TFII-I [T0	1020	1025	0	GGACAG	1.46484	1.48598
cg1146814	DIP2C	TFII-I [T0	1312	1317	0	CTGTCC	1.46484	1.48598
cg1146814	DIP2C	TFII-I [T0	1725	1730	0	GGACAG	1.46484	1.48598
cg1146814	DIP2C	c-Myb [T0	1487	1494	0	GGCAGT	0.03052	0.03205
cg1146814	DIP2C	ER-alpha [	123	127	0	GGTCA	1.95312	1.99744
cg1146814	DIP2C	ER-alpha [	250	254	0	TGACC	1.95312	1.99744
cg1146814	DIP2C	ER-alpha [	791	795	0	TGACC	1.95312	1.99744
cg1146814	DIP2C	ER-alpha [	1271	1275	0	GGTCA	1.95312	1.99744
cg1146814	DIP2C	ER-alpha [	1675	1679	0	TGACC	1.95312	1.99744

cg1146814	DIP2C	ER-alpha [	1735	1739	0	TGACC	1.95312	1.99744
cg1146814	DIP2C	RXR-alph	912	918	0	TGAACC	0.24414	0.24342
cg1146814	DIP2C	TCF-4E [T	359	365	0	CTTTGCT	0.12207	0.11933
cg1146814	DIP2C	NFI/CTF [	885	892	0	ACGCTT	0.18311	0.191
cg1146814	DIP2C	GR [T050	494	500	0	CAAAAA	0.36621	0.33174
cg1146814	DIP2C	Pax-5 [T0	148	154	0	GGGCTC	1.09863	1.24633
cg1146814	DIP2C	Pax-5 [T0	229	235	0	CCAGCC	1.09863	1.24633
cg1146814	DIP2C	Pax-5 [T0	692	698	0	CCAGCC	1.09863	1.24633
cg1146814	DIP2C	Pax-5 [T0	703	709	0	GGGCCC	1.09863	1.24633
cg1146814	DIP2C	Pax-5 [T0	1149	1155	0	GGGCAG	1.09863	1.24633
cg1146814	DIP2C	Pax-5 [T0	1162	1168	0	CCAGCC	1.09863	1.24633
cg1146814	DIP2C	Pax-5 [T0	1328	1334	0	CAAGCC	1.09863	1.24633
cg1146814	DIP2C	Pax-5 [T0	1638	1644	0	CCTGCC	1.09863	1.24633
cg1146814	DIP2C	p53 [T006	1149	1155	0	GGGCAG	0.36621	0.40082
cg1146814	DIP2C	p53 [T006	1638	1644	0	CCTGCC	0.36621	0.40082
cg1146814	DIP2C	AP-2alpha	828	833	0	GCAGGC	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	1094	1099	0	GCAGGC	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	1618	1623	0	GCAGGC	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	1637	1642	0	GCCTGC	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	1711	1716	0	GCAGGC	0.97656	1.07867
cg1146814	DIP2C	AP-2alpha	1744	1749	0	GCCTGC	0.97656	1.07867
cg1146814	DIP2C	IRF-2 [T01	0	5	0	AAGTGA	0.48828	0.46235
cg1146814	DIP2C	IRF-2 [T01	1732	1737	0	AAGTGA	0.48828	0.46235
cg1146814	DIP2C	HNF-1A [	1216	1223	0	ATATTA	0.24414	0.20853
cg1006492	DIP2C	GR-beta [T	257	261	0	AATGT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	302	306	0	AAATT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	830	834	0	AATGT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	1186	1190	0	AAATT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	1187	1191	0	AATTT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	1222	1226	0	ACATT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	1264	1268	0	ACATT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	1324	1328	0	AATGT	3.90625	3.51525
cg1006492	DIP2C	GR-beta [T	1612	1616	0	AATGT	3.90625	3.51525
cg1006492	DIP2C	XBP-1 [T0	515	520	0	AGTCAT	0.97656	0.94838
cg1006492	DIP2C	XBP-1 [T0	1070	1075	0	CGTCAT	0.97656	0.94838
cg1006492	DIP2C	TFIID [T0	742	748	0	TTTTTTA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	743	749	0	TTTTTAA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	917	923	0	TTAAAA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	918	924	0	TAAAAA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	932	938	0	TCTAAA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	934	940	0	TAAAAA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	1328	1334	0	TTTTCA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	1363	1369	0	TTTTCA	1.09863	0.95175
cg1006492	DIP2C	TFIID [T0	1598	1604	0	TTTTCA	1.09863	0.95175
cg1006492	DIP2C	AP-1 [T00	820	828	0	TGACTC	0.03052	0.03037
cg1006492	DIP2C	c-Jun [T00	820	826	0	TGACTC	0.12207	0.11843
cg1006492	DIP2C	c-Jun [T00	982	988	0	TGACTC	0.12207	0.11843
cg1006492	DIP2C	GR-alpha [	1136	1140	0	CCTAT	7.8125	7.79817

cg1006492	DIP2C	GR-alpha [	1144	1148	0	CCTGT	7.8125	7.79817
cg1006492	DIP2C	GR-alpha [	1678	1682	0	ACAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha [	1727	1731	0	ACAGG	7.8125	7.79817
cg1006492	DIP2C	GR-alpha [	1966	1970	0	CCTGT	7.8125	7.79817
cg1006492	DIP2C	FOXP3 [T	249	254	0	CACAAC	1.46484	1.44953
cg1006492	DIP2C	FOXP3 [T	345	350	0	GTTGTG	1.46484	1.44953
cg1006492	DIP2C	FOXP3 [T	1458	1463	0	AACAAC	1.46484	1.44953
cg1006492	DIP2C	PR B [T00	443	449	0	CACTGT	0.36621	0.35051
cg1006492	DIP2C	PR B [T00	1930	1936	0	AACAGT	0.36621	0.35051
cg1006492	DIP2C	PR A [T01	443	449	0	CACTGT	0.36621	0.35051
cg1006492	DIP2C	PR A [T01	1930	1936	0	AACAGT	0.36621	0.35051
cg1006492	DIP2C	HNF-3alp	1605	1612	0	TGAAAA	0.09155	0.07727
cg1006492	DIP2C	C/EBPbeta	100	103	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	146	149	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	197	200	0	GCAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	233	236	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	239	242	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	250	253	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	279	282	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	282	285	0	TTGC	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	346	349	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	464	467	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	474	477	0	GCAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	497	500	0	GCAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	510	513	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	611	614	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	672	675	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	706	709	0	TTGC	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	726	729	0	GCAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	738	741	0	TTGC	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	775	778	0	GCAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	893	896	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1003	1006	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1022	1025	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1039	1042	0	GCAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1239	1242	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1322	1325	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1341	1344	0	TTGC	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1347	1350	0	GCAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1459	1462	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1527	1530	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1530	1533	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1573	1576	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1769	1772	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1785	1788	0	TTGT	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1823	1826	0	ACAA	15.625	15.26275
cg1006492	DIP2C	C/EBPbeta	1871	1874	0	GCAA	15.625	15.26275
cg1006492	DIP2C	YY1 [T00	24	27	0	CCAT	7.8125	7.79459

cg1006492	DIP2C	YY1 [T00	81	84	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	468	471	0	ATGG	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	530	533	0	ATGG	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	654	657	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	702	705	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	794	797	0	ATGG	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	903	906	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	950	953	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	1017	1020	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	1074	1077	0	ATGG	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	1139	1142	0	ATGG	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	1386	1389	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	1756	1759	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	1840	1843	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	YY1 [T00	1894	1897	0	CCAT	7.8125	7.79459
cg1006492	DIP2C	TFII-I [T0	61	66	0	GGACAG	1.46484	1.48598
cg1006492	DIP2C	TFII-I [T0	75	80	0	CTTTCC	1.46484	1.48598
cg1006492	DIP2C	TFII-I [T0	269	274	0	CTTTCC	1.46484	1.48598
cg1006492	DIP2C	TFII-I [T0	685	690	0	CTTTCC	1.46484	1.48598
cg1006492	DIP2C	TFII-I [T0	1167	1172	0	CTTTCC	1.46484	1.48598
cg1006492	DIP2C	TFII-I [T0	1535	1540	0	CTGTCC	1.46484	1.48598
cg1006492	DIP2C	TFII-I [T0	1562	1567	0	CTTTCC	1.46484	1.48598
cg1006492	DIP2C	c-Ets-1 [T	597	603	0	CAGGAA	0.24414	0.24982
cg1006492	DIP2C	c-Ets-1 [T	1176	1182	0	CTTCCTC	0.24414	0.24982
cg1006492	DIP2C	ER-alpha [	623	627	0	GGTCA	1.95312	1.99744
cg1006492	DIP2C	ER-alpha [	1318	1322	0	GGTCA	1.95312	1.99744
cg1006492	DIP2C	ER-alpha [	1502	1506	0	TGACC	1.95312	1.99744
cg1006492	DIP2C	ER-alpha [	1665	1669	0	GGTCA	1.95312	1.99744
cg1006492	DIP2C	ER-alpha [	1780	1784	0	TGACC	1.95312	1.99744
cg1006492	DIP2C	RXR-alpha	1493	1499	0	TGAACC	0.24414	0.24342
cg1006492	DIP2C	GATA-1 [	1409	1414	0	TATCTG	0.97656	0.92541
cg1006492	DIP2C	GATA-1 [	1434	1439	0	TATCTG	0.97656	0.92541
cg1006492	DIP2C	GATA-1 [	1447	1452	0	CAGATA	0.97656	0.92541
cg1006492	DIP2C	GATA-1 [	1774	1779	0	TATCTG	0.97656	0.92541
cg1006492	DIP2C	Pax-5 [T0	813	819	0	GGGCTG	1.09863	1.24633
cg1006492	DIP2C	Pax-5 [T0	1110	1116	0	CGGGCC	1.09863	1.24633
cg1006492	DIP2C	Pax-5 [T0	1141	1147	0	GGGCCT	1.09863	1.24633
cg1006492	DIP2C	Pax-5 [T0	1730	1736	0	GGGCTG	1.09863	1.24633
cg1006492	DIP2C	AP-2alpha	350	355	0	GCAGGC	0.97656	1.07867
cg1006492	DIP2C	AP-2alpha	1878	1883	0	GCAGGC	0.97656	1.07867
cg0545033	DIP2C	GR-beta [	187	191	0	AATGT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	232	236	0	AAATT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	760	764	0	AATGT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	1116	1120	0	AAATT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	1117	1121	0	AATTT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	1152	1156	0	ACATT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	1194	1198	0	ACATT	3.90625	3.51525
cg0545033	DIP2C	GR-beta [	1254	1258	0	AATGT	3.90625	3.51525

cg0545033	DIP2C	GR-beta [T	1542	1546	0	AATGT	3.90625	3.51525
cg0545033	DIP2C	XBP-1 [T	445	450	0	AGTCAT	0.97656	0.94838
cg0545033	DIP2C	XBP-1 [T	1000	1005	0	CGTCAT	0.97656	0.94838
cg0545033	DIP2C	TFIID [T0	672	678	0	TTTTTTA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	673	679	0	TTTTTAA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	847	853	0	TTAAAA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	848	854	0	TAAAAA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	862	868	0	TCTAAA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	864	870	0	TAAAAA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	1258	1264	0	TTTTCAA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	1293	1299	0	TTTTCAA	1.09863	0.95175
cg0545033	DIP2C	TFIID [T0	1528	1534	0	TTTTCAA	1.09863	0.95175
cg0545033	DIP2C	AP-1 [T00	750	758	0	TGACTC	0.03052	0.03037
cg0545033	DIP2C	c-Jun [T00	750	756	0	TGACTC	0.12207	0.11843
cg0545033	DIP2C	c-Jun [T00	912	918	0	TGACTC	0.12207	0.11843
cg0545033	DIP2C	GR-alpha [	1066	1070	0	CCTAT	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	1074	1078	0	CCTGT	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	1608	1612	0	ACAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	1657	1661	0	ACAGG	7.8125	7.79817
cg0545033	DIP2C	GR-alpha [	1896	1900	0	CCTGT	7.8125	7.79817
cg0545033	DIP2C	FOXP3 [T	179	184	0	CACAAC	1.46484	1.44953
cg0545033	DIP2C	FOXP3 [T	275	280	0	GTTGTG	1.46484	1.44953
cg0545033	DIP2C	FOXP3 [T	1388	1393	0	AACAAC	1.46484	1.44953
cg0545033	DIP2C	PR B [T00	373	379	0	CACTGT	0.36621	0.35051
cg0545033	DIP2C	PR B [T00	1860	1866	0	AACAGT	0.36621	0.35051
cg0545033	DIP2C	PR A [T01	373	379	0	CACTGT	0.36621	0.35051
cg0545033	DIP2C	PR A [T01	1860	1866	0	AACAGT	0.36621	0.35051
cg0545033	DIP2C	HNF-3alph	1535	1542	0	TGAAAA	0.09155	0.07727
cg0545033	DIP2C	C/EBPbeta	30	33	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	76	79	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	127	130	0	GCAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	163	166	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	169	172	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	180	183	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	209	212	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	212	215	0	TTGC	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	276	279	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	394	397	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	404	407	0	GCAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	427	430	0	GCAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	440	443	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	541	544	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	602	605	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	636	639	0	TTGC	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	656	659	0	GCAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	668	671	0	TTGC	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	705	708	0	GCAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	823	826	0	ACAA	15.625	15.26275

cg0545033	DIP2C	C/EBPbeta	933	936	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	952	955	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	969	972	0	GCAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1169	1172	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1252	1255	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1271	1274	0	TTGC	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1277	1280	0	GCAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1389	1392	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1457	1460	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1460	1463	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1503	1506	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1699	1702	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1715	1718	0	TTGT	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1753	1756	0	ACAA	15.625	15.26275
cg0545033	DIP2C	C/EBPbeta	1801	1804	0	GCAA	15.625	15.26275
cg0545033	DIP2C	YY1 [T00	11	14	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	398	401	0	ATGG	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	460	463	0	ATGG	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	584	587	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	632	635	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	724	727	0	ATGG	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	833	836	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	880	883	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	947	950	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1004	1007	0	ATGG	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1069	1072	0	ATGG	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1316	1319	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1686	1689	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1770	1773	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1824	1827	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1973	1976	0	ATGG	7.8125	7.79459
cg0545033	DIP2C	YY1 [T00	1984	1987	0	CCAT	7.8125	7.79459
cg0545033	DIP2C	TFII-I [T0	5	10	0	CTTTCC	1.46484	1.48598
cg0545033	DIP2C	TFII-I [T0	199	204	0	CTTTCC	1.46484	1.48598
cg0545033	DIP2C	TFII-I [T0	615	620	0	CTTTCC	1.46484	1.48598
cg0545033	DIP2C	TFII-I [T0	1097	1102	0	CTTTCC	1.46484	1.48598
cg0545033	DIP2C	TFII-I [T0	1465	1470	0	CTGTCC	1.46484	1.48598
cg0545033	DIP2C	TFII-I [T0	1492	1497	0	CTTTCC	1.46484	1.48598
cg0545033	DIP2C	c-Ets-1 [T	527	533	0	CAGGAA	0.24414	0.24982
cg0545033	DIP2C	c-Ets-1 [T	1106	1112	0	CTTCCTC	0.24414	0.24982
cg0545033	DIP2C	ER-alpha [	553	557	0	GGTCA	1.95312	1.99744
cg0545033	DIP2C	ER-alpha [	1248	1252	0	GGTCA	1.95312	1.99744
cg0545033	DIP2C	ER-alpha [	1432	1436	0	TGACC	1.95312	1.99744
cg0545033	DIP2C	ER-alpha [	1595	1599	0	GGTCA	1.95312	1.99744
cg0545033	DIP2C	ER-alpha [	1710	1714	0	TGACC	1.95312	1.99744
cg0545033	DIP2C	ER-alpha [	1943	1947	0	GGTCA	1.95312	1.99744
cg0545033	DIP2C	RXR-alph	1423	1429	0	TGAACC	0.24414	0.24342
cg0545033	DIP2C	GATA-1 [	1339	1344	0	TATCTG	0.97656	0.92541

cg0545033	DIP2C	GATA-1 [	1364	1369	0	TATCTG	0.97656	0.92541
cg0545033	DIP2C	GATA-1 [	1377	1382	0	CAGATA	0.97656	0.92541
cg0545033	DIP2C	GATA-1 [	1704	1709	0	TATCTG	0.97656	0.92541
cg0545033	DIP2C	Pax-5 [T0	743	749	0	GGGCTG	1.09863	1.24633
cg0545033	DIP2C	Pax-5 [T0	1040	1046	0	CGGGCC	1.09863	1.24633
cg0545033	DIP2C	Pax-5 [T0	1071	1077	0	GGGCCT	1.09863	1.24633
cg0545033	DIP2C	Pax-5 [T0	1660	1666	0	GGGCTG	1.09863	1.24633
cg0545033	DIP2C	AP-2alpha	280	285	0	GCAGGC	0.97656	1.07867
cg0545033	DIP2C	AP-2alpha	1808	1813	0	GCAGGC	0.97656	1.07867
cg0646158	DNAJC5	RAR-beta:	116	127	9.97066	TTCATG	0.06974	0.06822
cg0646158	DNAJC5	XBP-1 [T	218	223	9.789909	AGACAT	1.95312	1.95208
cg0646158	DNAJC5	XBP-1 [T	1519	1524	9.789909	ATGGCG	1.95312	1.95208
cg0646158	DNAJC5	NF-AT2 [	1147	1156	9.755755	ATTTGT	0.08774	0.08903
cg0646158	DNAJC5	PR B [T00	155	161	9.743489	AACACC	1.09863	1.10292
cg0646158	DNAJC5	PR B [T00	320	326	9.743489	GTGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR B [T00	482	488	9.743489	GTGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR B [T00	500	506	9.743489	GGGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR B [T00	898	904	9.743489	GTGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR B [T00	916	922	9.743489	GGGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR B [T00	1156	1162	9.743489	CTGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR A [T01	155	161	9.743489	AACACC	1.09863	1.10292
cg0646158	DNAJC5	PR A [T01	320	326	9.743489	GTGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR A [T01	482	488	9.743489	GTGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR A [T01	500	506	9.743489	GGGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR A [T01	898	904	9.743489	GTGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR A [T01	916	922	9.743489	GGGTGT	1.09863	1.10292
cg0646158	DNAJC5	PR A [T01	1156	1162	9.743489	CTGTGT	1.09863	1.10292
cg0646158	DNAJC5	c-Myb [T0	466	473	9.729271	TTCAGT	0.36621	0.37054
cg0646158	DNAJC5	c-Jun [T00	933	939	9.717135	CAGGTC	0.73242	0.73031
cg0646158	DNAJC5	c-Ets-1 [T	657	663	9.585075	CGGGAA	0.36621	0.36441
cg0646158	DNAJC5	Pax-5 [T0	847	853	9.552105	GGGCAA	1.46484	1.43083
cg0646158	DNAJC5	Pax-5 [T0	1799	1805	9.552105	GTGGCC	1.46484	1.43083
cg0646158	DNAJC5	TFIID [T0	565	571	9.552105	TTTGCC	1.46484	1.48472
cg0646158	DNAJC5	TFIID [T0	711	717	9.552105	TACCAA	1.46484	1.48472
cg0646158	DNAJC5	TFIID [T0	1007	1013	9.552105	TGAGAA	1.46484	1.48472
cg0646158	DNAJC5	TFIID [T0	1403	1409	9.552105	TCCCAA	1.46484	1.48472
cg0646158	DNAJC5	TFIID [T0	1539	1545	9.552105	TGGCAA	1.46484	1.48472
cg0646158	DNAJC5	NF-1 [T00	1741	1748	9.535536	TTGGAC	0.73242	0.73053
cg0646158	DNAJC5	NF-1 [T00	1478	1485	9.513281	TTGGGG	0.73242	0.73053
cg0646158	DNAJC5	NF-1 [T00	1736	1743	9.513281	TTGGGT	0.73242	0.73053
cg0646158	DNAJC5	TFII-I [T0	22	27	9.512894	GGAAAA	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	287	292	9.512894	GGATTT	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	356	361	9.512894	GTTTCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	659	664	9.512894	GGAATT	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	974	979	9.512894	TTTTCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1044	1049	9.512894	TTATCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1083	1088	9.512894	TTGTCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1120	1125	9.512894	GGATTT	7.32422	7.29728

cg0646158	DNAJC5	TFII-I [T0	1151	1156	9.512894	GTTTCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1384	1389	9.512894	CGGTCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1596	1601	9.512894	AAGTCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1743	1748	9.512894	GGACAA	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1774	1779	9.512894	AAGTCC	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1791	1796	9.512894	GGACAA	7.32422	7.29728
cg0646158	DNAJC5	TFII-I [T0	1880	1885	9.512894	TTATCC	7.32422	7.29728
cg0646158	DNAJC5	FOXP3 [T	33	38	9.512894	GCCAAC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	110	115	9.512894	GTTGGC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	412	417	9.512894	GTTTAT	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	486	491	9.512894	GTTCTC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	497	502	9.512894	GTTGGG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	504	509	9.512894	GTTCTG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	678	683	9.512894	GCCAAC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	848	853	9.512894	GGCAAC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	902	907	9.512894	GTTCTC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	913	918	9.512894	GTTGGG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	920	925	9.512894	GTTCTG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	960	965	9.512894	CAGAAC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	993	998	9.512894	GTTCTG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1028	1033	9.512894	GTTGGG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1227	1232	9.512894	GTTGCT	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1253	1258	9.512894	GTTTAT	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1280	1285	9.512894	GTTTAT	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1463	1468	9.512894	GTTCTT	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1747	1752	9.512894	AAGAAC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1752	1757	9.512894	CGCAAC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1842	1847	9.512894	GTTTAG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1861	1866	9.512894	AAGAAC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1960	1965	9.512894	GTTATG	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1974	1979	9.512894	GTTCTC	7.32422	7.35678
cg0646158	DNAJC5	FOXP3 [T	1982	1987	9.512894	GCCAAC	7.32422	7.35678
cg0646158	DNAJC5	TCF-4E [T	296	302	9.453578	CTTTGA	0.48828	0.49215
cg0646158	DNAJC5	TCF-4E [T	1926	1932	9.453578	CTTTGT	0.48828	0.49215
cg0646158	DNAJC5	NFI/CTF [	1732	1739	9.352332	GTCCTT	0.54932	0.54821
cg0646158	DNAJC5	SRY [T00	296	304	9.264664	CTTTGA	0.12207	0.12265
cg0646158	DNAJC5	VDR [T00	957	965	9.234242	GTTCAG	0.12207	0.12335
cg0646158	DNAJC5	MEF-2A [	702	712	9.220261	TACTAA	0.07343	0.07563
cg0646158	DNAJC5	HNF-1B [	225	233	9.170219	AAATTA	0.08392	0.0857
cg0646158	DNAJC5	STAT5A [	1176	1188	9.080962	ATTTTTC	0.02816	0.02876
cg0646158	DNAJC5	c-Ets-1 [T	402	408	9.065503	ATTCCA	0.85449	0.85523
cg0646158	DNAJC5	c-Ets-1 [T	1588	1594	9.065503	ATGGAA	0.85449	0.85523
cg0646158	DNAJC5	USF2 [T0	134	143	9.056375	CAGGTG	0.1545	0.15287
cg0646158	DNAJC5	USF2 [T0	1422	1431	9.056375	CAGGTG	0.1545	0.15287
cg0646158	DNAJC5	NFI/CTF [	107	114	9.042931	GCAGTT	0.48828	0.48804
cg0646158	DNAJC5	c-Myb [T0	893	900	9.024874	AAACTG	0.39673	0.40028
cg0646158	DNAJC5	c-Ets-1 [T	278	284	9.020687	GTTCCC	0.85449	0.85523
cg0646158	DNAJC5	c-Jun [T00	517	523	9.013496	CACGTC	0.61035	0.61059

cg0646158	DNAJC5	PXR-1:RX	954	961	8.998824	GTTGTT	0.24414	0.2439
cg0646158	DNAJC5	GR [T050	562	568	8.971049	GTATT	0.61035	0.61632
cg0646158	DNAJC5	HNF-1C [	537	545	8.969184	GTTAGA	0.12207	0.12495
cg0646158	DNAJC5	c-Ets-2 [T	1814	1822	8.912323	CCCCAG	0.27466	0.27495
cg0646158	DNAJC5	NFI/CTF [	1474	1481	8.814757	TCTCTT	0.48828	0.48804
cg0646158	DNAJC5	NF-1 [T00	1401	1408	8.790071	CCTCCC	0.24414	0.24467
cg0646158	DNAJC5	NF-1 [T00	1979	1986	8.790071	CTTGCC	0.24414	0.24467
cg0646158	DNAJC5	AR [T000	1791	1799	8.762682	GGACAA	0.04578	0.04533
cg0646158	DNAJC5	LEF-1 [T0	1206	1213	8.759086	CTTTGC	0.54932	0.55326
cg0646158	DNAJC5	LEF-1 [T0	1633	1640	8.759086	CTTTGT	0.54932	0.55326
cg0646158	DNAJC5	LEF-1 [T0	1926	1933	8.759086	CTTTGT	0.54932	0.55326
cg0646158	DNAJC5	XBP-1 [T	186	191	8.75604	TTTCAT	2.92969	2.9674
cg0646158	DNAJC5	XBP-1 [T	222	227	8.75604	ATGAAA	2.92969	2.9674
cg0646158	DNAJC5	XBP-1 [T	1172	1177	8.75604	TTTCAT	2.92969	2.9674
cg0646158	DNAJC5	XBP-1 [T	1345	1350	8.75604	GATCAT	2.92969	2.9674
cg0646158	DNAJC5	XBP-1 [T	1622	1627	8.75604	TTTCAT	2.92969	2.9674
cg0646158	DNAJC5	MAZ [T00	157	169	8.752298	CACCCT	0.01413	0.01385
cg0646158	DNAJC5	NF-AT1 [	22	30	8.599808	GGAAAA	0.10681	0.10725
cg0646158	DNAJC5	RAR-beta	353	362	8.55975	TGGGTT	0.26703	0.26657
cg0646158	DNAJC5	RAR-beta	687	696	8.541284	GAGAAA	0.26703	0.26657
cg0646158	DNAJC5	AP-1 [T00	370	378	8.513775	GCTAAG	0.03052	0.03084
cg0646158	DNAJC5	c-Myb [T0	359	366	8.412632	TCCAGT	0.30518	0.30924
cg0646158	DNAJC5	HNF-1B [	536	544	8.379818	AGTTAG	0.11444	0.11669
cg0646158	DNAJC5	PR B [T00	989	995	8.338824	GTCTGT	1.09863	1.10009
cg0646158	DNAJC5	PR B [T00	1306	1312	8.338824	AACAGG	1.09863	1.10009
cg0646158	DNAJC5	PR A [T01	989	995	8.338824	GTCTGT	1.09863	1.10009
cg0646158	DNAJC5	PR A [T01	1306	1312	8.338824	AACAGG	1.09863	1.10009
cg0646158	DNAJC5	PXR-1:RX	1577	1584	8.304332	TGAACG	0.12207	0.12266
cg0646158	DNAJC5	GR-alpha	19	23	8.281568	GAAGG	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	40	44	8.281568	CCTCC	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	43	47	8.281568	CCTCC	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	160	164	8.281568	CCTCC	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	316	320	8.281568	GGAGG	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	348	352	8.281568	CCTCC	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	608	612	8.281568	GGAGG	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	798	802	8.281568	GGAGG	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	804	808	8.281568	GGAGG	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	1388	1392	8.281568	CCTCC	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	1401	1405	8.281568	CCTCC	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	1551	1555	8.281568	CAAGG	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	1613	1617	8.281568	CCTTG	7.8125	7.72956
cg0646158	DNAJC5	GR-alpha	1734	1738	8.281568	CCTTG	7.8125	7.72956
cg0646158	DNAJC5	GCF [T00	105	113	8.256755	GCGCAG	0.09155	0.09002
cg0646158	DNAJC5	c-Jun [T00	395	401	8.242207	TGACCT	0.48828	0.49076
cg0646158	DNAJC5	NFI/CTF [	1737	1744	8.241664	TGGGTT	0.18311	0.1823
cg0646158	DNAJC5	NF-AT2 [	970	979	8.21356	ATGTTT	0.08965	0.09068
cg0646158	DNAJC5	ENKTF-1	674	681	8.19852	CCTGGC	0.73242	0.71737
cg0646158	DNAJC5	NF-1 [T00	986	993	8.191058	TTGGTC	0.24414	0.24409

cg0646158	DNAJC5	c-Jun [T00	1764	1770	8.128539	TGACAT	0.48828	0.49076
cg0646158	DNAJC5	GR-alpha [	11	15	8.073878	GCAGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	29	33	8.073878	CCAGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	92	96	8.073878	CCTGC	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	164	168	8.073878	CCAGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	283	287	8.073878	CCTGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	351	355	8.073878	CCTGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	569	573	8.073878	CCAGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	618	622	8.073878	GCAGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	674	678	8.073878	CCTGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	776	780	8.073878	GCAGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	844	848	8.073878	CCTGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	1322	1326	8.073878	CCTGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	1372	1376	8.073878	CCTGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	1816	1820	8.073878	CCAGG	7.8125	7.72238
cg0646158	DNAJC5	GR-alpha [	1884	1888	8.073878	CCTGG	7.8125	7.72238
cg0646158	DNAJC5	Pax-5 [T0	100	106	8.014558	GGGCAG	2.19727	2.14502
cg0646158	DNAJC5	Pax-5 [T0	121	127	8.014558	GGAGCC	2.19727	2.14502
cg0646158	DNAJC5	Pax-5 [T0	195	201	8.014558	GGTGCC	2.19727	2.14502
cg0646158	DNAJC5	Pax-5 [T0	430	436	8.014558	GAAGCC	2.19727	2.14502
cg0646158	DNAJC5	Pax-5 [T0	1325	1331	8.014558	GGGCTC	2.19727	2.14502
cg0646158	DNAJC5	Pax-5 [T0	1375	1381	8.014558	GGGCTC	2.19727	2.14502
cg0646158	DNAJC5	Pax-5 [T0	1428	1434	8.014558	TGAGCC	2.19727	2.14502
cg0646158	DNAJC5	Pax-5 [T0	1608	1614	8.014558	TCTGCC	2.19727	2.14502
cg0646158	DNAJC5	TFIID [T0	271	277	8.014558	TTTCTA	2.19727	2.24348
cg0646158	DNAJC5	TFIID [T0	538	544	8.014558	TTAGAA	2.19727	2.24348
cg0646158	DNAJC5	TFIID [T0	1003	1009	8.014558	TTTCTG	2.19727	2.24348
cg0646158	DNAJC5	TFIID [T0	1634	1640	8.014558	TTTGTG	2.19727	2.24348
cg0646158	DNAJC5	C/EBPalph	1721	1727	8.006685	CATTGT	0.24414	0.24674
cg0646158	DNAJC5	c-Myb [T0	639	646	8.005241	GGGAGT	0.21362	0.21454
cg0646158	DNAJC5	c-Ets-2 [T	976	984	7.84116	TTCCTG	0.32043	0.32298
cg0646158	DNAJC5	p53 [T006	121	127	7.833758	GGAGCC	0.48828	0.47377
cg0646158	DNAJC5	p53 [T006	1325	1331	7.833758	GGGCTC	0.48828	0.47377
cg0646158	DNAJC5	RXR-alpha	1481	1487	7.815913	GGGTGG	0.24414	0.24104
cg0646158	DNAJC5	c-Ets-2 [T	1153	1161	7.76635	TTCCTG	0.32043	0.32298
cg0646158	DNAJC5	NF-AT1 [	1148	1156	7.72101	TTTGTTT	0.19836	0.19941
cg0646158	DNAJC5	NF-1 [T00	1615	1622	7.693985	TTGGTA	0.24414	0.24565
cg0646158	DNAJC5	c-Jun [T00	510	516	7.686747	TGACTG	0.48828	0.48775
cg0646158	DNAJC5	GR [T050	714	720	7.527031	CAAAAT	1.83105	1.86007
cg0646158	DNAJC5	GR [T050	1114	1120	7.527031	ATGTTT	1.83105	1.86007
cg0646158	DNAJC5	GR [T050	1145	1151	7.527031	CTATTT	1.83105	1.86007
cg0646158	DNAJC5	GR [T050	1274	1280	7.527031	TATTTT	1.83105	1.86007
cg0646158	DNAJC5	GR [T050	1290	1296	7.527031	ATATTT	1.83105	1.86007
cg0646158	DNAJC5	GR [T050	1406	1412	7.527031	CAAAAT	1.83105	1.86007
cg0646158	DNAJC5	GR [T050	1567	1573	7.527031	TCTTTTG	1.83105	1.86007
cg0646158	DNAJC5	GR [T050	1572	1578	7.527031	TGCTTT	1.83105	1.86007
cg0646158	DNAJC5	AR [T000	1743	1751	7.467081	GGACAA	0.25177	0.25079
cg0646158	DNAJC5	C/EBPalph	831	837	7.465744	CATTGC	0.48828	0.49653

cg0646158	DNAJC5	C/EBPalph	1094	1100	7.465744	CATTGA	0.48828	0.49653
cg0646158	DNAJC5	C/EBPalph	1867	1873	7.465744	CATTGC	0.48828	0.49653
cg0646158	DNAJC5	PEA3 [T0	1806	1814	7.421728	CCACAT	0.34332	0.34161
cg0646158	DNAJC5	C/EBPalph	1071	1077	7.396431	AATTGG	0.48828	0.49653
cg0646158	DNAJC5	PPAR-alph	1411	1421	7.370536	TGCTGG	0.04482	0.04393
cg0646158	DNAJC5	SRY [T00	208	216	7.175614	GCAGCA	0.30518	0.30739
cg0646158	DNAJC5	SRY [T00	1574	1582	7.175614	CTTTGA	0.30518	0.30739
cg0646158	DNAJC5	XBP-1 [T	115	120	7.172312	CTTCAT	2.92969	2.97018
cg0646158	DNAJC5	XBP-1 [T	398	403	7.172312	CCTCAT	2.92969	2.97018
cg0646158	DNAJC5	XBP-1 [T	1968	1973	7.172312	ATTCAT	2.92969	2.97018
cg0646158	DNAJC5	p53 [T006	1799	1805	7.150251	GTGGCC	1.09863	1.07125
cg0646158	DNAJC5	c-Myb [T0	1902	1909	7.127234	GAACTG	0.18311	0.18399
cg0646158	DNAJC5	Ik-1 [T027	45	57	7.122895	TCCCAC	0.01064	0.01049
cg0646158	DNAJC5	Ik-1 [T027	749	761	7.122895	TCCCAG	0.01064	0.01049
cg0646158	DNAJC5	Ik-1 [T027	1406	1418	7.122895	CAAAAT	0.01064	0.01049
cg0646158	DNAJC5	HNF-3alph	247	254	7.000129	TATTTAT	0.82397	0.84946
cg0646158	DNAJC5	HNF-3alph	1039	1046	7.000129	CATTTTT	0.82397	0.84946
cg0646158	DNAJC5	HNF-3alph	1139	1146	7.000129	AATTTTC	0.82397	0.84946
cg0646158	DNAJC5	NF-1 [T00	1029	1036	6.948522	TTGGGTC	0.48828	0.4856
cg0646158	DNAJC5	ENKTF-1	29	36	6.942764	CCAGGC	1.46484	1.44228
cg0646158	DNAJC5	ENKTF-1	1512	1519	6.942764	CCATGC	1.46484	1.44228
cg0646158	DNAJC5	ENKTF-1	1520	1527	6.942764	TGGCGT	1.46484	1.44228
cg0646158	DNAJC5	VDR [T00	1573	1581	6.925682	GCTTTG	0.42725	0.43062
cg0646158	DNAJC5	NF-AT1 [	353	362	6.890694	TGGGTT	0.01907	0.01922
cg0646158	DNAJC5	C/EBPalph	256	262	6.85549	TTCAAT	0.73242	0.74337
cg0646158	DNAJC5	STAT5A [	1000	1012	6.810722	CGATTTC	0.01341	0.01369
cg0646158	DNAJC5	c-Jun [T00	1052	1058	6.787369	TCTGTC	0.73242	0.73173
cg0646158	DNAJC5	C/EBPalph	1241	1247	6.786177	TACAAT	0.73242	0.74337
cg0646158	DNAJC5	p53 [T006	1375	1381	6.778774	GGGCTC	1.09863	1.07125
cg0646158	DNAJC5	p53 [T006	1428	1434	6.778774	TGAGCC	1.09863	1.07125
cg0646158	DNAJC5	AR [T000	1080	1088	6.760234	TTTTTGT	0.23651	0.23551
cg0646158	DNAJC5	LEF-1 [T0	296	303	6.75468	CTTTGAC	0.06104	0.06131
cg0646158	DNAJC5	LEF-1 [T0	1574	1581	6.75468	CTTTGA	0.06104	0.06131
cg0646158	DNAJC5	ATF3 [T01	516	523	6.744803	TCACGT	0.27466	0.27656
cg0646158	DNAJC5	TCF-4 [T0	295	304	6.735684	TCTTTGA	0.04959	0.05016
cg0646158	DNAJC5	NF-1 [T00	675	682	6.722386	CTGGCC	0.24414	0.24147
cg0646158	DNAJC5	HNF-1C [	470	478	6.596946	GTTAAA	0.05341	0.05475
cg0646158	DNAJC5	TFII-I [T0	836	841	6.581441	CACTCC	0.97656	0.97366
cg0646158	DNAJC5	TFII-I [T0	1340	1345	6.581441	GGAGTG	0.97656	0.97366
cg0646158	DNAJC5	FOXP3 [T	327	332	6.581441	GTTGAA	0.97656	0.99397
cg0646158	DNAJC5	FOXP3 [T	1899	1904	6.581441	GTTGAA	0.97656	0.99397
cg0646158	DNAJC5	p53 [T006	430	436	6.563521	GAAGCC	0.48828	0.47541
cg0646158	DNAJC5	XBP-1 [T	1514	1519	6.478682	ATGCCA	0.97656	0.97062
cg0646158	DNAJC5	XBP-1 [T	1830	1835	6.478682	ATGCCC	0.97656	0.97062
cg0646158	DNAJC5	RAR-beta	22	31	6.39673	GGAAAA	0.18311	0.183
cg0646158	DNAJC5	MEF-2A [	1985	1995	6.342474	AACAAA	0.02384	0.02461
cg0646158	DNAJC5	TCF-4E [T	1574	1580	6.302385	CTTTGA	0.61035	0.61344
cg0646158	DNAJC5	GR-alpha [	398	402	6.263098	CCTCA	3.90625	3.91061

cg0646158	DNAJC5	GR-alpha [	614	618	6.263098	TGAGG	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	632	636	6.263098	TGAGG	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	651	655	6.263098	TGAGG	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	766	770	6.263098	TGAGG	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	772	776	6.263098	TGAGG	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	1062	1066	6.263098	CCTTA	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	1234	1238	6.263098	TAAGG	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	1301	1305	6.263098	TAAGG	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	1363	1367	6.263098	CCTCA	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	1395	1399	6.263098	CCTCA	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	1757	1761	6.263098	CCTCA	3.90625	3.91061
cg0646158	DNAJC5	GR-alpha [	1946	1950	6.263098	CCTTA	3.90625	3.91061
cg0646158	DNAJC5	c-Myb [T0	1459	1466	6.259888	TGCAGT	0.30518	0.3056
cg0646158	DNAJC5	ETF [T002	124	134	6.253495	GCCCCC	0.00954	0.00918
cg0646158	DNAJC5	C/EBPalph	415	421	6.245236	TATTGA	0.97656	0.99
cg0646158	DNAJC5	SRY [T00	1633	1641	6.176442	CTTTGTC	0.15259	0.15366
cg0646158	DNAJC5	PPAR-alph	75	85	6.14093	GACTGG	0.02003	0.01956
cg0646158	DNAJC5	GR-alpha [	3	7	6.055408	TCAGG	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	133	137	6.055408	TCAGG	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	174	178	6.055408	CCTGA	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	376	380	6.055408	TCAGG	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	435	439	6.055408	CCTAA	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	630	634	6.055408	CCTGA	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	649	653	6.055408	CCTGA	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	932	936	6.055408	TCAGG	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	978	982	6.055408	CCTGA	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	1468	1472	6.055408	TCAGG	3.90625	3.9065
cg0646158	DNAJC5	GR-alpha [	1672	1676	6.055408	CCTAA	3.90625	3.9065
cg0646158	DNAJC5	c-Myb [T0	861	868	6.04018	AAACTG	0.21362	0.21535
cg0646158	DNAJC5	c-Ets-1 [T	357	363	6.039428	TTTCCAC	0.36621	0.36731
cg0646158	DNAJC5	C/EBPalph	476	482	5.996794	AACAAT	0.97656	0.99
cg0646158	DNAJC5	C/EBPalph	543	549	5.996794	AACAAT	0.97656	0.99
cg0646158	DNAJC5	C/EBPalph	554	560	5.996794	AACAAT	0.97656	0.99
cg0646158	DNAJC5	RXR-alpha	194	200	5.937582	GGGTGC	0.73242	0.72249
cg0646158	DNAJC5	GCF [T00	573	581	5.917256	GCGCTG	0.64087	0.6219
cg0646158	DNAJC5	GCF [T00	1690	1698	5.917256	AGACAG	0.64087	0.6219
cg0646158	DNAJC5	IRF-1 [T0	1152	1160	5.861409	TTTCCTC	0.16785	0.16909
cg0646158	DNAJC5	VDR [T00	786	794	5.771401	TGCTTGA	0.42725	0.42999
cg0646158	DNAJC5	RXR-alpha	155	161	5.715466	AACACC	0.61035	0.6044
cg0646158	DNAJC5	RXR-alpha	500	506	5.715466	GGGTGT	0.61035	0.6044
cg0646158	DNAJC5	RXR-alpha	916	922	5.715466	GGGTGT	0.61035	0.6044
cg0646158	DNAJC5	NF-AT1 [	971	979	5.604085	TGTTTTT	0.03815	0.03856
cg0646158	DNAJC5	NFI/CTF [	1114	1121	5.558661	ATGTTTC	0.54932	0.55038
cg0646158	DNAJC5	TFIID [T0	702	708	5.544826	TACTAA	0.73242	0.75085
cg0646158	DNAJC5	TFIID [T0	1855	1861	5.544826	TTTACCA	0.73242	0.75085
cg0646158	DNAJC5	C/EBPalph	783	789	5.455853	CATTGCT	0.73242	0.74391
cg0646158	DNAJC5	IRF-1 [T0	975	983	5.404935	TTTCCTC	0.22888	0.23087
cg0646158	DNAJC5	C/EBPalph	1104	1110	5.38654	AATTGTT	0.73242	0.74391

cg0646158	DNAJC5	NF-1 [T00	30	37	5.377909	CAGGCC	0.24414	0.24258
cg0646158	DNAJC5	RAR-beta	1737	1746	5.333686	TGGGTT	0.15259	0.15189
cg0646158	DNAJC5	RXR-alpha	46	52	5.271235	CCCACC	0.61035	0.6044
cg0646158	DNAJC5	c-Jun [T00	177	183	5.193102	GAAGTC	0.61035	0.61057
cg0646158	DNAJC5	SRY [T00	1926	1934	5.086565	CTTTGT	0.06104	0.06209
cg0646158	DNAJC5	USF2 [T0	86	95	5.052423	CACTCA	0.103	0.10178
cg0646158	DNAJC5	GR-beta [	246	250	5.042296	GTATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	287	291	5.042296	GGATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	562	566	5.042296	GTATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	709	713	5.042296	AATAC	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	747	751	5.042296	AATCC	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	1014	1018	5.042296	GTATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	1120	1124	5.042296	GGATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	1237	1241	5.042296	GGATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	1489	1493	5.042296	GTATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	1563	1567	5.042296	GGATT	3.90625	3.95351
cg0646158	DNAJC5	GR-beta [	1966	1970	5.042296	GTATT	3.90625	3.95351
cg0646158	DNAJC5	E2F-1 [T0	1388	1395	5.042045	CCTCCC	0.18311	0.17901
cg0646158	DNAJC5	c-Ets-1 [T	1130	1136	5.038739	CTTCCA	0.48828	0.49031
cg0646158	DNAJC5	HNF-1B [	469	477	4.953067	AGTTAA	0.04578	0.04699
cg0646158	DNAJC5	XBP-1 [T	739	744	4.894955	ATGCCT	0.97656	0.96979
cg0646158	DNAJC5	AP-2alpha	1671	1676	4.890408	GCCTAA	0.97656	0.97567
cg0646158	DNAJC5	NF-Y [T0	1072	1079	4.867193	ATTGGA	0.36621	0.36847
cg0646158	DNAJC5	GCF [T00	100	108	4.846987	GGGCAG	0.27466	0.26486
cg0646158	DNAJC5	HNF-3alp	1017	1024	4.842999	TTAAAA	0.09155	0.09582
cg0646158	DNAJC5	TFII-I [T0	74	79	4.756447	GGACTG	2.92969	2.93695
cg0646158	DNAJC5	TFII-I [T0	401	406	4.756447	CATTCC	2.92969	2.93695
cg0646158	DNAJC5	TFII-I [T0	1057	1062	4.756447	CAGTCC	2.92969	2.93695
cg0646158	DNAJC5	FOXP3 [T	23	28	4.756447	GAAAAC	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	263	268	4.756447	CAAAAC	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	473	478	4.756447	AAAAAC	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	529	534	4.756447	GTTGAT	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	859	864	4.756447	CAAAAC	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	945	950	4.756447	GTTGAT	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	972	977	4.756447	GTTTTT	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	1078	1083	4.756447	GTTTTT	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	1108	1113	4.756447	GTTGAT	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	1160	1165	4.756447	GTTGAG	2.92969	2.96063
cg0646158	DNAJC5	FOXP3 [T	1296	1301	4.756447	GTTTTT	2.92969	2.96063
cg0646158	DNAJC5	VDR [T00	1897	1905	4.617121	GCGTTG	0.37384	0.37445
cg0646158	DNAJC5	AP-1 [T00	1714	1722	4.606866	GGGGAG	0.03052	0.03019
cg0646158	DNAJC5	c-Fos [T00	1717	1726	4.563121	GAGTCA	0.04578	0.04591
cg0646158	DNAJC5	USF2 [T0	624	633	4.528187	GGATCA	0.06866	0.06782
cg0646158	DNAJC5	GATA-2 [	1877	1885	4.444445	ACTTTA	0.24414	0.24541
cg0646158	DNAJC5	STAT4 [T	344	349	4.411765	TCTTCC	1.95312	1.94235
cg0646158	DNAJC5	STAT4 [T	401	406	4.411765	CATTCC	1.95312	1.94235
cg0646158	DNAJC5	STAT4 [T	1129	1134	4.411765	TCTTCC	1.95312	1.94235
cg0646158	DNAJC5	STAT4 [T	1819	1824	4.411765	GGAAGA	1.95312	1.94235

cg0646158	DNAJC5	HOXD9 [T	1646	1655	4.321431	TCTTTTT	0.03433	0.03596
cg0646158	DNAJC5	HOXD10 [	1646	1655	4.321431	TCTTTTT	0.03433	0.03596
cg0646158	DNAJC5	RXR-alph	63	69	4.24113	GGGACC	0.97656	0.9671
cg0646158	DNAJC5	RXR-alph	1310	1316	4.24113	GGGTCC	0.97656	0.9671
cg0646158	DNAJC5	PXR-1:RX	790	797	4.213958	TGAACC	0.12207	0.12119
cg0646158	DNAJC5	GR-beta [T	57	61	4.201913	CTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	250	254	4.201913	TTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	253	257	4.201913	TTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	414	418	4.201913	TTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	531	535	4.201913	TGATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	980	984	4.201913	TGATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1000	1004	4.201913	CGATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1145	1149	4.201913	CTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1255	1259	4.201913	TTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1273	1277	4.201913	TTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1282	1286	4.201913	TTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1592	1596	4.201913	AATAA	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1651	1655	4.201913	TTATT	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1667	1671	4.201913	AATAG	7.8125	7.94607
cg0646158	DNAJC5	GR-beta [T	1992	1996	4.201913	AATAG	7.8125	7.94607
cg0646158	DNAJC5	ATF-2 [T0	515	524	4.17677	GTCACG	0.03433	0.03472
cg0646158	DNAJC5	p53 [T006	1440	1446	4.125254	CCGGCC	0.73242	0.71379
cg0646158	DNAJC5	c-Ets-2 [T	1299	1307	4.091811	TTTAAG	0.16022	0.16243
cg0646158	DNAJC5	p53 [T006	195	201	4.083527	GGTGCC	0.73242	0.71379
cg0646158	DNAJC5	IRF-1 [T0	357	365	4.043231	TTTCCA	0.1297	0.13087
cg0646158	DNAJC5	RXR-alph	169	175	4.019014	CACACC	0.97656	0.9671
cg0646158	DNAJC5	RXR-alph	354	360	4.019014	GGGTTT	0.97656	0.9671
cg0646158	DNAJC5	RXR-alph	689	695	4.019014	GAAACC	0.97656	0.9671
cg0646158	DNAJC5	RXR-alph	725	731	4.019014	GGGTGT	0.97656	0.9671
cg0646158	DNAJC5	RXR-alph	1031	1037	4.019014	GGGTCT	0.97656	0.9671
cg0646158	DNAJC5	EBF [T05	280	290	4.016439	TCCCCT	0.0248	0.02398
cg0646158	DNAJC5	TFIID [T0	249	255	4.007279	TTTATTA	1.09863	1.13456
cg0646158	DNAJC5	TFIID [T0	1015	1021	4.007279	TATTAA	1.09863	1.13456
cg0646158	DNAJC5	AP-2alpha	1551	1556	3.970052	CAAGGC	0.97656	0.96469
cg0646158	DNAJC5	NFI/CTF [	1611	1618	3.793671	GCCCTT	0.18311	0.18109
cg0646158	DNAJC5	USF1 [T0	1531	1540	3.775819	TGTGCA	0.08011	0.07901
cg0646158	DNAJC5	GR [T050	263	269	3.763516	CAAAAC	0.73242	0.74251
cg0646158	DNAJC5	GR [T050	294	300	3.763516	TTCTTTG	0.73242	0.74251
cg0646158	DNAJC5	GR [T050	859	865	3.763516	CAAAAC	0.73242	0.74251
cg0646158	DNAJC5	GR [T050	1204	1210	3.763516	CTCTTT	0.73242	0.74251
cg0646158	DNAJC5	c-Ets-1 [T	1302	1308	3.71855	AAGGAA	0.61035	0.60765
cg0646158	DNAJC5	c-Ets-2 [T	17	25	3.518824	GAGAAG	0.18311	0.18304
cg0646158	DNAJC5	HNF-3alp	1274	1281	3.500065	TATTTT	0.27466	0.28532
cg0646158	DNAJC5	HNF-3alp	1283	1290	3.500065	TATTTAT	0.27466	0.28532
cg0646158	DNAJC5	HNF-3alp	1652	1659	3.500065	TATTTTT	0.27466	0.28532
cg0646158	DNAJC5	HNF-3alp	1988	1995	3.500065	AAAAAA	0.27466	0.28532
cg0646158	DNAJC5	VDR [T00	643	651	3.462841	GTTCAG	0.21362	0.21341
cg0646158	DNAJC5	GR-beta [T	331	335	3.361531	AATAT	3.90625	3.99611

cg0646158	DNAJC5	GR-beta [T	1244	1248	3.361531	AATAT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1290	1294	3.361531	ATATT	3.90625	3.99611
cg0646158	DNAJC5	GATA-2 [	380	388	3.333333	GGATAG	0.30518	0.30786
cg0646158	DNAJC5	GATA-2 [	947	955	3.333333	TGATAG	0.30518	0.30786
cg0646158	DNAJC5	PR B [T00	266	272	3.29756	AACATT	0.24414	0.25122
cg0646158	DNAJC5	PR B [T00	1104	1110	3.29756	AATTGT	0.24414	0.25122
cg0646158	DNAJC5	PR A [T01	266	272	3.29756	AACATT	0.24414	0.25122
cg0646158	DNAJC5	PR A [T01	1104	1110	3.29756	AATTGT	0.24414	0.25122
cg0646158	DNAJC5	USF1 [T0	1535	1544	3.289896	CACGTG	0.0515	0.05082
cg0646158	DNAJC5	RXR-alph	24	30	3.170788	AAAACC	0.24414	0.24522
cg0646158	DNAJC5	TCF-4E [T	1206	1212	3.151193	CTTTGC	0.24414	0.24672
cg0646158	DNAJC5	p53 [T006	847	853	3.024997	GGGCAA	0.48828	0.47786
cg0646158	DNAJC5	c-Myb [T0	106	113	2.984694	CGCAGT	0.03052	0.03013
cg0646158	DNAJC5	STAT4 [T	1304	1309	2.941176	GGAACA	2.92969	2.929
cg0646158	DNAJC5	STAT4 [T	1590	1595	2.941176	GGAATA	2.92969	2.929
cg0646158	DNAJC5	IRF-1 [T0	18	26	2.890712	AGAAGG	0.07629	0.07756
cg0646158	DNAJC5	p53 [T006	100	106	2.813291	GGGCAG	0.48828	0.47786
cg0646158	DNAJC5	PR B [T00	476	482	2.80933	AACAAT	0.73242	0.74818
cg0646158	DNAJC5	PR B [T00	543	549	2.80933	AACAAT	0.73242	0.74818
cg0646158	DNAJC5	PR B [T00	554	560	2.80933	AACAAT	0.73242	0.74818
cg0646158	DNAJC5	PR B [T00	1092	1098	2.80933	AACATT	0.73242	0.74818
cg0646158	DNAJC5	PR A [T01	476	482	2.80933	AACAAT	0.73242	0.74818
cg0646158	DNAJC5	PR A [T01	543	549	2.80933	AACAAT	0.73242	0.74818
cg0646158	DNAJC5	PR A [T01	554	560	2.80933	AACAAT	0.73242	0.74818
cg0646158	DNAJC5	PR A [T01	1092	1098	2.80933	AACATT	0.73242	0.74818
cg0646158	DNAJC5	AR [T000	861	869	2.733525	AAACTG	0.11444	0.11507
cg0646158	DNAJC5	RXR-alph	1738	1744	2.726556	GGGTTG	0.85449	0.84796
cg0646158	DNAJC5	CREB [T0	515	523	2.664517	GTCACG	0.06104	0.06135
cg0646158	DNAJC5	c-Jun [T00	1716	1722	2.654872	GGAGTC	0.48828	0.48929
cg0646158	DNAJC5	PXR-1:RX	640	647	2.577808	GGAGTT	0.12207	0.12266
cg0646158	DNAJC5	AP-2alpha	614	619	2.550491	TGAGGC	0.48828	0.48266
cg0646158	DNAJC5	AP-2alpha	766	771	2.550491	TGAGGC	0.48828	0.48266
cg0646158	DNAJC5	AP-2alpha	772	777	2.550491	TGAGGC	0.48828	0.48266
cg0646158	DNAJC5	AP-2alpha	1362	1367	2.550491	GCCTCA	0.48828	0.48266
cg0646158	DNAJC5	AP-2alpha	1394	1399	2.550491	GCCTCA	0.48828	0.48266
cg0646158	DNAJC5	RXR-alph	591	597	2.544678	ATAACC	0.85449	0.84796
cg0646158	DNAJC5	c-Jun [T00	372	378	2.538231	TAAGTC	0.48828	0.48929
cg0646158	DNAJC5	LEF-1 [T0	209	216	2.345041	CAGCAA	0.09155	0.09192
cg0646158	DNAJC5	Elk-1 [T00	1815	1823	2.299314	CCCAGG	0.09155	0.09114
cg0646158	DNAJC5	T3R-beta1	89	97	2.240658	TCACCT	0.15259	0.15262
cg0646158	DNAJC5	T3R-beta1	809	817	2.240658	TTGTGG	0.15259	0.15262
cg0646158	DNAJC5	T3R-beta1	627	635	2.221365	TCACCT	0.15259	0.15262
cg0646158	DNAJC5	GATA-1 [	1045	1050	2.176375	TATCCA	3.90625	3.92756
cg0646158	DNAJC5	GATA-1 [	1881	1886	2.176375	TATCCT	3.90625	3.92756
cg0646158	DNAJC5	GATA-1 [	379	384	2.001358	GGGATA	3.90625	3.92756
cg0646158	DNAJC5	GATA-1 [	1780	1785	1.896347	TATCGG	3.90625	3.92756
cg0646158	DNAJC5	AP-2alpha	608	613	1.871933	GGAGGC	0.97656	0.95407
cg0646158	DNAJC5	AP-2alpha	798	803	1.871933	GGAGGC	0.97656	0.95407

cg0646158	DNAJC5	AP-2alpha	1400	1405	1.871933	GCCTCC	0.97656	0.95407
cg0646158	DNAJC5	HIF-1 [T0	1531	1539	1.839875	TGTGCA	0.1297	0.12851
cg0646158	DNAJC5	p53 [T006	1608	1614	1.758307	TCTGCC	0.36621	0.36261
cg0646158	DNAJC5	GR-beta [	259	263	1.680765	AATTC	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	463	467	1.680765	GCATT	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	660	664	1.680765	GAATT	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	661	665	1.680765	AATTC	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	782	786	1.680765	GCATT	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	1038	1042	1.680765	GCATT	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	1098	1102	1.680765	GAATT	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	1210	1214	1.680765	GCATT	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	1409	1413	1.680765	AATGC	3.90625	3.94936
cg0646158	DNAJC5	GR-beta [	1851	1855	1.680765	GCATT	3.90625	3.94936
cg0646158	DNAJC5	c-Ets-2 [T	346	354	1.64415	TTCCTC	0.04578	0.04579
cg0646158	DNAJC5	c-Ets-1 [T	20	26	1.641124	AAGGAA	0.36621	0.36952
cg0646158	DNAJC5	C/EBPbeta	34	37	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	111	114	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	149	152	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	498	501	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	679	682	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	713	716	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	876	879	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	914	917	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	986	989	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1029	1032	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1073	1076	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1118	1121	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1133	1136	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1405	1408	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1478	1481	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1561	1564	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1615	1618	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1736	1739	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1741	1744	1.639871	TTGG	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1859	1862	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1983	1986	1.639871	CCAA	15.625	15.72563
cg0646158	DNAJC5	XBP-1 [T	935	940	1.583727	GGTCAT	0.97656	0.98146
cg0646158	DNAJC5	XBP-1 [T	1763	1768	1.583727	ATGACA	0.97656	0.98146
cg0646158	DNAJC5	TFIID [T0	261	267	1.537547	TTCAAA	0.73242	0.75096
cg0646158	DNAJC5	TFIID [T0	1170	1176	1.537547	TTTTTCA	0.73242	0.75096
cg0646158	DNAJC5	STAT4 [T	22	27	1.470588	GGAAAA	1.95312	1.96333
cg0646158	DNAJC5	STAT4 [T	277	282	1.470588	AGTTCC	1.95312	1.96333
cg0646158	DNAJC5	STAT4 [T	356	361	1.470588	GTTTCC	1.95312	1.96333
cg0646158	DNAJC5	STAT4 [T	659	664	1.470588	GGAATT	1.95312	1.96333
cg0646158	DNAJC5	STAT4 [T	974	979	1.470588	TTTTCC	1.95312	1.96333
cg0646158	DNAJC5	STAT4 [T	1151	1156	1.470588	GTTTCC	1.95312	1.96333
cg0646158	DNAJC5	PR B [T00	950	956	1.404665	TAGTGT	0.36621	0.37023
cg0646158	DNAJC5	PR B [T00	1556	1562	1.404665	CAGTGT	0.36621	0.37023

cg0646158	DNAJC5	PR A [T01	950	956	1.404665	TAGTGT	0.36621	0.37023
cg0646158	DNAJC5	PR A [T01	1556	1562	1.404665	CAGTGT	0.36621	0.37023
cg0646158	DNAJC5	c-Ets-1 [T	975	981	1.384951	TTTCCTC	0.36621	0.36952
cg0646158	DNAJC5	c-Ets-1 [T	1152	1158	1.384951	TTTCCTC	0.36621	0.36952
cg0646158	DNAJC5	C/EBPbeta	257	260	1.366559	TCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	262	265	1.366559	TCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	298	301	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	328	331	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	335	338	1.366559	TCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	417	420	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	428	431	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	530	533	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	664	667	1.366559	TCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	789	792	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	946	949	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1096	1099	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1109	1112	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1161	1164	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1365	1368	1.366559	TCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1379	1382	1.366559	TCAA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1576	1579	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	C/EBPbeta	1900	1903	1.366559	TTGA	15.625	15.72563
cg0646158	DNAJC5	AP-2alpha	741	746	1.357116	GCCTGT	0.48828	0.48203
cg0646158	DNAJC5	HNF-3alph	1256	1263	1.342935	TATTTTA	0.03052	0.03194
cg0646158	DNAJC5	GATA-1 [	333	338	1.038567	TATCAA	1.95312	1.98662
cg0646158	DNAJC5	GATA-1 [	946	951	1.038567	TTGATA	1.95312	1.98662
cg0646158	DNAJC5	GATA-1 [	1109	1114	1.038567	TTGATA	1.95312	1.98662
cg0646158	DNAJC5	PXR-1:RX	1901	1908	0.941658	TGAACT	0.12207	0.12266
cg0646158	DNAJC5	TCF-4 [T0	1573	1582	0.925008	GCTTTG	0.05722	0.05784
cg0646158	DNAJC5	GATA-1 [	1637	1642	0.863549	GTGATA	1.95312	1.98662
cg0646158	DNAJC5	GR-beta [	226	230	0.840383	AATTA	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	258	262	0.840383	CAATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	400	404	0.840383	TCATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	405	409	0.840383	CCATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	717	721	0.840383	AATTA	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	830	834	0.840383	CCATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1021	1025	0.840383	AATTA	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1048	1052	0.840383	CCATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1070	1074	0.840383	TAATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1071	1075	0.840383	AATTG	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1103	1107	0.840383	TAATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1104	1108	0.840383	AATTG	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1138	1142	0.840383	TAATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1174	1178	0.840383	TCATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1261	1265	0.840383	TAATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1262	1266	0.840383	AATTA	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1265	1269	0.840383	TAATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [	1266	1270	0.840383	AATTA	7.8125	7.94706

cg0646158	DNAJC5	GR-beta [T	1269	1273	0.840383	TAATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [T	1720	1724	0.840383	TCATT	7.8125	7.94706
cg0646158	DNAJC5	GR-beta [T	1866	1870	0.840383	CCATT	7.8125	7.94706
cg0646158	DNAJC5	ATF [T00	516	527	0.83717	TCACGT	0.00286	0.00287
cg0646158	DNAJC5	AP-2alpha	3	8	0.678558	TCAGGC	0.48828	0.48199
cg0646158	DNAJC5	AP-2alpha	648	653	0.678558	GCCTGA	0.48828	0.48199
cg0646158	DNAJC5	GATA-1 [	342	347	0.280028	TATCTT	0.97656	0.99875
cg0646158	DNAJC5	AP-2alpha	29	34	0.226186	CCAGGC	0.97656	0.95305
cg0646158	DNAJC5	AP-2alpha	164	169	0.226186	CCAGGC	0.97656	0.95305
cg0646158	DNAJC5	AP-2alpha	569	574	0.226186	CCAGGC	0.97656	0.95305
cg0646158	DNAJC5	AP-2alpha	673	678	0.226186	GCCTGG	0.97656	0.95305
cg0646158	DNAJC5	AP-2alpha	843	848	0.226186	GCCTGG	0.97656	0.95305
cg0646158	DNAJC5	GR-alpha [	52	56	0.207689	CCTTT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	213	217	0.207689	AAAGG	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1203	1207	0.207689	CCTCT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1223	1227	0.207689	AGAGG	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1709	1713	0.207689	CCTCT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1925	1929	0.207689	CCTTT	7.8125	7.81264
cg0646158	DNAJC5	HNF-1A [	225	232	0.143882	AAATTA	0.24414	0.25261
cg0646158	DNAJC5	Elk-1 [T00	345	353	0.134348	CTTCCTC	0.06104	0.06047
cg0646158	DNAJC5	c-Ets-1 [T	345	351	0.128087	CTTCCTC	0.24414	0.2429
cg0646158	DNAJC5	GR-alpha [	97	101	0	ACAGG	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	588	592	0	CCTAT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	742	746	0	CCTGT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	760	764	0	CCTGT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1155	1159	0	CCTGT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1307	1311	0	ACAGG	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1315	1319	0	CCTGT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1421	1425	0	ACAGG	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1434	1438	0	CCTGT	7.8125	7.81264
cg0646158	DNAJC5	GR-alpha [	1778	1782	0	CCTAT	7.8125	7.81264
cg0646158	DNAJC5	AP-2alpha	11	16	0	GCAGGC	0.97656	0.95305
cg0646158	DNAJC5	AP-2alpha	618	623	0	GCAGGC	0.97656	0.95305
cg0646158	DNAJC5	XBP-1 [T	179	184	0	AGTCAT	0.97656	0.98127
cg0646158	DNAJC5	XBP-1 [T	233	238	0	CGTCAT	0.97656	0.98127
cg0646158	DNAJC5	XBP-1 [T	519	524	0	CGTCAT	0.97656	0.98127
cg0646158	DNAJC5	XBP-1 [T	1718	1723	0	AGTCAT	0.97656	0.98127
cg0646158	DNAJC5	Pax-5 [T0	1440	1446	0	CCGGCC	1.09863	1.06846
cg0646158	DNAJC5	Pax-5 [T0	1829	1835	0	CATGCC	1.09863	1.06846
cg0646158	DNAJC5	p53 [T006	1829	1835	0	CATGCC	0.36621	0.35912
cg0646158	DNAJC5	TFII-I [T0	380	385	0	GGATAG	1.46484	1.45997
cg0646158	DNAJC5	TFII-I [T0	864	869	0	CTGTCC	1.46484	1.45997
cg0646158	DNAJC5	c-Ets-1 [T	1817	1823	0	CAGGAA	0.24414	0.2429
cg0646158	DNAJC5	YY1 [T00	119	122	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	405	408	0	CCAT	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	523	526	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	684	687	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	695	698	0	CCAT	7.8125	7.81711

cg0646158	DNAJC5	YY1 [T00	830	833	0	CCAT	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	939	942	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1048	1051	0	CCAT	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1512	1515	0	CCAT	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1517	1520	0	CCAT	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1519	1522	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1588	1591	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1600	1603	0	CCAT	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1678	1681	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1866	1869	0	CCAT	7.8125	7.81711
cg0646158	DNAJC5	YY1 [T00	1963	1966	0	ATGG	7.8125	7.81711
cg0646158	DNAJC5	ER-alpha [	395	399	0	TGACC	1.95312	1.9404
cg0646158	DNAJC5	ER-alpha [	935	939	0	GGTCA	1.95312	1.9404
cg0646158	DNAJC5	ER-alpha [	1907	1911	0	GGTCA	1.95312	1.9404
cg0646158	DNAJC5	C/EBPbeta	211	214	0	GCAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	325	328	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	365	368	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	448	451	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	477	480	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	544	547	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	555	558	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	566	569	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	785	788	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	809	812	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	833	836	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	849	852	0	GCAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	852	855	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	858	861	0	GCAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	955	958	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1036	1039	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1083	1086	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1106	1109	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1149	1152	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1183	1186	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1208	1211	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1228	1231	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1242	1245	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1278	1281	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1294	1297	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1541	1544	0	GCAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1550	1553	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1571	1574	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1635	1638	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1723	1726	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1745	1748	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1753	1756	0	GCAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1793	1796	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1869	1872	0	TTGC	15.625	15.71349

cg0646158	DNAJC5	C/EBPbeta	1928	1931	0	TTGT	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1980	1983	0	TTGC	15.625	15.71349
cg0646158	DNAJC5	C/EBPbeta	1986	1989	0	ACAA	15.625	15.71349
cg0646158	DNAJC5	TFIID [T0	270	276	0	TTTTCTA	1.09863	1.13474
cg0646158	DNAJC5	TFIID [T0	471	477	0	TTAAAA	1.09863	1.13474
cg0646158	DNAJC5	TFIID [T0	1141	1147	0	TTTTCTA	1.09863	1.13474
cg0646158	DNAJC5	TFIID [T0	1213	1219	0	TTTTTTA	1.09863	1.13474
cg0646158	DNAJC5	TFIID [T0	1297	1303	0	TTTTTAA	1.09863	1.13474
cg0646158	DNAJC5	TFIID [T0	1769	1775	0	TTAAAA	1.09863	1.13474
cg0646158	DNAJC5	FOXP3 [T	324	329	0	GTTGTT	1.46484	1.47315
cg0646158	DNAJC5	FOXP3 [T	808	813	0	GTTGTG	1.46484	1.47315
cg0646158	DNAJC5	FOXP3 [T	954	959	0	GTTGTT	1.46484	1.47315
cg0646158	DNAJC5	GR-beta [T	225	229	0	AAATT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	267	271	0	ACATT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	479	483	0	AATGT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	546	550	0	AATGT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	557	561	0	AATGT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	716	720	0	AAATT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1020	1024	0	AAATT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1093	1097	0	ACATT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1099	1103	0	AATTT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1139	1143	0	AATTT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1270	1274	0	AATTT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1766	1770	0	ACATT	3.90625	3.99611
cg0646158	DNAJC5	GR-beta [T	1938	1942	0	AATGT	3.90625	3.99611
cg0646158	DNAJC5	GR [T050	877	883	0	CAAAAA	0.36621	0.37562
cg0646158	DNAJC5	GR [T050	982	988	0	ATTTTTC	0.36621	0.37562
cg0646158	DNAJC5	GR [T050	1079	1085	0	TTTTTTG	0.36621	0.37562
cg0646158	DNAJC5	GR [T050	1987	1993	0	CAAAAA	0.36621	0.37562
cg0646158	DNAJC5	HNF-3alph	705	712	0	TAAAAA	0.09155	0.09511
cg0646158	DNAJC5	TCF-4E [T	210	216	0	AGCAAA	0.12207	0.12262
cg0646158	DNAJC5	HNF-1A [	470	477	0	GTTAAA	0.24414	0.25261
cg0646158	DNAJC5	TBP [T007	1285	1294	0	TTTATAT	0.03052	0.03159
cg0646158	DNAJC5	c-Myc [T0	1535	1540	0	CACGTG	0.48828	0.48199
cg0163748	FAHD1	LEF-1 [T0	325	332	9.937995	AGCCAA	0.12207	0.12154
cg0163748	FAHD1	LEF-1 [T0	914	921	9.937995	CTTTGGC	0.12207	0.12154
cg0163748	FAHD1	STAT1beta	779	788	9.807397	TTTTCCT	0.14877	0.1495
cg0163748	FAHD1	XBP-1 [T	449	454	9.789909	ATGGCG	1.95312	1.95208
cg0163748	FAHD1	XBP-1 [T	1437	1442	9.789909	CGCCAT	1.95312	1.95208
cg0163748	FAHD1	XBP-1 [T	1459	1464	9.789909	AGACAT	1.95312	1.95208
cg0163748	FAHD1	XBP-1 [T	1807	1812	9.789909	ATGGCT	1.95312	1.95208
cg0163748	FAHD1	PR B [T00	296	302	9.743489	AACACC	1.09863	1.10292
cg0163748	FAHD1	PR B [T00	1689	1695	9.743489	TTGTGTT	1.09863	1.10292
cg0163748	FAHD1	PR A [T01	296	302	9.743489	AACACC	1.09863	1.10292
cg0163748	FAHD1	PR A [T01	1689	1695	9.743489	TTGTGTT	1.09863	1.10292
cg0163748	FAHD1	AhR:Arnt	951	960	9.738501	AAGGGC	0.17929	0.17456
cg0163748	FAHD1	LEF-1 [T0	1154	1161	9.72404	CTTTGTC	0.21362	0.2139
cg0163748	FAHD1	c-Jun [T00	1771	1777	9.717135	CAGGTC	0.73242	0.73031

cg0163748	FAHD1	Pax-5 [T0	465	471	9.552105	TTTGCC	1.46484	1.43083
cg0163748	FAHD1	Pax-5 [T0	679	685	9.552105	GGGCGT	1.46484	1.43083
cg0163748	FAHD1	TFIID [T0	684	690	9.552105	TCCCAA	1.46484	1.48472
cg0163748	FAHD1	TFIID [T0	1155	1161	9.552105	TTTGTC	1.46484	1.48472
cg0163748	FAHD1	TFIID [T0	1517	1523	9.552105	TTTGGA	1.46484	1.48472
cg0163748	FAHD1	TFIID [T0	1670	1676	9.552105	TTTGAC	1.46484	1.48472
cg0163748	FAHD1	NF-1 [T00	631	638	9.535536	TTGGTC	0.73242	0.73053
cg0163748	FAHD1	NF-AT1 [	1520	1528	9.521781	GGAAAT	0.16785	0.1682
cg0163748	FAHD1	TFII-I [T0	180	185	9.512894	GGATTT	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	779	784	9.512894	TTTTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	909	914	9.512894	TTTTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1199	1204	9.512894	AAGTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1235	1240	9.512894	AAGTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1244	1249	9.512894	AATTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1296	1301	9.512894	TTTTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1403	1408	9.512894	TTGTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1427	1432	9.512894	CCTTCC	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1532	1537	9.512894	GGATGG	7.32422	7.29728
cg0163748	FAHD1	TFII-I [T0	1634	1639	9.512894	AATTCC	7.32422	7.29728
cg0163748	FAHD1	FOXP3 [T	52	57	9.512894	CAGAAC	7.32422	7.35678
cg0163748	FAHD1	FOXP3 [T	350	355	9.512894	GTTCTT	7.32422	7.35678
cg0163748	FAHD1	FOXP3 [T	630	635	9.512894	GTTGGT	7.32422	7.35678
cg0163748	FAHD1	FOXP3 [T	1288	1293	9.512894	GATAAC	7.32422	7.35678
cg0163748	FAHD1	FOXP3 [T	1680	1685	9.512894	GTTCTT	7.32422	7.35678
cg0163748	FAHD1	c-Jun [T00	67	73	9.511322	TGACCA	0.73242	0.73031
cg0163748	FAHD1	TCF-4E [T	1043	1049	9.453578	GTCAAA	0.48828	0.49215
cg0163748	FAHD1	NFI/CTF [	327	334	9.352332	CCAAAG	0.54932	0.54821
cg0163748	FAHD1	c-Ets-1 [T	924	930	9.276861	GTTCCC	0.36621	0.36441
cg0163748	FAHD1	NF-AT2 [	775	784	9.228174	ATCTTT	0.05341	0.05386
cg0163748	FAHD1	MEF-2A [	601	611	9.220261	TATTTT	0.07343	0.07563
cg0163748	FAHD1	AP-1 [T00	1972	1980	9.168921	CTTCAG	0.24414	0.24693
cg0163748	FAHD1	LEF-1 [T0	1042	1049	9.082175	AGTCAA	0.54932	0.55326
cg0163748	FAHD1	HNF-1B [	331	339	9.080623	AGTTAA	0.08392	0.0857
cg0163748	FAHD1	USF2 [T0	1183	1192	9.056375	CAGGTG	0.1545	0.15287
cg0163748	FAHD1	NF-AT1 [	1602	1610	9.042733	GGAAAT	0.22888	0.22959
cg0163748	FAHD1	E2F-1 [T0	1432	1439	9.028527	CTCCCC	0.27466	0.26875
cg0163748	FAHD1	LEF-1 [T0	684	691	8.973041	TCCCAA	0.54932	0.55326
cg0163748	FAHD1	c-Ets-1 [T	1635	1641	8.937416	ATTCCA	0.85449	0.85523
cg0163748	FAHD1	Elk-1 [T00	964	972	8.931691	TGCTGG	0.24414	0.24034
cg0163748	FAHD1	c-Ets-1 [T	1862	1868	8.8926	GTTCCC	0.85449	0.85523
cg0163748	FAHD1	PR B [T00	1676	1682	8.827054	ATCTGT	0.36621	0.36944
cg0163748	FAHD1	PR A [T01	1676	1682	8.827054	ATCTGT	0.36621	0.36944
cg0163748	FAHD1	NF-1 [T00	548	555	8.790071	CCTCCC	0.24414	0.24467
cg0163748	FAHD1	NF-1 [T00	1572	1579	8.790071	TCTCCC	0.24414	0.24467
cg0163748	FAHD1	LEF-1 [T0	1194	1201	8.759086	ACACAA	0.54932	0.55326
cg0163748	FAHD1	XBP-1 [T	196	201	8.75604	TATCAT	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T	230	235	8.75604	TTTCAT	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T	307	312	8.75604	TTTCAT	2.92969	2.9674

cg0163748	FAHD1	XBP-1 [T0	397	402	8.75604	GCTCAT	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T0	708	713	8.75604	ATGAGC	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T0	815	820	8.75604	TTTCAT	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T0	959	964	8.75604	GCTCAT	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T0	1325	1330	8.75604	ATGAAA	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T0	1350	1355	8.75604	ATGAAC	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T0	1606	1611	8.75604	ATGAGA	2.92969	2.9674
cg0163748	FAHD1	XBP-1 [T0	1821	1826	8.75604	GATCAT	2.92969	2.9674
cg0163748	FAHD1	STAT1beta	1296	1305	8.695301	TTTTCCA	0.22316	0.22446
cg0163748	FAHD1	IRF-1 [T0	1516	1524	8.497322	TTTTGGA	0.20599	0.20664
cg0163748	FAHD1	RBP-Jkapp	923	934	8.425028	GGTTCCC	0.02074	0.02078
cg0163748	FAHD1	HNF-1B [	1048	1056	8.379818	AGTTATA	0.11444	0.11669
cg0163748	FAHD1	PR B [T00	902	908	8.338824	TGCTGTT	1.09863	1.10009
cg0163748	FAHD1	PR B [T00	1223	1229	8.338824	AACAGA	1.09863	1.10009
cg0163748	FAHD1	PR B [T00	1684	1690	8.338824	TTCTGTT	1.09863	1.10009
cg0163748	FAHD1	PR A [T01	902	908	8.338824	TGCTGTT	1.09863	1.10009
cg0163748	FAHD1	PR A [T01	1223	1229	8.338824	AACAGA	1.09863	1.10009
cg0163748	FAHD1	PR A [T01	1684	1690	8.338824	TTCTGTT	1.09863	1.10009
cg0163748	FAHD1	PXR-1:RX	1128	1135	8.304332	AGTGTTC	0.12207	0.12266
cg0163748	FAHD1	GR-alpha [	516	520	8.281568	CCTCC	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	548	552	8.281568	CCTCC	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	783	787	8.281568	CCTTG	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	847	851	8.281568	CCTCC	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	861	865	8.281568	CCTTG	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	1427	1431	8.281568	CCTTC	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	1431	1435	8.281568	CCTCC	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	1878	1882	8.281568	GAAGG	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	1938	1942	8.281568	CAAGG	7.8125	7.72956
cg0163748	FAHD1	GR-alpha [	1992	1996	8.281568	CAAGG	7.8125	7.72956
cg0163748	FAHD1	NF-AT2 [	1762	1771	8.245775	ACATATT	0.08965	0.09068
cg0163748	FAHD1	c-Jun [T00	655	661	8.242207	TGACCTC	0.48828	0.49076
cg0163748	FAHD1	ENKTF-1	917	924	8.19852	TGGCTAC	0.73242	0.71737
cg0163748	FAHD1	NF-1 [T00	1711	1718	8.191058	TTGGCCT	0.24414	0.24409
cg0163748	FAHD1	SRY [T00	1193	1201	8.174786	CACACA	0.15259	0.15383
cg0163748	FAHD1	GR-alpha [	77	81	8.073878	GCAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	470	474	8.073878	CCAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	520	524	8.073878	CCAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	538	542	8.073878	CCTGC	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	676	680	8.073878	CCTGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	920	924	8.073878	CTAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	991	995	8.073878	CCAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1081	1085	8.073878	CCTAG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1085	1089	8.073878	GTAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1119	1123	8.073878	CCTGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1182	1186	8.073878	GCAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1188	1192	8.073878	GTAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1274	1278	8.073878	CCTAG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1415	1419	8.073878	CCTAC	7.8125	7.72238

cg0163748	FAHD1	GR-alpha [	1595	1599	8.073878	CCTAC	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1770	1774	8.073878	CCAGG	7.8125	7.72238
cg0163748	FAHD1	GR-alpha [	1923	1927	8.073878	GCAGG	7.8125	7.72238
cg0163748	FAHD1	Pax-5 [T0	1076	1082	8.014558	GCAGCC	2.19727	2.14502
cg0163748	FAHD1	Pax-5 [T0	1360	1366	8.014558	TATGCC	2.19727	2.14502
cg0163748	FAHD1	TFIID [T0	266	272	8.014558	TCAGAA	2.19727	2.24348
cg0163748	FAHD1	TFIID [T0	443	449	8.014558	TTTGAG	2.19727	2.24348
cg0163748	FAHD1	TFIID [T0	882	888	8.014558	TTTGCT	2.19727	2.24348
cg0163748	FAHD1	TFIID [T0	1159	1165	8.014558	TCACAA	2.19727	2.24348
cg0163748	FAHD1	TFIID [T0	1324	1330	8.014558	TATGAA	2.19727	2.24348
cg0163748	FAHD1	TFIID [T0	1518	1524	8.014558	TTGGAA	2.19727	2.24348
cg0163748	FAHD1	TFIID [T0	1625	1631	8.014558	TAAGAA	2.19727	2.24348
cg0163748	FAHD1	C/EBPalph	1346	1352	8.006685	TACAAT	0.24414	0.24674
cg0163748	FAHD1	HNF-1C [	1049	1057	7.717465	GTTATA	0.08392	0.08549
cg0163748	FAHD1	HNF-1C [	332	340	7.623927	GTTAAG	0.08392	0.08549
cg0163748	FAHD1	c-Jun [T00	1169	1175	7.538568	TGACAT	0.48828	0.48775
cg0163748	FAHD1	c-Jun [T00	1672	1678	7.538568	TGACAT	0.48828	0.48775
cg0163748	FAHD1	GR [T050	594	600	7.527031	AATTTC	1.83105	1.86007
cg0163748	FAHD1	GR [T050	1152	1158	7.527031	AGCTTT	1.83105	1.86007
cg0163748	FAHD1	GR [T050	1162	1168	7.527031	CAAACA	1.83105	1.86007
cg0163748	FAHD1	GR [T050	1399	1405	7.527031	ATGTTT	1.83105	1.86007
cg0163748	FAHD1	GR [T050	1514	1520	7.527031	TATTTT	1.83105	1.86007
cg0163748	FAHD1	C/EBPalph	1178	1184	7.465744	CATTGC	0.48828	0.49653
cg0163748	FAHD1	CTF [T001	1706	1717	7.455692	GTTGAT	0.01431	0.01434
cg0163748	FAHD1	C/EBPalph	176	182	7.396431	AATTGG	0.48828	0.49653
cg0163748	FAHD1	C/EBPalph	372	378	7.396431	AATTGT	0.48828	0.49653
cg0163748	FAHD1	C/EBPalph	407	413	7.396431	TACAAT	0.48828	0.49653
cg0163748	FAHD1	C/EBPalph	734	740	7.396431	TACAAT	0.48828	0.49653
cg0163748	FAHD1	XBP-1 [T	161	166	7.172312	ATGAGG	2.92969	2.97018
cg0163748	FAHD1	XBP-1 [T	878	883	7.172312	ATGATT	2.92969	2.97018
cg0163748	FAHD1	XBP-1 [T	1262	1267	7.172312	AATCAT	2.92969	2.97018
cg0163748	FAHD1	XBP-1 [T	1729	1734	7.172312	ATGAGT	2.92969	2.97018
cg0163748	FAHD1	XBP-1 [T	1909	1914	7.172312	ATGAAG	2.92969	2.97018
cg0163748	FAHD1	c-Jun [T00	1538	1544	7.096776	TGACTG	0.73242	0.73173
cg0163748	FAHD1	TFIID [T0	1256	1262	7.082373	TGCTAA	0.12207	0.12407
cg0163748	FAHD1	NF-AT1 [	1763	1771	7.072017	CATATT	0.15259	0.1548
cg0163748	FAHD1	HNF-3alph	378	385	7.000129	AATTTT	0.82397	0.84946
cg0163748	FAHD1	HNF-3alph	410	417	7.000129	AATTTC	0.82397	0.84946
cg0163748	FAHD1	HNF-3alph	594	601	7.000129	AATTTC	0.82397	0.84946
cg0163748	FAHD1	HNF-3alph	1514	1521	7.000129	TATTTC	0.82397	0.84946
cg0163748	FAHD1	HNF-3alph	1765	1772	7.000129	TATTTC	0.82397	0.84946
cg0163748	FAHD1	NF-1 [T00	943	950	6.948522	TTGGAT	0.48828	0.4856
cg0163748	FAHD1	ENKTF-1	16	23	6.942764	TGGCAG	1.46484	1.44228
cg0163748	FAHD1	ENKTF-1	240	247	6.942764	TGGCAA	1.46484	1.44228
cg0163748	FAHD1	c-Jun [T00	631	637	6.856451	TTGGTC	0.73242	0.73173
cg0163748	FAHD1	c-Jun [T00	1028	1034	6.787369	TGACAG	0.73242	0.73173
cg0163748	FAHD1	NFI/CTF [	235	242	6.786076	TTGCTT	0.73242	0.73214
cg0163748	FAHD1	NFI/CTF [	1707	1714	6.786076	TTGATT	0.73242	0.73214

cg0163748	FAHD1	RXR-alph	1793	1799	6.785809	GGTACC	0.36621	0.36214
cg0163748	FAHD1	c-Ets-2 [T	1246	1254	6.769996	TTCCTG	0.03052	0.03102
cg0163748	FAHD1	ATF3 [T0	1169	1176	6.744803	TGACAT	0.27466	0.27656
cg0163748	FAHD1	T3R-beta1	623	631	6.702681	TCACCA	0.21362	0.21147
cg0163748	FAHD1	GATA-2 [	1250	1258	6.666667	TGATAT	0.24414	0.24583
cg0163748	FAHD1	TFII-I [T0	477	482	6.581441	GGAGTG	0.97656	0.97366
cg0163748	FAHD1	TFII-I [T0	1571	1576	6.581441	ATCTCC	0.97656	0.97366
cg0163748	FAHD1	TFII-I [T0	1881	1886	6.581441	GGAGTG	0.97656	0.97366
cg0163748	FAHD1	FOXP3 [T	1376	1381	6.581441	TTCAAC	0.97656	0.99397
cg0163748	FAHD1	FOXP3 [T	1698	1703	6.581441	TAAAAC	0.97656	0.99397
cg0163748	FAHD1	p53 [T006	1076	1082	6.563521	GCAGCC	0.48828	0.47541
cg0163748	FAHD1	NF-AT1 [	776	784	6.562181	TCTTTTT	0.03815	0.03835
cg0163748	FAHD1	c-Myb [T0	1022	1029	6.539977	CCAAGT	0.30518	0.3056
cg0163748	FAHD1	AR [T000	1400	1408	6.50872	TGTTTG	0.19836	0.19597
cg0163748	FAHD1	IRF-1 [T0	1297	1305	6.497844	TTTCCA	0.19073	0.19127
cg0163748	FAHD1	XBP-1 [T	1361	1366	6.478682	ATGCCC	0.97656	0.97062
cg0163748	FAHD1	C/EBPalp	241	247	6.460799	GGCAAT	0.48828	0.49071
cg0163748	FAHD1	C/EBPalp	1166	1172	6.460799	CATTGA	0.48828	0.49071
cg0163748	FAHD1	c-Ets-1 [T	1518	1524	6.423689	TTGGAA	0.48828	0.48798
cg0163748	FAHD1	C/EBPalp	1241	1247	6.391486	GACAAT	0.48828	0.49071
cg0163748	FAHD1	c-Ets-1 [T	1600	1606	6.295602	ATGGAA	0.48828	0.48798
cg0163748	FAHD1	GR-alpha [	162	166	6.263098	TGAGG	3.90625	3.91061
cg0163748	FAHD1	GR-alpha [	542	546	6.263098	CCTCA	3.90625	3.91061
cg0163748	FAHD1	GR-alpha [	658	662	6.263098	CCTCA	3.90625	3.91061
cg0163748	FAHD1	GR-alpha [	1203	1207	6.263098	CCTTA	3.90625	3.91061
cg0163748	FAHD1	C/EBPalp	342	348	6.245236	TATTGC	0.97656	0.99
cg0163748	FAHD1	p53 [T006	679	685	6.188498	GGGCGT	0.61035	0.594
cg0163748	FAHD1	SRY [T00	1154	1162	6.176442	CTTTGT	0.15259	0.15366
cg0163748	FAHD1	c-Ets-1 [T	1297	1303	6.167515	TTTCCA	0.36621	0.36731
cg0163748	FAHD1	c-Myb [T0	811	818	6.157321	CAACTT	0.21362	0.21535
cg0163748	FAHD1	c-Jun [T00	1155	1161	6.152811	TTTGTC	0.36621	0.37082
cg0163748	FAHD1	NF-AT1 [	906	914	6.150044	GTTTTTT	0.06866	0.06922
cg0163748	FAHD1	GR-alpha [	121	125	6.055408	TTAGG	3.90625	3.9065
cg0163748	FAHD1	GR-alpha [	653	657	6.055408	CCTGA	3.90625	3.9065
cg0163748	FAHD1	GR-alpha [	1248	1252	6.055408	CCTGA	3.90625	3.9065
cg0163748	FAHD1	GR-alpha [	1583	1587	6.055408	TCAGG	3.90625	3.9065
cg0163748	FAHD1	GR-alpha [	1844	1848	6.055408	CCTAA	3.90625	3.9065
cg0163748	FAHD1	GR-alpha [	1890	1894	6.055408	TCAGG	3.90625	3.9065
cg0163748	FAHD1	c-Ets-1 [T	1767	1773	6.039428	TTTCCA	0.36621	0.36731
cg0163748	FAHD1	TCF-4 [T0	1041	1050	6.036797	AAGTCA	0.04578	0.04635
cg0163748	FAHD1	HOXD9 [	219	228	5.898575	TAGTAT	0.05722	0.0598
cg0163748	FAHD1	HOXD10 [	219	228	5.898575	TAGTAT	0.05722	0.0598
cg0163748	FAHD1	STAT4 [T	1427	1432	5.882353	CCTTCC	0.48828	0.48408
cg0163748	FAHD1	STAT1bet	1516	1525	5.796867	TTTTGG	0.1545	0.1557
cg0163748	FAHD1	c-Jun [T00	1040	1046	5.783074	AAAGTC	0.36621	0.37082
cg0163748	FAHD1	VDR [T00	524	532	5.771401	GTTCAA	0.42725	0.42999
cg0163748	FAHD1	VDR [T00	1347	1355	5.771401	ACAATG	0.42725	0.42999
cg0163748	FAHD1	c-Jun [T00	1122	1128	5.703976	GGGGTC	0.48828	0.48665

cg0163748	FAHD1	HNF-1C [	739	747	5.695506	TTATTTA	0.07629	0.07817
cg0163748	FAHD1	ENKTF-1	450	457	5.687009	TGGCGT	0.73242	0.7249
cg0163748	FAHD1	ENKTF-1	574	581	5.687009	ATACGC	0.73242	0.7249
cg0163748	FAHD1	c-Ets-1 [T	1554	1560	5.686398	CTTCCC	0.36621	0.3623
cg0163748	FAHD1	IRF-1 [T0	1767	1775	5.65977	TTTCCA	0.22888	0.23087
cg0163748	FAHD1	NF-1 [T00	856	863	5.626299	TTGGAC	0.24414	0.24258
cg0163748	FAHD1	NF-AT1 [	1293	1301	5.604085	CGTTTT	0.03815	0.03856
cg0163748	FAHD1	GATA-2 [	1011	1019	5.555555	AGATAT	0.18311	0.1835
cg0163748	FAHD1	GATA-2 [	1810	1818	5.555555	GCTGTA	0.18311	0.1835
cg0163748	FAHD1	TFIID [T0	217	223	5.544826	TTTAGT	0.73242	0.75085
cg0163748	FAHD1	TFIID [T0	605	611	5.544826	TTTAGT	0.73242	0.75085
cg0163748	FAHD1	NF-AT1 [	1601	1610	5.512555	TGGAAA	0.05913	0.05965
cg0163748	FAHD1	C/EBPalp	233	239	5.455853	CATTGC	0.73242	0.74391
cg0163748	FAHD1	C/EBPalp	1379	1385	5.38654	AACAAT	0.73242	0.74391
cg0163748	FAHD1	RXR-alph	132	138	5.271235	GCAACC	0.61035	0.6044
cg0163748	FAHD1	RXR-alph	312	318	5.271235	TCTACC	0.61035	0.6044
cg0163748	FAHD1	c-Jun [T00	838	844	5.193102	GAAGTC	0.61035	0.61057
cg0163748	FAHD1	POU2F2 (	1694	1704	5.123481	TTTTTAA	0.02432	0.02504
cg0163748	FAHD1	HNF-1A [	332	339	5.116518	GTTAAG	0.36621	0.37179
cg0163748	FAHD1	AP-2alpha	1714	1719	5.100982	GCCTTT	0.97656	0.97567
cg0163748	FAHD1	AP-1 [T00	260	268	5.059986	GAAGAG	0.12207	0.12162
cg0163748	FAHD1	GR-beta [	180	184	5.042296	GGATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	221	225	5.042296	GTATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	600	604	5.042296	GTATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	697	701	5.042296	GGATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	821	825	5.042296	GGATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	974	978	5.042296	GTATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	1271	1275	5.042296	AATCC	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	1310	1314	5.042296	AATAC	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	1344	1348	5.042296	AATAC	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	1645	1649	5.042296	GTATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	1733	1737	5.042296	GTATT	3.90625	3.95351
cg0163748	FAHD1	GR-beta [	1854	1858	5.042296	GGATT	3.90625	3.95351
cg0163748	FAHD1	c-Ets-1 [T	353	359	5.038739	CTTCCA	0.48828	0.49031
cg0163748	FAHD1	PXR-1:RX	999	1006	5.032032	ACGGTT	0.12207	0.12266
cg0163748	FAHD1	C/EBPalp	822	828	5.024728	GATTGC	0.97656	0.99332
cg0163748	FAHD1	NFI/CTF [	912	919	5.021086	TCCTTT	0.24414	0.24103
cg0163748	FAHD1	NFI/CTF [	1991	1998	5.021086	CCAAGG	0.24414	0.24103
cg0163748	FAHD1	XBP-1 [T	570	575	4.894955	AGGCAT	0.97656	0.96979
cg0163748	FAHD1	XBP-1 [T	704	709	4.894955	AGGCAT	0.97656	0.96979
cg0163748	FAHD1	AP-2alpha	1843	1848	4.890408	GCCTAA	0.97656	0.97567
cg0163748	FAHD1	C/EBPalp	282	288	4.845599	AGCAAT	0.97656	0.99332
cg0163748	FAHD1	HNF-3alp	383	390	4.842999	TTTAAA	0.09155	0.09582
cg0163748	FAHD1	c-Myb [T0	346	353	4.840682	GCAAGT	0.30518	0.30568
cg0163748	FAHD1	c-Myb [T0	744	751	4.840682	TAACTT	0.30518	0.30568
cg0163748	FAHD1	NF-AT1 [	1519	1528	4.823485	TGGAAA	0.07629	0.07704
cg0163748	FAHD1	p53 [T006	1113	1119	4.786849	AGTGCC	0.48828	0.47747
cg0163748	FAHD1	c-Ets-1 [T	934	940	4.782565	GTGGAA	0.48828	0.49031

cg0163748	FAHD1	C/EBPalph	1341	1347	4.776286	ACCAAT	0.97656	0.99332
cg0163748	FAHD1	TFII-I [T0	366	371	4.756447	GGATAT	2.92969	2.93695
cg0163748	FAHD1	TFII-I [T0	821	826	4.756447	GGATTG	2.92969	2.93695
cg0163748	FAHD1	TFII-I [T0	1520	1525	4.756447	GGAAAT	2.92969	2.93695
cg0163748	FAHD1	TFII-I [T0	1586	1591	4.756447	GGATAT	2.92969	2.93695
cg0163748	FAHD1	TFII-I [T0	1602	1607	4.756447	GGAAAT	2.92969	2.93695
cg0163748	FAHD1	TFII-I [T0	1766	1771	4.756447	ATTTCC	2.92969	2.93695
cg0163748	FAHD1	TFII-I [T0	1963	1968	4.756447	GGATAT	2.92969	2.93695
cg0163748	FAHD1	FOXP3 [T	63	68	4.756447	GTTTTG	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	293	298	4.756447	CAAAAC	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	906	911	4.756447	GTTTTT	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	1026	1031	4.756447	GTTGAC	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	1220	1225	4.756447	AAAAAC	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	1294	1299	4.756447	GTTTTT	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	1304	1309	4.756447	GTTTTG	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	1337	1342	4.756447	AAAAAC	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	1693	1698	4.756447	GTTTTT	2.92969	2.96063
cg0163748	FAHD1	FOXP3 [T	1706	1711	4.756447	GTTGAT	2.92969	2.96063
cg0163748	FAHD1	HNF-1A [	205	212	4.684871	ATCTTA	0.12207	0.12485
cg0163748	FAHD1	c-Ets-1 [T0	966	972	4.654478	CTGGAA	0.85449	0.85764
cg0163748	FAHD1	VDR [T00	1002	1010	4.617121	GTTCAG	0.37384	0.37445
cg0163748	FAHD1	VDR [T00	1131	1139	4.617121	GTTCAC	0.37384	0.37445
cg0163748	FAHD1	C/EBPalph	867	873	4.560723	GATTGT	0.24414	0.24411
cg0163748	FAHD1	C/EBPalph	1709	1715	4.560723	GATTGG	0.24414	0.24411
cg0163748	FAHD1	T3R-beta1	1532	1540	4.481316	GGATGG	0.27466	0.27551
cg0163748	FAHD1	GATA-2 [	1612	1620	4.444445	CCATTA	0.24414	0.24541
cg0163748	FAHD1	c-Jun [T00	1974	1980	4.441904	TCAGTC	0.12207	0.12266
cg0163748	FAHD1	RXR-alph	668	674	4.423008	TCCACC	0.24414	0.24292
cg0163748	FAHD1	STAT4 [T	352	357	4.411765	TCTTCC	1.95312	1.94235
cg0163748	FAHD1	STAT4 [T	936	941	4.411765	GGAAGA	1.95312	1.94235
cg0163748	FAHD1	STAT4 [T	1553	1558	4.411765	TCTTCC	1.95312	1.94235
cg0163748	FAHD1	STAT4 [T	1941	1946	4.411765	GGAAGA	1.95312	1.94235
cg0163748	FAHD1	PEA3 [T0	1738	1746	4.30818	ACACAT	0.13733	0.13791
cg0163748	FAHD1	RAR-beta	617	626	4.252176	AGGGTT	0.14496	0.1447
cg0163748	FAHD1	C/EBPalph	1253	1259	4.235345	TATTGC	0.48828	0.49358
cg0163748	FAHD1	AP-2alpha	1188	1193	4.211849	GTAGGC	0.97656	0.96469
cg0163748	FAHD1	GR-beta [	111	115	4.201913	AATCA	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	188	192	4.201913	TTATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	224	228	4.201913	TTATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	272	276	4.201913	AATAG	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	341	345	4.201913	TTATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	387	391	4.201913	AATAG	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	531	535	4.201913	TGATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	739	743	4.201913	TTATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	752	756	4.201913	TTATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	879	883	4.201913	TGATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	977	981	4.201913	TTATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [	1035	1039	4.201913	CTATT	7.8125	7.94607

cg0163748	FAHD1	GR-beta [T	1216	1220	4.201913	AATCA	7.8125	7.94607
cg0163748	FAHD1	GR-beta [T	1262	1266	4.201913	AATCA	7.8125	7.94607
cg0163748	FAHD1	GR-beta [T	1370	1374	4.201913	AATAG	7.8125	7.94607
cg0163748	FAHD1	GR-beta [T	1581	1585	4.201913	AATCA	7.8125	7.94607
cg0163748	FAHD1	GR-beta [T	1631	1635	4.201913	AATAA	7.8125	7.94607
cg0163748	FAHD1	GR-beta [T	1708	1712	4.201913	TGATT	7.8125	7.94607
cg0163748	FAHD1	GR-beta [T	1869	1873	4.201913	TGATT	7.8125	7.94607
cg0163748	FAHD1	c-Ets-1 [T	1245	1251	4.154851	ATTCCT	0.24414	0.24526
cg0163748	FAHD1	c-Ets-2 [T	781	789	4.091811	TTCCTT	0.16022	0.16243
cg0163748	FAHD1	c-Ets-2 [T	1936	1944	4.091811	TCCAAG	0.16022	0.16243
cg0163748	FAHD1	PXR-1:RX	521	528	4.090374	CAGGTT	0.12207	0.12119
cg0163748	FAHD1	HOXD9 [T	1781	1790	4.080895	AATATA	0.03052	0.03168
cg0163748	FAHD1	HOXD10 [	1781	1790	4.080895	AATATA	0.03052	0.03168
cg0163748	FAHD1	RXR-alpha	583	589	4.019014	CACACC	0.97656	0.9671
cg0163748	FAHD1	RXR-alpha	618	624	4.019014	GGGTTT	0.97656	0.9671
cg0163748	FAHD1	RXR-alpha	1506	1512	4.019014	CACACC	0.97656	0.9671
cg0163748	FAHD1	c-Ets-2 [T	911	919	4.017001	TTCCTTT	0.16022	0.16243
cg0163748	FAHD1	STAT1beta	1598	1607	4.01053	ACATGG	0.03433	0.03457
cg0163748	FAHD1	Pax-5 [T0	1113	1119	4.007279	AGTGCC	1.09863	1.07975
cg0163748	FAHD1	TFIID [T0	187	193	4.007279	TTTATTA	1.09863	1.13456
cg0163748	FAHD1	TFIID [T0	382	388	4.007279	TTTTAA	1.09863	1.13456
cg0163748	FAHD1	TFIID [T0	1036	1042	4.007279	TATTAA	1.09863	1.13456
cg0163748	FAHD1	TFIID [T0	1050	1056	4.007279	TTATAA	1.09863	1.13456
cg0163748	FAHD1	TFIID [T0	1367	1373	4.007279	TTTAAT	1.09863	1.13456
cg0163748	FAHD1	TFIID [T0	1695	1701	4.007279	TTTTAA	1.09863	1.13456
cg0163748	FAHD1	TFIID [T0	1718	1724	4.007279	TTTATA	1.09863	1.13456
cg0163748	FAHD1	TFIID [T0	1719	1725	4.007279	TTATAA	1.09863	1.13456
cg0163748	FAHD1	GR [T050	62	68	3.763516	AGTTTC	0.73242	0.74251
cg0163748	FAHD1	GR [T050	293	299	3.763516	CAAAAC	0.73242	0.74251
cg0163748	FAHD1	GR [T050	1303	1309	3.763516	CGTTTC	0.73242	0.74251
cg0163748	FAHD1	p53 [T006	1958	1964	3.750231	GGGCTG	0.73242	0.71379
cg0163748	FAHD1	NF-Y [T0	177	184	3.732121	ATTGGA	0.48828	0.48904
cg0163748	FAHD1	PU.1 [T02	160	172	3.723988	TATGAG	0.00173	0.00172
cg0163748	FAHD1	HNF-3alph	225	232	3.500065	TATTTTT	0.27466	0.28532
cg0163748	FAHD1	HNF-3alph	268	275	3.500065	AGAAAA	0.27466	0.28532
cg0163748	FAHD1	HNF-3alph	1627	1634	3.500065	AGAAAA	0.27466	0.28532
cg0163748	FAHD1	PXR-1:RX	1986	1993	3.395883	TGAACC	0.12207	0.12271
cg0163748	FAHD1	RXR-alpha	31	37	3.392904	GTAACC	1.09863	1.08572
cg0163748	FAHD1	RXR-alpha	1826	1832	3.392904	TGTACC	1.09863	1.08572
cg0163748	FAHD1	Elk-1 [T00	161	169	3.381796	ATGAGG	0.04578	0.04588
cg0163748	FAHD1	p53 [T006	953	959	3.375208	GGGCGT	0.73242	0.7189
cg0163748	FAHD1	T3R-beta1	1980	1988	3.370634	AGCTGG	0.27466	0.2755
cg0163748	FAHD1	GR-beta [T	153	157	3.361531	AATAT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	277	281	3.361531	AGATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	492	496	3.361531	AATCT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	563	567	3.361531	AGATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	764	768	3.361531	ATATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	831	835	3.361531	AGATT	3.90625	3.99611

cg0163748	FAHD1	GR-beta [T	866	870	3.361531	AGATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1252	1256	3.361531	ATATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1513	1517	3.361531	ATATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1588	1592	3.361531	ATATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1661	1665	3.361531	AATAT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1750	1754	3.361531	AATAT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1764	1768	3.361531	ATATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1781	1785	3.361531	AATAT	3.90625	3.99611
cg0163748	FAHD1	IRF-1 [T0	910	918	3.347186	TTTCCTT	0.06866	0.06927
cg0163748	FAHD1	GATA-2 [	1287	1295	3.333333	AGATAA	0.30518	0.30786
cg0163748	FAHD1	HNF-1B [	740	748	3.302045	TATTTA	0.04578	0.0471
cg0163748	FAHD1	PR B [T00	1379	1385	3.29756	AACAAT	0.24414	0.25122
cg0163748	FAHD1	PR A [T01	1379	1385	3.29756	AACAAT	0.24414	0.25122
cg0163748	FAHD1	c-Jun [T00	262	268	3.244843	AGAGTC	0.24414	0.24403
cg0163748	FAHD1	TCF-4E [T	947	953	3.151193	ATCAAA	0.24414	0.24672
cg0163748	FAHD1	IRF-1 [T0	1598	1606	3.145547	ACATGG	0.07629	0.07756
cg0163748	FAHD1	Elk-1 [T00	1937	1945	3.121991	CCAAGG	0.07629	0.07656
cg0163748	FAHD1	SRY [T00	945	953	3.088221	GGATCA	0.06104	0.06203
cg0163748	FAHD1	C/EBPalph	71	77	2.981957	CACAAT	0.48828	0.4911
cg0163748	FAHD1	STAT4 [T	165	170	2.941176	GGAAGT	2.92969	2.929
cg0163748	FAHD1	STAT4 [T	923	928	2.941176	GGTTCC	2.92969	2.929
cg0163748	FAHD1	STAT4 [T	968	973	2.941176	GGAAGT	2.92969	2.929
cg0163748	FAHD1	STAT4 [T	1861	1866	2.941176	TGTTCC	2.92969	2.929
cg0163748	FAHD1	STAT1bet	1766	1775	2.898434	ATTTCC	0.0515	0.05191
cg0163748	FAHD1	IRF-1 [T0	780	788	2.890712	TTTCCTT	0.07629	0.07756
cg0163748	FAHD1	PR B [T00	1164	1170	2.80933	AACATT	0.73242	0.74818
cg0163748	FAHD1	PR A [T01	1164	1170	2.80933	AACATT	0.73242	0.74818
cg0163748	FAHD1	TBP [T00	1716	1725	2.807313	CTTTTAT	0.12207	0.12635
cg0163748	FAHD1	TBP [T00	1718	1727	2.807313	TTTATA	0.12207	0.12635
cg0163748	FAHD1	NF-AT1 [T	1293	1302	2.756277	CGTTTTT	0.05913	0.05995
cg0163748	FAHD1	c-Ets-2 [T	1429	1437	2.715313	TTCCTCC	0.07629	0.07593
cg0163748	FAHD1	PXR-1:RX	1351	1358	2.577808	TGAACT	0.12207	0.12266
cg0163748	FAHD1	AP-2alpha	541	546	2.550491	GCCTCA	0.48828	0.48266
cg0163748	FAHD1	ENKTF-1	1434	1441	2.511511	CCCCGC	0.12207	0.11894
cg0163748	FAHD1	Ik-1 [T027	687	699	2.374299	CAAAGT	0.00063	0.00061
cg0163748	FAHD1	c-Jun [T00	793	799	2.345465	TGACAC	0.48828	0.48929
cg0163748	FAHD1	VDR [T00	1982	1990	2.308561	CTGGTG	0.10681	0.10609
cg0163748	FAHD1	GATA-1 [	365	370	2.176375	TGGATA	3.90625	3.92756
cg0163748	FAHD1	GATA-1 [	1585	1590	2.176375	AGGATA	3.90625	3.92756
cg0163748	FAHD1	GATA-1 [	1962	1967	2.176375	TGGATA	3.90625	3.92756
cg0163748	FAHD1	RAR-beta	1984	1993	2.144554	GGTGAA	0.07629	0.07625
cg0163748	FAHD1	NF-1 [T00	682	689	2.067686	CGTCCC	0.12207	0.12133
cg0163748	FAHD1	NF-AT1 [T	1763	1772	2.067208	CATATT	0.03815	0.03874
cg0163748	FAHD1	p53 [T006	465	471	1.970013	TTTGCCC	0.36621	0.36261
cg0163748	FAHD1	AP-2alpha	515	520	1.871933	GCCTCC	0.97656	0.95407
cg0163748	FAHD1	AP-2alpha	547	552	1.871933	GCCTCC	0.97656	0.95407
cg0163748	FAHD1	AP-2alpha	846	851	1.871933	GCCTCC	0.97656	0.95407
cg0163748	FAHD1	TFII-I [T0	1422	1427	1.824994	CTCTCC	0.48828	0.48408

cg0163748	FAHD1	FOXP3 [T	809	814	1.824994	TACAAC	0.48828	0.49451
cg0163748	FAHD1	C/EBPalph	765	771	1.761449	TATTGTC	0.48828	0.49438
cg0163748	FAHD1	p53 [T006	1360	1366	1.758307	TATGCCC	0.36621	0.36261
cg0163748	FAHD1	NF-Y [T0	1710	1717	1.749852	ATTGGCC	0.18311	0.18459
cg0163748	FAHD1	RXR-alpha	1123	1129	1.696452	GGGTCA	0.48828	0.48222
cg0163748	FAHD1	GR-beta [T	74	78	1.680765	AATGC	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	244	248	1.680765	AATGC	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	337	341	1.680765	GCATT	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	1177	1181	1.680765	GCATT	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	1244	1248	1.680765	AATTC	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	1278	1282	1.680765	GCATT	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	1390	1394	1.680765	GCATT	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	1523	1527	1.680765	AATGC	3.90625	3.94936
cg0163748	FAHD1	GR-beta [T	1634	1638	1.680765	AATTC	3.90625	3.94936
cg0163748	FAHD1	c-Ets-1 [T	780	786	1.641124	TTTCCTT	0.36621	0.36952
cg0163748	FAHD1	c-Ets-1 [T	910	916	1.641124	TTTCCTT	0.36621	0.36952
cg0163748	FAHD1	C/EBPbeta	45	48	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	178	181	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	239	242	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	300	303	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	327	330	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	356	359	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	552	555	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	631	634	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	686	689	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	856	859	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	916	919	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	943	946	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1022	1025	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1233	1236	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1342	1345	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1518	1521	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1576	1579	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1711	1714	1.639871	TTGG	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1937	1940	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1991	1994	1.639871	CCAA	15.625	15.72563
cg0163748	FAHD1	Pax-5 [T0	953	959	1.537547	GGGCGT	0.73242	0.71311
cg0163748	FAHD1	TFIID [T0	228	234	1.537547	TTTTTCA	0.73242	0.75096
cg0163748	FAHD1	TFIID [T0	596	602	1.537547	TTTTGTA	0.73242	0.75096
cg0163748	FAHD1	TFIID [T0	854	860	1.537547	TTTTGGA	0.73242	0.75096
cg0163748	FAHD1	TFIID [T0	1296	1302	1.537547	TTTTCCA	0.73242	0.75096
cg0163748	FAHD1	TFIID [T0	1305	1311	1.537547	TTTTGAA	0.73242	0.75096
cg0163748	FAHD1	TFIID [T0	1326	1332	1.537547	TGAAAA	0.73242	0.75096
cg0163748	FAHD1	TFIID [T0	1516	1522	1.537547	TTTTGGA	0.73242	0.75096
cg0163748	FAHD1	STAT4 [T	779	784	1.470588	TTTTCC	1.95312	1.96333
cg0163748	FAHD1	STAT4 [T	909	914	1.470588	TTTTCC	1.95312	1.96333
cg0163748	FAHD1	STAT4 [T	1244	1249	1.470588	AATTCC	1.95312	1.96333
cg0163748	FAHD1	STAT4 [T	1296	1301	1.470588	TTTTCC	1.95312	1.96333

cg0163748	FAHD1	STAT4 [T	1634	1639	1.470588	AATTCC	1.95312	1.96333
cg0163748	FAHD1	GR [T050	1219	1225	1.444018	CAAAAA	0.12207	0.1245
cg0163748	FAHD1	PR B [T00	1127	1133	1.404665	CAGTGT	0.36621	0.37023
cg0163748	FAHD1	PR A [T01	1127	1133	1.404665	CAGTGT	0.36621	0.37023
cg0163748	FAHD1	C/EBPbeta	66	69	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	444	447	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	526	529	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	635	638	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	660	663	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	842	845	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	863	866	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	948	951	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1027	1030	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1044	1047	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1168	1171	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1218	1221	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1307	1310	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1377	1380	1.366559	TCAA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1671	1674	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	C/EBPbeta	1707	1710	1.366559	TTGA	15.625	15.72563
cg0163748	FAHD1	AP-2alpha	568	573	1.357116	ACAGGC	0.48828	0.48203
cg0163748	FAHD1	AP-2alpha	702	707	1.357116	ACAGGC	0.48828	0.48203
cg0163748	FAHD1	p53 [T006	717	723	1.270236	CGTGCC	0.12207	0.11849
cg0163748	FAHD1	HNF-1A [	453	460	1.213286	CGTTTA	0.48828	0.49664
cg0163748	FAHD1	c-Ets-2 [T	160	168	1.145973	TATGAG	0.06104	0.06166
cg0163748	FAHD1	T3R-beta1	1133	1141	1.110682	TCACCA	0.07629	0.07585
cg0163748	FAHD1	EBF [T05	1116	1126	1.088777	GCCCCT	0.00763	0.00736
cg0163748	FAHD1	NF-Y [T0	1339	1346	1.058936	AAACCA	0.12207	0.12315
cg0163748	FAHD1	GATA-1 [	196	201	1.038567	TATCAT	1.95312	1.98662
cg0163748	FAHD1	TBP [T00	1047	1056	0.935771	AAGTTA	0.12207	0.12628
cg0163748	FAHD1	GATA-1 [	1616	1621	0.863549	TATCAC	1.95312	1.98662
cg0163748	FAHD1	GATA-1 [	1754	1759	0.863549	TATCAC	1.95312	1.98662
cg0163748	FAHD1	GR-beta [	147	151	0.840383	AATTA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	175	179	0.840383	TAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	176	180	0.840383	AATTG	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	232	236	0.840383	TCATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	252	256	0.840383	TAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	253	257	0.840383	AATTA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	284	288	0.840383	CAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	285	289	0.840383	AATTA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	371	375	0.840383	TAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	372	376	0.840383	AATTG	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	377	381	0.840383	TAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	409	413	0.840383	CAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	593	597	0.840383	TAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	736	740	0.840383	CAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	737	741	0.840383	AATTA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [	850	854	0.840383	CCATT	7.8125	7.94706

cg0163748	FAHD1	GR-beta [T	877	881	0.840383	AATGA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1243	1247	0.840383	CAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1349	1353	0.840383	AATGA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1381	1385	0.840383	CAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1382	1386	0.840383	AATTA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1605	1609	0.840383	AATGA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1612	1616	0.840383	CCATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1633	1637	0.840383	TAATT	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1728	1732	0.840383	AATGA	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1806	1810	0.840383	AATGG	7.8125	7.94706
cg0163748	FAHD1	GR-beta [T	1908	1912	0.840383	AATGA	7.8125	7.94706
cg0163748	FAHD1	c-Fos [T00	263	272	0.768508	GAGTCA	0.00763	0.00766
cg0163748	FAHD1	TCF-4 [T0	945	954	0.76243	GGATCA	0.05722	0.05784
cg0163748	FAHD1	GATA-1 [	890	895	0.758539	TATCAG	1.95312	1.98662
cg0163748	FAHD1	GATA-1 [	1249	1254	0.758539	CTGATA	1.95312	1.98662
cg0163748	FAHD1	GATA-1 [	1966	1971	0.758539	TATCAG	1.95312	1.98662
cg0163748	FAHD1	C/EBPalph	489	495	0.540941	CACAAT	0.24414	0.24507
cg0163748	FAHD1	GATA-1 [	96	101	0.280028	TAGATA	0.97656	0.99875
cg0163748	FAHD1	GATA-1 [	204	209	0.280028	TATCTT	0.97656	0.99875
cg0163748	FAHD1	GATA-1 [	1286	1291	0.280028	AAGATA	0.97656	0.99875
cg0163748	FAHD1	c-Ets-1 [T	1939	1945	0.256174	AAGGAA	0.24414	0.24569
cg0163748	FAHD1	AP-2alpha	470	475	0.226186	CCAGGC	0.97656	0.95305
cg0163748	FAHD1	AP-2alpha	675	680	0.226186	GCCTGG	0.97656	0.95305
cg0163748	FAHD1	GR-alpha [	510	514	0.207689	CCTCT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	913	917	0.207689	CCTTT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	950	954	0.207689	AAAGG	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1365	1369	0.207689	CCTTT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1407	1411	0.207689	CCTCT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1468	1472	0.207689	CCTCT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1558	1562	0.207689	CCTTT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1715	1719	0.207689	CCTTT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1799	1803	0.207689	CCTTT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1918	1922	0.207689	AAAGG	7.8125	7.81264
cg0163748	FAHD1	HNF-1A [	740	747	0.143882	TATTTA	0.24414	0.25261
cg0163748	FAHD1	c-Ets-1 [T	163	169	0.128087	GAGGAA	0.24414	0.2429
cg0163748	FAHD1	c-Ets-1 [T	1428	1434	0.128087	CTTCCTC	0.24414	0.2429
cg0163748	FAHD1	GATA-1 [	1010	1015	0.105011	GAGATA	0.97656	0.98738
cg0163748	FAHD1	GATA-1 [	1814	1819	0.105011	TATCTC	0.97656	0.98738
cg0163748	FAHD1	GR-alpha [	568	572	0	ACAGG	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	615	619	0	ACAGG	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	702	706	0	ACAGG	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1322	1326	0	CCTAT	7.8125	7.81264
cg0163748	FAHD1	GR-alpha [	1790	1794	0	ACAGG	7.8125	7.81264
cg0163748	FAHD1	AP-2alpha	77	82	0	GCAGGC	0.97656	0.95305
cg0163748	FAHD1	RXR-alpha	1986	1992	0	TGAACC	0.24414	0.2444
cg0163748	FAHD1	Pax-5 [T0	717	723	0	CGTGCC	1.09863	1.06846
cg0163748	FAHD1	Pax-5 [T0	1921	1927	0	GGGCAG	1.09863	1.06846
cg0163748	FAHD1	Pax-5 [T0	1958	1964	0	GGGCTG	1.09863	1.06846

cg0163748	FAHD1	p53 [T006	1921	1927	0	GGGCAG	0.36621	0.35912
cg0163748	FAHD1	STAT4 [T	1520	1525	0	GGAAAT	0.48828	0.49387
cg0163748	FAHD1	STAT4 [T	1602	1607	0	GGAAAT	0.48828	0.49387
cg0163748	FAHD1	STAT4 [T	1766	1771	0	ATTTCC	0.48828	0.49387
cg0163748	FAHD1	YY1 [T00	138	141	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	172	175	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	404	407	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	449	452	0	ATGG	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	626	629	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	731	734	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	773	776	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	819	822	0	ATGG	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	850	853	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	928	931	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1357	1360	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1439	1442	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1511	1514	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1534	1537	0	ATGG	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1600	1603	0	ATGG	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1612	1615	0	CCAT	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1666	1669	0	ATGG	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1807	1810	0	ATGG	7.8125	7.81711
cg0163748	FAHD1	YY1 [T00	1850	1853	0	ATGG	7.8125	7.81711
cg0163748	FAHD1	Elk-1 [T00	1428	1436	0	CTTCCTC	0.06104	0.06047
cg0163748	FAHD1	ER-alpha [	67	71	0	TGACC	1.95312	1.9404
cg0163748	FAHD1	ER-alpha [	633	637	0	GGTCA	1.95312	1.9404
cg0163748	FAHD1	ER-alpha [	655	659	0	TGACC	1.95312	1.9404
cg0163748	FAHD1	ER-alpha [	770	774	0	TGACC	1.95312	1.9404
cg0163748	FAHD1	ER-alpha [	1124	1128	0	GGTCA	1.95312	1.9404
cg0163748	FAHD1	ER-alpha [	1773	1777	0	GGTCA	1.95312	1.9404
cg0163748	FAHD1	C/EBPbeta	72	75	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	89	92	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	132	135	0	GCAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	235	238	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	242	245	0	GCAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	283	286	0	GCAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	292	295	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	344	347	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	346	349	0	GCAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	374	377	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	395	398	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	408	411	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	466	469	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	490	493	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	506	509	0	GCAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	598	601	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	735	738	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	748	751	0	TTGC	15.625	15.71349

cg0163748	FAHD1	C/EBPbeta	767	770	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	785	788	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	810	813	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	824	827	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	869	872	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	883	886	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1094	1097	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1149	1152	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1156	1159	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1161	1164	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1180	1183	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1196	1199	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1211	1214	0	GCAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1242	1245	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1255	1258	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1347	1350	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1380	1383	0	ACAA	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1403	1406	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1689	1692	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1860	1863	0	TTGT	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1873	1876	0	TTGC	15.625	15.71349
cg0163748	FAHD1	C/EBPbeta	1930	1933	0	GCAA	15.625	15.71349
cg0163748	FAHD1	TFIID [T0	380	386	0	TTTTTTA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	381	387	0	TTTTTAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	441	447	0	TTTTTGA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1218	1224	0	TCAAAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1334	1340	0	TTTAAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1335	1341	0	TTAAAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1694	1700	0	TTTTTAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1696	1702	0	TTTAAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1717	1723	0	TTTTATA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1720	1726	0	TATAAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1722	1728	0	TAAAAA	1.09863	1.13474
cg0163748	FAHD1	TFIID [T0	1801	1807	0	TTTTTAA	1.09863	1.13474
cg0163748	FAHD1	FOXP3 [T	1688	1693	0	GTTGTG	1.46484	1.47315
cg0163748	FAHD1	GR-beta [T	146	150	0	AAATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	304	308	0	AAATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	305	309	0	AATTT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	378	382	0	AATTT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	410	414	0	AATTT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	594	598	0	AATTT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	797	801	0	ACATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1165	1169	0	ACATT	3.90625	3.99611
cg0163748	FAHD1	GR-beta [T	1313	1317	0	ACATT	3.90625	3.99611
cg0163748	FAHD1	GR [T050	301	307	0	CAAAAA	0.36621	0.37562
cg0163748	FAHD1	GR [T050	440	446	0	CTTTTTG	0.36621	0.37562
cg0163748	FAHD1	GR [T050	462	468	0	CTTTTTG	0.36621	0.37562
cg0163748	FAHD1	GR [T050	852	858	0	ATTTTT	0.36621	0.37562

cg0163748	FAHD1	HNF-3alp	601	608	0	TATTTTT	0.09155	0.09511
cg0163748	FAHD1	LEF-1 [T0	946	953	0	GATCAA	0.03052	0.03083
cg0163748	FAHD1	IRF-2 [T0	528	533	0	AAGTGA	0.48828	0.49387
cg0163748	FAHD1	IRF-2 [T0	662	667	0	AAGTGA	0.48828	0.49387
cg2707039	FAM188B	Elk-1 [T00	789	797	9.979803	ATGCGG	0.10681	0.10604
cg2707039	FAM188B	Elk-1 [T00	1874	1882	9.979803	CTTCCG	0.10681	0.10604
cg0783131	FAM188B	RAR-beta:	1106	1117	9.97066	TCAGCC	0.06974	0.06822
cg0783131	FAM188B	STAT1bet	1531	1540	9.807397	ATAGGG	0.14877	0.1495
cg0783131	FAM188B	XBP-1 [T	154	159	9.789909	ATGGCT	1.95312	1.95208
cg0783131	FAM188B	XBP-1 [T	288	293	9.789909	AGCCAT	1.95312	1.95208
cg0783131	FAM188B	XBP-1 [T	970	975	9.789909	AGACAT	1.95312	1.95208
cg0783131	FAM188B	XBP-1 [T	1828	1833	9.789909	ATGGCT	1.95312	1.95208
cg0783131	FAM188B	XBP-1 [T	1886	1891	9.789909	ATGGCT	1.95312	1.95208
cg2707039	FAM188B	XBP-1 [T	546	551	9.789909	ATGTCT	1.95312	1.95208
cg2707039	FAM188B	XBP-1 [T	1262	1267	9.789909	ATGTCT	1.95312	1.95208
cg2707039	FAM188B	XBP-1 [T	1602	1607	9.789909	AGCCAT	1.95312	1.95208
cg2707039	FAM188B	RelA [T00	1825	1835	9.775716	AGGGGA	0.02623	0.02606
cg0783131	FAM188B	NF-1 [T00	75	82	9.761671	AGCTCC	0.24414	0.24405
cg0783131	FAM188B	NF-1 [T00	420	427	9.761671	TTGGTG	0.24414	0.24405
cg0783131	FAM188B	NF-1 [T00	1094	1101	9.761671	TTGGAG	0.24414	0.24405
cg2707039	FAM188B	NF-1 [T00	1053	1060	9.761671	GGCACC	0.24414	0.24405
cg0783131	FAM188B	Elk-1 [T00	1545	1553	9.754368	TGAGGG	0.10681	0.10604
cg0783131	FAM188B	PR B [T00	959	965	9.743489	GTGTGT	1.09863	1.10292
cg0783131	FAM188B	PR A [T01	959	965	9.743489	GTGTGT	1.09863	1.10292
cg2707039	FAM188B	PR B [T00	102	108	9.743489	CTGTGT	1.09863	1.10292
cg2707039	FAM188B	PR B [T00	429	435	9.743489	CCGTGT	1.09863	1.10292
cg2707039	FAM188B	PR B [T00	468	474	9.743489	CTGTGT	1.09863	1.10292
cg2707039	FAM188B	PR A [T01	102	108	9.743489	CTGTGT	1.09863	1.10292
cg2707039	FAM188B	PR A [T01	429	435	9.743489	CCGTGT	1.09863	1.10292
cg2707039	FAM188B	PR A [T01	468	474	9.743489	CTGTGT	1.09863	1.10292
cg0783131	FAM188B	c-Myb [T0	1705	1712	9.729271	GAACTG	0.36621	0.37054
cg2707039	FAM188B	c-Myb [T0	58	65	9.729271	TAACTG	0.36621	0.37054
cg0783131	FAM188B	LEF-1 [T0	1987	1994	9.72404	CTTTGT	0.21362	0.2139
cg2707039	FAM188B	LEF-1 [T0	798	805	9.72404	TGGCAA	0.21362	0.2139
cg0783131	FAM188B	c-Ets-1 [T	234	240	9.713162	GGGGAA	0.36621	0.36441
cg0783131	FAM188B	NF-AT1 [	1119	1127	9.691726	GGAAAC	0.16785	0.1682
cg2707039	FAM188B	EBF [T05	1380	1390	9.678925	ACACCA	0.06866	0.06676
cg2707039	FAM188B	RAR-beta	68	77	9.641259	GGGGTT	0.21362	0.21243
cg2707039	FAM188B	EBF [T05	1731	1741	9.625349	TCCCCT	0.06866	0.06676
cg2707039	FAM188B	RAR-beta	861	870	9.622793	TAGAAA	0.21362	0.21243
cg2707039	FAM188B	Elk-1 [T00	1443	1451	9.62002	CTTCCC	0.07629	0.07577
cg2707039	FAM188B	c-Ets-1 [T	425	431	9.585075	ATTCCC	0.36621	0.36441
cg0783131	FAM188B	Pax-5 [T0	45	51	9.552105	TTTGCC	1.46484	1.43083
cg0783131	FAM188B	Pax-5 [T0	589	595	9.552105	GGGCCA	1.46484	1.43083
cg0783131	FAM188B	Pax-5 [T0	713	719	9.552105	GTGGCC	1.46484	1.43083
cg0783131	FAM188B	Pax-5 [T0	1161	1167	9.552105	GGGCCA	1.46484	1.43083
cg0783131	FAM188B	TFIID [T0	191	197	9.552105	TTTCGA	1.46484	1.48472
cg0783131	FAM188B	TFIID [T0	296	302	9.552105	TTTGAC	1.46484	1.48472

cg0783131	FAM188B	TFIID [T0	550	556	9.552105	TTTGTCA	1.46484	1.48472
cg0783131	FAM188B	TFIID [T0	1338	1344	9.552105	TGGGAA	1.46484	1.48472
cg0783131	FAM188B	TFIID [T0	1802	1808	9.552105	TGAGAA	1.46484	1.48472
cg0783131	FAM188B	TFIID [T0	1945	1951	9.552105	TCCCAA	1.46484	1.48472
cg0783131	FAM188B	TFIID [T0	1988	1994	9.552105	TTTGTCA	1.46484	1.48472
cg2707039	FAM188B	Pax-5 [T0	163	169	9.552105	GGGCGG	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	260	266	9.552105	GGGCGC	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	691	697	9.552105	GTAGCC	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	949	955	9.552105	GGGCCA	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	1159	1165	9.552105	GTGGCC	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	1386	1392	9.552105	GGGCGC	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	1387	1393	9.552105	GGCGCC	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	1759	1765	9.552105	GGGCGC	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	1760	1766	9.552105	GGCGCC	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	1932	1938	9.552105	GGGCGG	1.46484	1.43083
cg2707039	FAM188B	Pax-5 [T0	1986	1992	9.552105	GGGCGC	1.46484	1.43083
cg2707039	FAM188B	TFIID [T0	147	153	9.552105	TTTGGG	1.46484	1.48472
cg2707039	FAM188B	TFIID [T0	798	804	9.552105	TGGCAA	1.46484	1.48472
cg2707039	FAM188B	TFIID [T0	873	879	9.552105	TTTCCCA	1.46484	1.48472
cg2707039	FAM188B	TFIID [T0	1838	1844	9.552105	TTTCCCA	1.46484	1.48472
cg0783131	FAM188B	NF-1 [T00	822	829	9.535536	TTGGTC	0.73242	0.73053
cg2707039	FAM188B	NF-1 [T00	1090	1097	9.535536	GTGCCC	0.73242	0.73053
cg2707039	FAM188B	NF-1 [T00	1642	1649	9.535536	TTGGTC	0.73242	0.73053
cg2707039	FAM188B	NF-AT1 [	504	512	9.521781	GGAAAT	0.16785	0.1682
cg0783131	FAM188B	TFII-I [T0	33	38	9.512894	GGAAGG	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	258	263	9.512894	GGAAAA	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	488	493	9.512894	GGAAAC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	542	547	9.512894	CCTTCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	616	621	9.512894	CCATCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	634	639	9.512894	CCATCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	731	736	9.512894	GGACAC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	992	997	9.512894	TTTTCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1119	1124	9.512894	GGAAAC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1169	1174	9.512894	AAGTCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1417	1422	9.512894	CCTTCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1549	1554	9.512894	GGAAGG	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1639	1644	9.512894	CGTTCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1689	1694	9.512894	GGAAGG	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1776	1781	9.512894	GGACAC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1891	1896	9.512894	TTTTCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1911	1916	9.512894	CCATCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1967	1972	9.512894	CGATCC	7.32422	7.29728
cg0783131	FAM188B	TFII-I [T0	1979	1984	9.512894	TTGTCC	7.32422	7.29728
cg0783131	FAM188B	FOXP3 [T	91	96	9.512894	GTTATT	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	329	334	9.512894	GTTTAG	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	358	363	9.512894	GTTGGT	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	384	389	9.512894	GTTGGT	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	388	393	9.512894	GTTGGT	7.32422	7.35678

cg0783131	FAM188B	FOXP3 [T	454	459	9.512894	GTAAAC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	498	503	9.512894	AGCAAC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	537	542	9.512894	CAGAAC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	898	903	9.512894	AGCAAC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	1063	1068	9.512894	AGCAAC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	1278	1283	9.512894	ATAAAC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	1633	1638	9.512894	GTTCTC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	1821	1826	9.512894	CAGAAC	7.32422	7.35678
cg0783131	FAM188B	FOXP3 [T	1857	1862	9.512894	GTTCTC	7.32422	7.35678
cg2707039	FAM188B	TFII-I [T0	33	38	9.512894	GGATTT	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	269	274	9.512894	AAATCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	424	429	9.512894	AATTCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	437	442	9.512894	AAGTCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	568	573	9.512894	GGACAC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	584	589	9.512894	GGACGG	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	662	667	9.512894	CCATCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	840	845	9.512894	GGAAAA	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	929	934	9.512894	GTGTCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1269	1274	9.512894	GGAAAA	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1300	1305	9.512894	TTGTCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1363	1368	9.512894	GGACGG	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1442	1447	9.512894	CCTTCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1474	1479	9.512894	GGAAGG	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1766	1771	9.512894	CGTTCC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1828	1833	9.512894	GGAAAC	7.32422	7.29728
cg2707039	FAM188B	TFII-I [T0	1898	1903	9.512894	CCGTCC	7.32422	7.29728
cg2707039	FAM188B	FOXP3 [T	106	111	9.512894	GTTGGG	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	201	206	9.512894	GGCAAC	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	699	704	9.512894	CAGAAC	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	867	872	9.512894	CCCAAC	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	951	956	9.512894	GCCAAC	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	1155	1160	9.512894	GTTGGT	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	1218	1223	9.512894	GTTTAG	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	1486	1491	9.512894	GTTCTT	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	1517	1522	9.512894	GGCAAC	7.32422	7.35678
cg2707039	FAM188B	FOXP3 [T	1550	1555	9.512894	GTTGCC	7.32422	7.35678
cg2707039	FAM188B	Ik-1 [T027	272	284	9.497194	TCCCAG	0.02941	0.02907
cg0783131	FAM188B	TCF-4E [T	295	301	9.453578	CTTTGA	0.48828	0.49215
cg0783131	FAM188B	TCF-4E [T	1561	1567	9.453578	CTTTGTA	0.48828	0.49215
cg2707039	FAM188B	TCF-4E [T	749	755	9.453578	CTTTGTA	0.48828	0.49215
cg2707039	FAM188B	TCF-4E [T	1685	1691	9.453578	TCCAAA	0.48828	0.49215
cg2707039	FAM188B	HNF-1C [	780	788	9.379404	ATAGGT	0.19836	0.20229
cg0783131	FAM188B	NFI/CTF [	168	175	9.352332	AACCTT	0.54932	0.54821
cg0783131	FAM188B	NFI/CTF [	559	566	9.352332	CCAAGG	0.54932	0.54821
cg0783131	FAM188B	NFI/CTF [	592	599	9.352332	CCAAGG	0.54932	0.54821
cg0783131	FAM188B	NFI/CTF [	636	643	9.352332	ATCCTT	0.54932	0.54821
cg0783131	FAM188B	NFI/CTF [	1333	1340	9.352332	GGCCTT	0.54932	0.54821
cg0783131	FAM188B	NFI/CTF [	1759	1766	9.352332	CCAAGG	0.54932	0.54821

cg2707039	FAM188B	NFI/CTF [	1141	1148	9.352332	CCAAGG	0.54932	0.54821
cg2707039	FAM188B	NFI/CTF [	1686	1693	9.352332	CCAAAG	0.54932	0.54821
cg2707039	FAM188B	LEF-1 [T0	1684	1691	9.313676	CTCCAA	0.21362	0.2139
cg2707039	FAM188B	HNF-1B [	858	866	9.308068	GGTTAG	0.09155	0.09374
cg0783131	FAM188B	SRY [T00	295	303	9.264664	CTTTGA	0.12207	0.12265
cg0783131	FAM188B	MEF-2A [	77	87	9.220261	CTCCAA	0.07343	0.07563
cg2707039	FAM188B	AP-1 [T00	827	835	9.203282	TGACTA	0.24414	0.24693
cg2707039	FAM188B	c-Ets-1 [T	531	537	9.19359	ATTCCA	0.85449	0.85523
cg2707039	FAM188B	NF-AT1 [	1810	1818	9.18189	CCGCTT	0.22888	0.22959
cg2707039	FAM188B	PPAR-alp	1160	1170	9.158357	TGGCCC	0.0515	0.04986
cg0783131	FAM188B	RelA [T00	1546	1556	9.155011	GAGGGA	0.02432	0.0241
cg2707039	FAM188B	c-Ets-1 [T	1767	1773	9.148774	GTTCCC	0.85449	0.85523
cg0783131	FAM188B	HNF-1C [	941	949	9.116395	GTTACT	0.12207	0.12495
cg0783131	FAM188B	LEF-1 [T0	1164	1171	9.099721	CCACAA	0.54932	0.55326
cg2707039	FAM188B	LEF-1 [T0	1742	1749	9.099721	CTTTGC	0.54932	0.55326
cg0783131	FAM188B	LEF-1 [T0	295	302	9.082175	CTTTGA	0.54932	0.55326
cg0783131	FAM188B	USF2 [T0	721	730	9.056375	CCCACA	0.1545	0.15287
cg0783131	FAM188B	MAZ [T00	1767	1779	9.043062	TGTCGG	0.01413	0.01385
cg2707039	FAM188B	NFI/CTF [	952	959	9.042931	CCAACA	0.48828	0.48804
cg2707039	FAM188B	NF-AT1 [	1834	1842	9.042733	TACATT	0.22888	0.22959
cg2707039	FAM188B	PXR-1:RX	324	331	8.998824	GTTGTT	0.24414	0.2439
cg2707039	FAM188B	LEF-1 [T0	146	153	8.973041	CTTTGG	0.54932	0.55326
cg0783131	FAM188B	GR [T050	23	29	8.971049	CAAAGC	0.61035	0.61632
cg2707039	FAM188B	GR [T050	903	909	8.971049	CAAAAT	0.61035	0.61632
cg2707039	FAM188B	GR [T050	1687	1693	8.971049	CAAAGC	0.61035	0.61632
cg2707039	FAM188B	GR [T050	1740	1746	8.971049	GGCTTT	0.61035	0.61632
cg2707039	FAM188B	HNF-1C [	859	867	8.969184	GTTAGA	0.12207	0.12495
cg0783131	FAM188B	EBF [T05	47	57	8.948874	TGCCCA	0.01526	0.01496
cg2707039	FAM188B	RBP-Jkap	872	883	8.942683	CTTTCC	0.00763	0.00768
cg0783131	FAM188B	Elk-1 [T0	1418	1426	8.931691	CTTCCA	0.24414	0.24034
cg0783131	FAM188B	c-Ets-2 [T	1114	1122	8.912323	GCCCAG	0.27466	0.27495
cg2707039	FAM188B	c-Ets-2 [T	968	976	8.912323	AGCCAG	0.27466	0.27495
cg2707039	FAM188B	c-Ets-2 [T	1264	1272	8.912323	GTCTAG	0.27466	0.27495
cg2707039	FAM188B	c-Ets-2 [T	1691	1699	8.912323	GCCCAG	0.27466	0.27495
cg2707039	FAM188B	p53 [T006	1368	1374	8.912104	GGGCCC	0.12207	0.11837
cg0783131	FAM188B	HOXD9 [	1488	1497	8.847863	AATACC	0.04578	0.0476
cg0783131	FAM188B	HOXD10 [	1488	1497	8.847863	AATACC	0.04578	0.0476
cg0783131	FAM188B	EBF [T05	26	36	8.844893	AGCCCA	0.01526	0.01496
cg0783131	FAM188B	c-Jun [T00	3	9	8.832178	AAGGTC	0.61035	0.61059
cg0783131	FAM188B	c-Jun [T00	1551	1557	8.832178	AAGGTC	0.61035	0.61059
cg2707039	FAM188B	c-Jun [T00	1143	1149	8.832178	AAGGTC	0.61035	0.61059
cg0783131	FAM188B	PR B [T00	186	192	8.827054	AGCTGT	0.36621	0.36944
cg0783131	FAM188B	PR A [T01	186	192	8.827054	AGCTGT	0.36621	0.36944
cg0783131	FAM188B	NFI/CTF [	56	63	8.814757	TCACTT	0.48828	0.48804
cg0783131	FAM188B	NFI/CTF [	1090	1097	8.814757	CCTTTT	0.48828	0.48804
cg2707039	FAM188B	NFI/CTF [	329	336	8.814757	TCACTT	0.48828	0.48804
cg0783131	FAM188B	c-Ets-1 [T	1644	1650	8.809329	CTGGAA	0.85449	0.85523
cg2707039	FAM188B	c-Ets-1 [T	362	368	8.809329	ATTCCA	0.85449	0.85523

cg2707039	FAM188B	c-Ets-1 [T	454	460	8.809329	ATTCCA	0.85449	0.85523
cg2707039	FAM188B	c-Jun [T00	1860	1866	8.807683	GTCGTC	0.61035	0.61059
cg0783131	FAM188B	NF-1 [T00	640	647	8.790071	TTGGGA	0.24414	0.24467
cg0783131	FAM188B	NF-1 [T00	1337	1344	8.790071	TTGGGA	0.24414	0.24467
cg0783131	FAM188B	NF-1 [T00	1943	1950	8.790071	CCTCCC	0.24414	0.24467
cg2707039	FAM188B	NF-1 [T00	148	155	8.790071	TTGGGA	0.24414	0.24467
cg0783131	FAM188B	NF-AT1 [	1340	1348	8.769753	GGAAAG	0.22888	0.22959
cg2707039	FAM188B	LEF-1 [T0	749	756	8.759086	CTTTGT	0.54932	0.55326
cg0783131	FAM188B	XBP-1 [T	72	77	8.75604	ATGAGC	2.92969	2.9674
cg0783131	FAM188B	XBP-1 [T	130	135	8.75604	ATGAAC	2.92969	2.9674
cg0783131	FAM188B	XBP-1 [T	793	798	8.75604	TCTCAT	2.92969	2.9674
cg0783131	FAM188B	XBP-1 [T	805	810	8.75604	TCTCAT	2.92969	2.9674
cg0783131	FAM188B	XBP-1 [T	887	892	8.75604	GATCAT	2.92969	2.9674
cg0783131	FAM188B	XBP-1 [T	1288	1293	8.75604	ATGAGA	2.92969	2.9674
cg0783131	FAM188B	XBP-1 [T	1429	1434	8.75604	ATGAGC	2.92969	2.9674
cg0783131	FAM188B	XBP-1 [T	1509	1514	8.75604	TCTCAT	2.92969	2.9674
cg2707039	FAM188B	XBP-1 [T	1035	1040	8.75604	TCTCAT	2.92969	2.9674
cg2707039	FAM188B	XBP-1 [T	1718	1723	8.75604	GATCAT	2.92969	2.9674
cg2707039	FAM188B	STAT1bet	500	509	8.695301	AAGTGG	0.22316	0.22446
cg2707039	FAM188B	STAT1bet	1041	1050	8.695301	TACGGG	0.22316	0.22446
cg2707039	FAM188B	STAT1bet	1813	1822	8.695301	CTTTCC	0.22316	0.22446
cg2707039	FAM188B	STAT1bet	1837	1846	8.695301	ATTTCC	0.22316	0.22446
cg0783131	FAM188B	NF-AT1 [	1888	1896	8.599808	GGCTTT	0.10681	0.10725
cg0783131	FAM188B	c-Jun [T00	178	184	8.571705	CCAGTC	0.12207	0.12139
cg0783131	FAM188B	c-Jun [T00	1083	1089	8.571705	CCAGTC	0.12207	0.12139
cg0783131	FAM188B	IRF-1 [T0	484	492	8.570857	CTGTGG	0.20599	0.20664
cg0783131	FAM188B	p53 [T006	623	629	8.537081	GGGCTC	0.12207	0.11986
cg2707039	FAM188B	NF-AT1 [	1269	1277	8.532897	GGAAAA	0.10681	0.10725
cg0783131	FAM188B	c-Ets-1 [T	1702	1708	8.501115	TTGGAA	0.24414	0.24529
cg2707039	FAM188B	c-Myb [T0	540	547	8.443873	CAACTG	0.30518	0.30924
cg0783131	FAM188B	EBF [T05	577	587	8.430724	CTCCCT	0.03052	0.02952
cg0783131	FAM188B	LEF-1 [T0	1977	1984	8.361499	CTTTGT	0.15259	0.15214
cg0783131	FAM188B	PR B [T00	313	319	8.338824	AACAGA	1.09863	1.10009
cg0783131	FAM188B	PR B [T00	1055	1061	8.338824	GCCTGT	1.09863	1.10009
cg0783131	FAM188B	PR B [T00	1677	1683	8.338824	AACAGA	1.09863	1.10009
cg0783131	FAM188B	PR B [T00	1871	1877	8.338824	AACAGC	1.09863	1.10009
cg0783131	FAM188B	PR A [T01	313	319	8.338824	AACAGA	1.09863	1.10009
cg0783131	FAM188B	PR A [T01	1055	1061	8.338824	GCCTGT	1.09863	1.10009
cg0783131	FAM188B	PR A [T01	1677	1683	8.338824	AACAGA	1.09863	1.10009
cg0783131	FAM188B	PR A [T01	1871	1877	8.338824	AACAGC	1.09863	1.10009
cg0783131	FAM188B	ATF3 [T0	298	305	8.313799	TGACAT	0.27466	0.27431
cg0783131	FAM188B	GR-alpha [	2	6	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha [	34	38	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha [	170	174	8.281568	CCTTG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha [	505	509	8.281568	CCTTC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha [	521	525	8.281568	CCTTC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha [	542	546	8.281568	CCTTC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha [	560	564	8.281568	CAAGG	7.8125	7.72956

cg0783131	FAM188B	GR-alpha |	576	580	8.281568	CCTCC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	593	597	8.281568	CAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	638	642	8.281568	CCTTG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	643	647	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	667	671	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	671	675	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	863	867	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	880	884	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	996	1000	8.281568	CCTTC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1135	1139	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1144	1148	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1158	1162	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1190	1194	8.281568	CAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1238	1242	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1335	1339	8.281568	CCTTG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1352	1356	8.281568	CCTTG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1364	1368	8.281568	CCTCC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1417	1421	8.281568	CCTTC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1550	1554	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1593	1597	8.281568	CCTTG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1672	1676	8.281568	CAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1690	1694	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1747	1751	8.281568	GAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1760	1764	8.281568	CAAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1772	1776	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1836	1840	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1898	1902	8.281568	GGAGG	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1924	1928	8.281568	CCTCC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1928	1932	8.281568	CCTCC	7.8125	7.72956
cg0783131	FAM188B	GR-alpha |	1943	1947	8.281568	CCTCC	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	151	155	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	157	161	8.281568	CGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	285	289	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	295	299	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	317	321	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	613	617	8.281568	GAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	676	680	8.281568	CCTCG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	811	815	8.281568	GAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1058	1062	8.281568	CAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1066	1070	8.281568	CGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1117	1121	8.281568	CCTTG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1132	1136	8.281568	CAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1142	1146	8.281568	CAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1225	1229	8.281568	CCTCC	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1235	1239	8.281568	CAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1238	1242	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1280	1284	8.281568	CCTCG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha |	1403	1407	8.281568	CCTCC	7.8125	7.72956

cg2707039	FAM188B	GR-alpha [	1442	1446	8.281568	CCTTC	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1447	1451	8.281568	CCTCC	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1475	1479	8.281568	GAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1480	1484	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1578	1582	8.281568	CCTCG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1623	1627	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1626	1630	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1637	1641	8.281568	CCTCC	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1640	1644	8.281568	CCTTG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1683	1687	8.281568	CCTCC	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1737	1741	8.281568	GAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1756	1760	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1845	1849	8.281568	CGAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1880	1884	8.281568	CAAGG	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1909	1913	8.281568	CCTCC	7.8125	7.72956
cg2707039	FAM188B	GR-alpha [	1948	1952	8.281568	GGAGG	7.8125	7.72956
cg2707039	FAM188B	GCF [T00	1529	1537	8.256755	ATACTG	0.09155	0.09002
cg2707039	FAM188B	c-Ets-1 [T	815	821	8.244941	GTGGAA	0.24414	0.2425
cg2707039	FAM188B	IRF-1 [T0	1265	1273	8.242487	TCTAGG	0.25177	0.25263
cg0783131	FAM188B	c-Jun [T00	162	168	8.242207	GAGGTC	0.48828	0.49076
cg2707039	FAM188B	c-Jun [T00	176	182	8.242207	GAGGTC	0.48828	0.49076
cg0783131	FAM188B	NFI/CTF [	385	392	8.241664	TTGGTT	0.18311	0.1823
cg2707039	FAM188B	NF-kappa	1715	1725	8.229803	GGGGAT	0.0329	0.03218
cg2707039	FAM188B	p53 [T006	1367	1373	8.208781	GGGGCC	0.48828	0.47377
cg2707039	FAM188B	ENKTF-1	965	972	8.19852	CCTAGC	0.73242	0.71737
cg2707039	FAM188B	ENKTF-1	1136	1143	8.19852	GCCCGC	0.73242	0.71737
cg2707039	FAM188B	ENKTF-1	1459	1466	8.19852	GCCCGC	0.73242	0.71737
cg2707039	FAM188B	ENKTF-1	1522	1529	8.19852	CGCGGC	0.73242	0.71737
cg2707039	FAM188B	NF-1 [T00	684	691	8.191058	TTGGTC	0.24414	0.24409
cg2707039	FAM188B	AhR [T01	125	135	8.184723	CTCACG	0.04864	0.04833
cg2707039	FAM188B	SRY [T00	764	772	8.174786	CAAGCA	0.15259	0.15383
cg2707039	FAM188B	p53 [T006	1869	1875	8.162057	GGGCGC	0.48828	0.47377
cg0783131	FAM188B	NF-AT1 [	258	266	8.12076	GGAAAA	0.1297	0.12988
cg0783131	FAM188B	c-Ets-1 [T	963	969	8.116854	GTTCCA	0.24414	0.2425
cg0783131	FAM188B	c-Ets-1 [T	1651	1657	8.116854	GTTCCA	0.24414	0.2425
cg0783131	FAM188B	VDR [T00	127	135	8.079962	TAAATG	0.24414	0.24712
cg2707039	FAM188B	VDR [T00	186	194	8.079962	GTTCAA	0.24414	0.24712
cg0783131	FAM188B	IRF-1 [T0	1892	1900	8.078284	TTTCCA	0.25177	0.25263
cg0783131	FAM188B	GR-alpha [	29	33	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	50	54	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	231	235	8.073878	GCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	272	276	8.073878	CCTAG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	414	418	8.073878	GCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	442	446	8.073878	CCTAG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	580	584	8.073878	CCTGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	620	624	8.073878	CCTGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	684	688	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	727	731	8.073878	CCTGG	7.8125	7.72238

cg0783131	FAM188B	GR-alpha [	750	754	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	781	785	8.073878	CCTGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	928	932	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1020	1024	8.073878	CCTGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1070	1074	8.073878	CCTGC	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1116	1120	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1140	1144	8.073878	GCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1173	1177	8.073878	CCTGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1320	1324	8.073878	CCTAC	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1328	1332	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1370	1374	8.073878	GCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1378	1382	8.073878	GCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1440	1444	8.073878	CTAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1643	1647	8.073878	CCTGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1876	1880	8.073878	CCTGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1895	1899	8.073878	CCAGG	7.8125	7.72238
cg0783131	FAM188B	GR-alpha [	1939	1943	8.073878	CCTGC	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	448	452	8.073878	CCTGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	637	641	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	822	826	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	965	969	8.073878	CCTAG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	970	974	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1050	1054	8.073878	GCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1242	1246	8.073878	GCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1266	1270	8.073878	CTAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1304	1308	8.073878	CCTAG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1305	1309	8.073878	CTAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1322	1326	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1328	1332	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1372	1376	8.073878	CCTAG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1373	1377	8.073878	CTAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1383	1387	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1470	1474	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1554	1558	8.073878	CCTGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1693	1697	8.073878	CCAGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1771	1775	8.073878	CCTAC	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1775	1779	8.073878	CCTAC	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1782	1786	8.073878	CCTGC	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1912	1916	8.073878	CCTGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1956	1960	8.073878	CCTGG	7.8125	7.72238
cg2707039	FAM188B	GR-alpha [	1978	1982	8.073878	CCTAG	7.8125	7.72238
cg0783131	FAM188B	Pax-5 [T0	422	428	8.014558	GGTGCC	2.19727	2.14502
cg0783131	FAM188B	Pax-5 [T0	678	684	8.014558	GGGCTG	2.19727	2.14502
cg0783131	FAM188B	Pax-5 [T0	688	694	8.014558	GAAGCC	2.19727	2.14502
cg0783131	FAM188B	Pax-5 [T0	1373	1379	8.014558	GGGCTG	2.19727	2.14502
cg0783131	FAM188B	Pax-5 [T0	1412	1418	8.014558	TCAGCC	2.19727	2.14502
cg0783131	FAM188B	Pax-5 [T0	1588	1594	8.014558	TATGCC	2.19727	2.14502
cg0783131	FAM188B	Pax-5 [T0	1878	1884	8.014558	TGGGCC	2.19727	2.14502

cg0783131	FAM188B	TFIID [T0	117	123	8.014558	TTTCTAA	2.19727	2.24348
cg0783131	FAM188B	TFIID [T0	148	154	8.014558	TTTCAA	2.19727	2.24348
cg0783131	FAM188B	TFIID [T0	251	257	8.014558	TTTGAA	2.19727	2.24348
cg0783131	FAM188B	TFIID [T0	1229	1235	8.014558	TAAGAA	2.19727	2.24348
cg0783131	FAM188B	TFIID [T0	1577	1583	8.014558	TTTGCA	2.19727	2.24348
cg0783131	FAM188B	TFIID [T0	1578	1584	8.014558	TTGCAA	2.19727	2.24348
cg0783131	FAM188B	TFIID [T0	1712	1718	8.014558	TTTCAG	2.19727	2.24348
cg2707039	FAM188B	Pax-5 [T0	76	82	8.014558	GGGCTG	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	372	378	8.014558	GGGCAC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	758	764	8.014558	GCAGCC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	894	900	8.014558	GGGCCT	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1089	1095	8.014558	GGTGCC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1111	1117	8.014558	GGGCTT	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1341	1347	8.014558	GAGGCC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1367	1373	8.014558	GGGGCC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1563	1569	8.014558	GCGGCC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1575	1581	8.014558	GGGCCT	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1584	1590	8.014558	GGGCAG	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1793	1799	8.014558	GATGCC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1904	1910	8.014558	GCTGCC	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1916	1922	8.014558	GGGCAT	2.19727	2.14502
cg2707039	FAM188B	Pax-5 [T0	1961	1967	8.014558	GGGCCG	2.19727	2.14502
cg2707039	FAM188B	TFIID [T0	91	97	8.014558	TTTCAA	2.19727	2.24348
cg2707039	FAM188B	TFIID [T0	393	399	8.014558	TCTCAA	2.19727	2.24348
cg2707039	FAM188B	TFIID [T0	860	866	8.014558	TTAGAA	2.19727	2.24348
cg2707039	FAM188B	TFIID [T0	916	922	8.014558	TTTCTGA	2.19727	2.24348
cg2707039	FAM188B	TFIID [T0	1267	1273	8.014558	TAGGAA	2.19727	2.24348
cg2707039	FAM188B	PU.1 [T02	1691	1703	8.010215	GCCCAG	0.00191	0.00188
cg2707039	FAM188B	c-Myb [T0	959	966	8.005241	TAACTA	0.21362	0.21454
cg2707039	FAM188B	c-Myb [T0	1649	1656	8.005241	GGGAGT	0.21362	0.21454
cg0783131	FAM188B	HNF-1B [	940	948	7.973785	GGTTAC	0.06866	0.07026
cg2707039	FAM188B	ETF [T002	1946	1956	7.870358	GGGGAG	0.07153	0.06862
cg0783131	FAM188B	p53 [T006	1908	1914	7.853573	GGGCCA	0.48828	0.47377
cg0783131	FAM188B	c-Ets-2 [T	682	690	7.84116	TGCCAG	0.32043	0.32298
cg0783131	FAM188B	c-Ets-2 [T	1641	1649	7.84116	TTCCTGC	0.32043	0.32298
cg0783131	FAM188B	T3R-beta1	1812	1820	7.79407	TCACCC	0.27466	0.27236
cg0783131	FAM188B	NF-AT2 [	608	617	7.779688	AATCCT	0.08965	0.09068
cg0783131	FAM188B	GATA-2 [	1682	1690	7.777778	AGATAC	0.30518	0.30758
cg0783131	FAM188B	c-Ets-2 [T	1684	1692	7.76635	ATACAG	0.32043	0.32298
cg2707039	FAM188B	NF-AT1 [	869	877	7.744746	CAACTT	0.19836	0.19941
cg2707039	FAM188B	NF-AT1 [	1045	1053	7.744746	GGAAAG	0.19836	0.19941
cg0783131	FAM188B	NF-1 [T00	1702	1709	7.693985	TTGGAA	0.24414	0.24565
cg0783131	FAM188B	c-Jun [T00	404	410	7.686747	ACAGTC	0.48828	0.48775
cg2707039	FAM188B	c-Jun [T00	465	471	7.686747	TGACTG	0.48828	0.48775
cg0783131	FAM188B	c-Myb [T0	275	282	7.662426	AGAAGT	0.42725	0.43114
cg0783131	FAM188B	p53 [T006	1332	1338	7.641867	GGGCCT	0.73242	0.7186
cg2707039	FAM188B	p53 [T006	1133	1139	7.641867	AAGGCC	0.73242	0.7186
cg2707039	FAM188B	p53 [T006	1172	1178	7.641867	GGGCCG	0.73242	0.7186

cg2707039	FAM188B	AR [T0004	1297	1305	7.623968	AATTTGT	0.25177	0.25079
cg0783131	FAM188B	NFI/CTF [	1492	1499	7.587343	CCAATT	0.36621	0.36674
cg0783131	FAM188B	GR [T0507	42	48	7.527031	ATATTT	1.83105	1.86007
cg0783131	FAM188B	GR [T0507	293	299	7.527031	TGCTTT	1.83105	1.86007
cg0783131	FAM188B	GR [T0507	311	317	7.527031	CAAACA	1.83105	1.86007
cg0783131	FAM188B	GR [T0507	547	553	7.527031	CCTTTT	1.83105	1.86007
cg0783131	FAM188B	GR [T0507	903	909	7.527031	CATTTT	1.83105	1.86007
cg0783131	FAM188B	GR [T0507	1090	1096	7.527031	CCTTTT	1.83105	1.86007
cg0783131	FAM188B	GR [T0507	1251	1257	7.527031	CAAATA	1.83105	1.86007
cg2707039	FAM188B	GR [T0507	236	242	7.527031	CAAATA	1.83105	1.86007
cg0783131	FAM188B	IRF-1 [T0	1115	1123	7.477948	CCCAGG	0.14496	0.14449
cg0783131	FAM188B	C/EBPalph	1483	1489	7.465744	CATTGA	0.48828	0.49653
cg2707039	FAM188B	p53 [T006	260	266	7.458735	GGGCGC	0.73242	0.7186
cg2707039	FAM188B	p53 [T006	1386	1392	7.458735	GGGCGC	0.73242	0.7186
cg2707039	FAM188B	p53 [T006	1387	1393	7.458735	GGCGCC	0.73242	0.7186
cg2707039	FAM188B	p53 [T006	1759	1765	7.458735	GGGCGC	0.73242	0.7186
cg2707039	FAM188B	p53 [T006	1760	1766	7.458735	GGCGCC	0.73242	0.7186
cg0783131	FAM188B	NF-1 [T00	555	562	7.445595	CATGCC	0.24414	0.24565
cg0783131	FAM188B	NF-1 [T00	1514	1521	7.445595	TATGCC	0.24414	0.24565
cg0783131	FAM188B	RAR-alpha	52	64	7.429021	AGGGTC	0.00036	0.00035
cg0783131	FAM188B	PEA3 [T0	632	640	7.421728	CACCAT	0.34332	0.34161
cg0783131	FAM188B	PEA3 [T0	1426	1434	7.421728	TGGATG	0.34332	0.34161
cg0783131	FAM188B	PEA3 [T0	1900	1908	7.421728	AGGATG	0.34332	0.34161
cg0783131	FAM188B	RelA [T00	233	243	7.401574	AGGGGA	0.01335	0.01319
cg0783131	FAM188B	LEF-1 [T0	1561	1568	7.396545	CTTTGTA	0.21362	0.21302
cg0783131	FAM188B	C/EBPalph	1521	1527	7.396431	AATTGG	0.48828	0.49653
cg2707039	FAM188B	C/EBPalph	14	20	7.396431	AATTGT	0.48828	0.49653
cg2707039	FAM188B	IRF-1 [T0	836	844	7.387351	TCGGGG	0.14496	0.14449
cg0783131	FAM188B	NF-kappa	1180	1190	7.340726	TGTGTCT	0.04435	0.04347
cg2707039	FAM188B	E2F-1 [T0	791	798	7.336545	GCGGAA	0.45776	0.44878
cg2707039	FAM188B	E2F-1 [T0	1873	1880	7.336545	GCTTCC	0.45776	0.44878
cg2707039	FAM188B	E2F-1 [T0	1937	1944	7.336545	GCGGCA	0.45776	0.44878
cg0783131	FAM188B	p53 [T006	24	30	7.266844	AAAGCC	0.73242	0.7186
cg2707039	FAM188B	p53 [T006	1688	1694	7.266844	AAAGCC	0.73242	0.7186
cg0783131	FAM188B	NF-AT1 [	1786	1794	7.211175	GGAAAG	0.15259	0.1548
cg0783131	FAM188B	c-Ets-1 [T	1338	1344	7.199436	TGGGAA	0.73242	0.73099
cg2707039	FAM188B	c-Ets-1 [T	873	879	7.199436	TTTCCCA	0.73242	0.73099
cg2707039	FAM188B	c-Ets-1 [T	1838	1844	7.199436	TTTCCCA	0.73242	0.73099
cg0783131	FAM188B	SRY [T00	1163	1171	7.175614	GCCACA	0.30518	0.30739
cg0783131	FAM188B	SRY [T00	1977	1985	7.175614	CTTTGT	0.30518	0.30739
cg0783131	FAM188B	XBP-1 [T	160	165	7.172312	ATGAGG	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	266	271	7.172312	CTTCAT	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	736	741	7.172312	CCTCAT	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	809	814	7.172312	ATGATG	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	878	883	7.172312	ATGAAG	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	949	954	7.172312	ATGAAT	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	977	982	7.172312	CTTCAT	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	1236	1241	7.172312	ATGAAG	2.92969	2.97018

cg0783131	FAM188B	XBP-1 [T	1544	1549	7.172312	ATGAGG	2.92969	2.97018
cg0783131	FAM188B	XBP-1 [T	1993	1998	7.172312	CATCAT	2.92969	2.97018
cg2707039	FAM188B	XBP-1 [T	497	502	7.172312	ATGAAG	2.92969	2.97018
cg0783131	FAM188B	p53 [T006	1878	1884	7.153797	TGGGCC	1.09863	1.07125
cg0783131	FAM188B	p53 [T006	713	719	7.150251	GTGGCC	1.09863	1.07125
cg0783131	FAM188B	p53 [T006	1161	1167	7.150251	GGGCCA	1.09863	1.07125
cg2707039	FAM188B	p53 [T006	1159	1165	7.150251	GTGGCC	1.09863	1.07125
cg2707039	FAM188B	AR [T000	1821	1829	7.107265	GGACAG	0.23651	0.23551
cg0783131	FAM188B	p53 [T006	1964	1970	7.103527	GGGCGA	1.09863	1.07125
cg2707039	FAM188B	c-Jun [T00	510	516	7.096776	GCAGTC	0.73242	0.73173
cg2707039	FAM188B	c-Jun [T00	1394	1400	7.096776	TGACTG	0.73242	0.73173
cg0783131	FAM188B	NF-AT1 [	989	997	7.095752	CACTTT	0.15259	0.1548
cg0783131	FAM188B	Pax-5 [T0	1964	1970	7.082373	GGGCGA	0.12207	0.12014
cg0783131	FAM188B	c-Ets-1 [T	1533	1539	7.071349	AGGGAA	0.73242	0.73099
cg2707039	FAM188B	AR [T000	568	576	7.049779	GGACAC	0.23651	0.23551
cg0783131	FAM188B	HNF-3alp	80	87	7.000129	CAAAAA	0.82397	0.84946
cg0783131	FAM188B	HNF-3alp	258	265	7.000129	GGAAAA	0.82397	0.84946
cg0783131	FAM188B	HNF-3alp	1008	1015	7.000129	TATTTT	0.82397	0.84946
cg2707039	FAM188B	HNF-3alp	234	241	7.000129	TACAAA	0.82397	0.84946
cg2707039	FAM188B	HNF-3alp	420	427	7.000129	AAAAAA	0.82397	0.84946
cg2707039	FAM188B	GCF [T00	1807	1815	6.987525	GCGCCG	0.45776	0.44706
cg2707039	FAM188B	GCF [T00	1919	1927	6.987525	CATCCG	0.45776	0.44706
cg0783131	FAM188B	AR [T000	1950	1958	6.974607	AATCTG	0.23651	0.23551
cg0783131	FAM188B	NF-1 [T00	359	366	6.948522	TTGGTG	0.48828	0.4856
cg0783131	FAM188B	NF-1 [T00	1221	1228	6.948522	TTGGGT	0.48828	0.4856
cg2707039	FAM188B	c-Ets-1 [T	838	844	6.943262	GGGGAA	0.73242	0.73099
cg2707039	FAM188B	c-Ets-1 [T	1826	1832	6.943262	GGGGAA	0.73242	0.73099
cg0783131	FAM188B	ENKTF-1	155	162	6.942764	TGGCTA	1.46484	1.44228
cg0783131	FAM188B	ENKTF-1	928	935	6.942764	CCAGGC	1.46484	1.44228
cg0783131	FAM188B	ENKTF-1	1906	1913	6.942764	CGGGGC	1.46484	1.44228
cg2707039	FAM188B	ENKTF-1	334	341	6.942764	TGGCAG	1.46484	1.44228
cg2707039	FAM188B	ENKTF-1	798	805	6.942764	TGGCAA	1.46484	1.44228
cg2707039	FAM188B	p53 [T006	894	900	6.938545	GGGCCT	1.09863	1.07125
cg2707039	FAM188B	p53 [T006	1341	1347	6.938545	GAGGCC	1.09863	1.07125
cg2707039	FAM188B	p53 [T006	1563	1569	6.938545	GCGGCC	1.09863	1.07125
cg2707039	FAM188B	p53 [T006	1575	1581	6.938545	GGGCCT	1.09863	1.07125
cg2707039	FAM188B	p53 [T006	1961	1967	6.938545	GGGCCG	1.09863	1.07125
cg2707039	FAM188B	AhR:Arnt	1567	1576	6.928166	CCCGGC	0.0515	0.04974
cg0783131	FAM188B	NF-AT1 [	609	618	6.890694	ATCCTT	0.01907	0.01922
cg0783131	FAM188B	c-Jun [T00	822	828	6.856451	TTGGTC	0.73242	0.73173
cg2707039	FAM188B	c-Jun [T00	1642	1648	6.856451	TTGGTC	0.73242	0.73173
cg2707039	FAM188B	HOXD9 [	536	545	6.852796	AATACA	0.07629	0.0789
cg2707039	FAM188B	HOXD10 [	536	545	6.852796	AATACA	0.07629	0.0789
cg0783131	FAM188B	PEA3 [T0	793	801	6.824411	TCTCAT	0.22888	0.22933
cg0783131	FAM188B	COUP-TF	1548	1560	6.820034	GGGAAG	0.00894	0.00886
cg2707039	FAM188B	c-Ets-1 [T	1043	1049	6.815175	CGGGAA	0.73242	0.73099
cg2707039	FAM188B	c-Ets-1 [T	1814	1820	6.815175	TTTCCC	0.73242	0.73099
cg2707039	FAM188B	C/EBPalp	533	539	6.786177	TCCAAT	0.73242	0.74337

cg2707039	FAM188B	C/EBPalph	776	782	6.786177	TACAAT	0.73242	0.74337
cg0783131	FAM188B	NFI/CTF [	310	317	6.786076	CCAAAC	0.73242	0.73214
cg0783131	FAM188B	NFI/CTF [	907	914	6.786076	TTGCTTC	0.73242	0.73214
cg2707039	FAM188B	NFI/CTF [	763	770	6.786076	CCAAGC	0.73242	0.73214
cg2707039	FAM188B	NFI/CTF [	1887	1894	6.786076	CGGTTT	0.73242	0.73214
cg2707039	FAM188B	NFI/CTF [	1969	1976	6.786076	CCAAGC	0.73242	0.73214
cg0783131	FAM188B	RXR-alpha	1024	1030	6.785809	GGGTAA	0.36621	0.36214
cg2707039	FAM188B	p53 [T006	691	697	6.775228	GTAGCC	1.09863	1.07125
cg0783131	FAM188B	AR [T000	1776	1784	6.760234	GGACAC	0.23651	0.23551
cg2707039	FAM188B	AR [T000	1608	1616	6.723093	GGACAG	0.19836	0.19597
cg2707039	FAM188B	T3R-beta1	205	213	6.702681	ACATGG	0.21362	0.21147
cg2707039	FAM188B	E2F [T002	1136	1145	6.649462	GCCCGC	0.02289	0.02238
cg0783131	FAM188B	IRF-1 [T0	1336	1344	6.622811	CTTGGG	0.19073	0.19127
cg2707039	FAM188B	IRF-1 [T0	1838	1846	6.622811	TTTCCC	0.19073	0.19127
cg2707039	FAM188B	E2F-1 [T0	1292	1299	6.611004	GCGGTA	0.12207	0.12031
cg0783131	FAM188B	TFII-I [T0	460	465	6.581441	ATCTCC	0.97656	0.97366
cg0783131	FAM188B	TFII-I [T0	517	522	6.581441	CACTCC	0.97656	0.97366
cg0783131	FAM188B	TFII-I [T0	884	889	6.581441	GGAGAT	0.97656	0.97366
cg0783131	FAM188B	FOXP3 [T	282	287	6.581441	GTTTTA	0.97656	0.99397
cg0783131	FAM188B	FOXP3 [T	1304	1309	6.581441	TAAAAC	0.97656	0.99397
cg2707039	FAM188B	TFII-I [T0	1074	1079	6.581441	ATCTCC	0.97656	0.97366
cg2707039	FAM188B	TFII-I [T0	1408	1413	6.581441	CACTCC	0.97656	0.97366
cg2707039	FAM188B	FOXP3 [T	19	24	6.581441	TAAAAC	0.97656	0.99397
cg2707039	FAM188B	FOXP3 [T	433	438	6.581441	GTTGAA	0.97656	0.99397
cg2707039	FAM188B	FOXP3 [T	936	941	6.581441	GTTTTA	0.97656	0.99397
cg0783131	FAM188B	p53 [T006	678	684	6.563521	GGGCTG	0.48828	0.47541
cg0783131	FAM188B	p53 [T006	688	694	6.563521	GAAGCC	0.48828	0.47541
cg0783131	FAM188B	p53 [T006	1373	1379	6.563521	GGGCTG	0.48828	0.47541
cg2707039	FAM188B	p53 [T006	758	764	6.563521	GCAGCC	0.48828	0.47541
cg2707039	FAM188B	p53 [T006	1111	1117	6.563521	GGGCTT	0.48828	0.47541
cg2707039	FAM188B	PPAR-alph	1465	1475	6.51544	CAGCCC	0.03719	0.03639
cg0783131	FAM188B	XBP-1 [T	556	561	6.478682	ATGCCA	0.97656	0.97062
cg0783131	FAM188B	XBP-1 [T	1515	1520	6.478682	ATGCCA	0.97656	0.97062
cg0783131	FAM188B	XBP-1 [T	1589	1594	6.478682	ATGCCC	0.97656	0.97062
cg2707039	FAM188B	XBP-1 [T	1794	1799	6.478682	ATGCCC	0.97656	0.97062
cg2707039	FAM188B	XBP-1 [T	1916	1921	6.478682	GGGCAT	0.97656	0.97062
cg0783131	FAM188B	c-Jun [T00	378	384	6.475265	TGACAC	0.61035	0.60769
cg2707039	FAM188B	RAR-beta	210	219	6.415195	GTGAAA	0.18311	0.183
cg2707039	FAM188B	p53 [T006	1986	1992	6.403751	GGGCGC	0.48828	0.47541
cg0783131	FAM188B	MAZ [T00	1925	1937	6.387406	CTCCCTC	0.00316	0.00309
cg2707039	FAM188B	MAZ [T00	1444	1456	6.387406	TTCCCTC	0.00316	0.00309
cg2707039	FAM188B	TCF-4E [T	799	805	6.302385	GGCAAA	0.61035	0.61344
cg0783131	FAM188B	c-Ets-1 [T	613	619	6.295602	TTTCCAT	0.48828	0.48798
cg0783131	FAM188B	c-Jun [T00	52	58	6.293948	AGGGTC	0.61035	0.60769
cg2707039	FAM188B	c-Jun [T00	1330	1336	6.293948	AGGGTC	0.61035	0.60769
cg0783131	FAM188B	GR-alpha [	161	165	6.263098	TGAGG	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	242	246	6.263098	CCTTA	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	399	403	6.263098	TAAGG	3.90625	3.91061

cg0783131	FAM188B	GR-alpha [	651	655	6.263098	CCTCA	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	708	712	6.263098	CCTTA	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	736	740	6.263098	CCTCA	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	1248	1252	6.263098	CCTCA	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	1460	1464	6.263098	CCTCA	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	1545	1549	6.263098	TGAGG	3.90625	3.91061
cg0783131	FAM188B	GR-alpha [	1957	1961	6.263098	CCTCA	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	73	77	6.263098	TAAGG	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	175	179	6.263098	TGAGG	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	291	295	6.263098	TGAGG	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	650	654	6.263098	CCTCA	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	696	700	6.263098	CCTCA	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	897	901	6.263098	CCTCA	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	981	985	6.263098	TAAGG	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	1184	1188	6.263098	TGAGG	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	1196	1200	6.263098	TGAGG	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	1340	1344	6.263098	TGAGG	3.90625	3.91061
cg2707039	FAM188B	GR-alpha [	1656	1660	6.263098	CCTCA	3.90625	3.91061
cg0783131	FAM188B	c-Myb [T0	916	923	6.259888	GAACTG	0.30518	0.3056
cg2707039	FAM188B	NF-AT2 [	840	849	6.245826	GGAAAA	0.04196	0.04255
cg0783131	FAM188B	c-Fos [T00	1351	1360	6.236188	TCCTTG	0.09155	0.09126
cg0783131	FAM188B	PEA3 [T0	614	622	6.227095	TTCCAT	0.03815	0.03849
cg0783131	FAM188B	HNF-1B [	90	98	6.211503	TGTTAT	0.09918	0.10196
cg2707039	FAM188B	IRF-1 [T0	1814	1822	6.203774	TTTCCC	0.16785	0.16909
cg2707039	FAM188B	NF-AT1 [	503	512	6.201624	TGGAAA	0.03815	0.03846
cg2707039	FAM188B	p53 [T006	1932	1938	6.188498	GGGCGG	0.61035	0.594
cg0783131	FAM188B	SRY [T00	1987	1995	6.176442	CTTTGT	0.15259	0.15366
cg0783131	FAM188B	c-Ets-1 [T	486	492	6.167515	GTGGAA	0.36621	0.36731
cg2707039	FAM188B	c-Ets-1 [T	502	508	6.167515	GTGGAA	0.36621	0.36731
cg2707039	FAM188B	c-Myb [T0	869	876	6.157321	CAACTT	0.21362	0.21535
cg0783131	FAM188B	c-Jun [T00	550	556	6.152811	TTTGTC	0.36621	0.37082
cg0783131	FAM188B	c-Jun [T00	1988	1994	6.152811	TTTGTC	0.36621	0.37082
cg0783131	FAM188B	PPAR-alph	173	183	6.14093	TGGACC	0.02003	0.01956
cg0783131	FAM188B	HNF-1C [	91	99	6.127396	GTTATT	0.14496	0.14811
cg0783131	FAM188B	p53 [T006	589	595	6.095267	GGGCCA	0.61035	0.594
cg2707039	FAM188B	p53 [T006	949	955	6.095267	GGGCCA	0.61035	0.594
cg0783131	FAM188B	GR-alpha [	320	324	6.055408	CCTAA	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	376	380	6.055408	CCTGA	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	508	512	6.055408	TCAGG	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	524	528	6.055408	TCAGG	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	693	697	6.055408	CCTAA	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	826	830	6.055408	TCAGG	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	1128	1132	6.055408	CCTGA	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	1209	1213	6.055408	CCTAA	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	1295	1299	6.055408	TCAGG	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	1665	1669	6.055408	CCTGA	3.90625	3.9065
cg0783131	FAM188B	GR-alpha [	1833	1837	6.055408	TTAGG	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	173	177	6.055408	CCTGA	3.90625	3.9065

cg2707039	FAM188B	GR-alpha [	180	184	6.055408	TCAGG	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	265	269	6.055408	CCTGA	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	282	286	6.055408	TCAGG	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	377	381	6.055408	CCTGA	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	441	445	6.055408	CCTAA	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	517	521	6.055408	TTAGG	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	565	569	6.055408	TTAGG	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	652	656	6.055408	TCAGG	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	1194	1198	6.055408	CCTGA	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	1392	1396	6.055408	CCTGA	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	1646	1650	6.055408	TCAGG	3.90625	3.9065
cg2707039	FAM188B	GR-alpha [	1734	1738	6.055408	CCTGA	3.90625	3.9065
cg0783131	FAM188B	c-Ets-1 [T	1892	1898	6.039428	TTTCCA	0.36621	0.36731
cg0783131	FAM188B	C/EBPalph	1824	1830	5.996794	AACAAT	0.97656	0.99
cg0783131	FAM188B	RXR-alpha	753	759	5.937582	GGCACC	0.73242	0.72249
cg2707039	FAM188B	RXR-alpha	879	885	5.937582	AGTACC	0.73242	0.72249
cg2707039	FAM188B	GCF [T00	1490	1498	5.917256	TTGCCG	0.64087	0.6219
cg2707039	FAM188B	GCF [T00	1495	1503	5.917256	GCGCCG	0.64087	0.6219
cg0783131	FAM188B	AR [T000	731	739	5.8965	GGACAC	0.24414	0.24229
cg0783131	FAM188B	STAT4 [T	33	38	5.882353	GGAAGG	0.48828	0.48408
cg0783131	FAM188B	STAT4 [T	542	547	5.882353	CCTTCC	0.48828	0.48408
cg0783131	FAM188B	STAT4 [T	1417	1422	5.882353	CCTTCC	0.48828	0.48408
cg0783131	FAM188B	STAT4 [T	1549	1554	5.882353	GGAAGG	0.48828	0.48408
cg0783131	FAM188B	STAT4 [T	1689	1694	5.882353	GGAAGG	0.48828	0.48408
cg2707039	FAM188B	STAT4 [T	1442	1447	5.882353	CCTTCC	0.48828	0.48408
cg2707039	FAM188B	STAT4 [T	1474	1479	5.882353	GGAAGG	0.48828	0.48408
cg2707039	FAM188B	E2F-1 [T0	1489	1496	5.846171	CTTGCC	0.18311	0.18044
cg2707039	FAM188B	USF1 [T0	595	604	5.845905	CACGTG	0.01526	0.01523
cg2707039	FAM188B	c-Ets-1 [T	1251	1257	5.814485	CTTCCC	0.36621	0.36731
cg0783131	FAM188B	STAT1bet	1891	1900	5.796867	TTTTCCA	0.1545	0.1557
cg2707039	FAM188B	STAT1bet	836	845	5.796867	TCGGGG	0.1545	0.1557
cg2707039	FAM188B	STAT1bet	872	881	5.796867	CTTTCC	0.1545	0.1557
cg2707039	FAM188B	STAT1bet	1265	1274	5.796867	TCTAGG	0.1545	0.1557
cg0783131	FAM188B	c-Jun [T00	566	572	5.783074	TGACTT	0.36621	0.37082
cg2707039	FAM188B	C/EBPalph	710	716	5.781231	GACAAT	0.97656	0.99
cg2707039	FAM188B	HNF-1A [	71	78	5.754274	GTTAAG	0.24414	0.24409
cg0783131	FAM188B	AR [T000	1976	1984	5.754178	TCTTTGT	0.24414	0.24229
cg2707039	FAM188B	PPAR-alph	1794	1804	5.741676	ATGCCC	0.03529	0.03451
cg2707039	FAM188B	PPAR-alph	1911	1921	5.741676	TCCTGG	0.03529	0.03451
cg2707039	FAM188B	c-Jun [T00	1200	1206	5.703976	GGGGTC	0.48828	0.48665
cg0783131	FAM188B	ENKTF-1	587	594	5.687009	CAGGGC	0.73242	0.7249
cg0783131	FAM188B	ENKTF-1	777	784	5.687009	TGGCCC	0.73242	0.7249
cg0783131	FAM188B	ENKTF-1	1727	1734	5.687009	TGGCTC	0.73242	0.7249
cg0783131	FAM188B	ENKTF-1	1829	1836	5.687009	TGGCTT	0.73242	0.7249
cg2707039	FAM188B	ENKTF-1	350	357	5.687009	TTGCGC	0.73242	0.7249
cg2707039	FAM188B	ENKTF-1	1323	1330	5.687009	CAGGGC	0.73242	0.7249
cg2707039	FAM188B	ENKTF-1	1587	1594	5.687009	CAGAGC	0.73242	0.7249
cg2707039	FAM188B	ENKTF-1	1593	1600	5.687009	CAGAGC	0.73242	0.7249

cg2707039	FAM188B	ENKTF-1	1599	1606	5.687009	CAGAGC	0.73242	0.7249
cg0783131	FAM188B	c-Ets-1 [T	31	37	5.686398	AGGGAA	0.36621	0.3623
cg0783131	FAM188B	c-Ets-1 [T	372	378	5.686398	CTTCCCT	0.36621	0.3623
cg0783131	FAM188B	c-Ets-1 [T	543	549	5.686398	CTTCCCT	0.36621	0.3623
cg0783131	FAM188B	c-Ets-1 [T	1192	1198	5.686398	AGGGAA	0.36621	0.3623
cg0783131	FAM188B	c-Ets-1 [T	1547	1553	5.686398	AGGGAA	0.36621	0.3623
cg2707039	FAM188B	c-Ets-1 [T	1207	1213	5.686398	CTTCCCT	0.36621	0.3623
cg2707039	FAM188B	c-Ets-1 [T	1443	1449	5.686398	CTTCCCT	0.36621	0.3623
cg2707039	FAM188B	c-Ets-1 [T	1472	1478	5.686398	AGGGAA	0.36621	0.3623
cg0783131	FAM188B	NF-1 [T00	172	179	5.626299	TTGGAC	0.24414	0.24258
cg2707039	FAM188B	NF-1 [T00	1891	1898	5.626299	TTGGAC	0.24414	0.24258
cg0783131	FAM188B	T3R-beta1	112	120	5.591999	TCACCTT	0.21362	0.21287
cg0783131	FAM188B	T3R-beta1	909	917	5.591999	GCTTGG	0.21362	0.21287
cg0783131	FAM188B	T3R-beta1	1087	1095	5.591999	TCACCTT	0.21362	0.21287
cg2707039	FAM188B	T3R-beta1	1012	1020	5.591999	GCTTGG	0.21362	0.21287
cg0783131	FAM188B	IRF-1 [T0	613	621	5.564062	TTTCCAT	0.22888	0.23087
cg0783131	FAM188B	NFI/CTF [	416	423	5.558661	AGGATT	0.54932	0.55038
cg0783131	FAM188B	NFI/CTF [	818	825	5.558661	GGGCTT	0.54932	0.55038
cg2707039	FAM188B	NFI/CTF [	852	859	5.558661	GGGCTT	0.54932	0.55038
cg2707039	FAM188B	NFI/CTF [	1010	1017	5.558661	GAGCTT	0.54932	0.55038
cg0783131	FAM188B	GATA-2 [	1433	1441	5.555555	GCTGTA	0.18311	0.1835
cg0783131	FAM188B	AP-1 [T00	1289	1297	5.54906	TGAGAG	0.09155	0.09214
cg0783131	FAM188B	Pax-5 [T0	1908	1914	5.544826	GGGCCA	0.73242	0.72046
cg0783131	FAM188B	TFIID [T0	118	124	5.544826	TTCTAA	0.73242	0.75085
cg0783131	FAM188B	TFIID [T0	1623	1629	5.544826	TGGTAA	0.73242	0.75085
cg2707039	FAM188B	Pax-5 [T0	1869	1875	5.544826	GGGCGC	0.73242	0.72046
cg2707039	FAM188B	TFIID [T0	225	231	5.544826	TACTAA	0.73242	0.75085
cg0783131	FAM188B	p53 [T006	1412	1418	5.508538	TCAGCC	0.61035	0.59991
cg2707039	FAM188B	p53 [T006	76	82	5.508538	GGGCTG	0.61035	0.59991
cg2707039	FAM188B	HNF-1A [	1005	1012	5.466509	GTTAAG	0.24414	0.2469
cg2707039	FAM188B	IRF-1 [T0	1824	1832	5.42531	CAGGGG	0.22888	0.23087
cg2707039	FAM188B	E2F [T002	1964	1973	5.395922	CCGCGC	0.01526	0.0149
cg0783131	FAM188B	p53 [T006	1879	1885	5.39549	GGGCCC	0.61035	0.59991
cg0783131	FAM188B	C/EBPalph	1491	1497	5.38654	ACCAAT	0.73242	0.74391
cg2707039	FAM188B	NF-1 [T00	759	766	5.377909	CAGCCA	0.24414	0.24258
cg2707039	FAM188B	RAR-beta	815	824	5.333686	GTGGAA	0.15259	0.15189
cg0783131	FAM188B	MEF-2A [	1270	1280	5.321562	AGATTA	0.02003	0.02072
cg2707039	FAM188B	EBF [T05	1467	1477	5.295103	GCCCCA	0.01907	0.0183
cg0783131	FAM188B	RXR-alpha	717	723	5.271235	CCCACC	0.61035	0.6044
cg0783131	FAM188B	RXR-alpha	814	820	5.271235	GGGTGG	0.61035	0.6044
cg0783131	FAM188B	RXR-alpha	1037	1043	5.271235	TCTACC	0.61035	0.6044
cg0783131	FAM188B	RXR-alpha	1041	1047	5.271235	CCCACC	0.61035	0.6044
cg2707039	FAM188B	ELF-1 [T0	968	980	5.256555	AGCCAG	0.00453	0.00454
cg0783131	FAM188B	c-Jun [T00	1101	1107	5.193102	TGACTT	0.61035	0.61057
cg0783131	FAM188B	c-Ets-2 [T	1670	1678	5.162974	CTCAAG	0.13733	0.13828
cg2707039	FAM188B	c-Ets-2 [T	1115	1123	5.162974	TTCCTTC	0.13733	0.13828
cg0783131	FAM188B	c-Myb [T0	1152	1159	5.137438	GAACTG	0.30518	0.30568
cg2707039	FAM188B	c-Myb [T0	701	708	5.137438	GAACTG	0.30518	0.30568

cg2707039	FAM188B	p53 [T006	163	169	5.133514	GGGCGG	0.48828	0.47747
cg0783131	FAM188B	HNF-1A [	1795	1802	5.116518	GTTAAG	0.36621	0.37179
cg0783131	FAM188B	TCF-4 [T0	294	303	5.111789	GCTTTG	0.03433	0.03427
cg0783131	FAM188B	AP-2alpha	66	71	5.100982	AAAGGC	0.97656	0.97567
cg0783131	FAM188B	AP-2alpha	1406	1411	5.100982	GCCTTT	0.97656	0.97567
cg2707039	FAM188B	AP-2alpha	913	918	5.100982	GCCTTT	0.97656	0.97567
cg0783131	FAM188B	NF-Y [T0	1522	1529	5.094053	ATTGGA	0.36621	0.36847
cg0783131	FAM188B	RXR-alph	1811	1817	5.089356	ATCACC	0.48828	0.484
cg2707039	FAM188B	SRY [T00	749	757	5.086565	CTTTGT	0.06104	0.06209
cg0783131	FAM188B	AP-1 [T00	1355	1363	5.043062	TGACTC	0.12207	0.12162
cg0783131	FAM188B	GR-beta [	262	266	5.042296	AATAC	3.90625	3.95351
cg0783131	FAM188B	GR-beta [	417	421	5.042296	GGATT	3.90625	3.95351
cg0783131	FAM188B	GR-beta [	608	612	5.042296	AATCC	3.90625	3.95351
cg0783131	FAM188B	GR-beta [	1381	1385	5.042296	GGATT	3.90625	3.95351
cg0783131	FAM188B	GR-beta [	1400	1404	5.042296	GGATT	3.90625	3.95351
cg0783131	FAM188B	GR-beta [	1488	1492	5.042296	AATAC	3.90625	3.95351
cg0783131	FAM188B	GR-beta [	1658	1662	5.042296	AATCC	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	33	37	5.042296	GGATT	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	48	52	5.042296	AATAC	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	136	140	5.042296	AATCC	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	270	274	5.042296	AATCC	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	311	315	5.042296	AATCC	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	452	456	5.042296	GTATT	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	536	540	5.042296	AATAC	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	774	778	5.042296	AATAC	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	984	988	5.042296	GGATT	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	1246	1250	5.042296	GTATT	3.90625	3.95351
cg2707039	FAM188B	GR-beta [	1975	1979	5.042296	AATCC	3.90625	3.95351
cg0783131	FAM188B	E2F-1 [T0	1928	1935	5.042045	CCTCCC	0.18311	0.17901
cg2707039	FAM188B	E2F-1 [T0	1447	1454	5.042045	CCTCCC	0.18311	0.17901
cg0783131	FAM188B	c-Ets-1 [T	1523	1529	5.038739	TTGGAA	0.48828	0.49031
cg0783131	FAM188B	NFI/CTF [	1189	1196	5.021086	CCAAGG	0.24414	0.24103
cg2707039	FAM188B	NFI/CTF [	1057	1064	5.021086	CCAAGG	0.24414	0.24103
cg2707039	FAM188B	c-Jun [T00	671	677	5.000337	TGACAC	0.61035	0.61057
cg2707039	FAM188B	AR [T000	1539	1547	4.995624	GGACAG	0.11444	0.11247
cg0783131	FAM188B	IRF-1 [T0	993	1001	4.963725	TTTCCTT	0.1297	0.1302
cg0783131	FAM188B	AR [T000	584	592	4.947929	GGACAG	0.11444	0.11247
cg2707039	FAM188B	IRF-1 [T0	1041	1049	4.932737	TACGGG	0.1297	0.1302
cg0783131	FAM188B	EBF [T05	1017	1027	4.906683	CTCCCT	0.02289	0.02224
cg0783131	FAM188B	XBP-1 [T0	68	73	4.894955	AGGCAT	0.97656	0.96979
cg0783131	FAM188B	XBP-1 [T0	239	244	4.894955	ATGCCT	0.97656	0.96979
cg2707039	FAM188B	XBP-1 [T0	445	450	4.894955	ATGCCT	0.97656	0.96979
cg0783131	FAM188B	AP-2alpha	319	324	4.890408	GCCTAA	0.97656	0.97567
cg0783131	FAM188B	c-Jun [T00	298	304	4.883696	TGACAT	0.61035	0.61057
cg2707039	FAM188B	IRF-1 [T0	500	508	4.881305	AAGTGG	0.1297	0.1302
cg0783131	FAM188B	RXR-alph	922	928	4.86724	CATACC	0.48828	0.484
cg0783131	FAM188B	RXR-alph	1506	1512	4.86724	GGGTCT	0.48828	0.484
cg2707039	FAM188B	RXR-alph	1726	1732	4.86724	GGGTCT	0.48828	0.484

cg2707039	FAM188B	NF-Y [T0	531	538	4.867193	ATTCCAA	0.36621	0.36847
cg2707039	FAM188B	GCF [T00	1961	1969	4.846987	GGGCCG	0.27466	0.26486
cg0783131	FAM188B	TFII-I [T0	236	241	4.756447	GGAATG	2.92969	2.93695
cg0783131	FAM188B	TFII-I [T0	417	422	4.756447	GGATTG	2.92969	2.93695
cg0783131	FAM188B	TFII-I [T0	477	482	4.756447	CAGTCC	2.92969	2.93695
cg0783131	FAM188B	TFII-I [T0	607	612	4.756447	CAATCC	2.92969	2.93695
cg0783131	FAM188B	TFII-I [T0	1205	1210	4.756447	CAGTCC	2.92969	2.93695
cg0783131	FAM188B	TFII-I [T0	1254	1259	4.756447	ATATCC	2.92969	2.93695
cg0783131	FAM188B	TFII-I [T0	1535	1540	4.756447	GGAAAT	2.92969	2.93695
cg0783131	FAM188B	TFII-I [T0	1646	1651	4.756447	GGAATG	2.92969	2.93695
cg0783131	FAM188B	FOXP3 [T	165	170	4.756447	GTCAAC	2.92969	2.96063
cg0783131	FAM188B	FOXP3 [T	336	341	4.756447	GTTTTG	2.92969	2.96063
cg0783131	FAM188B	FOXP3 [T	1059	1064	4.756447	GTTGAG	2.92969	2.96063
cg0783131	FAM188B	FOXP3 [T	1570	1575	4.756447	GTTTTG	2.92969	2.96063
cg0783131	FAM188B	FOXP3 [T	1575	1580	4.756447	GTTTTG	2.92969	2.96063
cg0783131	FAM188B	FOXP3 [T	1600	1605	4.756447	GAAAAC	2.92969	2.96063
cg2707039	FAM188B	TFII-I [T0	167	172	4.756447	GGACTG	2.92969	2.93695
cg2707039	FAM188B	TFII-I [T0	361	366	4.756447	CATTCC	2.92969	2.93695
cg2707039	FAM188B	TFII-I [T0	504	509	4.756447	GGAAAT	2.92969	2.93695
cg2707039	FAM188B	TFII-I [T0	1837	1842	4.756447	ATTTCC	2.92969	2.93695
cg2707039	FAM188B	TFII-I [T0	1974	1979	4.756447	CAATCC	2.92969	2.93695
cg2707039	FAM188B	FOXP3 [T	94	99	4.756447	CAAAAC	2.92969	2.96063
cg0783131	FAM188B	c-Ets-1 [T	1784	1790	4.74411	ACGGAA	0.85449	0.85764
cg0783131	FAM188B	c-Ets-1 [T	1418	1424	4.654478	CTTCCAC	0.85449	0.85764
cg0783131	FAM188B	c-Ets-1 [T	1466	1472	4.654478	CTTCCAC	0.85449	0.85764
cg0783131	FAM188B	VDR [T00	911	919	4.617121	TTGGTGA	0.37384	0.37445
cg0783131	FAM188B	VDR [T00	1147	1155	4.617121	GGTGTGA	0.37384	0.37445
cg2707039	FAM188B	HNF-1B [	54	62	4.569001	TAAGTAA	0.05341	0.0549
cg2707039	FAM188B	IRF-1 [T0	873	881	4.549799	TTTCCCA	0.05341	0.05405
cg2707039	FAM188B	E2F-1 [T0	382	389	4.545253	GCGGGA	0.15259	0.14941
cg2707039	FAM188B	E2F-1 [T0	1427	1434	4.545253	GCGGGA	0.15259	0.14941
cg2707039	FAM188B	USF2 [T0	371	380	4.528187	CGGGCA	0.06866	0.06782
cg0783131	FAM188B	MAZ [T00	1921	1933	4.524062	CTCCCTC	0.00188	0.00184
cg0783131	FAM188B	T3R-beta1	33	41	4.481316	GGAAGG	0.27466	0.27551
cg0783131	FAM188B	T3R-beta1	1439	1447	4.462023	TCTAGGT	0.27466	0.27551
cg2707039	FAM188B	AP-2alpha	1305	1310	4.438035	CTAGGC	0.97656	0.96979
cg2707039	FAM188B	AP-2alpha	1373	1378	4.438035	CTAGGC	0.97656	0.96979
cg0783131	FAM188B	RXR-alpha	859	865	4.423008	GGGTGG	0.24414	0.24292
cg2707039	FAM188B	RXR-alpha	520	526	4.423008	GGGTGG	0.24414	0.24292
cg2707039	FAM188B	RXR-alpha	1187	1193	4.423008	GGGTGG	0.24414	0.24292
cg2707039	FAM188B	RXR-alpha	1436	1442	4.423008	TCCACCC	0.24414	0.24292
cg0783131	FAM188B	AP-2alpha	241	246	4.422424	GCCTTA	0.97656	0.96979
cg0783131	FAM188B	AP-2alpha	707	712	4.422424	GCCTTA	0.97656	0.96979
cg0783131	FAM188B	STAT4 [T	236	241	4.411765	GGAATG	1.95312	1.94235
cg0783131	FAM188B	STAT4 [T	687	692	4.411765	GGAAGC	1.95312	1.94235
cg0783131	FAM188B	STAT4 [T	1194	1199	4.411765	GGAAGA	1.95312	1.94235
cg0783131	FAM188B	STAT4 [T	1465	1470	4.411765	GCTTCC	1.95312	1.94235
cg0783131	FAM188B	STAT4 [T	1525	1530	4.411765	GGAAGA	1.95312	1.94235

cg0783131	FAM188B	STAT4 [T	1639	1644	4.411765	CGTTCC	1.95312	1.94235
cg0783131	FAM188B	STAT4 [T	1646	1651	4.411765	GGAATG	1.95312	1.94235
cg2707039	FAM188B	STAT4 [T	361	366	4.411765	CATTCC	1.95312	1.94235
cg2707039	FAM188B	STAT4 [T	1113	1118	4.411765	GCTTCC	1.95312	1.94235
cg2707039	FAM188B	STAT4 [T	1250	1255	4.411765	TCTTCC	1.95312	1.94235
cg2707039	FAM188B	STAT4 [T	1766	1771	4.411765	CGTTCC	1.95312	1.94235
cg2707039	FAM188B	STAT4 [T	1873	1878	4.411765	GCTTCC	1.95312	1.94235
cg2707039	FAM188B	c-Ets-1 [T	770	776	4.411026	AAGGAA	0.85449	0.85764
cg2707039	FAM188B	Sp1 [T007	162	171	4.357831	TGGGCG	0.08583	0.08339
cg0783131	FAM188B	p53 [T006	747	753	4.33696	GGGCCA	0.24414	0.23584
cg0783131	FAM188B	p53 [T006	776	782	4.33696	CTGGCC	0.24414	0.23584
cg2707039	FAM188B	p53 [T006	1325	1331	4.33696	GGGCCA	0.24414	0.23584
cg0783131	FAM188B	PEA3 [T0	562	570	4.30818	AGGATG	0.13733	0.13791
cg0783131	FAM188B	RAR-beta	129	138	4.289108	AATGAA	0.14496	0.1447
cg0783131	FAM188B	RXR-alph	53	59	4.24113	GGGTCA	0.97656	0.9671
cg2707039	FAM188B	RXR-alph	1201	1207	4.24113	GGGTCA	0.97656	0.9671
cg0783131	FAM188B	AR [T000	1345	1353	4.241082	GCTCTG	0.06866	0.06828
cg2707039	FAM188B	C/EBPalp	1020	1026	4.235345	ATCAAT	0.48828	0.49358
cg0783131	FAM188B	HNF-1B [	303	311	4.230295	TATTTA	0.01526	0.0157
cg0783131	FAM188B	AP-2alpha	1319	1324	4.211849	GCCTAC	0.97656	0.96469
cg0783131	FAM188B	GR-beta [T	20	24	4.201913	AATCA	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	84	88	4.201913	AATAA	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	92	96	4.201913	TTATT	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	696	700	4.201913	AATCA	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	1202	1206	4.201913	AATCA	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	1277	1281	4.201913	AATAA	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	1311	1315	4.201913	CTATT	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	1530	1534	4.201913	AATAG	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	1538	1542	4.201913	AATAA	7.8125	7.94607
cg0783131	FAM188B	GR-beta [T	1709	1713	4.201913	TGATT	7.8125	7.94607
cg2707039	FAM188B	GR-beta [T	10	14	4.201913	AATAA	7.8125	7.94607
cg2707039	FAM188B	GR-beta [T	45	49	4.201913	AATAA	7.8125	7.94607
cg2707039	FAM188B	GR-beta [T	529	533	4.201913	CTATT	7.8125	7.94607
cg2707039	FAM188B	GR-beta [T	629	633	4.201913	AATAG	7.8125	7.94607
cg2707039	FAM188B	GR-beta [T	713	717	4.201913	AATAA	7.8125	7.94607
cg2707039	FAM188B	GR-beta [T	779	783	4.201913	AATAG	7.8125	7.94607
cg2707039	FAM188B	GR-beta [T	1023	1027	4.201913	AATAA	7.8125	7.94607
cg2707039	FAM188B	NF-1 [T00	1965	1972	4.135372	CGCGCC	0.24414	0.24154
cg2707039	FAM188B	p53 [T006	109	115	4.125254	GGGCCG	0.73242	0.71379
cg2707039	FAM188B	p53 [T006	1953	1959	4.125254	GGGCCT	0.73242	0.71379
cg0783131	FAM188B	SRY [T00	19	27	4.087393	AAATCA	0.12207	0.12407
cg0783131	FAM188B	SRY [T00	1561	1569	4.087393	CTTTGT	0.12207	0.12407
cg0783131	FAM188B	p53 [T006	422	428	4.083527	GGTGCC	0.73242	0.71379
cg2707039	FAM188B	p53 [T006	372	378	4.083527	GGGCAC	0.73242	0.71379
cg2707039	FAM188B	p53 [T006	1089	1095	4.083527	GGTGCC	0.73242	0.71379
cg0783131	FAM188B	C/EBPalp	605	611	4.019783	GGCAAT	0.48828	0.49358
cg0783131	FAM188B	RXR-alph	1223	1229	4.019014	GGGTCT	0.97656	0.9671
cg2707039	FAM188B	RXR-alph	212	218	4.019014	GAAACC	0.97656	0.9671

cg2707039	FAM188B	RXR-alpha	480	486	4.019014	GGGTCTT	0.97656	0.9671
cg2707039	FAM188B	RXR-alpha	863	869	4.019014	GAAACC	0.97656	0.9671
cg2707039	FAM188B	c-Ets-2 [T0	767	775	4.017001	GCAAAG	0.16022	0.16243
cg0783131	FAM188B	Pax-5 [T00	24	30	4.007279	AAAGCC	1.09863	1.07975
cg0783131	FAM188B	Pax-5 [T00	623	629	4.007279	GGGCTCT	1.09863	1.07975
cg0783131	FAM188B	Pax-5 [T00	1332	1338	4.007279	GGGCCTT	1.09863	1.07975
cg0783131	FAM188B	TFIID [T0	395	401	4.007279	TTTATAA	1.09863	1.13456
cg2707039	FAM188B	Pax-5 [T00	1133	1139	4.007279	AAGGCC	1.09863	1.07975
cg2707039	FAM188B	Pax-5 [T00	1172	1178	4.007279	GGGCCG	1.09863	1.07975
cg2707039	FAM188B	Pax-5 [T00	1368	1374	4.007279	GGGCCC	1.09863	1.07975
cg2707039	FAM188B	Pax-5 [T00	1688	1694	4.007279	AAAGCC	1.09863	1.07975
cg2707039	FAM188B	TFIID [T0	4	10	4.007279	TTTTAAA	1.09863	1.13456
cg2707039	FAM188B	TFIID [T0	16	22	4.007279	TTGTAAA	1.09863	1.13456
cg2707039	FAM188B	TFIID [T0	551	557	4.007279	TTTATAA	1.09863	1.13456
cg2707039	FAM188B	TFIID [T0	937	943	4.007279	TTTTAAA	1.09863	1.13456
cg0783131	FAM188B	MAZ [T00	662	674	3.973255	ACTGGG	0.00587	0.00576
cg2707039	FAM188B	MAZ [T00	1943	1955	3.973255	GCTGGG	0.00587	0.00576
cg0783131	FAM188B	AP-2alpha	593	598	3.970052	CAAGGC	0.97656	0.96469
cg0783131	FAM188B	AP-2alpha	1334	1339	3.970052	GCCTTG	0.97656	0.96469
cg0783131	FAM188B	AP-2alpha	1760	1765	3.970052	CAAGGC	0.97656	0.96469
cg2707039	FAM188B	AP-2alpha	1132	1137	3.970052	CAAGGC	0.97656	0.96469
cg2707039	FAM188B	AP-2alpha	1880	1885	3.970052	CAAGGC	0.97656	0.96469
cg0783131	FAM188B	p53 [T006	843	849	3.961937	GGGCTA	0.73242	0.71379
cg0783131	FAM188B	p53 [T006	893	899	3.961937	GGGCTA	0.73242	0.71379
cg0783131	FAM188B	PPAR-alph	423	433	3.872523	GTGCCC	0.02575	0.02522
cg0783131	FAM188B	PPAR-alph	579	589	3.872523	CCCTGG	0.02575	0.02522
cg0783131	FAM188B	PPAR-alph	726	736	3.872523	ACCTGG	0.02575	0.02522
cg2707039	FAM188B	c-Myb [T0	1546	1553	3.85204	CCCAGTT	0.09155	0.09154
cg2707039	FAM188B	c-Jun [T00	827	833	3.807346	TGACTA	0.24414	0.24526
cg0783131	FAM188B	GR [T050	335	341	3.763516	TGTTTC	0.73242	0.74251
cg0783131	FAM188B	GR [T050	1559	1565	3.763516	ATCTTC	0.73242	0.74251
cg0783131	FAM188B	GR [T050	1569	1575	3.763516	AGTTTC	0.73242	0.74251
cg0783131	FAM188B	GR [T050	1574	1580	3.763516	TGTTTC	0.73242	0.74251
cg0783131	FAM188B	GR [T050	1975	1981	3.763516	ATCTTC	0.73242	0.74251
cg2707039	FAM188B	GR [T050	94	100	3.763516	CAAAAC	0.73242	0.74251
cg2707039	FAM188B	GR [T050	801	807	3.763516	CAAAGA	0.73242	0.74251
cg0783131	FAM188B	p53 [T006	818	824	3.750231	GGGCTT	0.73242	0.71379
cg2707039	FAM188B	p53 [T006	365	371	3.750231	CCAGCC	0.73242	0.71379
cg2707039	FAM188B	p53 [T006	852	858	3.750231	GGGCTT	0.73242	0.71379
cg2707039	FAM188B	p53 [T006	1456	1462	3.750231	CCAGCC	0.73242	0.71379
cg2707039	FAM188B	p53 [T006	1464	1470	3.750231	CCAGCC	0.73242	0.71379
cg0783131	FAM188B	AP-2alpha	1238	1243	3.743866	GAAGGC	0.48828	0.48238
cg2707039	FAM188B	AP-2alpha	1737	1742	3.743866	GAAGGC	0.48828	0.48238
cg0783131	FAM188B	TBP [T007	395	404	3.743085	TTTATAA	0.03052	0.03162
cg2707039	FAM188B	TBP [T007	551	560	3.743085	TTTATAA	0.03052	0.03162
cg0783131	FAM188B	NF-kappaB	234	244	3.742102	GGGGAA	0.01812	0.01756
cg0783131	FAM188B	c-Ets-1 [T0	1673	1679	3.71855	AAGGAA	0.61035	0.60765
cg0783131	FAM188B	PEA3 [T00	266	274	3.710864	CTTCATC	0.09155	0.09258

cg0783131	FAM188B	IRF-1 [T0	254	262	3.692688	GAAAGG	0.06866	0.06927
cg2707039	FAM188B	POU2F2 (	15	25	3.618429	ATTGTA	0.00572	0.00598
cg2707039	FAM188B	c-Ets-1 [T	1067	1073	3.590463	GAGGAA	0.61035	0.60765
cg2707039	FAM188B	c-Ets-1 [T	1653	1659	3.590463	GTTCCT	0.61035	0.60765
cg2707039	FAM188B	p53 [T006	1063	1069	3.586914	GGGCGA	0.73242	0.7189
cg2707039	FAM188B	p53 [T006	1676	1682	3.586914	CTCGCC	0.73242	0.7189
cg0783131	FAM188B	NF-AT2 [	1535	1544	3.571424	GGAAAT	0.03433	0.03499
cg2707039	FAM188B	HNF-1C [	53	61	3.558358	ATAAGT	0.04578	0.0471
cg0783131	FAM188B	C/EBPalph	418	424	3.555778	GATTGG	0.24414	0.24752
cg0783131	FAM188B	c-Ets-2 [T	994	1002	3.518824	TTCCTTC	0.18311	0.18304
cg2707039	FAM188B	HNF-3alph	41	48	3.500065	AGAAAA	0.27466	0.28532
cg2707039	FAM188B	VDR [T00	327	335	3.462841	GTTCAC	0.21362	0.21341
cg0783131	FAM188B	c-Ets-1 [T	1640	1646	3.462376	GTTCCT	0.61035	0.60765
cg0783131	FAM188B	NF-AT1 [	487	496	3.445347	TGGAAA	0.07629	0.07722
cg0783131	FAM188B	NF-AT1 [	1888	1897	3.445347	GGCTTT	0.07629	0.07722
cg0783131	FAM188B	c-Myb [T0	490	497	3.438142	AAACTG	0.12207	0.12203
cg2707039	FAM188B	NF-AT1 [	840	848	3.407861	GGAAAA	0.03052	0.03089
cg0783131	FAM188B	PXR-1:RX	131	138	3.395883	TGAACC	0.12207	0.12271
cg2707039	FAM188B	RXR-alpha	114	120	3.392904	GGGTGC	1.09863	1.08572
cg2707039	FAM188B	RXR-alpha	817	823	3.392904	GGAACC	1.09863	1.08572
cg0783131	FAM188B	p53 [T006	1931	1937	3.375208	CCCGCC	0.73242	0.7189
cg2707039	FAM188B	p53 [T006	1450	1456	3.375208	CCCGCC	0.73242	0.7189
cg2707039	FAM188B	T3R-beta1	489	497	3.370634	AAGAGG	0.27466	0.2755
cg0783131	FAM188B	GR-beta [	41	45	3.361531	AATAT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	42	46	3.361531	ATATT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	139	143	3.361531	AATCT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	302	306	3.361531	ATATT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	1007	1011	3.361531	ATATT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	1253	1257	3.361531	AATAT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	1270	1274	3.361531	AGATT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	1541	1545	3.361531	AATAT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [	1950	1954	3.361531	AATCT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [	238	242	3.361531	AATAT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [	239	243	3.361531	ATATT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [	347	351	3.361531	AGATT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [	562	566	3.361531	AGATT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [	804	808	3.361531	AGATT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [	906	910	3.361531	AATCT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [	922	926	3.361531	AATCT	3.90625	3.99611
cg2707039	FAM188B	GATA-2 [	475	483	3.333333	GGATAG	0.30518	0.30786
cg2707039	FAM188B	T3R-beta1	821	829	3.332047	CCCAGG	0.27466	0.2755
cg0783131	FAM188B	PR B [T00	901	907	3.29756	AACATT	0.24414	0.25122
cg0783131	FAM188B	PR B [T00	1697	1703	3.29756	AAATGT	0.24414	0.25122
cg0783131	FAM188B	PR A [T01	901	907	3.29756	AACATT	0.24414	0.25122
cg0783131	FAM188B	PR A [T01	1697	1703	3.29756	AAATGT	0.24414	0.25122
cg2707039	FAM188B	c-Ets-2 [T	1064	1072	3.2883	GGCGAG	0.18311	0.18304
cg2707039	FAM188B	c-Ets-2 [T	1654	1662	3.2883	TTCCTCA	0.18311	0.18304
cg0783131	FAM188B	c-Jun [T00	1291	1297	3.244843	AGAGTC	0.24414	0.24403

cg2707039	FAM188B	c-Ets-1 [T	791	797	3.231072	GCGGAA	0.24414	0.23981
cg2707039	FAM188B	c-Ets-1 [T	1874	1880	3.231072	CTTCCGC	0.24414	0.23981
cg0783131	FAM188B	AP-2alpha	106	111	3.229049	GCCTCT	0.48828	0.48238
cg0783131	FAM188B	AP-2alpha	351	356	3.229049	GCCTCT	0.48828	0.48238
cg0783131	FAM188B	AP-2alpha	602	607	3.229049	AGAGGC	0.48828	0.48238
cg0783131	FAM188B	AP-2alpha	700	705	3.229049	AGAGGC	0.48828	0.48238
cg0783131	FAM188B	AP-2alpha	1073	1078	3.229049	GCCTCT	0.48828	0.48238
cg2707039	FAM188B	AP-2alpha	632	637	3.229049	AGAGGC	0.48828	0.48238
cg2707039	FAM188B	AP-2alpha	645	650	3.229049	AGAGGC	0.48828	0.48238
cg2707039	FAM188B	AP-2alpha	1309	1314	3.229049	GCCTCT	0.48828	0.48238
cg2707039	FAM188B	AP-2alpha	1613	1618	3.229049	GCCTCT	0.48828	0.48238
cg0783131	FAM188B	TCF-4E [T	21	27	3.151193	ATCAAA	0.24414	0.24672
cg2707039	FAM188B	TCF-4E [T	1742	1748	3.151193	CTTTGCA	0.24414	0.24672
cg0783131	FAM188B	IRF-1 [T0	1782	1790	3.145547	ATACGG	0.07629	0.07756
cg0783131	FAM188B	TFIID [T0	1576	1582	3.075094	TTTTGCA	0.12207	0.12409
cg2707039	FAM188B	Pax-5 [T0	1063	1069	3.075094	GGGCGA	0.12207	0.11895
cg2707039	FAM188B	Pax-5 [T0	1676	1682	3.075094	CTCGCCC	0.12207	0.11895
cg0783131	FAM188B	C/EBPalph	1199	1205	3.014837	AGCAAT	0.48828	0.4911
cg2707039	FAM188B	C/EBPalph	1972	1978	3.014837	AGCAAT	0.48828	0.4911
cg2707039	FAM188B	Elk-1 [T00	1114	1122	2.987643	CTTCCTT	0.07629	0.07656
cg0783131	FAM188B	HOXD9 [T	87	96	2.949288	AAGTGT	0.02289	0.02401
cg0783131	FAM188B	HOXD10 [	87	96	2.949288	AAGTGT	0.02289	0.02401
cg0783131	FAM188B	c-Ets-2 [T	253	261	2.945838	TGAAAG	0.06104	0.06231
cg0783131	FAM188B	STAT4 [T	371	376	2.941176	ACTTCC	2.92969	2.929
cg0783131	FAM188B	STAT4 [T	612	617	2.941176	CTTTCC	2.92969	2.929
cg0783131	FAM188B	STAT4 [T	962	967	2.941176	TGTTCC	2.92969	2.929
cg0783131	FAM188B	STAT4 [T	1340	1345	2.941176	GGAAAG	2.92969	2.929
cg0783131	FAM188B	STAT4 [T	1650	1655	2.941176	TGTTCC	2.92969	2.929
cg0783131	FAM188B	STAT4 [T	1675	1680	2.941176	GGAACA	2.92969	2.929
cg0783131	FAM188B	STAT4 [T	1786	1791	2.941176	GGAAAG	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	453	458	2.941176	TATTCC	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	530	535	2.941176	TATTCC	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	772	777	2.941176	GGAATA	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	793	798	2.941176	GGAAGT	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	817	822	2.941176	GGAACC	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	872	877	2.941176	CTTTCC	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	973	978	2.941176	GGAAGT	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	1045	1050	2.941176	GGAAAG	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	1069	1074	2.941176	GGAACA	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	1206	1211	2.941176	ACTTCC	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	1696	1701	2.941176	GGAAGT	2.92969	2.929
cg2707039	FAM188B	STAT4 [T	1813	1818	2.941176	CTTTCC	2.92969	2.929
cg2707039	FAM188B	p53 [T006	1793	1799	2.813291	GATGCC	0.48828	0.47786
cg2707039	FAM188B	p53 [T006	1904	1910	2.813291	GCTGCCC	0.48828	0.47786
cg2707039	FAM188B	p53 [T006	1916	1922	2.813291	GGGCAT	0.48828	0.47786
cg0783131	FAM188B	NF-1 [T00	588	595	2.813149	AGGGCC	0.24414	0.24101
cg2707039	FAM188B	NF-1 [T00	948	955	2.813149	GGGGCC	0.24414	0.24101
cg0783131	FAM188B	PR B [T00	1647	1653	2.80933	GAATGT	0.73242	0.74818

cg0783131	FAM188B	PR B [T00	1824	1830	2.80933	AACAAT	0.73242	0.74818
cg0783131	FAM188B	PR A [T01	1647	1653	2.80933	GAATGT	0.73242	0.74818
cg0783131	FAM188B	PR A [T01	1824	1830	2.80933	AACAAT	0.73242	0.74818
cg2707039	FAM188B	c-Myb [T0	973	980	2.687937	GGAAGT	0.06104	0.06117
cg0783131	FAM188B	MEF-2A [	1008	1018	2.660781	TATTTTT	0.00572	0.00593
cg0783131	FAM188B	c-Jun [T00	1355	1361	2.654872	TGACTC	0.48828	0.48929
cg2707039	FAM188B	PPAR-alp	1542	1552	2.642917	CAGACC	0.00858	0.00847
cg0783131	FAM188B	NF-AT1 [	609	617	2.619709	ATCCTTT	0.09155	0.0926
cg0783131	FAM188B	c-Fos [T00	1663	1672	2.598489	AGCCTG	0.03052	0.03034
cg0783131	FAM188B	PXR-1:RX	915	922	2.577808	TGAACT	0.12207	0.12266
cg2707039	FAM188B	PXR-1:RX	183	190	2.577808	GGAGTT	0.12207	0.12266
cg0783131	FAM188B	AP-2alpha	650	655	2.550491	GCCTCA	0.48828	0.48266
cg0783131	FAM188B	AP-2alpha	1247	1252	2.550491	GCCTCA	0.48828	0.48266
cg2707039	FAM188B	AP-2alpha	649	654	2.550491	GCCTCA	0.48828	0.48266
cg2707039	FAM188B	AP-2alpha	896	901	2.550491	GCCTCA	0.48828	0.48266
cg2707039	FAM188B	AP-2alpha	1340	1345	2.550491	TGAGGC	0.48828	0.48266
cg2707039	FAM188B	ENKTF-1	1508	1515	2.511511	CGTCGC	0.12207	0.11894
cg2707039	FAM188B	RBP-Jkap	1837	1848	2.494498	ATTTCC	0.00477	0.00478
cg2707039	FAM188B	Sp1 [T007	1931	1940	2.491373	GGGGCG	0.04005	0.03892
cg0783131	FAM188B	C/EBPalp	945	951	2.441016	CTCAAT	0.48828	0.49114
cg2707039	FAM188B	Ik-1 [T027	138	150	2.374299	TCCCAG	0.00063	0.00061
cg2707039	FAM188B	C/EBPalp	82	88	2.371703	AATTGT	0.48828	0.49114
cg2707039	FAM188B	USF1 [T0	591	600	2.33584	TAGCCA	0.02861	0.02812
cg2707039	FAM188B	RXR-alpha	1542	1548	2.322562	CAGACC	0.85449	0.84796
cg0783131	FAM188B	Elk-1 [T00	1685	1693	2.299314	TACAGG	0.09155	0.09114
cg2707039	FAM188B	Elk-1 [T00	1692	1700	2.299314	CCCAGG	0.09155	0.09114
cg2707039	FAM188B	ELF-1 [T0	1691	1703	2.252809	GCCCAG	0.00215	0.00215
cg0783131	FAM188B	NF-Y [T0	419	426	2.194008	ATTGGT	0.21362	0.21508
cg0783131	FAM188B	NF-Y [T0	1489	1496	2.194008	ATACCA	0.21362	0.21508
cg0783131	FAM188B	GATA-1 [	1255	1260	2.176375	TATCCA	3.90625	3.92756
cg2707039	FAM188B	GATA-1 [	474	479	2.176375	TGGATA	3.90625	3.92756
cg0783131	FAM188B	Elk-1 [T00	683	691	2.164966	GCCAGG	0.05341	0.05317
cg2707039	FAM188B	Elk-1 [T00	969	977	2.164966	GCCAGG	0.05341	0.05317
cg2707039	FAM188B	AP-2alpha	1279	1284	2.098119	GCCTCG	0.97656	0.95407
cg2707039	FAM188B	AP-2alpha	1577	1582	2.098119	GCCTCG	0.97656	0.95407
cg2707039	FAM188B	AP-2alpha	1845	1850	2.098119	CGAGGC	0.97656	0.95407
cg0783131	FAM188B	NF-1 [T00	1755	1762	2.067686	TGTGCC	0.12207	0.12133
cg2707039	FAM188B	LEF-1 [T0	765	772	2.004405	AAGCAA	0.18311	0.18582
cg0783131	FAM188B	GATA-1 [	1265	1270	2.001358	GGGATA	3.90625	3.92756
cg0783131	FAM188B	p53 [T006	45	51	1.970013	TTTGCC	0.36621	0.36261
cg2707039	FAM188B	NF-kappa	1725	1735	1.951792	GGGGTC	0.00572	0.0055
cg0783131	FAM188B	NF-AT1 [	1535	1543	1.94698	GGAAAT	0.06866	0.07012
cg0783131	FAM188B	HNF-1C [	302	310	1.940349	ATATTT	0.02289	0.02363
cg0783131	FAM188B	PR B [T00	87	93	1.892895	AAGTGT	0.12207	0.12429
cg0783131	FAM188B	PR A [T01	87	93	1.892895	AAGTGT	0.12207	0.12429
cg2707039	FAM188B	c-Ets-2 [T	0	8	1.874674	TTCCTTT	0.16785	0.16856
cg0783131	FAM188B	AP-2alpha	643	648	1.871933	GGAGGC	0.97656	0.95407
cg0783131	FAM188B	AP-2alpha	671	676	1.871933	GGAGGC	0.97656	0.95407

cg0783131	FAM188B	AP-2alpha	1836	1841	1.871933	GGAGGC	0.97656	0.95407
cg0783131	FAM188B	AP-2alpha	1942	1947	1.871933	GCCTCC	0.97656	0.95407
cg2707039	FAM188B	AP-2alpha	151	156	1.871933	GGAGGC	0.97656	0.95407
cg2707039	FAM188B	AP-2alpha	285	290	1.871933	GGAGGC	0.97656	0.95407
cg2707039	FAM188B	AP-2alpha	1238	1243	1.871933	GGAGGC	0.97656	0.95407
cg2707039	FAM188B	AP-2alpha	1402	1407	1.871933	GCCTCC	0.97656	0.95407
cg2707039	FAM188B	AP-2alpha	1636	1641	1.871933	GCCTCC	0.97656	0.95407
cg0783131	FAM188B	TBP [T007	214	223	1.871542	CTTATAT	0.18311	0.18942
cg0783131	FAM188B	C/EBPalph	1494	1500	1.830762	AATTGC	0.48828	0.49438
cg0783131	FAM188B	TFII-I [T0	1015	1020	1.824994	CTCTCC	0.48828	0.48408
cg2707039	FAM188B	TFII-I [T0	641	646	1.824994	GGAGAG	0.48828	0.48408
cg2707039	FAM188B	FOXP3 [T	538	543	1.824994	TACAAC	0.48828	0.49451
cg2707039	FAM188B	FOXP3 [T	977	982	1.824994	GTTGTA	0.48828	0.49451
cg2707039	FAM188B	c-Ets-1 [T	1267	1273	1.769212	TAGGAA	0.12207	0.12414
cg0783131	FAM188B	p53 [T006	1588	1594	1.758307	TATGCC	0.36621	0.36261
cg2707039	FAM188B	p53 [T006	1584	1590	1.758307	GGGCAG	0.36621	0.36261
cg2707039	FAM188B	RXR-alpha	1331	1337	1.696452	GGGTCA	0.48828	0.48222
cg0783131	FAM188B	GR-beta [T	222	226	1.680765	AATGC	3.90625	3.94936
cg0783131	FAM188B	GR-beta [T	238	242	1.680765	AATGC	3.90625	3.94936
cg0783131	FAM188B	GR-beta [T	951	955	1.680765	GAATT	3.90625	3.94936
cg0783131	FAM188B	GR-beta [T	1212	1216	1.680765	AATGC	3.90625	3.94936
cg0783131	FAM188B	GR-beta [T	1215	1219	1.680765	GCATT	3.90625	3.94936
cg2707039	FAM188B	GR-beta [T	81	85	1.680765	GAATT	3.90625	3.94936
cg2707039	FAM188B	GR-beta [T	360	364	1.680765	GCATT	3.90625	3.94936
cg2707039	FAM188B	GR-beta [T	424	428	1.680765	AATTC	3.90625	3.94936
cg2707039	FAM188B	GR-beta [T	444	448	1.680765	AATGC	3.90625	3.94936
cg2707039	FAM188B	GR-beta [T	507	511	1.680765	AATGC	3.90625	3.94936
cg2707039	FAM188B	GR-beta [T	1105	1109	1.680765	AATGC	3.90625	3.94936
cg0783131	FAM188B	c-Ets-1 [T	256	262	1.641124	AAGGAA	0.36621	0.36952
cg0783131	FAM188B	c-Ets-1 [T	993	999	1.641124	TTTCCTT	0.36621	0.36952
cg0783131	FAM188B	C/EBPbeta	60	63	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	79	82	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	136	139	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	172	175	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	310	313	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	359	362	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	385	388	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	389	392	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	420	423	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	559	562	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	592	595	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	640	643	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	822	825	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	873	876	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	911	914	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1094	1097	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1189	1192	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1221	1224	1.639871	TTGG	15.625	15.72563

cg0783131	FAM188B	C/EBPbeta	1283	1286	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1337	1340	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1492	1495	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1518	1521	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1523	1526	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1702	1705	1.639871	TTGG	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1759	1762	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1947	1950	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	107	110	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	148	151	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	333	336	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	473	476	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	534	537	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	684	687	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	763	766	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	856	859	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	868	871	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	952	955	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1014	1017	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1057	1060	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1094	1097	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1141	1144	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1156	1159	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1642	1645	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1686	1689	1.639871	CCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1711	1714	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1891	1894	1.639871	TTGG	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1969	1972	1.639871	CCAA	15.625	15.72563
cg0783131	FAM188B	AR [T000	402	410	1.618276	GGACAG	0.09155	0.09119
cg0783131	FAM188B	IRF-1 [T0	1531	1539	1.616539	ATAGGG	0.04578	0.04655
cg0783131	FAM188B	XBP-1 [T	5	10	1.583727	GGTCAT	0.97656	0.98146
cg0783131	FAM188B	XBP-1 [T	552	557	1.583727	TGTCAT	0.97656	0.98146
cg0783131	FAM188B	XBP-1 [T	1990	1995	1.583727	TGTCAT	0.97656	0.98146
cg2707039	FAM188B	XBP-1 [T	1318	1323	1.583727	ATGACC	0.97656	0.98146
cg0783131	FAM188B	Pax-5 [T0	747	753	1.537547	GGGCCA	0.73242	0.71311
cg0783131	FAM188B	Pax-5 [T0	776	782	1.537547	CTGGCC	0.73242	0.71311
cg0783131	FAM188B	Pax-5 [T0	843	849	1.537547	GGGCTA	0.73242	0.71311
cg0783131	FAM188B	Pax-5 [T0	893	899	1.537547	GGGCTA	0.73242	0.71311
cg0783131	FAM188B	Pax-5 [T0	1931	1937	1.537547	CCCGCC	0.73242	0.71311
cg0783131	FAM188B	TFIID [T0	78	84	1.537547	TCCAAA	0.73242	0.75096
cg0783131	FAM188B	TFIID [T0	1092	1098	1.537547	TTTTGG	0.73242	0.75096
cg0783131	FAM188B	TFIID [T0	1891	1897	1.537547	TTTTCC	0.73242	0.75096
cg2707039	FAM188B	Pax-5 [T0	1118	1124	1.537547	CTTGCC	0.73242	0.71311
cg2707039	FAM188B	Pax-5 [T0	1325	1331	1.537547	GGGCCA	0.73242	0.71311
cg2707039	FAM188B	Pax-5 [T0	1450	1456	1.537547	CCCGCC	0.73242	0.71311
cg2707039	FAM188B	TFIID [T0	17	23	1.537547	TGTAAA	0.73242	0.75096
cg2707039	FAM188B	TFIID [T0	92	98	1.537547	TTCAAA	0.73242	0.75096
cg2707039	FAM188B	AR [T000	926	934	1.513096	TCAGTG	0.09155	0.09119

cg0783131	FAM188B	STAT4 [T	258	263	1.470588	GGAAAA	1.95312	1.96333
cg0783131	FAM188B	STAT4 [T	488	493	1.470588	GGAAAC	1.95312	1.96333
cg0783131	FAM188B	STAT4 [T	992	997	1.470588	TTTTCC	1.95312	1.96333
cg0783131	FAM188B	STAT4 [T	1119	1124	1.470588	GGAAAC	1.95312	1.96333
cg0783131	FAM188B	STAT4 [T	1704	1709	1.470588	GGAACT	1.95312	1.96333
cg0783131	FAM188B	STAT4 [T	1891	1896	1.470588	TTTTCC	1.95312	1.96333
cg2707039	FAM188B	STAT4 [T	424	429	1.470588	AATTCC	1.95312	1.96333
cg2707039	FAM188B	STAT4 [T	840	845	1.470588	GGAAAA	1.95312	1.96333
cg2707039	FAM188B	STAT4 [T	1269	1274	1.470588	GGAAAA	1.95312	1.96333
cg2707039	FAM188B	STAT4 [T	1652	1657	1.470588	AGTTCC	1.95312	1.96333
cg2707039	FAM188B	STAT4 [T	1828	1833	1.470588	GGAAAC	1.95312	1.96333
cg0783131	FAM188B	Sp1 [T007	1929	1938	1.469012	CTCCCG	0.03242	0.03129
cg2707039	FAM188B	Sp1 [T007	1448	1457	1.469012	CTCCCG	0.03242	0.03129
cg0783131	FAM188B	TCF-4 [T0	19	28	1.461318	AAATCA	0.04578	0.04635
cg0783131	FAM188B	PR B [T00	332	338	1.404665	TAGTGT	0.36621	0.37023
cg0783131	FAM188B	PR A [T01	332	338	1.404665	TAGTGT	0.36621	0.37023
cg0783131	FAM188B	c-Ets-1 [T	1117	1123	1.384951	CAGGAA	0.36621	0.36952
cg0783131	FAM188B	C/EBPbeta	22	25	1.366559	TCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	150	153	1.366559	TCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	166	169	1.366559	TCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	252	255	1.366559	TTGA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	297	300	1.366559	TTGA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	946	949	1.366559	TCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	955	958	1.366559	TTGA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1060	1063	1.366559	TTGA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1250	1253	1.366559	TCAA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1354	1357	1.366559	TTGA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1485	1488	1.366559	TTGA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1595	1598	1.366559	TTGA	15.625	15.72563
cg0783131	FAM188B	C/EBPbeta	1671	1674	1.366559	TCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	93	96	1.366559	TCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	188	191	1.366559	TCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	308	311	1.366559	TTGA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	395	398	1.366559	TCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	434	437	1.366559	TTGA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1021	1024	1.366559	TCAA	15.625	15.72563
cg2707039	FAM188B	C/EBPbeta	1131	1134	1.366559	TCAA	15.625	15.72563
cg0783131	FAM188B	LEF-1 [T0	20	27	1.362541	AATCAA	0.09155	0.09326
cg0783131	FAM188B	AP-2alpha	531	536	1.357116	GCCTGT	0.48828	0.48203
cg0783131	FAM188B	AP-2alpha	1055	1060	1.357116	GCCTGT	0.48828	0.48203
cg0783131	FAM188B	AP-2alpha	1764	1769	1.357116	GCCTGT	0.48828	0.48203
cg2707039	FAM188B	AP-2alpha	130	135	1.357116	GCCTGT	0.48828	0.48203
cg2707039	FAM188B	AP-2alpha	572	577	1.357116	ACAGGC	0.48828	0.48203
cg0783131	FAM188B	HNF-3alph	1273	1280	1.342935	TTAAAA	0.03052	0.03194
cg2707039	FAM188B	HNF-3alph	6	13	1.342935	TTAAAA	0.03052	0.03194
cg0783131	FAM188B	p53 [T006	1111	1117	1.270236	CGTGCC	0.12207	0.11849
cg0783131	FAM188B	p53 [T006	1499	1505	1.270236	CGTGCC	0.12207	0.11849
cg2707039	FAM188B	p53 [T006	248	254	1.270236	GGGCAC	0.12207	0.11849

cg2707039	FAM188B	ENKTF-1	1964	1971	1.255756	CCGCGC	0.24414	0.23904
cg0783131	FAM188B	T3R-beta1	862	870	1.129976	TGGAGG	0.07629	0.07585
cg0783131	FAM188B	GATA-2 [	1970	1978	1.111111	TCCCTAT	0.09155	0.09208
cg2707039	FAM188B	GCF [T00	1534	1542	1.070269	GCGCCG	0.18311	0.17647
cg2707039	FAM188B	GCF [T00	1982	1990	1.070269	GCGCGG	0.18311	0.17647
cg2707039	FAM188B	USF2 [T0	823	832	1.048473	CAGGTG	0.01717	0.01694
cg0783131	FAM188B	PXR-1:RX	1151	1158	0.941658	TGAACT	0.12207	0.12266
cg0783131	FAM188B	RXR-alph	173	179	0.848226	TGGACC	0.48828	0.48333
cg2707039	FAM188B	RXR-alph	523	529	0.848226	TGGACC	0.48828	0.48333
cg2707039	FAM188B	RXR-alph	1892	1898	0.848226	TGGACC	0.48828	0.48333
cg0783131	FAM188B	GR-beta [T	129	133	0.840383	AATGA	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	153	157	0.840383	AATGG	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	948	952	0.840383	AATGA	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	1235	1239	0.840383	AATGA	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	1482	1486	0.840383	CCATT	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	1493	1497	0.840383	CAATT	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	1494	1498	0.840383	AATTG	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	1521	1525	0.840383	AATTG	7.8125	7.94706
cg0783131	FAM188B	GR-beta [T	1827	1831	0.840383	AATGG	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	14	18	0.840383	AATTG	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	82	86	0.840383	AATTG	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	302	306	0.840383	AATGG	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	514	518	0.840383	TCATT	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	945	949	0.840383	AATGG	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	1027	1031	0.840383	AATGG	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	1037	1041	0.840383	TCATT	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	1082	1086	0.840383	TAATT	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	1255	1259	0.840383	CCATT	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	1273	1277	0.840383	AATGG	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	1296	1300	0.840383	TAATT	7.8125	7.94706
cg2707039	FAM188B	GR-beta [T	1707	1711	0.840383	TAATT	7.8125	7.94706
cg0783131	FAM188B	AP-2alpha	508	513	0.678558	TCAGGC	0.48828	0.48199
cg0783131	FAM188B	AP-2alpha	524	529	0.678558	TCAGGC	0.48828	0.48199
cg0783131	FAM188B	AP-2alpha	1127	1132	0.678558	GCCTGA	0.48828	0.48199
cg0783131	FAM188B	AP-2alpha	1664	1669	0.678558	GCCTGA	0.48828	0.48199
cg2707039	FAM188B	AP-2alpha	172	177	0.678558	GCCTGA	0.48828	0.48199
cg2707039	FAM188B	AP-2alpha	264	269	0.678558	GCCTGA	0.48828	0.48199
cg2707039	FAM188B	C/EBPalp	805	811	0.540941	GATTGT	0.24414	0.24507
cg0783131	FAM188B	AP-1 [T00	1667	1675	0.314596	TGACTC	0.09155	0.09215
cg0783131	FAM188B	GATA-1 [	1004	1009	0.280028	AAGATA	0.97656	0.99875
cg0783131	FAM188B	GATA-1 [	1437	1442	0.280028	TATCTA	0.97656	0.99875
cg0783131	FAM188B	GATA-1 [	1974	1979	0.280028	TATCTT	0.97656	0.99875
cg2707039	FAM188B	c-Ets-1 [T	1114	1120	0.256174	CTTCCT	0.24414	0.24569
cg0783131	FAM188B	AP-2alpha	750	755	0.226186	CCAGGC	0.97656	0.95305
cg0783131	FAM188B	AP-2alpha	928	933	0.226186	CCAGGC	0.97656	0.95305
cg0783131	FAM188B	AP-2alpha	1875	1880	0.226186	GCCTGG	0.97656	0.95305
cg2707039	FAM188B	AP-2alpha	447	452	0.226186	GCCTGG	0.97656	0.95305
cg2707039	FAM188B	AP-2alpha	1553	1558	0.226186	GCCTGG	0.97656	0.95305

cg2707039	FAM188B	AP-2alpha	1955	1960	0.226186	GCCTGG	0.97656	0.95305
cg2707039	FAM188B	p53 [T006	1118	1124	0.211706	CTTGCC	0.36621	0.35912
cg0783131	FAM188B	GR-alpha [	13	17	0.207689	AAAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	66	70	0.207689	AAAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	107	111	0.207689	CCTCT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	115	119	0.207689	CCTTT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	255	259	0.207689	AAAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	352	356	0.207689	CCTCT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	547	551	0.207689	CCTTT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	602	606	0.207689	AGAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	611	615	0.207689	CCTTT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	700	704	0.207689	AGAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	855	859	0.207689	AGAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1046	1050	0.207689	CCTTT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1074	1078	0.207689	CCTCT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1090	1094	0.207689	CCTTT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1407	1411	0.207689	CCTTT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1471	1475	0.207689	AGAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1986	1990	0.207689	CCTTT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	2	6	0.207689	CCTTT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	490	494	0.207689	AGAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	632	636	0.207689	AGAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	645	649	0.207689	AGAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	769	773	0.207689	AAAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	914	918	0.207689	CCTTT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	1078	1082	0.207689	CCTTT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	1167	1171	0.207689	AGAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	1310	1314	0.207689	CCTCT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	1614	1618	0.207689	CCTCT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	1665	1669	0.207689	AAAGG	7.8125	7.81264
cg0783131	FAM188B	HNF-1A [	303	310	0.143882	TATTTA	0.24414	0.25261
cg0783131	FAM188B	GATA-1 [	1681	1686	0.105011	GAGATA	0.97656	0.98738
cg0783131	FAM188B	GR-alpha [	532	536	0	CCTGT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	586	590	0	ACAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1056	1060	0	CCTGT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1531	1535	0	ATAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1686	1690	0	ACAGG	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1765	1769	0	CCTGT	7.8125	7.81264
cg0783131	FAM188B	GR-alpha [	1972	1976	0	CCTAT	7.8125	7.81264
cg0783131	FAM188B	XBP-1 [T	406	411	0	AGTCAT	0.97656	0.98127
cg0783131	FAM188B	XBP-1 [T	565	570	0	ATGACT	0.97656	0.98127
cg0783131	FAM188B	RXR-alpha	131	137	0	TGAACC	0.24414	0.2444
cg0783131	FAM188B	Pax-5 [T0	412	418	0	GGGCAG	1.09863	1.06846
cg0783131	FAM188B	Pax-5 [T0	818	824	0	GGGCTT	1.09863	1.06846
cg0783131	FAM188B	Pax-5 [T0	1111	1117	0	CGTGCC	1.09863	1.06846
cg0783131	FAM188B	Pax-5 [T0	1138	1144	0	GGGCAG	1.09863	1.06846
cg0783131	FAM188B	Pax-5 [T0	1499	1505	0	CGTGCC	1.09863	1.06846
cg0783131	FAM188B	Pax-5 [T0	1879	1885	0	GGGCCC	1.09863	1.06846

cg0783131	FAM188B	p53 [T006	412	418	0	GGGCAG	0.36621	0.35912
cg0783131	FAM188B	p53 [T006	1138	1144	0	GGGCAG	0.36621	0.35912
cg0783131	FAM188B	TFII-I [T0	402	407	0	GGACAG	1.46484	1.45997
cg0783131	FAM188B	TFII-I [T0	584	589	0	GGACAG	1.46484	1.45997
cg0783131	FAM188B	TFII-I [T0	612	617	0	CTTTCC	1.46484	1.45997
cg0783131	FAM188B	TFII-I [T0	1266	1271	0	GGATAG	1.46484	1.45997
cg0783131	FAM188B	TFII-I [T0	1340	1345	0	GGAAAG	1.46484	1.45997
cg0783131	FAM188B	TFII-I [T0	1348	1353	0	CTGTCC	1.46484	1.45997
cg0783131	FAM188B	TFII-I [T0	1786	1791	0	GGAAAG	1.46484	1.45997
cg0783131	FAM188B	TFII-I [T0	1953	1958	0	CTGTCC	1.46484	1.45997
cg0783131	FAM188B	STAT4 [T	1535	1540	0	GGAAAT	0.48828	0.49387
cg0783131	FAM188B	c-Ets-1 [T	685	691	0	CAGGAA	0.24414	0.2429
cg0783131	FAM188B	c-Ets-1 [T	1687	1693	0	CAGGAA	0.24414	0.2429
cg0783131	FAM188B	YY1 [T00	154	157	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	290	293	0	CCAT	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	410	413	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	616	619	0	CCAT	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	634	637	0	CCAT	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	759	762	0	CCAT	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	812	815	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	891	894	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	1263	1266	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	1393	1396	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	1482	1485	0	CCAT	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	1809	1812	0	CCAT	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	1828	1831	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	1886	1889	0	ATGG	7.8125	7.81711
cg0783131	FAM188B	YY1 [T00	1911	1914	0	CCAT	7.8125	7.81711
cg0783131	FAM188B	ER-alpha [	5	9	0	GGTCA	1.95312	1.9404
cg0783131	FAM188B	ER-alpha [	54	58	0	GGTCA	1.95312	1.9404
cg0783131	FAM188B	ER-alpha [	164	168	0	GGTCA	1.95312	1.9404
cg0783131	FAM188B	ER-alpha [	784	788	0	GGTCA	1.95312	1.9404
cg0783131	FAM188B	ER-alpha [	824	828	0	GGTCA	1.95312	1.9404
cg0783131	FAM188B	ER-alpha [	1553	1557	0	GGTCA	1.95312	1.9404
cg0783131	FAM188B	C/EBPbeta	46	49	0	TTGC	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	280	283	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	339	342	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	499	502	0	GCAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	551	554	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	606	609	0	GCAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	899	902	0	GCAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	907	910	0	TTGC	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1064	1067	0	GCAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1078	1081	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1166	1169	0	ACAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1200	1203	0	GCAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1496	1499	0	TTGC	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1563	1566	0	TTGT	15.625	15.71349

cg0783131	FAM188B	C/EBPbeta	1573	1576	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1578	1581	0	TTGC	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1580	1583	0	GCAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1631	1634	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1721	1724	0	TTGC	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1743	1746	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1825	1828	0	ACAA	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1979	1982	0	TTGT	15.625	15.71349
cg0783131	FAM188B	C/EBPbeta	1989	1992	0	TTGT	15.625	15.71349
cg0783131	FAM188B	c-Jun [T00	1667	1673	0	TGACTC	0.12207	0.12266
cg0783131	FAM188B	c-Fos [T00	1292	1301	0	GAGTCA	0.01144	0.01142
cg0783131	FAM188B	TFIID [T0	119	125	0	TCTAAA	1.09863	1.13474
cg0783131	FAM188B	TFIID [T0	147	153	0	TTTTCA	1.09863	1.13474
cg0783131	FAM188B	FOXP3 [T	279	284	0	GTTGTT	1.46484	1.47315
cg0783131	FAM188B	GR-beta [T	902	906	0	ACATT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [T	952	956	0	AATTT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [T	1520	1524	0	AAATT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [T	1627	1631	0	AAATT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [T	1628	1632	0	AATTT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [T	1648	1652	0	AATGT	3.90625	3.99611
cg0783131	FAM188B	GR-beta [T	1698	1702	0	AATGT	3.90625	3.99611
cg0783131	FAM188B	GR [T0507	80	86	0	CAAAAA	0.36621	0.37562
cg0783131	FAM188B	GR [T0507	1217	1223	0	ATTTTTC	0.36621	0.37562
cg0783131	FAM188B	IRF-2 [T01	56	61	0	TCACTT	0.48828	0.49387
cg0783131	FAM188B	IRF-2 [T01	323	328	0	AAGTGA	0.48828	0.49387
cg0783131	FAM188B	IRF-2 [T01	988	993	0	TCACTT	0.48828	0.49387
cg2707039	FAM188B	GR-alpha [	65	69	0	ATAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	101	105	0	CCTGT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	131	135	0	CCTGT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	477	481	0	ATAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	528	532	0	CCTAT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	572	576	0	ACAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	780	784	0	ATAGG	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	1211	1215	0	CCTGT	7.8125	7.81264
cg2707039	FAM188B	GR-alpha [	1823	1827	0	ACAGG	7.8125	7.81264
cg2707039	FAM188B	AP-2alpha	1050	1055	0	GCAGGC	0.97656	0.95305
cg2707039	FAM188B	AP-2alpha	1781	1786	0	GCCTGC	0.97656	0.95305
cg2707039	FAM188B	XBP-1 [T0	512	517	0	AGTCAT	0.97656	0.98127
cg2707039	FAM188B	RXR-alpha	69	75	0	GGGTTA	0.24414	0.2444
cg2707039	FAM188B	Pax-5 [T0	109	115	0	GGGCCG	1.09863	1.06846
cg2707039	FAM188B	Pax-5 [T0	248	254	0	GGGCAC	1.09863	1.06846
cg2707039	FAM188B	Pax-5 [T0	365	371	0	CCAGCC	1.09863	1.06846
cg2707039	FAM188B	Pax-5 [T0	852	858	0	GGGCTT	1.09863	1.06846
cg2707039	FAM188B	Pax-5 [T0	1456	1462	0	CCAGCC	1.09863	1.06846
cg2707039	FAM188B	Pax-5 [T0	1464	1470	0	CCAGCC	1.09863	1.06846
cg2707039	FAM188B	Pax-5 [T0	1953	1959	0	GGGCCT	1.09863	1.06846
cg2707039	FAM188B	TFII-I [T0	475	480	0	GGATAG	1.46484	1.45997
cg2707039	FAM188B	TFII-I [T0	872	877	0	CTTTCC	1.46484	1.45997

cg2707039	FAM188B	TFII-I [T0	1045	1050	0	GGAAAG	1.46484	1.45997
cg2707039	FAM188B	TFII-I [T0	1539	1544	0	GGACAG	1.46484	1.45997
cg2707039	FAM188B	TFII-I [T0	1608	1613	0	GGACAG	1.46484	1.45997
cg2707039	FAM188B	TFII-I [T0	1813	1818	0	CTTTCC	1.46484	1.45997
cg2707039	FAM188B	TFII-I [T0	1821	1826	0	GGACAG	1.46484	1.45997
cg2707039	FAM188B	STAT4 [T	504	509	0	GGAAAT	0.48828	0.49387
cg2707039	FAM188B	STAT4 [T	1837	1842	0	ATTTCC	0.48828	0.49387
cg2707039	FAM188B	c-Ets-1 [T	971	977	0	CAGGAA	0.24414	0.2429
cg2707039	FAM188B	c-Ets-1 [T	1694	1700	0	CAGGAA	0.24414	0.2429
cg2707039	FAM188B	YY1 [T00	207	210	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	303	306	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	621	624	0	CCAT	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	662	665	0	CCAT	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	736	739	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	755	758	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	946	949	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	1028	1031	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	1255	1258	0	CCAT	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	1274	1277	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	1527	1530	0	CCAT	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	1604	1607	0	CCAT	7.8125	7.81711
cg2707039	FAM188B	YY1 [T00	1606	1609	0	ATGG	7.8125	7.81711
cg2707039	FAM188B	ER-alpha [	178	182	0	GGTCA	1.95312	1.9404
cg2707039	FAM188B	ER-alpha [	1145	1149	0	GGTCA	1.95312	1.9404
cg2707039	FAM188B	ER-alpha [	1202	1206	0	GGTCA	1.95312	1.9404
cg2707039	FAM188B	ER-alpha [	1319	1323	0	TGACC	1.95312	1.9404
cg2707039	FAM188B	ER-alpha [	1332	1336	0	GGTCA	1.95312	1.9404
cg2707039	FAM188B	ER-alpha [	1644	1648	0	GGTCA	1.95312	1.9404
cg2707039	FAM188B	C/EBPbeta	16	19	0	TTGT	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	84	87	0	TTGT	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	202	205	0	GCAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	235	238	0	ACAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	325	328	0	TTGT	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	350	353	0	TTGC	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	539	542	0	ACAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	711	714	0	ACAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	723	726	0	TTGT	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	751	754	0	TTGT	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	767	770	0	GCAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	777	780	0	ACAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	800	803	0	GCAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	807	810	0	TTGT	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	902	905	0	GCAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	978	981	0	TTGT	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	995	998	0	GCAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1119	1122	0	TTGC	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1234	1237	0	ACAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1300	1303	0	TTGT	15.625	15.71349

cg2707039	FAM188B	C/EBPbeta	1425	1428	0	TTGC	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1490	1493	0	TTGC	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1518	1521	0	GCAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1551	1554	0	TTGC	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1744	1747	0	TTGC	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1879	1882	0	GCAA	15.625	15.71349
cg2707039	FAM188B	C/EBPbeta	1973	1976	0	GCAA	15.625	15.71349
cg2707039	FAM188B	NF-1 [T00	107	114	0	TTGGGC	0.12207	0.11983
cg2707039	FAM188B	TFIID [T0	5	11	0	TTTAAA	1.09863	1.13474
cg2707039	FAM188B	TFIID [T0	395	401	0	TCAAAA	1.09863	1.13474
cg2707039	FAM188B	FOXP3 [T	324	329	0	GTTGTT	1.46484	1.47315
cg2707039	FAM188B	FOXP3 [T	722	727	0	GTTGTT	1.46484	1.47315
cg2707039	FAM188B	GR-beta [T	13	17	0	AAATT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	423	427	0	AAATT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	461	465	0	AATGT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	717	721	0	AATGT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	844	848	0	AATGT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	1083	1087	0	AATTT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	1297	1301	0	AATTT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	1708	1712	0	AATTT	3.90625	3.99611
cg2707039	FAM188B	GR-beta [T	1835	1839	0	ACATT	3.90625	3.99611
cg2707039	FAM188B	C/EBPalph	348	354	0	GATTGC	0.24414	0.2444
cg2707039	FAM188B	PR B [T00	954	960	0	AACAGT	0.36621	0.36944
cg2707039	FAM188B	PR A [T01	954	960	0	AACAGT	0.36621	0.36944
cg2707039	FAM188B	GR [T050	396	402	0	CAAAAA	0.36621	0.37562
cg2707039	FAM188B	TCF-4E [T	766	772	0	AGCAAA	0.12207	0.12262
cg2707039	FAM188B	IRF-2 [T0	329	334	0	TCACTT	0.48828	0.49387
cg2707039	FAM188B	IRF-2 [T0	1204	1209	0	TCACTT	0.48828	0.49387
cg2707039	FAM188B	c-Myc [T0	595	600	0	CACGTG	0.48828	0.48199
cg0738020	FBN1	c-Ets-1 [T	1305	1311	9.969337	ATTCCC	0.24414	0.23698
cg2254337	FBN1	LEF-1 [T0	1511	1518	9.937995	AGCCAA	0.12207	0.1238
cg0738020	FBN1	PEA3 [T0	308	316	9.937959	GGGATG	0.18311	0.18382
cg0738020	FBN1	PEA3 [T0	1736	1744	9.937959	TCCCAT	0.18311	0.18382
cg0738020	FBN1	GATA-3 [	32	43	9.883336	AAAGAT	0.01037	0.00992
cg0738020	FBN1	c-Myb [T0	1930	1937	9.815171	ACAAGT	0.36621	0.34605
cg2254337	FBN1	c-Myb [T0	545	552	9.815171	TCAAGT	0.36621	0.34605
cg2254337	FBN1	STAT1bet	1297	1306	9.807397	CTTTCC	0.14877	0.14533
cg0738020	FBN1	XBP-1 [T	161	166	9.789909	AGACAT	1.95312	1.94901
cg0738020	FBN1	XBP-1 [T	1259	1264	9.789909	AGCCAT	1.95312	1.94901
cg2254337	FBN1	XBP-1 [T	314	319	9.789909	ATGGCT	1.95312	1.94901
cg2254337	FBN1	XBP-1 [T	647	652	9.789909	ATGTCT	1.95312	1.94901
cg0738020	FBN1	NF-AT2 [	510	519	9.787971	TCATTT	0.08774	0.08205
cg2254337	FBN1	NF-AT2 [	1489	1498	9.755755	CTTTCTT	0.08774	0.08205
cg0738020	FBN1	Elk-1 [T00	1387	1395	9.754368	CTTCCA	0.10681	0.11027
cg2254337	FBN1	Elk-1 [T00	71	79	9.754368	CTTCCA	0.10681	0.11027
cg0738020	FBN1	PR B [T00	379	385	9.743489	TTGTGT	1.09863	1.0981
cg0738020	FBN1	PR B [T00	805	811	9.743489	GTGTGT	1.09863	1.0981
cg0738020	FBN1	PR B [T00	1430	1436	9.743489	GTGTGT	1.09863	1.0981

cg0738020	FBN1	PR A [T01	379	385	9.743489	TTGTGTT	1.09863	1.0981
cg0738020	FBN1	PR A [T01	805	811	9.743489	GTGTGTT	1.09863	1.0981
cg0738020	FBN1	PR A [T01	1430	1436	9.743489	GTGTGTT	1.09863	1.0981
cg2254337	FBN1	LEF-1 [T0	160	167	9.72404	TGACAA	0.21362	0.21229
cg2254337	FBN1	LEF-1 [T0	552	559	9.72404	CTTTGTC	0.21362	0.21229
cg2254337	FBN1	LEF-1 [T0	680	687	9.72404	CTTTGTC	0.21362	0.21229
cg2254337	FBN1	LEF-1 [T0	1768	1775	9.72404	CTTTGTC	0.21362	0.21229
cg0738020	FBN1	NF-kappaI	207	218	9.707305	CAGAGG	0.01776	0.01845
cg0738020	FBN1	NF-AT1 [T	1176	1184	9.691726	GGAAAC	0.16785	0.16528
cg0738020	FBN1	HNF-1C [	826	834	9.601936	GTTATTC	0.19836	0.18179
cg0738020	FBN1	HNF-1C [	1587	1595	9.601936	AACACTA	0.19836	0.18179
cg0738020	FBN1	RAR-beta	249	258	9.567396	AGGGTT	0.21362	0.22369
cg0738020	FBN1	TFIID [T0	9	15	9.552105	TGTGAA	1.46484	1.37777
cg0738020	FBN1	TFIID [T0	1477	1483	9.552105	TGAGAA	1.46484	1.37777
cg0738020	FBN1	Pax-5 [T0	252	258	9.552105	GTTGCC	1.46484	1.61918
cg0738020	FBN1	Pax-5 [T0	538	544	9.552105	GGGCTA	1.46484	1.61918
cg2254337	FBN1	TFIID [T0	160	166	9.552105	TGACAA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	481	487	9.552105	TGAGAA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	553	559	9.552105	TTTGTCA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	880	886	9.552105	TGGCAA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1014	1020	9.552105	TTTCTCA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1051	1057	9.552105	TTTGTCA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1479	1485	9.552105	TTTCTCA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1495	1501	9.552105	TTCCAA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1681	1687	9.552105	TCCCAA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1769	1775	9.552105	TTTGTCA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1829	1835	9.552105	TTCCAA	1.46484	1.37777
cg2254337	FBN1	TFIID [T0	1930	1936	9.552105	TTTGGTA	1.46484	1.37777
cg0738020	FBN1	NF-1 [T00	884	891	9.535536	TTGTCCA	0.73242	0.74634
cg0738020	FBN1	NF-AT1 [T	467	475	9.521781	GGAAAT	0.16785	0.16528
cg2254337	FBN1	NF-1 [T00	1151	1158	9.513281	TTGGCTT	0.73242	0.74634
cg2254337	FBN1	NF-1 [T00	1509	1516	9.513281	CAAGCC	0.73242	0.74634
cg0738020	FBN1	FOXP3 [T	26	31	9.512894	AAGAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	64	69	9.512894	AATAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	252	257	9.512894	GTTGCC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	480	485	9.512894	ATAAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	577	582	9.512894	CAGAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	620	625	9.512894	ATAAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	809	814	9.512894	GTTGCT	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	826	831	9.512894	GTTATT	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	838	843	9.512894	GTAAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	1003	1008	9.512894	CTAAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	1212	1217	9.512894	GTTGGT	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	1500	1505	9.512894	ATAAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	1546	1551	9.512894	CATAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	1624	1629	9.512894	AATAAC	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	1819	1824	9.512894	GTTTAT	7.32422	7.22156
cg0738020	FBN1	FOXP3 [T	1908	1913	9.512894	GTTATT	7.32422	7.22156

cg0738020	FBN1	TFII-I [T0	195	200	9.512894	AATTCC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	304	309	9.512894	GGAAGG	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	406	411	9.512894	GGAAAA	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	514	519	9.512894	TTTTCC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	884	889	9.512894	TTGTCC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	937	942	9.512894	CGTTCC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	947	952	9.512894	GGACAA	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1041	1046	9.512894	GGACAC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1120	1125	9.512894	GGAAAA	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1176	1181	9.512894	GGAAAC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1358	1363	9.512894	CCTTCC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1738	1743	9.512894	CCATCC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1790	1795	9.512894	GGAAAC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1939	1944	9.512894	TTTTCC	7.32422	7.44385
cg0738020	FBN1	TFII-I [T0	1986	1991	9.512894	GGAATT	7.32422	7.44385
cg2254337	FBN1	FOXP3 [T	109	114	9.512894	CATAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	181	186	9.512894	AATAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	190	195	9.512894	GTTGCC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	199	204	9.512894	GATAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	262	267	9.512894	GTTATG	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	294	299	9.512894	GTAAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	320	325	9.512894	ACCAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	518	523	9.512894	GAGAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	549	554	9.512894	GTTCTT	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	594	599	9.512894	GTTATT	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1002	1007	9.512894	GTTCTG	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1232	1237	9.512894	GTTTAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1280	1285	9.512894	CAGAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1319	1324	9.512894	GTTCTG	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1631	1636	9.512894	ACCAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1653	1658	9.512894	GAGAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1686	1691	9.512894	AATAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1726	1731	9.512894	AATAAC	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1787	1792	9.512894	GTTGGG	7.32422	7.22156
cg2254337	FBN1	FOXP3 [T	1978	1983	9.512894	CCCAAC	7.32422	7.22156
cg2254337	FBN1	TFII-I [T0	409	414	9.512894	TTATCC	7.32422	7.44385
cg2254337	FBN1	TFII-I [T0	753	758	9.512894	TTTTCC	7.32422	7.44385
cg2254337	FBN1	TFII-I [T0	993	998	9.512894	TTATCC	7.32422	7.44385
cg2254337	FBN1	TFII-I [T0	1009	1014	9.512894	GGAATT	7.32422	7.44385
cg2254337	FBN1	TFII-I [T0	1440	1445	9.512894	GTTTCC	7.32422	7.44385
cg2254337	FBN1	TFII-I [T0	1606	1611	9.512894	AAATCC	7.32422	7.44385
cg2254337	FBN1	c-Jun [T00	46	52	9.511322	TGACCA	0.73242	0.7366
cg2254337	FBN1	Ik-1 [T027	1866	1878	9.497194	GGCAGG	0.02941	0.03137
cg0738020	FBN1	TCF-4E [T	929	935	9.453578	TCCAAA	0.48828	0.46934
cg2254337	FBN1	TCF-4E [T	1742	1748	9.453578	TACAAA	0.48828	0.46934
cg0738020	FBN1	EBF [T05	1094	1104	9.428348	GTCCCTC	0.06866	0.07687
cg0738020	FBN1	HOXD9 [T	1896	1905	9.356547	CTCTTAT	0.02289	0.02088
cg0738020	FBN1	HOXD10 [	1896	1905	9.356547	CTCTTAT	0.02289	0.02088

cg2254337	FBN1	HOXD9 [T	181	190	9.356547	AATAAC	0.02289	0.02088
cg2254337	FBN1	HOXD10 [	181	190	9.356547	AATAAC	0.02289	0.02088
cg0738020	FBN1	NFI/CTF [	258	265	9.352332	CCAAGG	0.54932	0.55369
cg0738020	FBN1	NFI/CTF [	1170	1177	9.352332	GGCATT	0.54932	0.55369
cg0738020	FBN1	AP-1 [T00	152	160	9.290522	TGACTG	0.09155	0.08441
cg0738020	FBN1	SRY [T00	1682	1690	9.264664	CTTTGC	0.12207	0.11857
cg2254337	FBN1	NF-AT1 [T	1294	1302	9.18189	TCACTT	0.22888	0.22581
cg0738020	FBN1	AP-1 [T00	862	870	9.168921	TGACTG	0.24414	0.23028
cg0738020	FBN1	c-Myb [T0	1208	1215	9.142015	CAAAGT	0.39673	0.37851
cg0738020	FBN1	AP-1 [T00	266	274	9.116043	TGACTA	0.24414	0.23028
cg2254337	FBN1	LEF-1 [T0	1246	1253	9.099721	CTGCAA	0.54932	0.53171
cg2254337	FBN1	LEF-1 [T0	1741	1748	9.099721	CTACAA	0.54932	0.53171
cg2254337	FBN1	USF2 [T0	923	932	9.056375	TTTACA	0.1545	0.16206
cg2254337	FBN1	USF2 [T0	1468	1477	9.056375	TTCACA	0.1545	0.16206
cg0738020	FBN1	c-Ets-1 [T	212	218	9.020687	GTTCCC	0.85449	0.84987
cg0738020	FBN1	c-Ets-1 [T	938	944	9.020687	GTTCCC	0.85449	0.84987
cg0738020	FBN1	c-Jun [T00	790	796	9.013496	TGACAT	0.61035	0.60549
cg0738020	FBN1	c-Jun [T00	866	872	9.013496	TGACGT	0.61035	0.60549
cg0738020	FBN1	PXR-1:RX	1811	1818	8.998824	GATGTT	0.24414	0.24356
cg0738020	FBN1	LEF-1 [T0	928	935	8.973041	ATCCAA	0.54932	0.53171
cg0738020	FBN1	GR [T050	111	117	8.971049	CAAATA	0.61035	0.5928
cg0738020	FBN1	GR [T050	526	532	8.971049	CAAATA	0.61035	0.5928
cg0738020	FBN1	GR [T050	1758	1764	8.971049	GTATTT	0.61035	0.5928
cg2254337	FBN1	GR [T050	1098	1104	8.971049	CAAAAT	0.61035	0.5928
cg0738020	FBN1	HNF-1C [	1643	1651	8.969184	TTTTCTA	0.12207	0.10938
cg2254337	FBN1	c-Ets-1 [T	356	362	8.937416	ATTCCA	0.85449	0.84987
cg2254337	FBN1	c-Ets-1 [T	1007	1013	8.937416	GTGGAA	0.85449	0.84987
cg0738020	FBN1	c-Ets-2 [T	175	183	8.912323	TTCCTA	0.27466	0.27171
cg2254337	FBN1	c-Ets-2 [T	1085	1093	8.912323	TTCCTG	0.27466	0.27171
cg0738020	FBN1	AP-1 [T00	440	448	8.854325	GATCAG	0.24414	0.23028
cg2254337	FBN1	c-Jun [T00	420	426	8.832178	AAGGTC	0.61035	0.60549
cg2254337	FBN1	PR B [T00	369	375	8.827054	ATCTGT	0.36621	0.35051
cg2254337	FBN1	PR B [T00	1580	1586	8.827054	ATCTGT	0.36621	0.35051
cg2254337	FBN1	PR A [T01	369	375	8.827054	ATCTGT	0.36621	0.35051
cg2254337	FBN1	PR A [T01	1580	1586	8.827054	ATCTGT	0.36621	0.35051
cg2254337	FBN1	NFI/CTF [	1831	1838	8.814757	CCAAAA	0.48828	0.48845
cg0738020	FBN1	c-Ets-1 [T	1218	1224	8.809329	ATTCCA	0.85449	0.84987
cg2254337	FBN1	c-Jun [T00	1623	1629	8.807683	TGACAA	0.61035	0.60549
cg2254337	FBN1	NF-1 [T00	1679	1686	8.790071	CTTCCC	0.24414	0.24339
cg0738020	FBN1	LEF-1 [T0	1682	1689	8.759086	CTTTGC	0.54932	0.53171
cg2254337	FBN1	LEF-1 [T0	901	908	8.759086	CTTTGC	0.54932	0.53171
cg0738020	FBN1	XBP-1 [T	17	22	8.75604	ATGAGA	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	170	175	8.75604	TCTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	283	288	8.75604	GTTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	383	388	8.75604	GTTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	508	513	8.75604	GTTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	641	646	8.75604	TTTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	1057	1062	8.75604	GTTCAT	2.92969	2.75329

cg0738020	FBN1	XBP-1 [T	1197	1202	8.75604	TCTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	1243	1248	8.75604	TCTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	1435	1440	8.75604	TTTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	1493	1498	8.75604	ATGATA	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	1852	1857	8.75604	TCTCAT	2.92969	2.75329
cg0738020	FBN1	XBP-1 [T	1934	1939	8.75604	GTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	7	12	8.75604	TTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	62	67	8.75604	TTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	106	111	8.75604	TATCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	155	160	8.75604	TTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	216	221	8.75604	TTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	310	315	8.75604	TTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	663	668	8.75604	ATGAAA	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	743	748	8.75604	TCTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	918	923	8.75604	GCTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	1016	1021	8.75604	TCTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	1021	1026	8.75604	TTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	1025	1030	8.75604	ATGAGC	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	1274	1279	8.75604	TTTCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	1717	1722	8.75604	GATCAT	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	1906	1911	8.75604	ATGATA	2.92969	2.75329
cg2254337	FBN1	XBP-1 [T	1961	1966	8.75604	ATGAAA	2.92969	2.75329
cg0738020	FBN1	STAT1bet	1786	1795	8.695301	ACCTGG	0.22316	0.2175
cg2254337	FBN1	STAT1bet	1814	1823	8.695301	ATGAGG	0.22316	0.2175
cg2254337	FBN1	GATA-3 [	787	798	8.678596	AGCTCT	0.01347	0.01297
cg0738020	FBN1	c-Jun [T00	518	524	8.571705	CCAGTC	0.12207	0.1249
cg0738020	FBN1	c-Jun [T00	1457	1463	8.571705	CCAGTC	0.12207	0.1249
cg2254337	FBN1	c-Jun [T00	1556	1562	8.571705	TGACTG	0.12207	0.1249
cg2254337	FBN1	RAR-beta	1972	1981	8.541284	AAAAAA	0.26703	0.27434
cg2254337	FBN1	p53 [T006	1252	1258	8.537081	AGAGCC	0.12207	0.13169
cg0738020	FBN1	NF-AT1 [	1936	1944	8.532897	TCATTTT	0.10681	0.10494
cg2254337	FBN1	USF2 [T0	953	962	8.532138	TGTCCAC	0.103	0.10815
cg0738020	FBN1	LEF-1 [T0	1162	1169	8.457856	CTTTGA	0.15259	0.154
cg2254337	FBN1	c-Myb [T0	688	695	8.412632	TCCAGTT	0.30518	0.28602
cg0738020	FBN1	HNF-1B [	1644	1652	8.379818	TTTCTAA	0.11444	0.10456
cg0738020	FBN1	c-Ets-1 [T	1710	1716	8.373028	GTTCCAT	0.24414	0.23702
cg0738020	FBN1	HNF-3alph	608	615	8.343064	ATAAAA	0.27466	0.23078
cg0738020	FBN1	HNF-3alph	1822	1829	8.343064	TATTTTA	0.27466	0.23078
cg0738020	FBN1	HNF-3alph	1879	1886	8.343064	CTAAAA	0.27466	0.23078
cg2254337	FBN1	HNF-3alph	1809	1816	8.343064	TTAAAA	0.27466	0.23078
cg0738020	FBN1	c-Ets-2 [T	1360	1368	8.339336	TTCCTAC	0.13733	0.13927
cg2254337	FBN1	c-Ets-2 [T	174	182	8.339336	ATGTAG	0.13733	0.13927
cg2254337	FBN1	c-Ets-2 [T	1380	1388	8.339336	TTCCTGC	0.13733	0.13927
cg0738020	FBN1	PR B [T00	575	581	8.338824	AACAGA	1.09863	1.09384
cg0738020	FBN1	PR B [T00	580	586	8.338824	AACAGA	1.09863	1.09384
cg0738020	FBN1	PR B [T00	704	710	8.338824	TGCTGTT	1.09863	1.09384
cg0738020	FBN1	PR B [T00	891	897	8.338824	AACAGC	1.09863	1.09384
cg0738020	FBN1	PR A [T01	575	581	8.338824	AACAGA	1.09863	1.09384

cg0738020	FBN1	PR A [T01	580	586	8.338824	AACAGA	1.09863	1.09384
cg0738020	FBN1	PR A [T01	704	710	8.338824	TGCTGTT	1.09863	1.09384
cg0738020	FBN1	PR A [T01	891	897	8.338824	AACAGC	1.09863	1.09384
cg2254337	FBN1	PR B [T00	126	132	8.338824	TTCTGTT	1.09863	1.09384
cg2254337	FBN1	PR B [T00	184	190	8.338824	AACAGA	1.09863	1.09384
cg2254337	FBN1	PR B [T00	1228	1234	8.338824	GCCTGTT	1.09863	1.09384
cg2254337	FBN1	PR A [T01	126	132	8.338824	TTCTGTT	1.09863	1.09384
cg2254337	FBN1	PR A [T01	184	190	8.338824	AACAGA	1.09863	1.09384
cg2254337	FBN1	PR A [T01	1228	1234	8.338824	GCCTGTT	1.09863	1.09384
cg0738020	FBN1	ATF3 [T01	1956	1963	8.313799	GTATGTC	0.27466	0.27379
cg0738020	FBN1	PXR-1:RX	1585	1592	8.304332	TGAACAC	0.12207	0.11843
cg0738020	FBN1	GR-alpha [	217	221	8.281568	CCTTC	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	247	251	8.281568	GAAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	259	263	8.281568	CAAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	305	309	8.281568	GAAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	402	406	8.281568	CGAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	690	694	8.281568	CCTCC	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1109	1113	8.281568	CAAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1166	1170	8.281568	GAAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1358	1362	8.281568	CCTTC	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1373	1377	8.281568	CCTTC	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1417	1421	8.281568	GAAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1511	1515	8.281568	CCTCC	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1595	1599	8.281568	CAAGG	7.8125	8.20394
cg0738020	FBN1	GR-alpha [	1944	1948	8.281568	CCTTC	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	286	290	8.281568	CCTCC	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	380	384	8.281568	CAAGG	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	413	417	8.281568	CCTTC	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	419	423	8.281568	GAAGG	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	604	608	8.281568	CCTCC	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	1164	1168	8.281568	CAAGG	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	1266	1270	8.281568	CCTCG	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	1331	1335	8.281568	CCTCC	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	1530	1534	8.281568	CAAGG	7.8125	8.20394
cg2254337	FBN1	GR-alpha [	1671	1675	8.281568	CCTTC	7.8125	8.20394
cg2254337	FBN1	c-Jun [T00	1263	1269	8.242207	TGACCTC	0.48828	0.47447
cg0738020	FBN1	NFI/CTF [	1742	1749	8.241664	CCAACCT	0.18311	0.1922
cg2254337	FBN1	NFI/CTF [	1784	1791	8.241664	CTGGTTC	0.18311	0.1922
cg2254337	FBN1	HOXD9 [T	246	255	8.224939	CTATTAT	0.08774	0.0777
cg2254337	FBN1	HOXD10 [	246	255	8.224939	CTATTAT	0.08774	0.0777
cg0738020	FBN1	ENKTF-1	874	881	8.19852	TGGCCAC	0.73242	0.80254
cg2254337	FBN1	ENKTF-1	377	384	8.19852	TGGCAAC	0.73242	0.80254
cg2254337	FBN1	ENKTF-1	1350	1357	8.19852	TGGCAGC	0.73242	0.80254
cg2254337	FBN1	ENKTF-1	1865	1872	8.19852	TGGCAGC	0.73242	0.80254
cg0738020	FBN1	NF-1 [T00	1912	1919	8.191058	TTGGCCT	0.24414	0.24485
cg0738020	FBN1	PXR-1:RX	829	836	8.180749	ATTGTTC	0.12207	0.11255
cg0738020	FBN1	SRY [T00	1162	1170	8.174786	CTTTGAA	0.15259	0.14791
cg2254337	FBN1	SRY [T00	475	483	8.174786	CTTTGCT	0.15259	0.14791

cg0738020	FBN1	c-Ets-1 [T	1051	1057	8.116854	GTTCCA	0.24414	0.2494
cg0738020	FBN1	VDR [T00	1057	1065	8.079962	GTTCAT	0.24414	0.22992
cg2254337	FBN1	VDR [T00	1892	1900	8.079962	TTTTGA	0.24414	0.22992
cg0738020	FBN1	GR-alpha [	177	181	8.073878	CCTAG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	185	189	8.073878	CCTGC	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	685	689	8.073878	GTAGG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	813	817	8.073878	CTAGG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	913	917	8.073878	CCAGG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	943	947	8.073878	CCAGG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	957	961	8.073878	GCAGG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	1082	1086	8.073878	CTAGG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	1362	1366	8.073878	CCTAC	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	1751	1755	8.073878	CCAGG	7.8125	8.20289
cg0738020	FBN1	GR-alpha [	1787	1791	8.073878	CCTGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	93	97	8.073878	CCAGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	176	180	8.073878	GTAGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	299	303	8.073878	CCTGC	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	386	390	8.073878	CCTGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	445	449	8.073878	CCTGC	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	945	949	8.073878	CCAGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1087	1091	8.073878	CCTGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1113	1117	8.073878	GTAGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1302	1306	8.073878	CCTGC	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1334	1338	8.073878	CCTGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1352	1356	8.073878	GCAGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1382	1386	8.073878	CCTGC	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1433	1437	8.073878	CCTAG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1434	1438	8.073878	CTAGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1451	1455	8.073878	CCTGC	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1474	1478	8.073878	CCTGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1537	1541	8.073878	GTAGG	7.8125	8.20289
cg2254337	FBN1	GR-alpha [	1867	1871	8.073878	GCAGG	7.8125	8.20289
cg0738020	FBN1	TFIID [T0	66	72	8.014558	TAACAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	232	238	8.014558	TTTGCT	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	626	632	8.014558	TAGCAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	779	785	8.014558	TTAGAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	846	852	8.014558	TTACAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	985	991	8.014558	TCTCAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	1174	1180	8.014558	TTGGAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	1205	1211	8.014558	TAACAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	1576	1582	8.014558	TAACAA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	1644	1650	8.014558	TTTCTA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	1683	1689	8.014558	TTTGCA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	1876	1882	8.014558	TTTCTA	2.19727	1.99811
cg0738020	FBN1	TFIID [T0	1919	1925	8.014558	TTTCTG	2.19727	1.99811
cg0738020	FBN1	Pax-5 [T0	133	139	8.014558	GATGCC	2.19727	2.42766
cg0738020	FBN1	Pax-5 [T0	148	154	8.014558	GGGCTG	2.19727	2.42766
cg0738020	FBN1	Pax-5 [T0	1598	1604	8.014558	GGGCAG	2.19727	2.42766

cg2254337	FBN1	TFIID [T0	7	13	8.014558	TTTCATA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	201	207	8.014558	TAACAA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	591	597	8.014558	TTTGTTA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	639	645	8.014558	TCACAA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	662	668	8.014558	TATGAA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	902	908	8.014558	TTTGCA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	1494	1500	8.014558	TTTCCA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	1752	1758	8.014558	TCAGAA	2.19727	1.99811
cg2254337	FBN1	TFIID [T0	1760	1766	8.014558	TAACAA	2.19727	1.99811
cg2254337	FBN1	Pax-5 [T0	1355	1361	8.014558	GGGCTG	2.19727	2.42766
cg2254337	FBN1	Pax-5 [T0	1370	1376	8.014558	GGGCTG	2.19727	2.42766
cg2254337	FBN1	Pax-5 [T0	1790	1796	8.014558	GGGCAG	2.19727	2.42766
cg0738020	FBN1	C/EBPalph	1172	1178	8.006685	CATTGG	0.24414	0.23098
cg2254337	FBN1	HOXD9 [T	1031	1040	7.984404	AATAGA	0.08774	0.0777
cg2254337	FBN1	HOXD10 [	1031	1040	7.984404	AATAGA	0.08774	0.0777
cg2254337	FBN1	MEF-2A [	596	606	7.982343	TATTTAT	0.04005	0.03447
cg2254337	FBN1	CTF [T001	1146	1157	7.899258	TAGAAT	0.02003	0.01872
cg0738020	FBN1	c-Ets-2 [T	1981	1989	7.84116	TTTCAG	0.32043	0.30792
cg2254337	FBN1	c-Ets-2 [T	91	99	7.84116	TCCCAG	0.32043	0.30792
cg2254337	FBN1	c-Myb [T0	258	265	7.825375	CCAAGT	0.21362	0.20997
cg2254337	FBN1	IRF-1 [T0	1084	1092	7.82345	TTTCCT	0.25177	0.2462
cg2254337	FBN1	RXR-alpha	459	465	7.815913	GCCACC	0.24414	0.26389
cg0738020	FBN1	NF-AT2 [	1790	1799	7.788021	GGAAAC	0.08965	0.08482
cg0738020	FBN1	c-Ets-2 [T	1398	1406	7.76635	CCACAG	0.32043	0.30792
cg0738020	FBN1	NF-AT1 [	1076	1084	7.744746	GGAAAG	0.19836	0.19379
cg2254337	FBN1	c-Myb [T0	1315	1322	7.739476	CTCAGT	0.42725	0.40917
cg0738020	FBN1	c-Ets-1 [T	196	202	7.642098	ATTCCG	0.48828	0.48642
cg0738020	FBN1	NFI/CTF [	356	363	7.587343	ACACTT	0.36621	0.36269
cg0738020	FBN1	NFI/CTF [	1629	1636	7.587343	CCAAAT	0.36621	0.36269
cg2254337	FBN1	NFI/CTF [	464	471	7.587343	CCAAAT	0.36621	0.36269
cg0738020	FBN1	NF-AT1 [	1120	1128	7.574801	GGAAAA	0.19836	0.19379
cg0738020	FBN1	c-Jun [T00	924	930	7.538568	TGACAT	0.48828	0.48672
cg0738020	FBN1	GR [T050	69	75	7.527031	CAAAAG	1.83105	1.71535
cg0738020	FBN1	GR [T050	699	705	7.527031	ATATTT	1.83105	1.71535
cg0738020	FBN1	GR [T050	799	805	7.527031	CAAACA	1.83105	1.71535
cg0738020	FBN1	GR [T050	889	895	7.527031	CAAACA	1.83105	1.71535
cg0738020	FBN1	GR [T050	970	976	7.527031	CAAAAG	1.83105	1.71535
cg0738020	FBN1	GR [T050	988	994	7.527031	CAAAAT	1.83105	1.71535
cg0738020	FBN1	GR [T050	992	998	7.527031	ATGTTT	1.83105	1.71535
cg0738020	FBN1	GR [T050	1139	1145	7.527031	CAAAAG	1.83105	1.71535
cg0738020	FBN1	GR [T050	1690	1696	7.527031	CAAAAG	1.83105	1.71535
cg2254337	FBN1	GR [T050	468	474	7.527031	ATGTTT	1.83105	1.71535
cg2254337	FBN1	GR [T050	473	479	7.527031	TGCTTT	1.83105	1.71535
cg2254337	FBN1	GR [T050	524	530	7.527031	ACTTTT	1.83105	1.71535
cg2254337	FBN1	GR [T050	656	662	7.527031	CAAATA	1.83105	1.71535
cg2254337	FBN1	GR [T050	678	684	7.527031	TGCTTT	1.83105	1.71535
cg2254337	FBN1	GR [T050	936	942	7.527031	TCTTTTG	1.83105	1.71535
cg2254337	FBN1	GR [T050	1288	1294	7.527031	CAAAAG	1.83105	1.71535

cg2254337	FBN1	GR [T050	1684	1690	7.527031	CAAATA	1.83105	1.71535
cg2254337	FBN1	GR [T050	1763	1769	7.527031	CAAAGC	1.83105	1.71535
cg2254337	FBN1	GR [T050	1766	1772	7.527031	AGCTTTC	1.83105	1.71535
cg2254337	FBN1	GR [T050	1832	1838	7.527031	CAAAAG	1.83105	1.71535
cg2254337	FBN1	GR [T050	1927	1933	7.527031	ATATTTC	1.83105	1.71535
cg2254337	FBN1	RAR-beta	1659	1668	7.47824	TCTCAAC	0.24414	0.25121
cg2254337	FBN1	C/EBPalph	400	406	7.465744	TTCAATC	0.48828	0.45033
cg2254337	FBN1	RAR-beta	1066	1075	7.459774	GAAAAA	0.24414	0.25121
cg2254337	FBN1	PEA3 [T0	324	332	7.421728	ACTCATC	0.34332	0.35389
cg0738020	FBN1	IRF-1 [T0	1072	1080	7.387351	TGGGGG	0.14496	0.14723
cg0738020	FBN1	E2F-1 [T0	1867	1874	7.336545	AATGCC	0.45776	0.49661
cg2254337	FBN1	E2F-1 [T0	448	455	7.336545	GCGGCA	0.45776	0.49661
cg0738020	FBN1	HOXD9 [	64	73	7.270719	AATAAC	0.06866	0.05771
cg0738020	FBN1	HOXD9 [	822	831	7.270719	TGTTGT	0.06866	0.05771
cg0738020	FBN1	HOXD10 [	64	73	7.270719	AATAAC	0.06866	0.05771
cg0738020	FBN1	HOXD10 [	822	831	7.270719	TGTTGT	0.06866	0.05771
cg2254337	FBN1	HOXD9 [	590	599	7.270719	TTTTGTT	0.06866	0.05771
cg2254337	FBN1	HOXD9 [	1726	1735	7.270719	AATAAC	0.06866	0.05771
cg2254337	FBN1	HOXD10 [	590	599	7.270719	TTTTGTT	0.06866	0.05771
cg2254337	FBN1	HOXD10 [	1726	1735	7.270719	AATAAC	0.06866	0.05771
cg0738020	FBN1	p53 [T006	754	760	7.266844	AAAGCC	0.73242	0.79826
cg2254337	FBN1	POU2F2 (	732	742	7.236857	TGTATTA	0.00238	0.00196
cg0738020	FBN1	SRY [T00	625	633	7.175614	CTAGCA	0.30518	0.29547
cg2254337	FBN1	SRY [T00	680	688	7.175614	CTTTGTC	0.30518	0.29547
cg0738020	FBN1	XBP-1 [T	245	250	7.172312	ATGAAG	2.92969	2.7512
cg0738020	FBN1	XBP-1 [T	500	505	7.172312	ACTCAT	2.92969	2.7512
cg0738020	FBN1	XBP-1 [T	899	904	7.172312	ATGATT	2.92969	2.7512
cg0738020	FBN1	XBP-1 [T	1439	1444	7.172312	ATTCAT	2.92969	2.7512
cg0738020	FBN1	XBP-1 [T	1485	1490	7.172312	ACTCAT	2.92969	2.7512
cg0738020	FBN1	XBP-1 [T	1715	1720	7.172312	ATGAGT	2.92969	2.7512
cg2254337	FBN1	XBP-1 [T	220	225	7.172312	ATGAAT	2.92969	2.7512
cg2254337	FBN1	XBP-1 [T	324	329	7.172312	ACTCAT	2.92969	2.7512
cg2254337	FBN1	XBP-1 [T	337	342	7.172312	AATCAT	2.92969	2.7512
cg2254337	FBN1	XBP-1 [T	404	409	7.172312	ATGAAT	2.92969	2.7512
cg2254337	FBN1	XBP-1 [T	1814	1819	7.172312	ATGAGG	2.92969	2.7512
cg0738020	FBN1	c-Myb [T0	1053	1060	7.127234	TCCAGT	0.18311	0.17765
cg2254337	FBN1	NF-AT1 [	750	758	7.095752	CTCTTTT	0.15259	0.14325
cg0738020	FBN1	c-Ets-1 [T	404	410	7.071349	AGGGAA	0.73242	0.73732
cg0738020	FBN1	c-Ets-1 [T	1940	1946	7.071349	TTTCCCT	0.73242	0.73732
cg2254337	FBN1	c-Ets-1 [T	1298	1304	7.071349	TTTCCCT	0.73242	0.73732
cg0738020	FBN1	IRF-1 [T0	19	27	7.044985	GAGAGG	0.1297	0.12685
cg0738020	FBN1	IRF-1 [T0	1116	1124	7.044985	TAGAGG	0.1297	0.12685
cg2254337	FBN1	C/EBPalph	170	176	7.00174	GACAAT	0.73242	0.68282
cg0738020	FBN1	HNF-3alph	987	994	7.000129	TCAAAA	0.82397	0.71909
cg0738020	FBN1	HNF-3alph	1759	1766	7.000129	TATTTGT	0.82397	0.71909
cg2254337	FBN1	HNF-3alph	1011	1018	7.000129	AATTTTC	0.82397	0.71909
cg2254337	FBN1	HNF-3alph	1857	1864	7.000129	ACTAAA	0.82397	0.71909
cg2254337	FBN1	HNF-3alph	1889	1896	7.000129	AATTTTT	0.82397	0.71909

cg2254337	FBN1	RXR-alph	1597	1603	6.967687	ACCACC	0.36621	0.38841
cg0738020	FBN1	NF-1 [T00	360	367	6.948522	TTGGCT	0.48828	0.50205
cg0738020	FBN1	c-Ets-1 [T	1074	1080	6.943262	GGGGAA	0.73242	0.73732
cg0738020	FBN1	ENKTF-1	1256	1263	6.942764	CGGAGC	1.46484	1.56616
cg2254337	FBN1	ENKTF-1	455	462	6.942764	CTCTGC	1.46484	1.56616
cg2254337	FBN1	ENKTF-1	1508	1515	6.942764	CCAAGC	1.46484	1.56616
cg0738020	FBN1	VDR [T00	283	291	6.925682	GTTCAT	0.42725	0.41
cg0738020	FBN1	VDR [T00	383	391	6.925682	GTTCAT	0.42725	0.41
cg0738020	FBN1	VDR [T00	508	516	6.925682	GTTCAT	0.42725	0.41
cg0738020	FBN1	VDR [T00	832	840	6.925682	GTTCAC	0.42725	0.41
cg0738020	FBN1	VDR [T00	1581	1589	6.925682	AAACTG	0.42725	0.41
cg0738020	FBN1	VDR [T00	1814	1822	6.925682	GTTCAG	0.42725	0.41
cg0738020	FBN1	VDR [T00	1934	1942	6.925682	GTTCAT	0.42725	0.41
cg0738020	FBN1	c-Jun [T00	795	801	6.856451	TGACCA	0.73242	0.73062
cg2254337	FBN1	C/EBPalp	1419	1425	6.85549	AATTGA	0.73242	0.68282
cg0738020	FBN1	ATF-2 [T0	865	874	6.803907	CTGACG	0.01907	0.01989
cg0738020	FBN1	NF-AT1 [	23	31	6.799037	GGAAAG	0.15259	0.14325
cg2254337	FBN1	C/EBPalp	18	24	6.786177	TATTGT	0.73242	0.68282
cg0738020	FBN1	NFI/CTF [	798	805	6.786076	CCAAAC	0.73242	0.74795
cg0738020	FBN1	NFI/CTF [	888	895	6.786076	CCAAAC	0.73242	0.74795
cg2254337	FBN1	NFI/CTF [	1508	1515	6.786076	CCAAGC	0.73242	0.74795
cg0738020	FBN1	p53 [T006	538	544	6.775228	GGGCTA	1.09863	1.22478
cg2254337	FBN1	NF-1 [T00	1788	1795	6.722386	TTGGGC	0.24414	0.2565
cg2254337	FBN1	c-Myb [T0	608	615	6.719843	CAACTA	0.30518	0.30272
cg2254337	FBN1	c-Myb [T0	1626	1633	6.719843	CAACTA	0.30518	0.30272
cg2254337	FBN1	IRF-1 [T0	1441	1449	6.699483	TTTCCT	0.19073	0.1875
cg0738020	FBN1	c-Ets-2 [T	462	470	6.695187	TTACAG	0.09155	0.08559
cg0738020	FBN1	PXR-1:RX	380	387	6.668182	TGTGTT	0.24414	0.23169
cg0738020	FBN1	PXR-1:RX	573	580	6.668182	TGAACA	0.24414	0.23169
cg2254337	FBN1	c-Jun [T00	1844	1850	6.668031	TGACTT	0.61035	0.6179
cg0738020	FBN1	AR [T000	881	889	6.603347	GACTTG	0.19836	0.20813
cg0738020	FBN1	AR [T000	947	955	6.603347	GGACAA	0.19836	0.20813
cg0738020	FBN1	FOXP3 [T	390	395	6.581441	GTTTTA	0.97656	0.904
cg0738020	FBN1	FOXP3 [T	571	576	6.581441	GTTGAA	0.97656	0.904
cg0738020	FBN1	TFII-I [T0	1453	1458	6.581441	ATCTCC	0.97656	0.9991
cg0738020	FBN1	TFII-I [T0	1733	1738	6.581441	CACTCC	0.97656	0.9991
cg2254337	FBN1	FOXP3 [T	895	900	6.581441	GTTGAA	0.97656	0.904
cg2254337	FBN1	FOXP3 [T	1694	1699	6.581441	GTTGAA	0.97656	0.904
cg2254337	FBN1	TFII-I [T0	793	798	6.581441	ATCTCC	0.97656	0.9991
cg2254337	FBN1	TFII-I [T0	806	811	6.581441	CACTCC	0.97656	0.9991
cg2254337	FBN1	TFII-I [T0	912	917	6.581441	GGAGTG	0.97656	0.9991
cg2254337	FBN1	RXR-alph	1167	1173	6.563693	GGGTGT	0.24414	0.25119
cg2254337	FBN1	p53 [T006	1355	1361	6.563521	GGGCTG	0.48828	0.54643
cg0738020	FBN1	PXR-1:RX	280	287	6.5446	TATGTT	0.24414	0.23169
cg0738020	FBN1	PXR-1:RX	505	512	6.5446	TTTGTT	0.24414	0.23169
cg2254337	FBN1	PXR-1:RX	497	504	6.5446	TGAACA	0.24414	0.23169
cg0738020	FBN1	IRF-1 [T0	1172	1180	6.535281	CATTGG	0.19073	0.1875
cg0738020	FBN1	PPAR-alp	1659	1669	6.51544	CTCTGG	0.03719	0.04058

cg0738020	FBN1	XBP-1 [T	134	139	6.478682	ATGCCC	0.97656	0.99906
cg0738020	FBN1	XBP-1 [T	323	328	6.478682	TGGCAT	0.97656	0.99906
cg0738020	FBN1	XBP-1 [T	1169	1174	6.478682	GGGCAT	0.97656	0.99906
cg0738020	FBN1	XBP-1 [T	1369	1374	6.478682	ATGCCC	0.97656	0.99906
cg2254337	FBN1	XBP-1 [T	832	837	6.478682	TGGCAT	0.97656	0.99906
cg2254337	FBN1	XBP-1 [T	970	975	6.478682	TGGCAT	0.97656	0.99906
cg0738020	FBN1	c-Jun [T00	547	553	6.475265	CGTGTC	0.61035	0.6179
cg2254337	FBN1	c-Jun [T00	632	638	6.462218	TGACTA	0.61035	0.6179
cg0738020	FBN1	IRF-1 [T0	515	523	6.461745	TTTCCA	0.19073	0.1875
cg0738020	FBN1	c-Fos [T00	201	210	6.448203	GAGTCA	0.04578	0.04485
cg0738020	FBN1	c-Fos [T00	1318	1327	6.448203	GAGTCA	0.04578	0.04485
cg0738020	FBN1	c-Ets-1 [T	1174	1180	6.423689	TTGGAA	0.48828	0.48842
cg2254337	FBN1	c-Ets-1 [T	1494	1500	6.423689	TTTCCA	0.48828	0.48842
cg2254337	FBN1	HOXD9 [	533	542	6.40726	CTCTTTT	0.01144	0.01024
cg2254337	FBN1	HOXD10 [	533	542	6.40726	CTCTTTT	0.01144	0.01024
cg2254337	FBN1	C/EBPalph	1149	1155	6.391486	AATTGG	0.48828	0.47407
cg0738020	FBN1	TCF-4E [	29	35	6.302385	AACAAA	0.61035	0.59686
cg0738020	FBN1	TCF-4E [	1162	1168	6.302385	CTTTGA	0.61035	0.59686
cg0738020	FBN1	TCF-4E [	1206	1212	6.302385	AACAAA	0.61035	0.59686
cg2254337	FBN1	TCF-4E [	202	208	6.302385	AACAAA	0.61035	0.59686
cg2254337	FBN1	TCF-4E [	1761	1767	6.302385	AACAAA	0.61035	0.59686
cg0738020	FBN1	GR-alpha [	189	193	6.263098	CCTTA	3.90625	3.89624
cg0738020	FBN1	GR-alpha [	270	274	6.263098	TAAGG	3.90625	3.89624
cg0738020	FBN1	GR-alpha [	332	336	6.263098	TGAGG	3.90625	3.89624
cg0738020	FBN1	GR-alpha [	1771	1775	6.263098	TAAGG	3.90625	3.89624
cg2254337	FBN1	GR-alpha [	1257	1261	6.263098	CCTTA	3.90625	3.89624
cg2254337	FBN1	GR-alpha [	1314	1318	6.263098	CCTCA	3.90625	3.89624
cg2254337	FBN1	GR-alpha [	1779	1783	6.263098	TAAGG	3.90625	3.89624
cg2254337	FBN1	GR-alpha [	1815	1819	6.263098	TGAGG	3.90625	3.89624
cg2254337	FBN1	GR-alpha [	1900	1904	6.263098	CCTTA	3.90625	3.89624
cg0738020	FBN1	AP-1 [T00	198	206	6.25518	TCCGAG	0.03052	0.03035
cg2254337	FBN1	IRF-1 [T0	1814	1822	6.24301	ATGAGG	0.16785	0.16217
cg2254337	FBN1	HNF-1B [	593	601	6.211503	TGTTAT	0.09918	0.08736
cg0738020	FBN1	IRF-1 [T0	463	471	6.206911	TACAGG	0.16785	0.16217
cg2254337	FBN1	NF-AT1 [	1490	1499	6.201624	TTTCTTT	0.03815	0.03661
cg0738020	FBN1	SRY [T00	231	239	6.176442	CTTTGC	0.15259	0.14742
cg2254337	FBN1	SRY [T00	159	167	6.176442	ATGACA	0.15259	0.14742
cg2254337	FBN1	SRY [T00	552	560	6.176442	CTTTGT	0.15259	0.14742
cg2254337	FBN1	SRY [T00	1768	1776	6.176442	CTTTGT	0.15259	0.14742
cg2254337	FBN1	c-Jun [T00	160	166	6.152811	TGACAA	0.36621	0.34478
cg2254337	FBN1	c-Jun [T00	553	559	6.152811	TTTGTC	0.36621	0.34478
cg2254337	FBN1	c-Jun [T00	1051	1057	6.152811	TTTGTC	0.36621	0.34478
cg2254337	FBN1	c-Jun [T00	1769	1775	6.152811	TTTGTC	0.36621	0.34478
cg0738020	FBN1	NF-AT1 [	406	414	6.150044	GGAAAA	0.06866	0.06621
cg2254337	FBN1	IRF-1 [T0	1494	1502	6.078807	TTTCCA	0.16785	0.16217
cg0738020	FBN1	GR-alpha [	369	373	6.055408	CCTGA	3.90625	3.89835
cg0738020	FBN1	GR-alpha [	490	494	6.055408	CCTGA	3.90625	3.89835
cg0738020	FBN1	GR-alpha [	551	555	6.055408	TCAGG	3.90625	3.89835

cg0738020	FBN1	GR-alpha [	563	567	6.055408	CCTAA	3.90625	3.89835
cg0738020	FBN1	GR-alpha [	1002	1006	6.055408	CCTAA	3.90625	3.89835
cg0738020	FBN1	GR-alpha [	1475	1479	6.055408	CCTGA	3.90625	3.89835
cg0738020	FBN1	GR-alpha [	1746	1750	6.055408	CCTGA	3.90625	3.89835
cg0738020	FBN1	GR-alpha [	1983	1987	6.055408	TCAGG	3.90625	3.89835
cg2254337	FBN1	GR-alpha [	117	121	6.055408	CCTAA	3.90625	3.89835
cg2254337	FBN1	GR-alpha [	278	282	6.055408	TCAGG	3.90625	3.89835
cg2254337	FBN1	GR-alpha [	959	963	6.055408	CCTGA	3.90625	3.89835
cg2254337	FBN1	GR-alpha [	1046	1050	6.055408	CCTAA	3.90625	3.89835
cg2254337	FBN1	GR-alpha [	1211	1215	6.055408	TCAGG	3.90625	3.89835
cg2254337	FBN1	GR-alpha [	1503	1507	6.055408	TCAGG	3.90625	3.89835
cg2254337	FBN1	GR-alpha [	1602	1606	6.055408	CCTGA	3.90625	3.89835
cg0738020	FBN1	c-Ets-1 [T	515	521	6.039428	TTTCCA	0.36621	0.36174
cg0738020	FBN1	c-Ets-1 [T	1788	1794	6.039428	CTGGAA	0.36621	0.36174
cg0738020	FBN1	NF-AT1 [	1790	1798	6.003834	GGAAAC	0.06866	0.06621
cg2254337	FBN1	HOXD9 [	349	358	5.898575	AATTTC	0.05722	0.04686
cg2254337	FBN1	HOXD10 [	349	358	5.898575	AATTTC	0.05722	0.04686
cg0738020	FBN1	c-Fos [T00	1405	1414	5.891709	AATGTG	0.09155	0.09198
cg0738020	FBN1	STAT4 [T	304	309	5.882353	GGAAGG	0.48828	0.51201
cg0738020	FBN1	STAT4 [T	1358	1363	5.882353	CCTTCC	0.48828	0.51201
cg0738020	FBN1	c-Ets-1 [T	1234	1240	5.814485	TGGGAA	0.36621	0.36174
cg2254337	FBN1	c-Ets-1 [T	1679	1685	5.814485	CTTCCC	0.36621	0.36174
cg0738020	FBN1	STAT1bet	463	472	5.796867	TACAGG	0.1545	0.14881
cg0738020	FBN1	STAT1bet	1072	1081	5.796867	TGGGGG	0.1545	0.14881
cg2254337	FBN1	STAT1bet	1083	1092	5.796867	ATTTCC	0.1545	0.14881
cg0738020	FBN1	c-Jun [T00	1159	1165	5.783074	TGACTT	0.36621	0.34478
cg2254337	FBN1	c-Jun [T00	436	442	5.783074	AAAGTC	0.36621	0.34478
cg2254337	FBN1	c-Jun [T00	1290	1296	5.783074	AAAGTC	0.36621	0.34478
cg0738020	FBN1	C/EBPalp	1910	1916	5.781231	TATTGG	0.97656	0.91422
cg2254337	FBN1	NF-AT1 [	1490	1498	5.77403	TTTCTTT	0.06866	0.06621
cg2254337	FBN1	NF-AT2 [	208	217	5.75046	GGAAAG	0.04196	0.03934
cg2254337	FBN1	ENKTF-1	1323	1330	5.687009	TGGCTC	0.73242	0.76357
cg0738020	FBN1	IRF-1 [T0	1786	1794	5.65977	ACCTGG	0.22888	0.21959
cg0738020	FBN1	HNF-1A [	1572	1579	5.610392	GACTTA	0.24414	0.23087
cg0738020	FBN1	c-Jun [T00	371	377	5.590308	TGACAC	0.48828	0.49294
cg2254337	FBN1	NFI/CTF [	1881	1888	5.558661	CCAAAC	0.54932	0.55504
cg2254337	FBN1	c-Ets-1 [T	362	368	5.558311	CTTCCC	0.36621	0.38732
cg2254337	FBN1	c-Ets-1 [T	1181	1187	5.558311	GGGGAA	0.36621	0.38732
cg0738020	FBN1	TFIID [T0	750	756	5.544826	TTCTAA	0.73242	0.65314
cg0738020	FBN1	TFIID [T0	1862	1868	5.544826	TTTAGA	0.73242	0.65314
cg0738020	FBN1	TFIID [T0	1877	1883	5.544826	TTCTAA	0.73242	0.65314
cg2254337	FBN1	TFIID [T0	254	260	5.544826	TTTACC	0.73242	0.65314
cg2254337	FBN1	TFIID [T0	576	582	5.544826	TTTATC	0.73242	0.65314
cg2254337	FBN1	TFIID [T0	1233	1239	5.544826	TTTACC	0.73242	0.65314
cg0738020	FBN1	NF-AT1 [	1175	1184	5.512555	TGGAAA	0.05913	0.05666
cg0738020	FBN1	p53 [T006	148	154	5.508538	GGGCTG	0.61035	0.65765
cg2254337	FBN1	p53 [T006	1370	1376	5.508538	GGGCTG	0.61035	0.65765
cg2254337	FBN1	HNF-1A [	130	137	5.466509	GTTAAG	0.24414	0.23087

cg0738020	FBN1	C/EBPalph	1855	1861	5.455853	CATTGAT	0.73242	0.68229
cg2254337	FBN1	HOXD9 [T	147	156	5.453039	AGCTTTT	0.04578	0.03952
cg2254337	FBN1	HOXD10 [	147	156	5.453039	AGCTTTT	0.04578	0.03952
cg0738020	FBN1	C/EBPalph	1530	1536	5.38654	AACAATT	0.73242	0.68229
cg2254337	FBN1	NF-1 [T00	1504	1511	5.377909	CAGGCCA	0.24414	0.25051
cg0738020	FBN1	RXR-alpha	250	256	5.271235	GGGTTGG	0.61035	0.65415
cg0738020	FBN1	GR [T0507	629	635	5.207533	CAAAGA	0.24414	0.24013
cg0738020	FBN1	GR [T0507	762	768	5.207533	CAAAAC	0.24414	0.24013
cg2254337	FBN1	GR [T0507	1946	1952	5.207533	CAAAAC	0.24414	0.24013
cg2254337	FBN1	c-Jun [T00	768	774	5.193102	TGACTTC	0.61035	0.60573
cg0738020	FBN1	NF-AT1 [T	511	519	5.125037	CATTTTT	0.05341	0.05073
cg0738020	FBN1	AP-2alpha	932	937	5.100982	AAAGGC	0.97656	0.97517
cg0738020	FBN1	AP-2alpha	1915	1920	5.100982	GCCTTT	0.97656	0.97517
cg2254337	FBN1	AP-2alpha	57	62	5.100982	GCCTTT	0.97656	0.97517
cg2254337	FBN1	AP-2alpha	1515	1520	5.100982	AAAGGC	0.97656	0.97517
cg2254337	FBN1	SRY [T00	1740	1748	5.086565	TCTACAA	0.06104	0.05662
cg0738020	FBN1	USF2 [T0	179	188	5.052423	TAGACAC	0.103	0.10797
cg0738020	FBN1	USF2 [T0	1781	1790	5.052423	CAGCCAC	0.103	0.10797
cg0738020	FBN1	AP-1 [T00	1315	1323	5.043062	TGGGAGT	0.12207	0.12309
cg0738020	FBN1	GR-beta [T	113	117	5.042296	AATAC	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	336	340	5.042296	GTATT	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	353	357	5.042296	AATAC	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	528	532	5.042296	AATAC	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	776	780	5.042296	GTATT	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	916	920	5.042296	GGATT	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	1112	1116	5.042296	GGATT	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	1216	1220	5.042296	GTATT	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	1482	1486	5.042296	AATAC	3.90625	3.7093
cg0738020	FBN1	GR-beta [T	1758	1762	5.042296	GTATT	3.90625	3.7093
cg2254337	FBN1	GR-beta [T	89	93	5.042296	AATCC	3.90625	3.7093
cg2254337	FBN1	GR-beta [T	442	446	5.042296	AATCC	3.90625	3.7093
cg2254337	FBN1	GR-beta [T	573	577	5.042296	GTATT	3.90625	3.7093
cg2254337	FBN1	GR-beta [T	733	737	5.042296	GTATT	3.90625	3.7093
cg2254337	FBN1	GR-beta [T	1607	1611	5.042296	AATCC	3.90625	3.7093
cg2254337	FBN1	GR-beta [T	1936	1940	5.042296	AATAC	3.90625	3.7093
cg0738020	FBN1	E2F-1 [T0	1421	1428	5.042045	GCGGGA	0.18311	0.20394
cg2254337	FBN1	c-Ets-1 [T0	1828	1834	5.038739	CTTCCAA	0.48828	0.48026
cg0738020	FBN1	C/EBPalph	219	225	5.024728	TTCAATC	0.97656	0.90302
cg0738020	FBN1	C/EBPalph	917	923	5.024728	GATTGCA	0.97656	0.90302
cg2254337	FBN1	C/EBPalph	86	92	5.024728	TTCAATC	0.97656	0.90302
cg0738020	FBN1	c-Jun [T00	997	1003	5.000337	TGACGCC	0.61035	0.60573
cg2254337	FBN1	AP-1 [T00	1041	1049	4.990183	TGACTCC	0.12207	0.12309
cg0738020	FBN1	c-Ets-1 [T0	302	308	4.910652	ATGGAAC	0.48828	0.48026
cg0738020	FBN1	c-Ets-1 [T0	1387	1393	4.910652	CTTCCAT	0.48828	0.48026
cg2254337	FBN1	c-Ets-1 [T0	71	77	4.910652	CTTCCAT	0.48828	0.48026
cg2254337	FBN1	c-Ets-1 [T0	1922	1928	4.910652	CTTCCAT	0.48828	0.48026
cg2254337	FBN1	PXR-1:RX	1896	1903	4.90845	TGAACCT	0.12207	0.11843
cg0738020	FBN1	EBF [T054	940	950	4.906683	TCCCCAC	0.02289	0.02569

cg0738020	FBN1	XBP-1 [T	487	492	4.894955	ATGCCT	0.97656	0.99839
cg0738020	FBN1	XBP-1 [T	553	558	4.894955	AGGCAT	0.97656	0.99839
cg0738020	FBN1	XBP-1 [T	959	964	4.894955	AGGCAT	0.97656	0.99839
cg0738020	FBN1	XBP-1 [T	1868	1873	4.894955	ATGCCG	0.97656	0.99839
cg2254337	FBN1	XBP-1 [T	449	454	4.894955	CGGCAT	0.97656	0.99839
cg2254337	FBN1	XBP-1 [T	601	606	4.894955	ATGCCT	0.97656	0.99839
cg2254337	FBN1	XBP-1 [T	1226	1231	4.894955	ATGCCT	0.97656	0.99839
cg0738020	FBN1	AP-2alpha	1001	1006	4.890408	GCCTAA	0.97656	0.97517
cg0738020	FBN1	c-Jun [T00	312	318	4.883696	TGACAT	0.61035	0.60573
cg0738020	FBN1	c-Jun [T00	1957	1963	4.883696	TATGTC	0.61035	0.60573
cg0738020	FBN1	AP-1 [T00	1409	1417	4.868583	TGACTC	0.12207	0.12309
cg2254337	FBN1	RXR-alph	10	16	4.86724	CATACC	0.48828	0.51407
cg0738020	FBN1	HNF-3alph	238	245	4.842999	ATAAAA	0.09155	0.07438
cg2254337	FBN1	HNF-3alph	706	713	4.842999	TTTAAA	0.09155	0.07438
cg2254337	FBN1	HNF-3alph	736	743	4.842999	TTAAAA	0.09155	0.07438
cg2254337	FBN1	HNF-1A [	668	675	4.828753	AACTTA	0.36621	0.34064
cg0738020	FBN1	C/EBPalph	695	701	4.776286	AACAAT	0.97656	0.90302
cg0738020	FBN1	C/EBPalph	828	834	4.776286	TATTGT	0.97656	0.90302
cg2254337	FBN1	C/EBPalph	726	732	4.776286	TATTGG	0.97656	0.90302
cg2254337	FBN1	C/EBPalph	1800	1806	4.776286	TATTGT	0.97656	0.90302
cg0738020	FBN1	FOXP3 [T	409	414	4.756447	AAAAAC	2.92969	2.82
cg0738020	FBN1	FOXP3 [T	493	498	4.756447	GAAAAC	2.92969	2.82
cg0738020	FBN1	FOXP3 [T	521	526	4.756447	GTCAAC	2.92969	2.82
cg0738020	FBN1	FOXP3 [T	762	767	4.756447	CAAAAC	2.92969	2.82
cg0738020	FBN1	FOXP3 [T	1579	1584	4.756447	CAAAAC	2.92969	2.82
cg0738020	FBN1	FOXP3 [T	1635	1640	4.756447	GTTTTG	2.92969	2.82
cg0738020	FBN1	TFII-I [T0	173	178	4.756447	CATTCC	2.92969	2.89715
cg0738020	FBN1	TFII-I [T0	262	267	4.756447	GGACTG	2.92969	2.89715
cg0738020	FBN1	TFII-I [T0	467	472	4.756447	GGAAAT	2.92969	2.89715
cg0738020	FBN1	TFII-I [T0	916	921	4.756447	GGATTG	2.92969	2.89715
cg0738020	FBN1	TFII-I [T0	1403	1408	4.756447	GGAATG	2.92969	2.89715
cg2254337	FBN1	FOXP3 [T	82	87	4.756447	GTTTTT	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	214	219	4.756447	GTTTTC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	303	308	4.756447	CTCAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	568	573	4.756447	GTTTTG	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	588	593	4.756447	GTTTTT	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	651	656	4.756447	CTCAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	665	670	4.756447	GAAAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	986	991	4.756447	AAAAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1067	1072	4.756447	AAAAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1525	1530	4.756447	AAAAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1645	1650	4.756447	ATCAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1660	1665	4.756447	CTCAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1946	1951	4.756447	CAAAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1954	1959	4.756447	AAAAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1973	1978	4.756447	AAAAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1983	1988	4.756447	CTCAAC	2.92969	2.82
cg2254337	FBN1	FOXP3 [T	1991	1996	4.756447	CAAAAC	2.92969	2.82

cg2254337	FBN1	TFII-I [T0(	88	93	4.756447	CAATCC	2.92969	2.89715
cg2254337	FBN1	TFII-I [T0(	441	446	4.756447	CAATCC	2.92969	2.89715
cg2254337	FBN1	TFII-I [T0(	1083	1088	4.756447	ATTTCC	2.92969	2.89715
cg2254337	FBN1	TFII-I [T0(	1238	1243	4.756447	CAGTCC	2.92969	2.89715
cg2254337	FBN1	TFII-I [T0(	1310	1315	4.756447	CATTCC	2.92969	2.89715
cg2254337	FBN1	TFII-I [T0(	1818	1823	4.756447	GGAAAT	2.92969	2.89715
cg2254337	FBN1	TFII-I [T0(	1909	1914	4.756447	ATATCC	2.92969	2.89715
cg0738020	FBN1	HNF-1A [	1201	1208	4.684871	ATCTTA	0.12207	0.10966
cg2254337	FBN1	c-Ets-1 [T(	686	692	4.654478	CTTCCA(	0.85449	0.8381
cg0738020	FBN1	VDR [T00	569	577	4.617121	ATGTTG	0.37384	0.36855
cg2254337	FBN1	VDR [T00	493	501	4.617121	AGACTG	0.37384	0.36855
cg2254337	FBN1	VDR [T00	893	901	4.617121	TCGTTG	0.37384	0.36855
cg0738020	FBN1	c-Ets-1 [T(	174	180	4.539113	ATTCCTA	0.85449	0.8381
cg2254337	FBN1	c-Ets-1 [T(	177	183	4.539113	TAGGAA	0.85449	0.8381
cg0738020	FBN1	T3R-beta1	669	677	4.481316	TCACCTA	0.27466	0.27245
cg2254337	FBN1	GATA-2 [	990	998	4.444445	ACATTA	0.24414	0.23857
cg0738020	FBN1	c-Jun [T00	152	158	4.441904	TGACTG	0.12207	0.11843
cg0738020	FBN1	c-Jun [T00	442	448	4.441904	TCAGTCA	0.12207	0.11843
cg0738020	FBN1	c-Jun [T00	862	868	4.441904	TGACTG	0.12207	0.11843
cg2254337	FBN1	AP-2alpha	1432	1437	4.438035	GCCTAG	0.97656	0.99839
cg2254337	FBN1	RXR-alpha	809	815	4.423008	TCCACC(	0.24414	0.25781
cg0738020	FBN1	AP-2alpha	188	193	4.422424	GCCTTA	0.97656	0.99839
cg2254337	FBN1	AP-2alpha	1779	1784	4.422424	TAAGGC	0.97656	0.99839
cg0738020	FBN1	STAT4 [T(	173	178	4.411765	CATTCC	1.95312	1.99838
cg0738020	FBN1	STAT4 [T(	937	942	4.411765	CGTTCC	1.95312	1.99838
cg0738020	FBN1	STAT4 [T(	1236	1241	4.411765	GGAAGA	1.95312	1.99838
cg0738020	FBN1	STAT4 [T(	1386	1391	4.411765	GCTTCC	1.95312	1.99838
cg0738020	FBN1	STAT4 [T(	1403	1408	4.411765	GGAATG	1.95312	1.99838
cg2254337	FBN1	STAT4 [T(	685	690	4.411765	TCTTCC	1.95312	1.99838
cg2254337	FBN1	STAT4 [T(	1183	1188	4.411765	GGAAGA	1.95312	1.99838
cg2254337	FBN1	STAT4 [T(	1310	1315	4.411765	CATTCC	1.95312	1.99838
cg2254337	FBN1	STAT4 [T(	1378	1383	4.411765	TCTTCC	1.95312	1.99838
cg2254337	FBN1	STAT4 [T(	1827	1832	4.411765	GCTTCC	1.95312	1.99838
cg2254337	FBN1	STAT4 [T(	1921	1926	4.411765	TCTTCC	1.95312	1.99838
cg2254337	FBN1	STAT4 [T(	1941	1946	4.411765	GGAAGC	1.95312	1.99838
cg2254337	FBN1	p53 [T006	1408	1414	4.33696	GGGCCA	0.24414	0.28373
cg2254337	FBN1	HNF-1C [	1709	1717	4.306318	GTTAAT(	0.07629	0.06715
cg2254337	FBN1	c-Ets-1 [T(	1311	1317	4.282938	ATTCCT(	0.85449	0.8381
cg0738020	FBN1	CREB [T0	866	874	4.261795	TGACGT(	0.04578	0.0464
cg0738020	FBN1	RXR-alpha	1834	1840	4.24113	GGGTAA	0.97656	1.02803
cg2254337	FBN1	RXR-alpha	1875	1881	4.24113	GGGACC	0.97656	1.02803
cg2254337	FBN1	AR [T000	949	957	4.241082	GCTCTG	0.06866	0.06981
cg2254337	FBN1	C/EBPalph	429	435	4.235345	AGCAAT	0.48828	0.46347
cg2254337	FBN1	C/EBPalph	1028	1034	4.235345	AGCAAT	0.48828	0.46347
cg0738020	FBN1	AP-2alpha	685	690	4.211849	GTAGGC	0.97656	1.02535
cg0738020	FBN1	GR-beta [	61	65	4.201913	AATAA	7.8125	7.23274
cg0738020	FBN1	GR-beta [	64	68	4.201913	AATAA	7.8125	7.23274
cg0738020	FBN1	GR-beta [	479	483	4.201913	AATAA	7.8125	7.23274

cg0738020	FBN1	GR-beta [T	586	590	4.201913	AATAG	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	619	623	4.201913	AATAA	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	664	668	4.201913	TGATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	673	677	4.201913	CTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	744	748	4.201913	TTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	827	831	4.201913	TTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	900	904	4.201913	TGATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1303	1307	4.201913	CTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1444	1448	4.201913	TTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1624	1628	4.201913	AATAA	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1639	1643	4.201913	TGATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1821	1825	4.201913	TTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1844	1848	4.201913	CTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1858	1862	4.201913	TGATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1883	1887	4.201913	AATAG	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1909	1913	4.201913	TTATT	7.8125	7.23274
cg0738020	FBN1	GR-beta [T	1925	1929	4.201913	AATAG	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	25	29	4.201913	CTATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	152	156	4.201913	TTATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	181	185	4.201913	AATAA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	246	250	4.201913	CTATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	270	274	4.201913	AATCA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	337	341	4.201913	AATCA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	354	358	4.201913	CTATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	432	436	4.201913	AATAA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	538	542	4.201913	TTATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	595	599	4.201913	TTATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	762	766	4.201913	AATAG	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1031	1035	4.201913	AATAG	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1138	1142	4.201913	TGATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1156	1160	4.201913	TTATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1161	1165	4.201913	AATCA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1374	1378	4.201913	TGATT	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1428	1432	4.201913	AATAG	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1644	1648	4.201913	AATCA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1686	1690	4.201913	AATAA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1712	1716	4.201913	AATCA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1726	1730	4.201913	AATAA	7.8125	7.23274
cg2254337	FBN1	GR-beta [T	1799	1803	4.201913	TTATT	7.8125	7.23274
cg0738020	FBN1	NF-Y [T0(	1173	1180	4.186615	ATTGGA	0.18311	0.17499
cg2254337	FBN1	NF-Y [T0(	1178	1185	4.186615	ATTGGG	0.18311	0.17499
cg0738020	FBN1	c-Ets-1 [T(	1401	1407	4.154851	CAGGAA	0.24414	0.23719
cg0738020	FBN1	c-Ets-1 [T(	1984	1990	4.154851	CAGGAA	0.24414	0.23719
cg0738020	FBN1	NF-1 [T00	254	261	4.135372	TGCCCC	0.24414	0.25714
cg0738020	FBN1	NF-AT1 [T	1789	1798	4.134416	TGGAAA	0.08392	0.07965
cg0738020	FBN1	c-Jun [T00	200	206	4.1298	CGAGTC	0.24414	0.23729
cg0738020	FBN1	RelA [T00	209	219	4.11851	GAGGTT	0.00811	0.0081
cg0738020	FBN1	NF-kappaI	934	944	4.078895	AGGCGT	0.01097	0.01194

cg2254337	FBN1	IRF-1 [T0	1298	1306	4.035054	TTTCCCT	0.1297	0.12468
cg2254337	FBN1	C/EBPalp	439	445	4.019783	GTCAAT	0.48828	0.46347
cg0738020	FBN1	RXR-alph	631	637	4.019014	AAGACC	0.97656	1.02803
cg2254337	FBN1	c-Ets-2 [T	203	211	4.017001	ACAAAG	0.16022	0.15061
cg0738020	FBN1	TFIID [T0	391	397	4.007279	TTTTAA	1.09863	0.94722
cg0738020	FBN1	TFIID [T0	618	624	4.007279	TAATAA	1.09863	0.94722
cg0738020	FBN1	Pax-5 [T0	754	760	4.007279	AAAGCC	1.09863	1.18533
cg0738020	FBN1	Pax-5 [T0	1169	1175	4.007279	GGGCAT	1.09863	1.18533
cg2254337	FBN1	TFIID [T0	734	740	4.007279	TATTAA	1.09863	0.94722
cg2254337	FBN1	TFIID [T0	759	765	4.007279	TTTAAT	1.09863	0.94722
cg2254337	FBN1	TFIID [T0	981	987	4.007279	TTTTAA	1.09863	0.94722
cg2254337	FBN1	Pax-5 [T0	1252	1258	4.007279	AGAGCC	1.09863	1.18533
cg0738020	FBN1	AR [T000	1041	1049	3.814754	GGACAC	0.06866	0.06981
cg0738020	FBN1	c-Jun [T00	266	272	3.807346	TGACTA	0.24414	0.23729
cg0738020	FBN1	NFI/CTF [	930	937	3.793671	CCAAAG	0.18311	0.19063
cg2254337	FBN1	NFI/CTF [	1513	1520	3.793671	CCAAAG	0.18311	0.19063
cg0738020	FBN1	GR [T050	31	37	3.763516	CAAAGA	0.73242	0.6946
cg0738020	FBN1	GR [T050	229	235	3.763516	CTCTTT	0.73242	0.6946
cg0738020	FBN1	GR [T050	1579	1585	3.763516	CAAAAC	0.73242	0.6946
cg0738020	FBN1	GR [T050	1634	1640	3.763516	TGTTTT	0.73242	0.6946
cg2254337	FBN1	GR [T050	163	169	3.763516	CAAAGA	0.73242	0.6946
cg2254337	FBN1	GR [T050	550	556	3.763516	TTCTTTG	0.73242	0.6946
cg2254337	FBN1	GR [T050	567	573	3.763516	TGTTTT	0.73242	0.6946
cg2254337	FBN1	GR [T050	1249	1255	3.763516	CAAAGA	0.73242	0.6946
cg2254337	FBN1	GR [T050	1991	1997	3.763516	CAAAAC	0.73242	0.6946
cg0738020	FBN1	HNF-1C [	1058	1066	3.755157	TTCATTA	0.04578	0.04045
cg2254337	FBN1	p53 [T006	1870	1876	3.750231	GGGCTG	0.73242	0.82434
cg0738020	FBN1	AP-2alpha	1357	1362	3.743866	GCCTTC	0.48828	0.5124
cg0738020	FBN1	AP-2alpha	1417	1422	3.743866	GAAGGC	0.48828	0.5124
cg0738020	FBN1	PEA3 [T0	924	932	3.710864	TGACAT	0.09155	0.08745
cg2254337	FBN1	IRF-1 [T0	754	762	3.692688	TTTCCTT	0.06866	0.0661
cg0738020	FBN1	IRF-1 [T0	402	410	3.689552	CGAGGG	0.06866	0.0661
cg2254337	FBN1	POU2F2 (	221	231	3.618429	TGAATT	0.00572	0.00469
cg0738020	FBN1	HNF-1B [	1059	1067	3.610263	TCATTA	0.04578	0.04011
cg0738020	FBN1	p53 [T006	1169	1175	3.516613	GGGCAT	0.73242	0.80362
cg0738020	FBN1	HNF-3alp	712	719	3.500065	AATTTC	0.27466	0.23175
cg2254337	FBN1	c-Ets-1 [T	94	100	3.462376	CAGGAA	0.61035	0.61936
cg0738020	FBN1	ATF3 [T0	312	319	3.372402	TGACAT	0.09155	0.08824
cg2254337	FBN1	T3R-beta1	142	150	3.370634	TCACCA	0.27466	0.27326
cg0738020	FBN1	GR-beta [	127	131	3.361531	AATAT	3.90625	3.51525
cg0738020	FBN1	GR-beta [	222	226	3.361531	AATCT	3.90625	3.51525
cg0738020	FBN1	GR-beta [	242	246	3.361531	AATAT	3.90625	3.51525
cg0738020	FBN1	GR-beta [	698	702	3.361531	AATAT	3.90625	3.51525
cg0738020	FBN1	GR-beta [	699	703	3.361531	ATATT	3.90625	3.51525
cg0738020	FBN1	GR-beta [	1128	1132	3.361531	AATCT	3.90625	3.51525
cg0738020	FBN1	GR-beta [	1901	1905	3.361531	ATATT	3.90625	3.51525
cg0738020	FBN1	GR-beta [	1977	1981	3.361531	AATCT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	17	21	3.361531	ATATT	3.90625	3.51525

cg2254337	FBN1	GR-beta [T	251	255	3.361531	ATATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	658	662	3.361531	AATAT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	710	714	3.361531	AATAT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	724	728	3.361531	AATAT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	725	729	3.361531	ATATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	827	831	3.361531	AATCT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	1101	1105	3.361531	AATCT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	1465	1469	3.361531	AGATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	1577	1581	3.361531	AATAT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	1796	1800	3.361531	ATATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	1836	1840	3.361531	AGATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	1861	1865	3.361531	AATAT	3.90625	3.51525
cg2254337	FBN1	GR-beta [T	1927	1931	3.361531	ATATT	3.90625	3.51525
cg2254337	FBN1	c-Ets-1 [T	1939	1945	3.359159	ACGGAA	0.61035	0.61936
cg2254337	FBN1	IRF-1 [T0	204	212	3.347186	CAAAGG	0.06866	0.0661
cg0738020	FBN1	PR B [T00	567	573	3.29756	AAATGT	0.24414	0.21408
cg0738020	FBN1	PR B [T00	990	996	3.29756	AAATGT	0.24414	0.21408
cg0738020	FBN1	PR B [T00	1530	1536	3.29756	AACAAT	0.24414	0.21408
cg0738020	FBN1	PR B [T00	1631	1637	3.29756	AAATGT	0.24414	0.21408
cg0738020	FBN1	PR A [T01	567	573	3.29756	AAATGT	0.24414	0.21408
cg0738020	FBN1	PR A [T01	990	996	3.29756	AAATGT	0.24414	0.21408
cg0738020	FBN1	PR A [T01	1530	1536	3.29756	AACAAT	0.24414	0.21408
cg0738020	FBN1	PR A [T01	1631	1637	3.29756	AAATGT	0.24414	0.21408
cg2254337	FBN1	PR B [T00	466	472	3.29756	AAATGT	0.24414	0.21408
cg2254337	FBN1	PR A [T01	466	472	3.29756	AAATGT	0.24414	0.21408
cg2254337	FBN1	c-Ets-2 [T	1312	1320	3.2883	TTCCTC	0.18311	0.18314
cg0738020	FBN1	RAR-beta	1615	1624	3.244529	TGGGTT	0.12207	0.12558
cg0738020	FBN1	AP-2alpha	1223	1228	3.229049	AGAGGC	0.48828	0.5124
cg2254337	FBN1	AP-2alpha	1918	1923	3.229049	GCCTCT	0.48828	0.5124
cg2254337	FBN1	HNF-4alpl	893	905	3.189869	TCGTTG	0.00209	0.00193
cg2254337	FBN1	RXR-alpha	1068	1074	3.170788	AAAACC	0.24414	0.24551
cg2254337	FBN1	RXR-alpha	1974	1980	3.170788	AAAACC	0.24414	0.24551
cg0738020	FBN1	TCF-4E [T	1682	1688	3.151193	CTTTGC	0.24414	0.23169
cg2254337	FBN1	TCF-4E [T	901	907	3.151193	CTTTGC	0.24414	0.23169
cg2254337	FBN1	TCF-4E [T	1247	1253	3.151193	TGCAAA	0.24414	0.23169
cg0738020	FBN1	POU2F2 (	458	468	3.116744	TGAATT	0.02575	0.02261
cg2254337	FBN1	POU2F2 (	620	630	3.116744	GATATA	0.02575	0.02261
cg0738020	FBN1	p53 [T006	252	258	3.024997	GTTGCC	0.48828	0.53227
cg2254337	FBN1	c-Fos [T00	867	876	3.022518	GAGTCA	0.06104	0.06233
cg0738020	FBN1	C/EBPalpl	1125	1131	3.014837	AGCAAT	0.48828	0.47526
cg0738020	FBN1	NF-kappaI	208	218	3.008169	AGAGGT	0.01669	0.01859
cg2254337	FBN1	C/EBPalpl	1177	1183	2.981957	CATTGG	0.48828	0.47526
cg2254337	FBN1	c-Ets-2 [T	755	763	2.945838	TTCCTTT	0.06104	0.05567
cg0738020	FBN1	STAT4 [T	23	28	2.941176	GGAAAG	2.92969	2.92382
cg0738020	FBN1	STAT4 [T	211	216	2.941176	GGTTCC	2.92969	2.92382
cg0738020	FBN1	STAT4 [T	1076	1081	2.941176	GGAAAG	2.92969	2.92382
cg0738020	FBN1	STAT4 [T	1217	1222	2.941176	TATTCC	2.92969	2.92382
cg0738020	FBN1	STAT4 [T	1304	1309	2.941176	TATTCC	2.92969	2.92382

cg0738020	FBN1	STAT4 [T	1709	1714	2.941176	GGTTCC	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	70	75	2.941176	ACTTCC	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	96	101	2.941176	GGAACC	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	179	184	2.941176	GGAATA	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	208	213	2.941176	GGAAAG	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	355	360	2.941176	TATTCC	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	361	366	2.941176	ACTTCC	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	1297	1302	2.941176	CTTTCC	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	1493	1498	2.941176	CTTTCC	2.92969	2.92382
cg2254337	FBN1	STAT4 [T	1678	1683	2.941176	ACTTCC	2.92969	2.92382
cg0738020	FBN1	p53 [T006	133	139	2.813291	GATGCC	0.48828	0.53227
cg0738020	FBN1	p53 [T006	1598	1604	2.813291	GGGCAG	0.48828	0.53227
cg2254337	FBN1	c-Fos [T00	1037	1046	2.810503	AGTCTG	0.06104	0.06233
cg0738020	FBN1	PR B [T00	695	701	2.80933	AACAAT	0.73242	0.66711
cg0738020	FBN1	PR B [T00	828	834	2.80933	TATTGTT	0.73242	0.66711
cg0738020	FBN1	PR A [T01	695	701	2.80933	AACAAT	0.73242	0.66711
cg0738020	FBN1	PR A [T01	828	834	2.80933	TATTGTT	0.73242	0.66711
cg2254337	FBN1	PR B [T00	564	570	2.80933	TAATGT	0.73242	0.66711
cg2254337	FBN1	PR B [T00	989	995	2.80933	AACATT	0.73242	0.66711
cg2254337	FBN1	PR B [T00	1800	1806	2.80933	TATTGTT	0.73242	0.66711
cg2254337	FBN1	PR A [T01	564	570	2.80933	TAATGT	0.73242	0.66711
cg2254337	FBN1	PR A [T01	989	995	2.80933	AACATT	0.73242	0.66711
cg2254337	FBN1	PR A [T01	1800	1806	2.80933	TATTGTT	0.73242	0.66711
cg0738020	FBN1	TBP [T007	233	242	2.807313	TTGCTAT	0.12207	0.10444
cg0738020	FBN1	c-Jun [T00	1317	1323	2.654872	GGAGTC	0.48828	0.48077
cg0738020	FBN1	c-Jun [T00	1409	1415	2.654872	TGACTC	0.48828	0.48077
cg2254337	FBN1	c-Jun [T00	1041	1047	2.654872	TGACTC	0.48828	0.48077
cg2254337	FBN1	NF-AT1 [T	208	216	2.619709	GGAAAG	0.09155	0.08666
cg2254337	FBN1	HNF-1B [	1708	1716	2.476533	AGTTAA	0.01526	0.01334
cg0738020	FBN1	C/EBPalph	1342	1348	2.441016	CTCAAT	0.48828	0.47439
cg0738020	FBN1	IRF-1 [T0	1940	1948	2.418514	TTTCCCT	0.02289	0.02196
cg2254337	FBN1	HNF-1C [	594	602	2.372238	GTTATTT	0.04578	0.04064
cg2254337	FBN1	LEF-1 [T0	475	482	2.345041	CTTTGCT	0.09155	0.09076
cg2254337	FBN1	RXR-alpha	779	785	2.322562	CAGACC	0.85449	0.89683
cg2254337	FBN1	T3R-beta1	1132	1140	2.240658	TTGTGG	0.15259	0.15303
cg2254337	FBN1	c-Ets-2 [T	1813	1821	2.217136	AATGAG	0.16785	0.16456
cg2254337	FBN1	NF-Y [T0	727	734	2.194008	ATTGGT	0.21362	0.20748
cg0738020	FBN1	GATA-1 [	1566	1571	2.176375	TGGATA	3.90625	3.79558
cg2254337	FBN1	GATA-1 [	410	415	2.176375	TATCCT	3.90625	3.79558
cg2254337	FBN1	GATA-1 [	994	999	2.176375	TATCCA	3.90625	3.79558
cg2254337	FBN1	GATA-1 [	1910	1915	2.176375	TATCCA	3.90625	3.79558
cg2254337	FBN1	c-Ets-2 [T	1442	1450	2.142327	TTCCTCT	0.16785	0.16456
cg2254337	FBN1	NF-Y [T0	1150	1157	2.12821	ATTGGC	0.21362	0.20748
cg2254337	FBN1	HOXD9 [T	432	441	2.085829	AATAAA	0.00381	0.00327
cg2254337	FBN1	HOXD10 [	432	441	2.085829	AATAAA	0.00381	0.00327
cg0738020	FBN1	LEF-1 [T0	231	238	2.004405	CTTTGCT	0.18311	0.17215
cg0738020	FBN1	LEF-1 [T0	626	633	2.004405	TAGCAA	0.18311	0.17215
cg0738020	FBN1	LEF-1 [T0	1205	1212	2.004405	TAACAA	0.18311	0.17215

cg2254337	FBN1	LEF-1 [T0	201	208	2.004405	TAACAA	0.18311	0.17215
cg2254337	FBN1	LEF-1 [T0	1760	1767	2.004405	TAACAA	0.18311	0.17215
cg0738020	FBN1	GATA-1 [	415	420	1.896347	TATCGG	3.90625	3.79558
cg0738020	FBN1	PR B [T00	341	347	1.892895	AACACT	0.12207	0.1127
cg0738020	FBN1	PR B [T00	1669	1675	1.892895	AACACT	0.12207	0.1127
cg0738020	FBN1	PR A [T01	341	347	1.892895	AACACT	0.12207	0.1127
cg0738020	FBN1	PR A [T01	1669	1675	1.892895	AACACT	0.12207	0.1127
cg2254337	FBN1	PR B [T00	521	527	1.892895	AACACT	0.12207	0.1127
cg2254337	FBN1	PR A [T01	521	527	1.892895	AACACT	0.12207	0.1127
cg2254337	FBN1	RXR-alpha	1661	1667	1.87833	TCAACC	0.12207	0.12517
cg0738020	FBN1	AP-2alpha	689	694	1.871933	GCCTCC	0.97656	1.07805
cg2254337	FBN1	AP-2alpha	285	290	1.871933	GCCTCC	0.97656	1.07805
cg2254337	FBN1	AP-2alpha	603	608	1.871933	GCCTCC	0.97656	1.07805
cg2254337	FBN1	AP-2alpha	1330	1335	1.871933	GCCTCC	0.97656	1.07805
cg0738020	FBN1	TCF-4 [T0	1161	1170	1.850015	ACTTTG	0.04196	0.03736
cg2254337	FBN1	C/EBPalp	1079	1085	1.830762	CTCAAT	0.48828	0.46352
cg2254337	FBN1	C/EBPalp	1821	1827	1.830762	AATTGA	0.48828	0.46352
cg2254337	FBN1	C/EBPalp	1886	1892	1.830762	CTCAAT	0.48828	0.46352
cg0738020	FBN1	FOXP3 [T	650	655	1.824994	TACAAC	0.48828	0.46414
cg0738020	FBN1	TFII-I [T0	592	597	1.824994	CTCTCC	0.48828	0.51201
cg0738020	FBN1	TFII-I [T0	1394	1399	1.824994	CTCTCC	0.48828	0.51201
cg2254337	FBN1	FOXP3 [T	719	724	1.824994	GTTGTA	0.48828	0.46414
cg2254337	FBN1	TFII-I [T0	1667	1672	1.824994	CTCTCC	0.48828	0.51201
cg0738020	FBN1	Elk-1 [T00	1359	1367	1.779702	CTTCCT	0.05341	0.05461
cg0738020	FBN1	C/EBPalp	674	680	1.761449	TATTGT	0.48828	0.46352
cg2254337	FBN1	p53 [T006	1790	1796	1.758307	GGGCAG	0.36621	0.38097
cg0738020	FBN1	NF-Y [T0	1911	1918	1.749852	ATTGGC	0.18311	0.17671
cg0738020	FBN1	GR-beta [	77	81	1.680765	AATGC	3.90625	3.70067
cg0738020	FBN1	GR-beta [	194	198	1.680765	GAATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	195	199	1.680765	AATTC	3.90625	3.70067
cg0738020	FBN1	GR-beta [	459	463	1.680765	GAATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	470	474	1.680765	AATTC	3.90625	3.70067
cg0738020	FBN1	GR-beta [	555	559	1.680765	GCATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	740	744	1.680765	GAATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	979	983	1.680765	GCATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	1031	1035	1.680765	GCATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	1171	1175	1.680765	GCATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	1867	1871	1.680765	AATGC	3.90625	3.70067
cg0738020	FBN1	GR-beta [	1873	1877	1.680765	GCATT	3.90625	3.70067
cg0738020	FBN1	GR-beta [	1987	1991	1.680765	GAATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [	2	6	1.680765	AATGC	3.90625	3.70067
cg2254337	FBN1	GR-beta [	222	226	1.680765	GAATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [	275	279	1.680765	AATTC	3.90625	3.70067
cg2254337	FBN1	GR-beta [	406	410	1.680765	GAATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [	503	507	1.680765	AATTC	3.90625	3.70067
cg2254337	FBN1	GR-beta [	625	629	1.680765	AATTC	3.90625	3.70067
cg2254337	FBN1	GR-beta [	740	744	1.680765	AATTC	3.90625	3.70067
cg2254337	FBN1	GR-beta [	834	838	1.680765	GCATT	3.90625	3.70067

cg2254337	FBN1	GR-beta [T	852	856	1.680765	AATGC	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	885	889	1.680765	AATTC	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	972	976	1.680765	GCATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1010	1014	1.680765	GAATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1148	1152	1.680765	GAATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1176	1180	1.680765	GCATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1309	1313	1.680765	GCATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1423	1427	1.680765	GAATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1500	1504	1.680765	AATTC	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1547	1551	1.680765	GAATT	3.90625	3.70067
cg2254337	FBN1	GR-beta [T	1588	1592	1.680765	GAATT	3.90625	3.70067
cg0738020	FBN1	HNF-1B [	57	65	1.651022	AGTTAAT	0.00763	0.00634
cg2254337	FBN1	c-Ets-1 [T	206	212	1.641124	AAGGAA	0.36621	0.35197
cg2254337	FBN1	c-Ets-1 [T	754	760	1.641124	TTTCCTT	0.36621	0.35197
cg0738020	FBN1	C/EBPbeta	121	124	1.639871	TTGG	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	258	261	1.639871	CCAA	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	360	363	1.639871	TTGG	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	693	696	1.639871	CCAA	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	798	801	1.639871	CCAA	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	888	891	1.639871	CCAA	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	930	933	1.639871	CCAA	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	1039	1042	1.639871	TTGG	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	1174	1177	1.639871	TTGG	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	1213	1216	1.639871	TTGG	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	1629	1632	1.639871	CCAA	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	1742	1745	1.639871	CCAA	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	1912	1915	1.639871	TTGG	15.625	15.23827
cg0738020	FBN1	C/EBPbeta	1993	1996	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	258	261	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	321	324	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	464	467	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	515	518	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	607	610	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	728	731	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	831	834	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1151	1154	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1179	1182	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1497	1500	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1508	1511	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1513	1516	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1632	1635	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1683	1686	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1788	1791	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1831	1834	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1881	1884	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1931	1934	1.639871	TTGG	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1951	1954	1.639871	CCAA	15.625	15.23827
cg2254337	FBN1	C/EBPbeta	1979	1982	1.639871	CCAA	15.625	15.23827

cg2254337	FBN1	PXR-1:RX	897	904	1.63615	TGAACT	0.06104	0.05484
cg0738020	FBN1	XBP-1 [T	311	316	1.583727	ATGACA	0.97656	0.94995
cg0738020	FBN1	XBP-1 [T	789	794	1.583727	ATGACA	0.97656	0.94995
cg0738020	FBN1	XBP-1 [T	794	799	1.583727	ATGACC	0.97656	0.94995
cg0738020	FBN1	XBP-1 [T	923	928	1.583727	ATGACA	0.97656	0.94995
cg2254337	FBN1	XBP-1 [T	159	164	1.583727	ATGACA	0.97656	0.94995
cg2254337	FBN1	XBP-1 [T	1053	1058	1.583727	TGTCAT	0.97656	0.94995
cg2254337	FBN1	XBP-1 [T	1262	1267	1.583727	ATGACC	0.97656	0.94995
cg0738020	FBN1	TFIID [T0	11	17	1.537547	TGAAAA	0.73242	0.65627
cg0738020	FBN1	TFIID [T0	455	461	1.537547	TTTTGA	0.73242	0.65627
cg0738020	FBN1	TFIID [T0	514	520	1.537547	TTTTCCA	0.73242	0.65627
cg0738020	FBN1	TFIID [T0	968	974	1.537547	TTCAAA	0.73242	0.65627
cg0738020	FBN1	TFIID [T0	1037	1043	1.537547	TTTTGG	0.73242	0.65627
cg2254337	FBN1	TFIID [T0	60	66	1.537547	TTTTTCA	0.73242	0.65627
cg2254337	FBN1	TFIID [T0	83	89	1.537547	TTTTTCA	0.73242	0.65627
cg2254337	FBN1	TFIID [T0	569	575	1.537547	TTTTGTA	0.73242	0.65627
cg2254337	FBN1	TFIID [T0	1286	1292	1.537547	TACAAA	0.73242	0.65627
cg2254337	FBN1	TFIID [T0	1830	1836	1.537547	TCCAAA	0.73242	0.65627
cg2254337	FBN1	TFIID [T0	1893	1899	1.537547	TTTTGA	0.73242	0.65627
cg2254337	FBN1	TFIID [T0	1962	1968	1.537547	TGAAAA	0.73242	0.65627
cg2254337	FBN1	Pax-5 [T0	1197	1203	1.537547	CTTGCC	0.73242	0.83087
cg2254337	FBN1	Pax-5 [T0	1408	1414	1.537547	GGGCCA	0.73242	0.83087
cg0738020	FBN1	c-Ets-1 [T	21	27	1.513038	GAGGAA	0.36621	0.35197
cg0738020	FBN1	c-Ets-1 [T	1118	1124	1.513038	GAGGAA	0.36621	0.35197
cg2254337	FBN1	c-Ets-1 [T	1441	1447	1.513038	TTTCCT	0.36621	0.35197
cg2254337	FBN1	c-Ets-1 [T	1816	1822	1.513038	GAGGAA	0.36621	0.35197
cg0738020	FBN1	STAT4 [T	195	200	1.470588	AATTCC	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	406	411	1.470588	GGAAAA	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	514	519	1.470588	TTTTCC	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	1050	1055	1.470588	AGTTCC	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	1120	1125	1.470588	GGAAAA	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	1176	1181	1.470588	GGAAAC	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	1790	1795	1.470588	GGAAAC	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	1939	1944	1.470588	TTTTCC	1.95312	1.90161
cg0738020	FBN1	STAT4 [T	1986	1991	1.470588	GGAATT	1.95312	1.90161
cg2254337	FBN1	STAT4 [T	753	758	1.470588	TTTTCC	1.95312	1.90161
cg2254337	FBN1	STAT4 [T	1009	1014	1.470588	GGAATT	1.95312	1.90161
cg2254337	FBN1	STAT4 [T	1440	1445	1.470588	GTTTCC	1.95312	1.90161
cg2254337	FBN1	GR [T050	588	594	1.444018	GTTTTT	0.12207	0.11476
cg2254337	FBN1	GR [T050	1524	1530	1.444018	CAAAAA	0.12207	0.11476
cg0738020	FBN1	PR B [T00	1587	1593	1.404665	AACACT	0.36621	0.35143
cg0738020	FBN1	PR A [T01	1587	1593	1.404665	AACACT	0.36621	0.35143
cg2254337	FBN1	PR B [T00	697	703	1.404665	TAGTGT	0.36621	0.35143
cg2254337	FBN1	PR A [T01	697	703	1.404665	TAGTGT	0.36621	0.35143
cg0738020	FBN1	c-Ets-1 [T	465	471	1.384951	CAGGAA	0.36621	0.35197
cg2254337	FBN1	c-Ets-1 [T	1084	1090	1.384951	TTTCCT	0.36621	0.35197
cg0738020	FBN1	NF-AT1 [	511	520	1.378139	CATTTT	0.01907	0.01758
cg0738020	FBN1	C/EBPbeta	0	3	1.366559	TCAA	15.625	15.23827

cg0738020 FBN1	C/EBPbeta	220	223	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	457	460	1.366559	TTGA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	473	476	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	522	525	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	572	575	1.366559	TTGA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	717	720	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	969	972	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	987	990	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	996	999	1.366559	TTGA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1047	1050	1.366559	TTGA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1147	1150	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1164	1167	1.366559	TTGA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1264	1267	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1343	1346	1.366559	TCAA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1605	1608	1.366559	TTGA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1638	1641	1.366559	TTGA	15.625	15.23827
cg0738020 FBN1	C/EBPbeta	1857	1860	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	87	90	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	272	275	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	304	307	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	401	404	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	424	427	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	440	443	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	490	493	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	528	531	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	545	548	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	652	655	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	849	852	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	865	868	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	896	899	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1080	1083	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1163	1166	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1421	1424	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1646	1649	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1661	1664	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1695	1698	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1823	1826	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1887	1890	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1895	1898	1.366559	TTGA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1984	1987	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	C/EBPbeta	1990	1993	1.366559	TCAA	15.625	15.23827
cg2254337 FBN1	AP-2alpha	1228	1233	1.357116	GCCTGT	0.48828	0.51319
cg0738020 FBN1	HNF-3alph	1620	1627	1.342935	TTAAAA	0.03052	0.02477
cg0738020 FBN1	GATA-2 [	34	42	1.111111	AGATAG	0.09155	0.08894
cg0738020 FBN1	GATA-2 [	979	987	1.111111	GCATTA	0.09155	0.08894
cg2254337 FBN1	GATA-2 [	788	796	1.111111	GCTCTA	0.09155	0.08894
cg0738020 FBN1	c-Ets-2 [T	18	26	1.071163	TGAGAG	0.06104	0.0583
cg0738020 FBN1	c-Ets-2 [T	1115	1123	1.071163	TTAGAG	0.06104	0.0583

cg0738020	FBN1	GATA-1 [	1493	1498	1.038567	ATGATA	1.95312	1.80234
cg2254337	FBN1	GATA-1 [	106	111	1.038567	TATCAT	1.95312	1.80234
cg2254337	FBN1	GATA-1 [	1906	1911	1.038567	ATGATA	1.95312	1.80234
cg0738020	FBN1	SRY [T00	1204	1212	0.999172	TTAACA	0.06104	0.0571
cg2254337	FBN1	SRY [T00	1759	1767	0.999172	CTAACA	0.06104	0.0571
cg0738020	FBN1	PXR-1:RX	1054	1061	0.941658	CCAGTT	0.12207	0.11843
cg0738020	FBN1	TBP [T007	603	612	0.935771	GGAGTA	0.12207	0.10448
cg2254337	FBN1	TBP [T007	38	47	0.935771	TTTATAT	0.12207	0.10448
cg0738020	FBN1	HNF-1C [	58	66	0.90144	GTTAAT	0.00763	0.00634
cg0738020	FBN1	GR-beta [	16	20	0.840383	AATGA	7.8125	7.2174
cg0738020	FBN1	GR-beta [	46	50	0.840383	AATTA	7.8125	7.2174
cg0738020	FBN1	GR-beta [	172	176	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	301	305	0.840383	AATGG	7.8125	7.2174
cg0738020	FBN1	GR-beta [	446	450	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	460	464	0.840383	AATTA	7.8125	7.2174
cg0738020	FBN1	GR-beta [	502	506	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	510	514	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	612	616	0.840383	AATTA	7.8125	7.2174
cg0738020	FBN1	GR-beta [	643	647	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	711	715	0.840383	TAATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	788	792	0.840383	AATGA	7.8125	7.2174
cg0738020	FBN1	GR-beta [	843	847	0.840383	CCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	898	902	0.840383	AATGA	7.8125	7.2174
cg0738020	FBN1	GR-beta [	965	969	0.840383	CCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1012	1016	0.840383	CCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1059	1063	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1437	1441	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1441	1445	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1461	1465	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1532	1536	0.840383	CAATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1699	1703	0.840383	AATGG	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1854	1858	0.840383	TCATT	7.8125	7.2174
cg0738020	FBN1	GR-beta [	1936	1940	0.840383	TCATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	64	68	0.840383	TCATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	223	227	0.840383	AATTA	7.8125	7.2174
cg2254337	FBN1	GR-beta [	348	352	0.840383	TAATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	403	407	0.840383	AATGA	7.8125	7.2174
cg2254337	FBN1	GR-beta [	407	411	0.840383	AATTA	7.8125	7.2174
cg2254337	FBN1	GR-beta [	624	628	0.840383	TAATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	745	749	0.840383	TCATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	920	924	0.840383	TCATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1018	1022	0.840383	TCATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1048	1052	0.840383	TAATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1081	1085	0.840383	CAATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1149	1153	0.840383	AATTG	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1261	1265	0.840383	AATGA	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1419	1423	0.840383	AATTG	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1424	1428	0.840383	AATTA	7.8125	7.2174

cg2254337	FBN1	GR-beta [	1589	1593	0.840383	AATTA	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1719	1723	0.840383	TCATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1813	1817	0.840383	AATGA	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1821	1825	0.840383	AATTG	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1842	1846	0.840383	AATGA	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1888	1892	0.840383	CAATT	7.8125	7.2174
cg2254337	FBN1	GR-beta [	1905	1909	0.840383	AATGA	7.8125	7.2174
cg0738020	FBN1	PXR-1:RX	1931	1938	0.818075	CAAGTT	0.12207	0.11843
cg0738020	FBN1	HNF-1A [	336	343	0.781639	GTATTA	0.48828	0.45029
cg2254337	FBN1	GATA-1 [	578	583	0.758539	TATCAG	1.95312	1.80234
cg0738020	FBN1	AP-2alpha	489	494	0.678558	GCCTGA	0.48828	0.51196
cg0738020	FBN1	AP-2alpha	551	556	0.678558	TCAGGC	0.48828	0.51196
cg0738020	FBN1	AP-2alpha	1474	1479	0.678558	GCCTGA	0.48828	0.51196
cg2254337	FBN1	AP-2alpha	1503	1508	0.678558	TCAGGC	0.48828	0.51196
cg0738020	FBN1	LEF-1 [T0	28	35	0.641865	GAACAA	0.06104	0.05974
cg0738020	FBN1	RXR-alpha	1616	1622	0.62611	GGGTTT	0.12207	0.11915
cg2254337	FBN1	POU2F2 (	264	274	0.501684	TATGTA	0.01287	0.01128
cg2254337	FBN1	HNF-1A [	1709	1716	0.431647	GTTAAT	0.24414	0.21942
cg0738020	FBN1	c-Ets-1 [T	1359	1365	0.384261	CTTCCTA	0.24414	0.23743
cg2254337	FBN1	AP-1 [T00	864	872	0.314596	CTTGAG	0.09155	0.08806
cg0738020	FBN1	HNF-1A [	1059	1066	0.287765	TCATTA	0.24414	0.21942
cg0738020	FBN1	GATA-1 [	33	38	0.280028	AAGATA	0.97656	0.8795
cg0738020	FBN1	GATA-1 [	52	57	0.280028	AAGATA	0.97656	0.8795
cg0738020	FBN1	GATA-1 [	855	860	0.280028	TATCTA	0.97656	0.8795
cg0738020	FBN1	GATA-1 [	1497	1502	0.280028	TAGATA	0.97656	0.8795
cg2254337	FBN1	GATA-1 [	235	240	0.280028	TATCTA	0.97656	0.8795
cg2254337	FBN1	GATA-1 [	239	244	0.280028	TATCTA	0.97656	0.8795
cg2254337	FBN1	GATA-1 [	243	248	0.280028	TATCTA	0.97656	0.8795
cg2254337	FBN1	GATA-1 [	618	623	0.280028	TAGATA	0.97656	0.8795
cg0738020	FBN1	AP-2alpha	1751	1756	0.226186	CCAGGC	0.97656	1.07867
cg2254337	FBN1	AP-2alpha	945	950	0.226186	CCAGGC	0.97656	1.07867
cg2254337	FBN1	p53 [T006	1197	1203	0.211706	CTTGCC	0.36621	0.40082
cg0738020	FBN1	GR-alpha [	4	8	0.207689	AAAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	20	24	0.207689	AGAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	71	75	0.207689	AAAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	208	212	0.207689	AGAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	723	727	0.207689	CCTTT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	932	936	0.207689	AAAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1117	1121	0.207689	AGAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1155	1159	0.207689	CCTCT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1223	1227	0.207689	AGAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1230	1234	0.207689	CCTCT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1339	1343	0.207689	CCTCT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1514	1518	0.207689	CCTCT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1558	1562	0.207689	CCTTT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1658	1662	0.207689	CCTCT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1681	1685	0.207689	CCTTT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1850	1854	0.207689	CCTCT	7.8125	7.79817

cg0738020	FBN1	GR-alpha [	1895	1899	0.207689	CCTCT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1916	1920	0.207689	CCTTT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	52	56	0.207689	CCTCT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	58	62	0.207689	CCTTT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	205	209	0.207689	AAAGG	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	210	214	0.207689	AAAGG	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	308	312	0.207689	CCTTT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	397	401	0.207689	CCTTT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	614	618	0.207689	CCTTT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	757	761	0.207689	CCTTT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	1444	1448	0.207689	CCTCT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	1515	1519	0.207689	AAAGG	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	1666	1670	0.207689	CCTCT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	1745	1749	0.207689	AAAGG	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	1919	1923	0.207689	CCTCT	7.8125	7.79817
cg2254337	FBN1	Elk-1 [T00	1379	1387	0.134348	CTTCCTC	0.06104	0.06399
cg0738020	FBN1	GATA-1 [	983	988	0.105011	TATCTC	0.97656	0.92541
cg2254337	FBN1	GATA-1 [	197	202	0.105011	GAGATA	0.97656	0.92541
cg2254337	FBN1	GATA-1 [	792	797	0.105011	TATCTC	0.97656	0.92541
cg0738020	FBN1	GR-beta [T	45	49	0	AAATT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	319	323	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	469	473	0	AAATT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	568	572	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	611	615	0	AAATT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	712	716	0	AATTT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	741	745	0	AATTT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	851	855	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	991	995	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1274	1278	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1289	1293	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1345	1349	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1405	1409	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1533	1537	0	AATTT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1608	1612	0	AAATT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1609	1613	0	AATTT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1632	1636	0	AATGT	3.90625	3.51525
cg0738020	FBN1	GR-beta [T	1988	1992	0	AATTT	3.90625	3.51525
cg0738020	FBN1	XBP-1 [T0	444	449	0	AGTCAT	0.97656	0.94838
cg0738020	FBN1	XBP-1 [T0	1459	1464	0	AGTCAT	0.97656	0.94838
cg0738020	FBN1	TFIID [T0	0	6	0	TCAAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	99	105	0	TCTAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	237	243	0	TATAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	392	398	0	TTTAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	393	399	0	TTAAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	454	460	0	TTTTTGA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	607	613	0	TATAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	714	720	0	TTTTCAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	725	731	0	TTTTAGA	1.09863	0.95175

cg0738020	FBN1	TFIID [T0	780	786	0	TAGAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	1283	1289	0	TAGAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	1619	1625	0	TTTAAA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	1643	1649	0	TTTTCTA	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	1861	1867	0	TTTTAG	1.09863	0.95175
cg0738020	FBN1	TFIID [T0	1878	1884	0	TCTAAA	1.09863	0.95175
cg0738020	FBN1	GR-alpha [	464	468	0	ACAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	672	676	0	CCTAT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1097	1101	0	CCTGT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1181	1185	0	CCTAT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1302	1306	0	CCTAT	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1400	1404	0	ACAGG	7.8125	7.79817
cg0738020	FBN1	GR-alpha [	1953	1957	0	CCTGT	7.8125	7.79817
cg0738020	FBN1	FOXP3 [T	378	383	0	GTTGTG	1.46484	1.44953
cg0738020	FBN1	FOXP3 [T	820	825	0	GTTGTT	1.46484	1.44953
cg0738020	FBN1	FOXP3 [T	823	828	0	GTTGTT	1.46484	1.44953
cg0738020	FBN1	PR B [T00	374	380	0	CACTGT	0.36621	0.35051
cg0738020	FBN1	PR B [T00	801	807	0	AACAGT	0.36621	0.35051
cg0738020	FBN1	PR A [T01	374	380	0	CACTGT	0.36621	0.35051
cg0738020	FBN1	PR A [T01	801	807	0	AACAGT	0.36621	0.35051
cg0738020	FBN1	C/EBPbeta	30	33	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	68	71	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	106	109	0	GCAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	110	113	0	GCAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	233	236	0	TTGC	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	253	256	0	TTGC	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	379	382	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	506	509	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	525	528	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	533	536	0	TTGC	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	628	631	0	GCAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	651	654	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	676	679	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	696	699	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	703	706	0	TTGC	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	761	764	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	810	813	0	TTGC	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	821	824	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	824	827	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	830	833	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	848	851	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	884	887	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	895	898	0	GCAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	919	922	0	TTGC	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	949	952	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1007	1010	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1018	1021	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1029	1032	0	TTGC	15.625	15.26275

cg0738020	FBN1	C/EBPbeta	1108	1111	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1126	1129	0	GCAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1138	1141	0	GCAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1207	1210	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1531	1534	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1578	1581	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1594	1597	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1612	1615	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1684	1687	0	TTGC	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1686	1689	0	GCAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1689	1692	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1762	1765	0	TTGT	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1930	1933	0	ACAA	15.625	15.26275
cg0738020	FBN1	C/EBPbeta	1974	1977	0	GCAA	15.625	15.26275
cg0738020	FBN1	YY1 [T00	139	142	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	302	305	0	ATGG	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	387	390	0	ATGG	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	434	437	0	ATGG	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	636	639	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	843	846	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	965	968	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1012	1015	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1247	1250	0	ATGG	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1261	1264	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1390	1393	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1565	1568	0	ATGG	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1700	1703	0	ATGG	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1707	1710	0	ATGG	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1713	1716	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1738	1741	0	CCAT	7.8125	7.79459
cg0738020	FBN1	YY1 [T00	1832	1835	0	ATGG	7.8125	7.79459
cg0738020	FBN1	TFII-I [T0	23	28	0	GGAAAG	1.46484	1.48598
cg0738020	FBN1	TFII-I [T0	1076	1081	0	GGAAAG	1.46484	1.48598
cg0738020	FBN1	TFII-I [T0	1567	1572	0	GGATAG	1.46484	1.48598
cg0738020	FBN1	STAT4 [T	467	472	0	GGAAAT	0.48828	0.46235
cg0738020	FBN1	ER-alpha [	795	799	0	TGACC	1.95312	1.99744
cg0738020	FBN1	ER-alpha [	1249	1253	0	GGTCA	1.95312	1.99744
cg0738020	FBN1	ER-alpha [	1748	1752	0	TGACC	1.95312	1.99744
cg0738020	FBN1	SRY [T00	27	35	0	AGAACA	0.03052	0.02847
cg0738020	FBN1	TCF-4E [T	231	237	0	CTTTGCT	0.12207	0.11933
cg0738020	FBN1	TCF-4E [T	627	633	0	AGCAAA	0.12207	0.11933
cg0738020	FBN1	GR [T050	1	7	0	CAAAAA	0.36621	0.33174
cg0738020	FBN1	GR [T050	453	459	0	TTTTTTG	0.36621	0.33174
cg0738020	FBN1	GR [T050	1014	1020	0	ATTTTT	0.36621	0.33174
cg0738020	FBN1	GR [T050	1035	1041	0	TTTTTTG	0.36621	0.33174
cg0738020	FBN1	GR [T050	1989	1995	0	ATTTTT	0.36621	0.33174
cg0738020	FBN1	Pax-5 [T0	1368	1374	0	CATGCC	1.09863	1.24633
cg0738020	FBN1	p53 [T006	1368	1374	0	CATGCC	0.36621	0.40082

cg0738020	FBN1	AP-2alpha	957	962	0	GCAGGC	0.97656	1.07867
cg0738020	FBN1	HNF-1A [	58	65	0	GTTAAT	0.24414	0.20853
cg2254337	FBN1	GR-beta [	173	177	0	AATGT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	274	278	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	349	353	0	AATTT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	467	471	0	AATGT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	502	506	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	565	569	0	AATGT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	646	650	0	AATGT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	739	743	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	884	888	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	990	994	0	ACATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1011	1015	0	AATTT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1049	1053	0	AATTT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1082	1086	0	AATTT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1271	1275	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1272	1276	0	AATTT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1418	1422	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1499	1503	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1548	1552	0	AATTT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1820	1824	0	AAATT	3.90625	3.51525
cg2254337	FBN1	GR-beta [	1889	1893	0	AATTT	3.90625	3.51525
cg2254337	FBN1	XBP-1 [T	1843	1848	0	ATGACT	0.97656	0.94838
cg2254337	FBN1	TFIID [T	84	90	0	TTTTCA	1.09863	0.95175
cg2254337	FBN1	TFIID [T	980	986	0	TTTTTA	1.09863	0.95175
cg2254337	FBN1	TFIID [T	982	988	0	TTTAAA	1.09863	0.95175
cg2254337	FBN1	TFIID [T	983	989	0	TTAAAA	1.09863	0.95175
cg2254337	FBN1	TFIID [T	984	990	0	TAAAAA	1.09863	0.95175
cg2254337	FBN1	TFIID [T	1695	1701	0	TTGAAA	1.09863	0.95175
cg2254337	FBN1	TFIID [T	1808	1814	0	TTTAAA	1.09863	0.95175
cg2254337	FBN1	TFIID [T	1892	1898	0	TTTTTGA	1.09863	0.95175
cg2254337	FBN1	c-Jun [T00	866	872	0	TGAGTC	0.12207	0.11843
cg2254337	FBN1	GR-alpha [	929	933	0	CCTGT	7.8125	7.79817
cg2254337	FBN1	GR-alpha [	1229	1233	0	CCTGT	7.8125	7.79817
cg2254337	FBN1	FOXP3 [T	373	378	0	GTTGTG	1.46484	1.44953
cg2254337	FBN1	FOXP3 [T	1624	1629	0	GACAAC	1.46484	1.44953
cg2254337	FBN1	FOXP3 [T	1729	1734	0	AACAAC	1.46484	1.44953
cg2254337	FBN1	FOXP3 [T	1804	1809	0	GTTGTT	1.46484	1.44953
cg2254337	FBN1	FOXP3 [T	1994	1999	0	AACAAC	1.46484	1.44953
cg2254337	FBN1	PR B [T00	78	84	0	CACTGT	0.36621	0.35051
cg2254337	FBN1	PR A [T01	78	84	0	CACTGT	0.36621	0.35051
cg2254337	FBN1	C/EBPbeta	20	23	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	162	165	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	171	174	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	191	194	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	203	206	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	374	377	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	379	382	0	GCAA	15.625	15.26275

cg2254337	FBN1	C/EBPbeta	390	393	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	430	433	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	472	475	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	477	480	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	500	503	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	508	511	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	554	557	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	571	574	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	586	589	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	592	595	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	641	644	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	655	658	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	682	685	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	694	697	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	720	723	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	882	885	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	903	906	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	905	908	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	940	943	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1029	1032	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1052	1055	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1062	1065	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1097	1100	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1132	1135	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1174	1177	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1198	1201	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1248	1251	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1287	1290	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1307	1310	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1396	1399	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1416	1419	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1523	1526	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1529	1532	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1625	1628	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1635	1638	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1730	1733	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1733	1736	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1743	1746	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1762	1765	0	ACAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1770	1773	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1802	1805	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1805	1808	0	TTGT	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1848	1851	0	TTGC	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1945	1948	0	GCAA	15.625	15.26275
cg2254337	FBN1	C/EBPbeta	1995	1998	0	ACAA	15.625	15.26275
cg2254337	FBN1	YY1 [T00	15	18	0	CCAT	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	74	77	0	CCAT	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	100	103	0	CCAT	7.8125	7.79459

cg2254337	FBN1	YY1 [T00	314	317	0	ATGG	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	367	370	0	CCAT	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	967	970	0	CCAT	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	969	972	0	ATGG	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	1242	1245	0	CCAT	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	1406	1409	0	ATGG	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	1569	1572	0	CCAT	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	1864	1867	0	ATGG	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	1925	1928	0	CCAT	7.8125	7.79459
cg2254337	FBN1	YY1 [T00	1959	1962	0	CCAT	7.8125	7.79459
cg2254337	FBN1	TFII-I [T0	208	213	0	GGAAAG	1.46484	1.48598
cg2254337	FBN1	TFII-I [T0	952	957	0	CTGTCC	1.46484	1.48598
cg2254337	FBN1	TFII-I [T0	1297	1302	0	CTTTCC	1.46484	1.48598
cg2254337	FBN1	TFII-I [T0	1493	1498	0	CTTTCC	1.46484	1.48598
cg2254337	FBN1	STAT4 [T	1083	1088	0	ATTTCC	0.48828	0.46235
cg2254337	FBN1	STAT4 [T	1818	1823	0	GGAAAT	0.48828	0.46235
cg2254337	FBN1	c-Ets-1 [T	1379	1385	0	CTTCCT	0.24414	0.24982
cg2254337	FBN1	ER-alpha [	46	50	0	TGACC	1.95312	1.99744
cg2254337	FBN1	ER-alpha [	422	426	0	GGTCA	1.95312	1.99744
cg2254337	FBN1	ER-alpha [	1263	1267	0	TGACC	1.95312	1.99744
cg2254337	FBN1	SRY [T00	200	208	0	ATAACA	0.03052	0.02847
cg2254337	FBN1	TCF-4E [T	475	481	0	CTTTGC	0.12207	0.11933
cg2254337	FBN1	GR [T050	642	648	0	CAAAAA	0.36621	0.33174
cg2254337	FBN1	GR [T050	1891	1897	0	TTTTTTG	0.36621	0.33174
cg2254337	FBN1	GR [T050	1952	1958	0	CAAAAA	0.36621	0.33174
cg2254337	FBN1	GATA-1 [	42	47	0	TATCTG	0.97656	0.92541
cg2254337	FBN1	GATA-1 [	331	336	0	CAGATA	0.97656	0.92541
cg2254337	FBN1	GATA-1 [	1552	1557	0	TATCTG	0.97656	0.92541
cg2254337	FBN1	GATA-1 [	1579	1584	0	TATCTG	0.97656	0.92541
cg2254337	FBN1	GATA-1 [	1793	1798	0	CAGATA	0.97656	0.92541
cg2254337	FBN1	Pax-5 [T0	1870	1876	0	GGGCTG	1.09863	1.24633
cg2254337	FBN1	AP-2alpha	1450	1455	0	GCCTGC	0.97656	1.07867
cg2254337	FBN1	IRF-2 [T01	68	73	0	TCACTT	0.48828	0.46235
cg2254337	FBN1	IRF-2 [T01	1294	1299	0	TCACTT	0.48828	0.46235
cg2709743	FLJ44606	Elk-1 [T00	1659	1667	9.979803	ATGCGG	0.10681	0.10604
cg0230409	FLJ44606	Elk-1 [T00	1585	1593	9.979803	ATGCGG	0.10681	0.10604
cg1020029	FLJ44606	Elk-1 [T00	1805	1813	9.979803	ATGCGG	0.10681	0.10604
cg2709743	FLJ44606	PEA3 [T0	1323	1331	9.937959	ATGCAT	0.18311	0.18304
cg0230409	FLJ44606	PEA3 [T0	1249	1257	9.937959	ATGCAT	0.18311	0.18304
cg1020029	FLJ44606	PEA3 [T0	1469	1477	9.937959	ATGCAT	0.18311	0.18304
cg2709743	FLJ44606	E2F-1 [T0	1310	1317	9.905405	TTAACC	0.33569	0.3277
cg0230409	FLJ44606	E2F-1 [T0	1236	1243	9.905405	TTAACC	0.33569	0.3277
cg1020029	FLJ44606	E2F-1 [T0	1456	1463	9.905405	TTAACC	0.33569	0.3277
cg2709743	FLJ44606	c-Ets-1 [T	263	269	9.841249	ATTCCC	0.24414	0.2459
cg2709743	FLJ44606	c-Ets-1 [T	1693	1699	9.841249	AGGGAA	0.24414	0.2459
cg0230409	FLJ44606	c-Ets-1 [T	189	195	9.841249	ATTCCC	0.24414	0.2459
cg0230409	FLJ44606	c-Ets-1 [T	1619	1625	9.841249	AGGGAA	0.24414	0.2459
cg1020029	FLJ44606	c-Ets-1 [T	409	415	9.841249	ATTCCC	0.24414	0.2459

cg1020029	FLJ44606	c-Ets-1 [T	1839	1845	9.841249	AGGGAA	0.24414	0.2459
cg2709743	FLJ44606	XBP-1 [T	560	565	9.789909	ATGGCT	1.95312	1.95208
cg2709743	FLJ44606	XBP-1 [T	846	851	9.789909	ATGGCT	1.95312	1.95208
cg2709743	FLJ44606	XBP-1 [T	1303	1308	9.789909	AGCCAT	1.95312	1.95208
cg2709743	FLJ44606	XBP-1 [T	1678	1683	9.789909	ATGGCT	1.95312	1.95208
cg0230409	FLJ44606	XBP-1 [T	486	491	9.789909	ATGGCT	1.95312	1.95208
cg0230409	FLJ44606	XBP-1 [T	772	777	9.789909	ATGGCT	1.95312	1.95208
cg0230409	FLJ44606	XBP-1 [T	1229	1234	9.789909	AGCCAT	1.95312	1.95208
cg0230409	FLJ44606	XBP-1 [T	1604	1609	9.789909	ATGGCT	1.95312	1.95208
cg1020029	FLJ44606	XBP-1 [T	706	711	9.789909	ATGGCT	1.95312	1.95208
cg1020029	FLJ44606	XBP-1 [T	992	997	9.789909	ATGGCT	1.95312	1.95208
cg1020029	FLJ44606	XBP-1 [T	1449	1454	9.789909	AGCCAT	1.95312	1.95208
cg1020029	FLJ44606	XBP-1 [T	1824	1829	9.789909	ATGGCT	1.95312	1.95208
cg1020029	FLJ44606	NF-1 [T00	54	61	9.761671	AGCTCC	0.24414	0.24405
cg1020029	FLJ44606	PR B [T00	6	12	9.743489	CCGTGT	1.09863	1.10292
cg1020029	FLJ44606	PR A [T01	6	12	9.743489	CCGTGT	1.09863	1.10292
cg2709743	FLJ44606	AhR:Arnt	895	904	9.738501	GCACGC	0.17929	0.17456
cg0230409	FLJ44606	AhR:Arnt	821	830	9.738501	GCACGC	0.17929	0.17456
cg1020029	FLJ44606	AhR:Arnt	1041	1050	9.738501	GCACGC	0.17929	0.17456
cg2709743	FLJ44606	c-Myb [T0	1818	1825	9.729271	GAACTG	0.36621	0.37054
cg0230409	FLJ44606	c-Myb [T0	1744	1751	9.729271	GAACTG	0.36621	0.37054
cg1020029	FLJ44606	c-Myb [T0	1964	1971	9.729271	GAACTG	0.36621	0.37054
cg2709743	FLJ44606	c-Ets-1 [T	1392	1398	9.713162	GGGGAA	0.36621	0.36441
cg0230409	FLJ44606	c-Ets-1 [T	1318	1324	9.713162	GGGGAA	0.36621	0.36441
cg1020029	FLJ44606	c-Ets-1 [T	1538	1544	9.713162	GGGGAA	0.36621	0.36441
cg2709743	FLJ44606	Pax-5 [T0	450	456	9.552105	TTTGCC	1.46484	1.43083
cg2709743	FLJ44606	Pax-5 [T0	1019	1025	9.552105	TCCGCC	1.46484	1.43083
cg2709743	FLJ44606	Pax-5 [T0	1039	1045	9.552105	TCCGCC	1.46484	1.43083
cg2709743	FLJ44606	Pax-5 [T0	1080	1086	9.552105	TCCGCC	1.46484	1.43083
cg2709743	FLJ44606	TFIID [T0	75	81	9.552105	TGGGAA	1.46484	1.48472
cg2709743	FLJ44606	TFIID [T0	269	275	9.552105	TGTGAA	1.46484	1.48472
cg2709743	FLJ44606	TFIID [T0	372	378	9.552105	TTTGTC	1.46484	1.48472
cg2709743	FLJ44606	TFIID [T0	1239	1245	9.552105	TTTGGG	1.46484	1.48472
cg2709743	FLJ44606	TFIID [T0	1448	1454	9.552105	TGAGAA	1.46484	1.48472
cg2709743	FLJ44606	TFIID [T0	1530	1536	9.552105	TGAGAA	1.46484	1.48472
cg2709743	FLJ44606	TFIID [T0	1856	1862	9.552105	TTTGGG	1.46484	1.48472
cg2709743	FLJ44606	TFIID [T0	1976	1982	9.552105	TGAGAA	1.46484	1.48472
cg0230409	FLJ44606	Pax-5 [T0	376	382	9.552105	TTTGCC	1.46484	1.43083
cg0230409	FLJ44606	Pax-5 [T0	945	951	9.552105	TCCGCC	1.46484	1.43083
cg0230409	FLJ44606	Pax-5 [T0	965	971	9.552105	TCCGCC	1.46484	1.43083
cg0230409	FLJ44606	Pax-5 [T0	1006	1012	9.552105	TCCGCC	1.46484	1.43083
cg0230409	FLJ44606	TFIID [T0	1	7	9.552105	TGGGAA	1.46484	1.48472
cg0230409	FLJ44606	TFIID [T0	195	201	9.552105	TGTGAA	1.46484	1.48472
cg0230409	FLJ44606	TFIID [T0	298	304	9.552105	TTTGTC	1.46484	1.48472
cg0230409	FLJ44606	TFIID [T0	1165	1171	9.552105	TTTGGG	1.46484	1.48472
cg0230409	FLJ44606	TFIID [T0	1374	1380	9.552105	TGAGAA	1.46484	1.48472
cg0230409	FLJ44606	TFIID [T0	1456	1462	9.552105	TGAGAA	1.46484	1.48472
cg0230409	FLJ44606	TFIID [T0	1782	1788	9.552105	TTTGGG	1.46484	1.48472

cg0230409	FLJ44606	TFIID [T0	1902	1908	9.552105	TGAGAA	1.46484	1.48472
cg1020029	FLJ44606	Pax-5 [T0	596	602	9.552105	TTTGCC	1.46484	1.43083
cg1020029	FLJ44606	Pax-5 [T0	1165	1171	9.552105	TCCGCC	1.46484	1.43083
cg1020029	FLJ44606	Pax-5 [T0	1185	1191	9.552105	TCCGCC	1.46484	1.43083
cg1020029	FLJ44606	Pax-5 [T0	1226	1232	9.552105	TCCGCC	1.46484	1.43083
cg1020029	FLJ44606	TFIID [T0	221	227	9.552105	TGGGAA	1.46484	1.48472
cg1020029	FLJ44606	TFIID [T0	415	421	9.552105	TGTGAA	1.46484	1.48472
cg1020029	FLJ44606	TFIID [T0	518	524	9.552105	TTTGTC	1.46484	1.48472
cg1020029	FLJ44606	TFIID [T0	1385	1391	9.552105	TTTGGG	1.46484	1.48472
cg1020029	FLJ44606	TFIID [T0	1594	1600	9.552105	TGAGAA	1.46484	1.48472
cg1020029	FLJ44606	TFIID [T0	1676	1682	9.552105	TGAGAA	1.46484	1.48472
cg2709743	FLJ44606	NF-AT1 [	77	85	9.521781	GGAAAT	0.16785	0.1682
cg0230409	FLJ44606	NF-AT1 [	3	11	9.521781	GGAAAT	0.16785	0.1682
cg1020029	FLJ44606	NF-AT1 [	223	231	9.521781	GGAAAT	0.16785	0.1682
cg2709743	FLJ44606	NF-1 [T00	540	547	9.513281	CACCCC	0.73242	0.73053
cg0230409	FLJ44606	NF-1 [T00	466	473	9.513281	CACCCC	0.73242	0.73053
cg1020029	FLJ44606	NF-1 [T00	39	46	9.513281	CACCCC	0.73242	0.73053
cg1020029	FLJ44606	NF-1 [T00	686	693	9.513281	CACCCC	0.73242	0.73053
cg2709743	FLJ44606	TFII-I [T0	136	141	9.512894	GGAATT	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	175	180	9.512894	GGATTT	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	326	331	9.512894	GGACTT	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	342	347	9.512894	GGACTT	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	655	660	9.512894	GGACGG	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	755	760	9.512894	TTTTCC	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	840	845	9.512894	GGATTT	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	865	870	9.512894	AATTCC	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1127	1132	9.512894	GTGTCC	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1220	1225	9.512894	GGAAAA	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1470	1475	9.512894	TTATCC	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1520	1525	9.512894	GGAAGG	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1623	1628	9.512894	GGAAGG	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1713	1718	9.512894	GGAAAC	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1807	1812	9.512894	GGAAGG	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1829	1834	9.512894	TTTTCC	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1871	1876	9.512894	GGAAGG	7.32422	7.29728
cg2709743	FLJ44606	TFII-I [T0	1988	1993	9.512894	GGATAA	7.32422	7.29728
cg2709743	FLJ44606	FOXP3 [T	231	236	9.512894	ATAAAC	7.32422	7.35678
cg2709743	FLJ44606	FOXP3 [T	813	818	9.512894	GTTTAT	7.32422	7.35678
cg2709743	FLJ44606	FOXP3 [T	1004	1009	9.512894	GCCAAC	7.32422	7.35678
cg2709743	FLJ44606	FOXP3 [T	1276	1281	9.512894	GCCAAC	7.32422	7.35678
cg2709743	FLJ44606	FOXP3 [T	1387	1392	9.512894	GTTATG	7.32422	7.35678
cg2709743	FLJ44606	FOXP3 [T	1495	1500	9.512894	GTTTAT	7.32422	7.35678
cg2709743	FLJ44606	FOXP3 [T	1596	1601	9.512894	GTTGGG	7.32422	7.35678
cg2709743	FLJ44606	FOXP3 [T	1877	1882	9.512894	GTTTAG	7.32422	7.35678
cg0230409	FLJ44606	TFII-I [T0	62	67	9.512894	GGAATT	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	101	106	9.512894	GGATTT	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	252	257	9.512894	GGACTT	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	268	273	9.512894	GGACTT	7.32422	7.29728

cg0230409	FLJ44606	TFII-I [T0	581	586	9.512894	GGACGG	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	681	686	9.512894	TTTTCC	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	766	771	9.512894	GGATTT	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	791	796	9.512894	AATTCC	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1053	1058	9.512894	GTGTCC	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1146	1151	9.512894	GGAAAA	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1396	1401	9.512894	TTATCC	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1446	1451	9.512894	GGAAGG	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1549	1554	9.512894	GGAAGG	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1639	1644	9.512894	GGAAAC	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1733	1738	9.512894	GGAAGG	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1755	1760	9.512894	TTTTCC	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1797	1802	9.512894	GGAAGG	7.32422	7.29728
cg0230409	FLJ44606	TFII-I [T0	1914	1919	9.512894	GGATAA	7.32422	7.29728
cg0230409	FLJ44606	FOXP3 [T	157	162	9.512894	ATAAAC	7.32422	7.35678
cg0230409	FLJ44606	FOXP3 [T	739	744	9.512894	GTTTAT	7.32422	7.35678
cg0230409	FLJ44606	FOXP3 [T	930	935	9.512894	GCCAAC	7.32422	7.35678
cg0230409	FLJ44606	FOXP3 [T	1202	1207	9.512894	GCCAAC	7.32422	7.35678
cg0230409	FLJ44606	FOXP3 [T	1313	1318	9.512894	GTTATG	7.32422	7.35678
cg0230409	FLJ44606	FOXP3 [T	1421	1426	9.512894	GTTTAT	7.32422	7.35678
cg0230409	FLJ44606	FOXP3 [T	1522	1527	9.512894	GTTGGG	7.32422	7.35678
cg0230409	FLJ44606	FOXP3 [T	1803	1808	9.512894	GTTTAG	7.32422	7.35678
cg1020029	FLJ44606	TFII-I [T0	0	5	9.512894	TTTTCC	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	282	287	9.512894	GGAATT	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	321	326	9.512894	GGATTT	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	472	477	9.512894	GGACTT	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	488	493	9.512894	GGACTT	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	801	806	9.512894	GGACGG	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	901	906	9.512894	TTTTCC	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	986	991	9.512894	GGATTT	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1011	1016	9.512894	AATTCC	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1273	1278	9.512894	GTGTCC	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1366	1371	9.512894	GGAAAA	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1616	1621	9.512894	TTATCC	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1666	1671	9.512894	GGAAGG	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1769	1774	9.512894	GGAAGG	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1859	1864	9.512894	GGAAAC	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1953	1958	9.512894	GGAAGG	7.32422	7.29728
cg1020029	FLJ44606	TFII-I [T0	1975	1980	9.512894	TTTTCC	7.32422	7.29728
cg1020029	FLJ44606	FOXP3 [T	377	382	9.512894	ATAAAC	7.32422	7.35678
cg1020029	FLJ44606	FOXP3 [T	959	964	9.512894	GTTTAT	7.32422	7.35678
cg1020029	FLJ44606	FOXP3 [T	1150	1155	9.512894	GCCAAC	7.32422	7.35678
cg1020029	FLJ44606	FOXP3 [T	1422	1427	9.512894	GCCAAC	7.32422	7.35678
cg1020029	FLJ44606	FOXP3 [T	1533	1538	9.512894	GTTATG	7.32422	7.35678
cg1020029	FLJ44606	FOXP3 [T	1641	1646	9.512894	GTTTAT	7.32422	7.35678
cg1020029	FLJ44606	FOXP3 [T	1742	1747	9.512894	GTTGGG	7.32422	7.35678
cg2709743	FLJ44606	Ik-1 [T027	1861	1873	9.497194	GAAGTA	0.02941	0.02907
cg0230409	FLJ44606	Ik-1 [T027	1787	1799	9.497194	GAAGTA	0.02941	0.02907

cg0230409	FLJ44606	TCF-4E [T	1934	1940	9.453578	CTCAAA	0.48828	0.49215
cg2709743	FLJ44606	RelA [T00	74	84	9.429339	CTGGGA	0.02813	0.0279
cg0230409	FLJ44606	RelA [T00	0	10	9.429339	CTGGGA	0.02813	0.0279
cg1020029	FLJ44606	RelA [T00	220	230	9.429339	CTGGGA	0.02813	0.0279
cg2709743	FLJ44606	NFI/CTF [	1193	1200	9.352332	CCAAGG	0.54932	0.54821
cg2709743	FLJ44606	NFI/CTF [	1566	1573	9.352332	AGCTTT	0.54932	0.54821
cg2709743	FLJ44606	NFI/CTF [	1853	1860	9.352332	AGCTTT	0.54932	0.54821
cg0230409	FLJ44606	NFI/CTF [	1119	1126	9.352332	CCAAGG	0.54932	0.54821
cg0230409	FLJ44606	NFI/CTF [	1492	1499	9.352332	AGCTTT	0.54932	0.54821
cg0230409	FLJ44606	NFI/CTF [	1779	1786	9.352332	AGCTTT	0.54932	0.54821
cg1020029	FLJ44606	NFI/CTF [	1339	1346	9.352332	CCAAGG	0.54932	0.54821
cg1020029	FLJ44606	NFI/CTF [	1712	1719	9.352332	AGCTTT	0.54932	0.54821
cg2709743	FLJ44606	LEF-1 [T0	1568	1575	9.313676	CTTTGG	0.21362	0.2139
cg0230409	FLJ44606	LEF-1 [T0	1494	1501	9.313676	CTTTGG	0.21362	0.2139
cg1020029	FLJ44606	LEF-1 [T0	1714	1721	9.313676	CTTTGG	0.21362	0.2139
cg2709743	FLJ44606	c-Ets-1 [T	1241	1247	9.276861	TGGGAA	0.36621	0.36441
cg0230409	FLJ44606	c-Ets-1 [T	1167	1173	9.276861	TGGGAA	0.36621	0.36441
cg1020029	FLJ44606	c-Ets-1 [T	1387	1393	9.276861	TGGGAA	0.36621	0.36441
cg2709743	FLJ44606	RAR-alph	151	163	9.192562	GGGGTC	0.02065	0.02038
cg0230409	FLJ44606	RAR-alph	77	89	9.192562	GGGGTC	0.02065	0.02038
cg1020029	FLJ44606	RAR-alph	297	309	9.192562	GGGGTC	0.02065	0.02038
cg2709743	FLJ44606	NF-AT1 [	1713	1721	9.158155	GGAAAC	0.22888	0.22959
cg0230409	FLJ44606	NF-AT1 [	1639	1647	9.158155	GGAAAC	0.22888	0.22959
cg1020029	FLJ44606	NF-AT1 [	1859	1867	9.158155	GGAAAC	0.22888	0.22959
cg2709743	FLJ44606	c-Ets-1 [T	513	519	9.148774	GTTCCC	0.85449	0.85523
cg2709743	FLJ44606	c-Ets-1 [T	979	985	9.148774	AGGGAA	0.85449	0.85523
cg0230409	FLJ44606	c-Ets-1 [T	439	445	9.148774	GTTCCC	0.85449	0.85523
cg0230409	FLJ44606	c-Ets-1 [T	905	911	9.148774	AGGGAA	0.85449	0.85523
cg1020029	FLJ44606	c-Ets-1 [T	659	665	9.148774	GTTCCC	0.85449	0.85523
cg1020029	FLJ44606	c-Ets-1 [T	1125	1131	9.148774	AGGGAA	0.85449	0.85523
cg2709743	FLJ44606	LEF-1 [T0	1512	1519	9.099721	CTTTGC	0.54932	0.55326
cg0230409	FLJ44606	LEF-1 [T0	1438	1445	9.099721	CTTTGC	0.54932	0.55326
cg1020029	FLJ44606	LEF-1 [T0	1658	1665	9.099721	CTTTGC	0.54932	0.55326
cg2709743	FLJ44606	USF2 [T0	1265	1274	9.056375	CAGGTG	0.1545	0.15287
cg0230409	FLJ44606	USF2 [T0	1191	1200	9.056375	CAGGTG	0.1545	0.15287
cg1020029	FLJ44606	USF2 [T0	1411	1420	9.056375	CAGGTG	0.1545	0.15287
cg2709743	FLJ44606	LEF-1 [T0	1855	1862	8.973041	CTTTGG	0.54932	0.55326
cg0230409	FLJ44606	LEF-1 [T0	1781	1788	8.973041	CTTTGG	0.54932	0.55326
cg2709743	FLJ44606	GR [T050	447	453	8.971049	GCTTTC	0.61035	0.61632
cg0230409	FLJ44606	GR [T050	373	379	8.971049	GCTTTC	0.61035	0.61632
cg0230409	FLJ44606	GR [T050	1963	1969	8.971049	CAAAAG	0.61035	0.61632
cg1020029	FLJ44606	GR [T050	593	599	8.971049	GCTTTC	0.61035	0.61632
cg2709743	FLJ44606	Elk-1 [T00	1619	1627	8.931691	TGGGGG	0.24414	0.24034
cg0230409	FLJ44606	Elk-1 [T00	1545	1553	8.931691	TGGGGG	0.24414	0.24034
cg1020029	FLJ44606	Elk-1 [T00	1765	1773	8.931691	TGGGGG	0.24414	0.24034
cg2709743	FLJ44606	c-Jun [T00	551	557	8.832178	AAGGTC	0.61035	0.61059
cg0230409	FLJ44606	c-Jun [T00	477	483	8.832178	AAGGTC	0.61035	0.61059
cg1020029	FLJ44606	c-Jun [T00	697	703	8.832178	AAGGTC	0.61035	0.61059

cg2709743	FLJ44606	PR B [T00	105	111	8.827054	AACAGA	0.36621	0.36944
cg2709743	FLJ44606	PR B [T00	388	394	8.827054	ATCTGT	0.36621	0.36944
cg2709743	FLJ44606	PR A [T01	105	111	8.827054	AACAGA	0.36621	0.36944
cg2709743	FLJ44606	PR A [T01	388	394	8.827054	ATCTGT	0.36621	0.36944
cg0230409	FLJ44606	PR B [T00	31	37	8.827054	AACAGA	0.36621	0.36944
cg0230409	FLJ44606	PR B [T00	314	320	8.827054	ATCTGT	0.36621	0.36944
cg0230409	FLJ44606	PR A [T01	31	37	8.827054	AACAGA	0.36621	0.36944
cg0230409	FLJ44606	PR A [T01	314	320	8.827054	ATCTGT	0.36621	0.36944
cg1020029	FLJ44606	PR B [T00	251	257	8.827054	AACAGA	0.36621	0.36944
cg1020029	FLJ44606	PR B [T00	534	540	8.827054	ATCTGT	0.36621	0.36944
cg1020029	FLJ44606	PR A [T01	251	257	8.827054	AACAGA	0.36621	0.36944
cg1020029	FLJ44606	PR A [T01	534	540	8.827054	ATCTGT	0.36621	0.36944
cg2709743	FLJ44606	NFI/CTF [	884	891	8.814757	CCAAAT	0.48828	0.48804
cg0230409	FLJ44606	NFI/CTF [	810	817	8.814757	CCAAAT	0.48828	0.48804
cg1020029	FLJ44606	NFI/CTF [	115	122	8.814757	CCAAAT	0.48828	0.48804
cg1020029	FLJ44606	NFI/CTF [	1030	1037	8.814757	CCAAAT	0.48828	0.48804
cg2709743	FLJ44606	c-Ets-1 [T	1929	1935	8.809329	ATTCCA	0.85449	0.85523
cg0230409	FLJ44606	c-Ets-1 [T	1855	1861	8.809329	ATTCCA	0.85449	0.85523
cg2709743	FLJ44606	NF-1 [T00	1857	1864	8.790071	TTGGGA	0.24414	0.24467
cg0230409	FLJ44606	NF-1 [T00	1783	1790	8.790071	TTGGGA	0.24414	0.24467
cg2709743	FLJ44606	MAZ [T00	1422	1434	8.779528	TACCCT	0.01413	0.01385
cg0230409	FLJ44606	MAZ [T00	1348	1360	8.779528	TACCCT	0.01413	0.01385
cg1020029	FLJ44606	MAZ [T00	1568	1580	8.779528	TACCCT	0.01413	0.01385
cg2709743	FLJ44606	XBP-1 [T	361	366	8.75604	ATGAGC	2.92969	2.9674
cg2709743	FLJ44606	XBP-1 [T	421	426	8.75604	TCTCAT	2.92969	2.9674
cg2709743	FLJ44606	XBP-1 [T	483	488	8.75604	GCTCAT	2.92969	2.9674
cg2709743	FLJ44606	XBP-1 [T	834	839	8.75604	GTTCAT	2.92969	2.9674
cg2709743	FLJ44606	XBP-1 [T	1402	1407	8.75604	ATGAGC	2.92969	2.9674
cg2709743	FLJ44606	XBP-1 [T	1529	1534	8.75604	ATGAGA	2.92969	2.9674
cg2709743	FLJ44606	XBP-1 [T	1975	1980	8.75604	ATGAGA	2.92969	2.9674
cg0230409	FLJ44606	XBP-1 [T	287	292	8.75604	ATGAGC	2.92969	2.9674
cg0230409	FLJ44606	XBP-1 [T	347	352	8.75604	TCTCAT	2.92969	2.9674
cg0230409	FLJ44606	XBP-1 [T	409	414	8.75604	GCTCAT	2.92969	2.9674
cg0230409	FLJ44606	XBP-1 [T	760	765	8.75604	GTTCAT	2.92969	2.9674
cg0230409	FLJ44606	XBP-1 [T	1328	1333	8.75604	ATGAGC	2.92969	2.9674
cg0230409	FLJ44606	XBP-1 [T	1455	1460	8.75604	ATGAGA	2.92969	2.9674
cg0230409	FLJ44606	XBP-1 [T	1901	1906	8.75604	ATGAGA	2.92969	2.9674
cg1020029	FLJ44606	XBP-1 [T	119	124	8.75604	ATGAGA	2.92969	2.9674
cg1020029	FLJ44606	XBP-1 [T	507	512	8.75604	ATGAGC	2.92969	2.9674
cg1020029	FLJ44606	XBP-1 [T	567	572	8.75604	TCTCAT	2.92969	2.9674
cg1020029	FLJ44606	XBP-1 [T	629	634	8.75604	GCTCAT	2.92969	2.9674
cg1020029	FLJ44606	XBP-1 [T	980	985	8.75604	GTTCAT	2.92969	2.9674
cg1020029	FLJ44606	XBP-1 [T	1548	1553	8.75604	ATGAGC	2.92969	2.9674
cg1020029	FLJ44606	XBP-1 [T	1675	1680	8.75604	ATGAGA	2.92969	2.9674
cg2709743	FLJ44606	STAT1bet	1461	1470	8.695301	ATTAGG	0.22316	0.22446
cg0230409	FLJ44606	STAT1bet	1387	1396	8.695301	ATTAGG	0.22316	0.22446
cg1020029	FLJ44606	STAT1bet	0	9	8.695301	TTTTCCC	0.22316	0.22446
cg1020029	FLJ44606	STAT1bet	1607	1616	8.695301	ATTAGG	0.22316	0.22446

cg2709743	FLJ44606	RXR-alpha	1776	1782	8.664139	GGGTAG	0.12207	0.12014
cg0230409	FLJ44606	RXR-alpha	1702	1708	8.664139	GGGTAG	0.12207	0.12014
cg1020029	FLJ44606	RXR-alpha	1922	1928	8.664139	GGGTAG	0.12207	0.12014
cg2709743	FLJ44606	RAR-beta	1593	1602	8.55975	TGGGTT	0.26703	0.26657
cg0230409	FLJ44606	RAR-beta	1519	1528	8.55975	TGGGTT	0.26703	0.26657
cg1020029	FLJ44606	RAR-beta	1739	1748	8.55975	TGGGTT	0.26703	0.26657
cg2709743	FLJ44606	p53 [T006	493	499	8.537081	AGAGCC	0.12207	0.11986
cg0230409	FLJ44606	p53 [T006	419	425	8.537081	AGAGCC	0.12207	0.11986
cg1020029	FLJ44606	p53 [T006	639	645	8.537081	AGAGCC	0.12207	0.11986
cg2709743	FLJ44606	NF-AT1 [	752	760	8.532897	TCCTTTT	0.10681	0.10725
cg0230409	FLJ44606	NF-AT1 [	678	686	8.532897	TCCTTTT	0.10681	0.10725
cg1020029	FLJ44606	NF-AT1 [	898	906	8.532897	TCCTTTT	0.10681	0.10725
cg2709743	FLJ44606	USF2 [T0	983	992	8.532138	AACCCA	0.103	0.10183
cg2709743	FLJ44606	USF2 [T0	1121	1130	8.532138	CAGGTG	0.103	0.10183
cg0230409	FLJ44606	USF2 [T0	909	918	8.532138	AACCCA	0.103	0.10183
cg0230409	FLJ44606	USF2 [T0	1047	1056	8.532138	CAGGTG	0.103	0.10183
cg1020029	FLJ44606	USF2 [T0	1129	1138	8.532138	AACCCA	0.103	0.10183
cg1020029	FLJ44606	USF2 [T0	1267	1276	8.532138	CAGGTG	0.103	0.10183
cg2709743	FLJ44606	c-Myb [T0	4	11	8.529773	CAACTT	0.30518	0.30924
cg1020029	FLJ44606	c-Myb [T0	150	157	8.529773	CAACTT	0.30518	0.30924
cg2709743	FLJ44606	AhR:Arnt	997	1006	8.431005	TCACGC	0.07439	0.07225
cg0230409	FLJ44606	AhR:Arnt	923	932	8.431005	TCACGC	0.07439	0.07225
cg1020029	FLJ44606	AhR:Arnt	1143	1152	8.431005	TCACGC	0.07439	0.07225
cg1020029	FLJ44606	POU2F2 (	30	40	8.346865	CCTATA	0.0515	0.05239
cg2709743	FLJ44606	HNF-3alph	195	202	8.343064	CTAAAA	0.27466	0.28528
cg2709743	FLJ44606	HNF-3alph	1306	1313	8.343064	CATTTA	0.27466	0.28528
cg2709743	FLJ44606	HNF-3alph	1479	1486	8.343064	ATTAAA	0.27466	0.28528
cg0230409	FLJ44606	HNF-3alph	121	128	8.343064	CTAAAA	0.27466	0.28528
cg0230409	FLJ44606	HNF-3alph	1232	1239	8.343064	CATTTA	0.27466	0.28528
cg0230409	FLJ44606	HNF-3alph	1405	1412	8.343064	ATTAAA	0.27466	0.28528
cg1020029	FLJ44606	HNF-3alph	341	348	8.343064	CTAAAA	0.27466	0.28528
cg1020029	FLJ44606	HNF-3alph	1452	1459	8.343064	CATTTA	0.27466	0.28528
cg1020029	FLJ44606	HNF-3alph	1625	1632	8.343064	ATTAAA	0.27466	0.28528
cg2709743	FLJ44606	PR B [T00	1716	1722	8.338824	AACAGG	1.09863	1.10009
cg2709743	FLJ44606	PR B [T00	1793	1799	8.338824	TTCTGTT	1.09863	1.10009
cg2709743	FLJ44606	PR A [T01	1716	1722	8.338824	AACAGG	1.09863	1.10009
cg2709743	FLJ44606	PR A [T01	1793	1799	8.338824	TTCTGTT	1.09863	1.10009
cg0230409	FLJ44606	PR B [T00	1642	1648	8.338824	AACAGG	1.09863	1.10009
cg0230409	FLJ44606	PR B [T00	1719	1725	8.338824	TTCTGTT	1.09863	1.10009
cg0230409	FLJ44606	PR B [T00	1983	1989	8.338824	GTCTGT	1.09863	1.10009
cg0230409	FLJ44606	PR A [T01	1642	1648	8.338824	AACAGG	1.09863	1.10009
cg0230409	FLJ44606	PR A [T01	1719	1725	8.338824	TTCTGTT	1.09863	1.10009
cg0230409	FLJ44606	PR A [T01	1983	1989	8.338824	GTCTGT	1.09863	1.10009
cg1020029	FLJ44606	PR B [T00	1862	1868	8.338824	AACAGG	1.09863	1.10009
cg1020029	FLJ44606	PR B [T00	1939	1945	8.338824	TTCTGTT	1.09863	1.10009
cg1020029	FLJ44606	PR A [T01	1862	1868	8.338824	AACAGG	1.09863	1.10009
cg1020029	FLJ44606	PR A [T01	1939	1945	8.338824	TTCTGTT	1.09863	1.10009
cg2709743	FLJ44606	GR-alpha [	26	30	8.281568	CAAGG	7.8125	7.72956

cg2709743	FLJ44606	GR-alpha |	130	134	8.281568	CCTTG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	338	342	8.281568	CCTTG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	678	682	8.281568	GGAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	963	967	8.281568	CCTCG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1145	1149	8.281568	CAAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1194	1198	8.281568	CAAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1358	1362	8.281568	CCTCC	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1361	1365	8.281568	CCTCC	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1425	1429	8.281568	CCTCC	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1521	1525	8.281568	GAAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1585	1589	8.281568	GAAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1624	1628	8.281568	GAAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1636	1640	8.281568	GGAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1808	1812	8.281568	GAAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1834	1838	8.281568	CCTTC	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1872	1876	8.281568	GAAGG	7.8125	7.72956
cg2709743	FLJ44606	GR-alpha |	1907	1911	8.281568	GGAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	56	60	8.281568	CCTTG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	264	268	8.281568	CCTTG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	604	608	8.281568	GGAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	889	893	8.281568	CCTCG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1071	1075	8.281568	CAAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1120	1124	8.281568	CAAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1284	1288	8.281568	CCTCC	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1287	1291	8.281568	CCTCC	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1351	1355	8.281568	CCTCC	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1447	1451	8.281568	GAAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1511	1515	8.281568	GAAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1550	1554	8.281568	GAAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1562	1566	8.281568	GGAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1734	1738	8.281568	GAAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1760	1764	8.281568	CCTTC	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1798	1802	8.281568	GAAGG	7.8125	7.72956
cg0230409	FLJ44606	GR-alpha |	1833	1837	8.281568	GGAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	172	176	8.281568	CAAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	276	280	8.281568	CCTTG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	484	488	8.281568	CCTTG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	824	828	8.281568	GGAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1109	1113	8.281568	CCTCG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1291	1295	8.281568	CAAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1340	1344	8.281568	CAAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1504	1508	8.281568	CCTCC	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1507	1511	8.281568	CCTCC	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1571	1575	8.281568	CCTCC	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1667	1671	8.281568	GAAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1731	1735	8.281568	GAAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1770	1774	8.281568	GAAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha |	1782	1786	8.281568	GGAGG	7.8125	7.72956

cg1020029	FLJ44606	GR-alpha [	1954	1958	8.281568	GAAGG	7.8125	7.72956
cg1020029	FLJ44606	GR-alpha [	1980	1984	8.281568	CCTTC	7.8125	7.72956
cg2709743	FLJ44606	NFI/CTF [	1593	1600	8.241664	TGGGTT(	0.18311	0.1823
cg0230409	FLJ44606	NFI/CTF [	1519	1526	8.241664	TGGGTT(	0.18311	0.1823
cg1020029	FLJ44606	NFI/CTF [	1739	1746	8.241664	TGGGTT(	0.18311	0.1823
cg2709743	FLJ44606	ENKTF-1	1151	1158	8.19852	TGGCCG(	0.73242	0.71737
cg0230409	FLJ44606	ENKTF-1	1077	1084	8.19852	TGGCCG(	0.73242	0.71737
cg1020029	FLJ44606	ENKTF-1	1297	1304	8.19852	TGGCCG(	0.73242	0.71737
cg2709743	FLJ44606	NF-1 [T00	1195	1202	8.191058	AAGGCC.	0.24414	0.24409
cg0230409	FLJ44606	NF-1 [T00	1121	1128	8.191058	AAGGCC.	0.24414	0.24409
cg1020029	FLJ44606	NF-1 [T00	1341	1348	8.191058	AAGGCC.	0.24414	0.24409
cg2709743	FLJ44606	PXR-1:RX	425	432	8.180749	ATTGTTC	0.12207	0.12407
cg0230409	FLJ44606	PXR-1:RX	351	358	8.180749	ATTGTTC	0.12207	0.12407
cg1020029	FLJ44606	PXR-1:RX	571	578	8.180749	ATTGTTC	0.12207	0.12407
cg2709743	FLJ44606	c-Jun [T00	312	318	8.128539	TGACAT	0.48828	0.49076
cg0230409	FLJ44606	c-Jun [T00	238	244	8.128539	TGACAT	0.48828	0.49076
cg1020029	FLJ44606	c-Jun [T00	458	464	8.128539	TGACAT	0.48828	0.49076
cg2709743	FLJ44606	E2F [T002	1000	1009	8.124323	CGCCGC(	0.02289	0.02249
cg0230409	FLJ44606	E2F [T002	926	935	8.124323	CGCCGC(	0.02289	0.02249
cg1020029	FLJ44606	E2F [T002	1146	1155	8.124323	CGCCGC(	0.02289	0.02249
cg0230409	FLJ44606	LEF-1 [T0	1933	1940	8.117221	ACTCAA	0.12207	0.1241
cg2709743	FLJ44606	VDR [T00	428	436	8.079962	GTTCAG	0.24414	0.24712
cg2709743	FLJ44606	VDR [T00	834	842	8.079962	GTTCAT(	0.24414	0.24712
cg0230409	FLJ44606	VDR [T00	354	362	8.079962	GTTCAG	0.24414	0.24712
cg0230409	FLJ44606	VDR [T00	760	768	8.079962	GTTCAT(	0.24414	0.24712
cg1020029	FLJ44606	VDR [T00	574	582	8.079962	GTTCAG	0.24414	0.24712
cg1020029	FLJ44606	VDR [T00	980	988	8.079962	GTTCAT(	0.24414	0.24712
cg2709743	FLJ44606	GR-alpha [	517	521	8.073878	CCTGC	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	922	926	8.073878	CCTGC	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1024	1028	8.073878	CCTGC	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1053	1057	8.073878	CCAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1066	1070	8.073878	CCAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1367	1371	8.073878	CTAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1383	1387	8.073878	CTAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1516	1520	8.073878	GCAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1613	1617	8.073878	GCAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1751	1755	8.073878	GCAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1903	1907	8.073878	GCAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1932	1936	8.073878	CCAGG	7.8125	7.72238
cg2709743	FLJ44606	GR-alpha [	1939	1943	8.073878	CTAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	443	447	8.073878	CCTGC	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	848	852	8.073878	CCTGC	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	950	954	8.073878	CCTGC	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	979	983	8.073878	CCAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	992	996	8.073878	CCAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	1293	1297	8.073878	CTAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	1309	1313	8.073878	CTAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	1442	1446	8.073878	GCAGG	7.8125	7.72238

cg0230409	FLJ44606	GR-alpha [	1539	1543	8.073878	GCAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	1677	1681	8.073878	GCAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	1829	1833	8.073878	GCAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	1858	1862	8.073878	CCAGG	7.8125	7.72238
cg0230409	FLJ44606	GR-alpha [	1865	1869	8.073878	CTAGG	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	663	667	8.073878	CCTGC	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1068	1072	8.073878	CCTGC	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1170	1174	8.073878	CCTGC	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1199	1203	8.073878	CCAGG	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1212	1216	8.073878	CCAGG	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1513	1517	8.073878	CTAGG	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1529	1533	8.073878	CTAGG	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1662	1666	8.073878	GCAGG	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1759	1763	8.073878	GCAGG	7.8125	7.72238
cg1020029	FLJ44606	GR-alpha [	1897	1901	8.073878	GCAGG	7.8125	7.72238
cg2709743	FLJ44606	Pax-5 [T0	442	448	8.014558	GGGCTG	2.19727	2.14502
cg2709743	FLJ44606	Pax-5 [T0	604	610	8.014558	GGGCTC	2.19727	2.14502
cg2709743	FLJ44606	Pax-5 [T0	660	666	8.014558	GGGCAT	2.19727	2.14502
cg2709743	FLJ44606	Pax-5 [T0	890	896	8.014558	GGGCAG	2.19727	2.14502
cg2709743	FLJ44606	TFIID [T0	283	289	8.014558	TTAGAA	2.19727	2.24348
cg2709743	FLJ44606	TFIID [T0	407	413	8.014558	TTTCTGA	2.19727	2.24348
cg2709743	FLJ44606	TFIID [T0	1463	1469	8.014558	TAGGAA	2.19727	2.24348
cg2709743	FLJ44606	TFIID [T0	1837	1843	8.014558	TCTGAA	2.19727	2.24348
cg0230409	FLJ44606	Pax-5 [T0	368	374	8.014558	GGGCTG	2.19727	2.14502
cg0230409	FLJ44606	Pax-5 [T0	530	536	8.014558	GGGCTC	2.19727	2.14502
cg0230409	FLJ44606	Pax-5 [T0	586	592	8.014558	GGGCAT	2.19727	2.14502
cg0230409	FLJ44606	Pax-5 [T0	816	822	8.014558	GGGCAG	2.19727	2.14502
cg0230409	FLJ44606	TFIID [T0	209	215	8.014558	TTAGAA	2.19727	2.24348
cg0230409	FLJ44606	TFIID [T0	333	339	8.014558	TTTCTGA	2.19727	2.24348
cg0230409	FLJ44606	TFIID [T0	1389	1395	8.014558	TAGGAA	2.19727	2.24348
cg0230409	FLJ44606	TFIID [T0	1763	1769	8.014558	TCTGAA	2.19727	2.24348
cg1020029	FLJ44606	Pax-5 [T0	588	594	8.014558	GGGCTG	2.19727	2.14502
cg1020029	FLJ44606	Pax-5 [T0	750	756	8.014558	GGGCTC	2.19727	2.14502
cg1020029	FLJ44606	Pax-5 [T0	806	812	8.014558	GGGCAT	2.19727	2.14502
cg1020029	FLJ44606	Pax-5 [T0	1036	1042	8.014558	GGGCAG	2.19727	2.14502
cg1020029	FLJ44606	TFIID [T0	20	26	8.014558	TTTCTAA	2.19727	2.24348
cg1020029	FLJ44606	TFIID [T0	429	435	8.014558	TTAGAA	2.19727	2.24348
cg1020029	FLJ44606	TFIID [T0	553	559	8.014558	TTTCTGA	2.19727	2.24348
cg1020029	FLJ44606	TFIID [T0	1609	1615	8.014558	TAGGAA	2.19727	2.24348
cg1020029	FLJ44606	TFIID [T0	1983	1989	8.014558	TCTGAA	2.19727	2.24348
cg2709743	FLJ44606	ETF [T002	1063	1073	7.870358	GCCCCA	0.07153	0.06862
cg0230409	FLJ44606	ETF [T002	989	999	7.870358	GCCCCA	0.07153	0.06862
cg1020029	FLJ44606	ETF [T002	1209	1219	7.870358	GCCCCA	0.07153	0.06862
cg2709743	FLJ44606	p53 [T006	604	610	7.833758	GGGCTC	0.48828	0.47377
cg0230409	FLJ44606	p53 [T006	530	536	7.833758	GGGCTC	0.48828	0.47377
cg1020029	FLJ44606	p53 [T006	750	756	7.833758	GGGCTC	0.48828	0.47377
cg2709743	FLJ44606	RXR-alpha	1148	1154	7.815913	GGGTGG	0.24414	0.24104
cg0230409	FLJ44606	RXR-alpha	1074	1080	7.815913	GGGTGG	0.24414	0.24104

cg1020029	FLJ44606	RXR-alph	1294	1300	7.815913	GGGTGG	0.24414	0.24104
cg2709743	FLJ44606	c-Jun [T00	289	295	7.686747	ACAGTC	0.48828	0.48775
cg0230409	FLJ44606	c-Jun [T00	215	221	7.686747	ACAGTC	0.48828	0.48775
cg1020029	FLJ44606	c-Jun [T00	435	441	7.686747	ACAGTC	0.48828	0.48775
cg2709743	FLJ44606	c-Myb [T0	687	694	7.662426	TGAAGT	0.42725	0.43114
cg0230409	FLJ44606	c-Myb [T0	613	620	7.662426	TGAAGT	0.42725	0.43114
cg1020029	FLJ44606	c-Myb [T0	833	840	7.662426	TGAAGT	0.42725	0.43114
cg2709743	FLJ44606	p53 [T006	1754	1760	7.641867	GGGCCT	0.73242	0.7186
cg0230409	FLJ44606	p53 [T006	1680	1686	7.641867	GGGCCT	0.73242	0.7186
cg1020029	FLJ44606	p53 [T006	1900	1906	7.641867	GGGCCT	0.73242	0.7186
cg2709743	FLJ44606	NFI/CTF [	610	617	7.587343	CCAAGT	0.36621	0.36674
cg0230409	FLJ44606	NFI/CTF [	536	543	7.587343	CCAAGT	0.36621	0.36674
cg0230409	FLJ44606	NFI/CTF [	1962	1969	7.587343	CCAAAA	0.36621	0.36674
cg1020029	FLJ44606	NFI/CTF [	756	763	7.587343	CCAAGT	0.36621	0.36674
cg2709743	FLJ44606	NF-AT1 [	1826	1834	7.574801	TGCTTTT	0.19836	0.19941
cg0230409	FLJ44606	NF-AT1 [	1752	1760	7.574801	TGCTTTT	0.19836	0.19941
cg1020029	FLJ44606	NF-AT1 [	1972	1980	7.574801	TGCTTTT	0.19836	0.19941
cg2709743	FLJ44606	GR [T050	369	375	7.527031	CTATTT	1.83105	1.86007
cg2709743	FLJ44606	GR [T050	1212	1218	7.527031	CAAAAT	1.83105	1.86007
cg2709743	FLJ44606	GR [T050	1236	1242	7.527031	ATGTTT	1.83105	1.86007
cg2709743	FLJ44606	GR [T050	1510	1516	7.527031	TGCTTT	1.83105	1.86007
cg2709743	FLJ44606	GR [T050	1566	1572	7.527031	AGCTTT	1.83105	1.86007
cg2709743	FLJ44606	GR [T050	1853	1859	7.527031	AGCTTT	1.83105	1.86007
cg0230409	FLJ44606	GR [T050	295	301	7.527031	CTATTT	1.83105	1.86007
cg0230409	FLJ44606	GR [T050	1138	1144	7.527031	CAAAAT	1.83105	1.86007
cg0230409	FLJ44606	GR [T050	1162	1168	7.527031	ATGTTT	1.83105	1.86007
cg0230409	FLJ44606	GR [T050	1436	1442	7.527031	TGCTTT	1.83105	1.86007
cg0230409	FLJ44606	GR [T050	1492	1498	7.527031	AGCTTT	1.83105	1.86007
cg0230409	FLJ44606	GR [T050	1779	1785	7.527031	AGCTTT	1.83105	1.86007
cg0230409	FLJ44606	GR [T050	1936	1942	7.527031	CAAAGC	1.83105	1.86007
cg1020029	FLJ44606	GR [T050	59	65	7.527031	CAAATA	1.83105	1.86007
cg1020029	FLJ44606	GR [T050	515	521	7.527031	CTATTT	1.83105	1.86007
cg1020029	FLJ44606	GR [T050	1358	1364	7.527031	CAAAAT	1.83105	1.86007
cg1020029	FLJ44606	GR [T050	1382	1388	7.527031	ATGTTT	1.83105	1.86007
cg1020029	FLJ44606	GR [T050	1656	1662	7.527031	TGCTTT	1.83105	1.86007
cg1020029	FLJ44606	GR [T050	1712	1718	7.527031	AGCTTT	1.83105	1.86007
cg2709743	FLJ44606	c-Ets-1 [T	866	872	7.514011	ATTCCG	0.48828	0.4878
cg0230409	FLJ44606	c-Ets-1 [T	792	798	7.514011	ATTCCG	0.48828	0.4878
cg1020029	FLJ44606	c-Ets-1 [T	1012	1018	7.514011	ATTCCG	0.48828	0.4878
cg2709743	FLJ44606	RAR-beta	979	988	7.47824	AGGGAA	0.24414	0.24343
cg0230409	FLJ44606	RAR-beta	905	914	7.47824	AGGGAA	0.24414	0.24343
cg1020029	FLJ44606	RAR-beta	1125	1134	7.47824	AGGGAA	0.24414	0.24343
cg2709743	FLJ44606	RAR-beta:	488	499	7.477995	TCCAGA	0.02861	0.02796
cg0230409	FLJ44606	RAR-beta:	414	425	7.477995	TCCAGA	0.02861	0.02796
cg1020029	FLJ44606	RAR-beta:	634	645	7.477995	TCCAGA	0.02861	0.02796
cg2709743	FLJ44606	NF-1 [T00	96	103	7.445595	TTGGGA	0.24414	0.24565
cg0230409	FLJ44606	NF-1 [T00	22	29	7.445595	TTGGGA	0.24414	0.24565
cg1020029	FLJ44606	NF-1 [T00	242	249	7.445595	TTGGGA	0.24414	0.24565

cg2709743	FLJ44606	PEA3 [T0	483	491	7.421728	GCTCAT	0.34332	0.34161
cg0230409	FLJ44606	PEA3 [T0	409	417	7.421728	GCTCAT	0.34332	0.34161
cg1020029	FLJ44606	PEA3 [T0	629	637	7.421728	GCTCAT	0.34332	0.34161
cg2709743	FLJ44606	PXR-1:RX	7	14	7.362674	CTTGTT	0.24414	0.24395
cg1020029	FLJ44606	PXR-1:RX	153	160	7.362674	CTTGTT	0.24414	0.24395
cg2709743	FLJ44606	E2F-1 [T0	1016	1023	7.336545	GCTTCC	0.45776	0.44878
cg2709743	FLJ44606	E2F-1 [T0	1036	1043	7.336545	ACTTCC	0.45776	0.44878
cg2709743	FLJ44606	E2F-1 [T0	1077	1084	7.336545	ACTTCC	0.45776	0.44878
cg2709743	FLJ44606	E2F-1 [T0	1099	1106	7.336545	ACTGCC	0.45776	0.44878
cg0230409	FLJ44606	E2F-1 [T0	942	949	7.336545	GCTTCC	0.45776	0.44878
cg0230409	FLJ44606	E2F-1 [T0	962	969	7.336545	ACTTCC	0.45776	0.44878
cg0230409	FLJ44606	E2F-1 [T0	1003	1010	7.336545	ACTTCC	0.45776	0.44878
cg0230409	FLJ44606	E2F-1 [T0	1025	1032	7.336545	ACTGCC	0.45776	0.44878
cg1020029	FLJ44606	E2F-1 [T0	1162	1169	7.336545	GCTTCC	0.45776	0.44878
cg1020029	FLJ44606	E2F-1 [T0	1182	1189	7.336545	ACTTCC	0.45776	0.44878
cg1020029	FLJ44606	E2F-1 [T0	1223	1230	7.336545	ACTTCC	0.45776	0.44878
cg1020029	FLJ44606	E2F-1 [T0	1245	1252	7.336545	ACTGCC	0.45776	0.44878
cg2709743	FLJ44606	HOXD9 [	199	208	7.270719	AATATA	0.06866	0.07152
cg2709743	FLJ44606	HOXD10 [	199	208	7.270719	AATATA	0.06866	0.07152
cg0230409	FLJ44606	HOXD9 [	125	134	7.270719	AATATA	0.06866	0.07152
cg0230409	FLJ44606	HOXD10 [	125	134	7.270719	AATATA	0.06866	0.07152
cg1020029	FLJ44606	HOXD9 [	345	354	7.270719	AATATA	0.06866	0.07152
cg1020029	FLJ44606	HOXD10 [	345	354	7.270719	AATATA	0.06866	0.07152
cg2709743	FLJ44606	c-Ets-1 [T	75	81	7.199436	TGGGAA	0.73242	0.73099
cg0230409	FLJ44606	c-Ets-1 [T	1	7	7.199436	TGGGAA	0.73242	0.73099
cg1020029	FLJ44606	c-Ets-1 [T	221	227	7.199436	TGGGAA	0.73242	0.73099
cg2709743	FLJ44606	XBP-1 [T	631	636	7.172312	CTTCAT	2.92969	2.97018
cg2709743	FLJ44606	XBP-1 [T	686	691	7.172312	ATGAAG	2.92969	2.97018
cg2709743	FLJ44606	XBP-1 [T	1983	1988	7.172312	ATGATG	2.92969	2.97018
cg0230409	FLJ44606	XBP-1 [T	557	562	7.172312	CTTCAT	2.92969	2.97018
cg0230409	FLJ44606	XBP-1 [T	612	617	7.172312	ATGAAG	2.92969	2.97018
cg0230409	FLJ44606	XBP-1 [T	1909	1914	7.172312	ATGATG	2.92969	2.97018
cg0230409	FLJ44606	XBP-1 [T	1975	1980	7.172312	ACTCAT	2.92969	2.97018
cg1020029	FLJ44606	XBP-1 [T	777	782	7.172312	CTTCAT	2.92969	2.97018
cg1020029	FLJ44606	XBP-1 [T	832	837	7.172312	ATGAAG	2.92969	2.97018
cg2709743	FLJ44606	c-Jun [T00	590	596	7.096776	GCAGTC	0.73242	0.73173
cg0230409	FLJ44606	c-Jun [T00	516	522	7.096776	GCAGTC	0.73242	0.73173
cg1020029	FLJ44606	c-Jun [T00	736	742	7.096776	GCAGTC	0.73242	0.73173
cg2709743	FLJ44606	NF-AT1 [	1220	1228	7.095752	GGAAAA	0.15259	0.1548
cg0230409	FLJ44606	NF-AT1 [	1146	1154	7.095752	GGAAAA	0.15259	0.1548
cg1020029	FLJ44606	NF-AT1 [	1366	1374	7.095752	GGAAAA	0.15259	0.1548
cg2709743	FLJ44606	c-Ets-1 [T	1830	1836	7.071349	TTTCCC	0.73242	0.73099
cg0230409	FLJ44606	c-Ets-1 [T	1756	1762	7.071349	TTTCCC	0.73242	0.73099
cg1020029	FLJ44606	c-Ets-1 [T	1976	1982	7.071349	TTTCCC	0.73242	0.73099
cg2709743	FLJ44606	C/EBPalp	57	63	7.00174	GACAAT	0.73242	0.74337
cg1020029	FLJ44606	C/EBPalp	203	209	7.00174	GACAAT	0.73242	0.74337
cg2709743	FLJ44606	HNF-3alp	222	229	7.000129	TATTTA	0.82397	0.84946
cg2709743	FLJ44606	HNF-3alp	569	576	7.000129	CAAAAA	0.82397	0.84946

cg2709743	FLJ44606	HNF-3alph	575	582	7.000129	TATTTAT	0.82397	0.84946
cg2709743	FLJ44606	HNF-3alph	772	779	7.000129	TATTTAC	0.82397	0.84946
cg2709743	FLJ44606	HNF-3alph	1349	1356	7.000129	TATTTAC	0.82397	0.84946
cg2709743	FLJ44606	HNF-3alph	1437	1444	7.000129	TGAAAA	0.82397	0.84946
cg2709743	FLJ44606	HNF-3alph	1967	1974	7.000129	AGTAAA	0.82397	0.84946
cg0230409	FLJ44606	HNF-3alph	148	155	7.000129	TATTTAT	0.82397	0.84946
cg0230409	FLJ44606	HNF-3alph	495	502	7.000129	CAAAAA	0.82397	0.84946
cg0230409	FLJ44606	HNF-3alph	501	508	7.000129	TATTTAT	0.82397	0.84946
cg0230409	FLJ44606	HNF-3alph	698	705	7.000129	TATTTAC	0.82397	0.84946
cg0230409	FLJ44606	HNF-3alph	1275	1282	7.000129	TATTTAC	0.82397	0.84946
cg0230409	FLJ44606	HNF-3alph	1363	1370	7.000129	TGAAAA	0.82397	0.84946
cg0230409	FLJ44606	HNF-3alph	1893	1900	7.000129	AGTAAA	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	57	64	7.000129	TCCAAA	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	85	92	7.000129	CATTTTT	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	368	375	7.000129	TATTTAT	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	715	722	7.000129	CAAAAA	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	721	728	7.000129	TATTTAT	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	918	925	7.000129	TATTTAC	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	1495	1502	7.000129	TATTTAC	0.82397	0.84946
cg1020029	FLJ44606	HNF-3alph	1583	1590	7.000129	TGAAAA	0.82397	0.84946
cg2709743	FLJ44606	AhR [T01	996	1006	6.981759	CTCACG	0.02289	0.02262
cg0230409	FLJ44606	AhR [T01	922	932	6.981759	CTCACG	0.02289	0.02262
cg1020029	FLJ44606	AhR [T01	1142	1152	6.981759	CTCACG	0.02289	0.02262
cg2709743	FLJ44606	IRF-1 [T0	73	81	6.968314	TCTGGG	0.1297	0.13036
cg1020029	FLJ44606	IRF-1 [T0	219	227	6.968314	TCTGGG	0.1297	0.13036
cg2709743	FLJ44606	NF-1 [T00	21	28	6.948522	TGCACC	0.48828	0.4856
cg2709743	FLJ44606	NF-1 [T00	1273	1280	6.948522	GGAGCC	0.48828	0.4856
cg2709743	FLJ44606	NF-1 [T00	1570	1577	6.948522	TTGGGG	0.48828	0.4856
cg0230409	FLJ44606	NF-1 [T00	1199	1206	6.948522	GGAGCC	0.48828	0.4856
cg0230409	FLJ44606	NF-1 [T00	1496	1503	6.948522	TTGGGG	0.48828	0.4856
cg1020029	FLJ44606	NF-1 [T00	167	174	6.948522	TGCACC	0.48828	0.4856
cg1020029	FLJ44606	NF-1 [T00	1419	1426	6.948522	GGAGCC	0.48828	0.4856
cg1020029	FLJ44606	NF-1 [T00	1716	1723	6.948522	TTGGGG	0.48828	0.4856
cg1020029	FLJ44606	c-Ets-1 [T	1	7	6.943262	TTTCCC	0.73242	0.73099
cg2709743	FLJ44606	ENKTF-1	1300	1307	6.942764	CCGAGC	1.46484	1.44228
cg2709743	FLJ44606	ENKTF-1	1679	1686	6.942764	TGGCTG	1.46484	1.44228
cg2709743	FLJ44606	ENKTF-1	1744	1751	6.942764	TGGCCA	1.46484	1.44228
cg0230409	FLJ44606	ENKTF-1	1226	1233	6.942764	CCGAGC	1.46484	1.44228
cg0230409	FLJ44606	ENKTF-1	1605	1612	6.942764	TGGCTG	1.46484	1.44228
cg0230409	FLJ44606	ENKTF-1	1670	1677	6.942764	TGGCCA	1.46484	1.44228
cg1020029	FLJ44606	ENKTF-1	1446	1453	6.942764	CCGAGC	1.46484	1.44228
cg1020029	FLJ44606	ENKTF-1	1825	1832	6.942764	TGGCTG	1.46484	1.44228
cg1020029	FLJ44606	ENKTF-1	1890	1897	6.942764	TGGCCA	1.46484	1.44228
cg2709743	FLJ44606	p53 [T006	1108	1114	6.891821	GGGCGT	1.09863	1.07125
cg0230409	FLJ44606	p53 [T006	1034	1040	6.891821	GGGCGT	1.09863	1.07125
cg1020029	FLJ44606	p53 [T006	1254	1260	6.891821	GGGCGT	1.09863	1.07125
cg1020029	FLJ44606	c-Jun [T00	112	118	6.856451	TGACCA	0.73242	0.73173
cg2709743	FLJ44606	C/EBPalph	641	647	6.85549	TTCAATT	0.73242	0.74337

cg0230409	FLJ44606	C/EBPalph	567	573	6.85549	TTCAATT	0.73242	0.74337
cg1020029	FLJ44606	C/EBPalph	787	793	6.85549	TTCAATT	0.73242	0.74337
cg2709743	FLJ44606	c-Ets-1 [T	756	762	6.815175	TTTCCCC	0.73242	0.73099
cg0230409	FLJ44606	c-Ets-1 [T	682	688	6.815175	TTTCCCC	0.73242	0.73099
cg1020029	FLJ44606	c-Ets-1 [T	902	908	6.815175	TTTCCCC	0.73242	0.73099
cg2709743	FLJ44606	NFI/CTF [	252	259	6.786076	CCAAGC	0.73242	0.73214
cg2709743	FLJ44606	NFI/CTF [	1199	1206	6.786076	CCAAAC	0.73242	0.73214
cg0230409	FLJ44606	NFI/CTF [	178	185	6.786076	CCAAGC	0.73242	0.73214
cg0230409	FLJ44606	NFI/CTF [	1125	1132	6.786076	CCAAAC	0.73242	0.73214
cg1020029	FLJ44606	NFI/CTF [	398	405	6.786076	CCAAGC	0.73242	0.73214
cg1020029	FLJ44606	NFI/CTF [	1345	1352	6.786076	CCAAAC	0.73242	0.73214
cg2709743	FLJ44606	c-Ets-2 [T	1460	1468	6.769996	TATTAGC	0.03052	0.03102
cg0230409	FLJ44606	c-Ets-2 [T	1386	1394	6.769996	TATTAGC	0.03052	0.03102
cg1020029	FLJ44606	c-Ets-2 [T	1606	1614	6.769996	TATTAGC	0.03052	0.03102
cg2709743	FLJ44606	NF-1 [T00	451	458	6.722386	TTGCCCA	0.24414	0.24147
cg0230409	FLJ44606	NF-1 [T00	377	384	6.722386	TTGCCCA	0.24414	0.24147
cg1020029	FLJ44606	NF-1 [T00	597	604	6.722386	TTGCCCA	0.24414	0.24147
cg2709743	FLJ44606	T3R-beta1	539	547	6.683388	TCACCCC	0.21362	0.21147
cg0230409	FLJ44606	T3R-beta1	465	473	6.683388	TCACCCC	0.21362	0.21147
cg1020029	FLJ44606	T3R-beta1	685	693	6.683388	TCACCCC	0.21362	0.21147
cg2709743	FLJ44606	T3R-beta1	248	256	6.664094	TCACCCA	0.21362	0.21147
cg2709743	FLJ44606	T3R-beta1	959	967	6.664094	TCACCCT	0.21362	0.21147
cg0230409	FLJ44606	T3R-beta1	174	182	6.664094	TCACCCA	0.21362	0.21147
cg0230409	FLJ44606	T3R-beta1	885	893	6.664094	TCACCCT	0.21362	0.21147
cg1020029	FLJ44606	T3R-beta1	394	402	6.664094	TCACCCA	0.21362	0.21147
cg1020029	FLJ44606	T3R-beta1	1105	1113	6.664094	TCACCCT	0.21362	0.21147
cg2709743	FLJ44606	Elk-1 [T00	1017	1025	6.598007	CTTCCGC	0.06104	0.05967
cg2709743	FLJ44606	Elk-1 [T00	1037	1045	6.598007	CTTCCGC	0.06104	0.05967
cg2709743	FLJ44606	Elk-1 [T00	1078	1086	6.598007	CTTCCGC	0.06104	0.05967
cg0230409	FLJ44606	Elk-1 [T00	943	951	6.598007	CTTCCGC	0.06104	0.05967
cg0230409	FLJ44606	Elk-1 [T00	963	971	6.598007	CTTCCGC	0.06104	0.05967
cg0230409	FLJ44606	Elk-1 [T00	1004	1012	6.598007	CTTCCGC	0.06104	0.05967
cg1020029	FLJ44606	Elk-1 [T00	1163	1171	6.598007	CTTCCGC	0.06104	0.05967
cg1020029	FLJ44606	Elk-1 [T00	1183	1191	6.598007	CTTCCGC	0.06104	0.05967
cg1020029	FLJ44606	Elk-1 [T00	1224	1232	6.598007	CTTCCGC	0.06104	0.05967
cg2709743	FLJ44606	TFII-I [T0	470	475	6.581441	GGAGAT	0.97656	0.97366
cg2709743	FLJ44606	TFII-I [T0	820	825	6.581441	ATCTCC	0.97656	0.97366
cg2709743	FLJ44606	FOXP3 [T	529	534	6.581441	TTCAAC	0.97656	0.99397
cg2709743	FLJ44606	FOXP3 [T	1555	1560	6.581441	GTTGAA	0.97656	0.99397
cg2709743	FLJ44606	FOXP3 [T	1797	1802	6.581441	GTTTTA	0.97656	0.99397
cg0230409	FLJ44606	TFII-I [T0	396	401	6.581441	GGAGAT	0.97656	0.97366
cg0230409	FLJ44606	TFII-I [T0	746	751	6.581441	ATCTCC	0.97656	0.97366
cg0230409	FLJ44606	FOXP3 [T	455	460	6.581441	TTCAAC	0.97656	0.99397
cg0230409	FLJ44606	FOXP3 [T	1481	1486	6.581441	GTTGAA	0.97656	0.99397
cg0230409	FLJ44606	FOXP3 [T	1723	1728	6.581441	GTTTTA	0.97656	0.99397
cg1020029	FLJ44606	TFII-I [T0	616	621	6.581441	GGAGAT	0.97656	0.97366
cg1020029	FLJ44606	TFII-I [T0	966	971	6.581441	ATCTCC	0.97656	0.97366
cg1020029	FLJ44606	FOXP3 [T	10	15	6.581441	GTTTTA	0.97656	0.99397

cg1020029	FLJ44606	FOXP3 [T	675	680	6.581441	TTCAAC	0.97656	0.99397
cg1020029	FLJ44606	FOXP3 [T	1701	1706	6.581441	GTTGAA	0.97656	0.99397
cg1020029	FLJ44606	FOXP3 [T	1943	1948	6.581441	GTTTTA	0.97656	0.99397
cg2709743	FLJ44606	p53 [T006	442	448	6.563521	GGGCTG	0.48828	0.47541
cg0230409	FLJ44606	p53 [T006	368	374	6.563521	GGGCTG	0.48828	0.47541
cg1020029	FLJ44606	p53 [T006	588	594	6.563521	GGGCTG	0.48828	0.47541
cg2709743	FLJ44606	IRF-1 [T0	756	764	6.549276	TTTCCC	0.19073	0.19127
cg0230409	FLJ44606	IRF-1 [T0	682	690	6.549276	TTTCCC	0.19073	0.19127
cg1020029	FLJ44606	IRF-1 [T0	902	910	6.549276	TTTCCC	0.19073	0.19127
cg2709743	FLJ44606	IRF-1 [T0	1709	1717	6.497844	AGGTGG	0.19073	0.19127
cg0230409	FLJ44606	IRF-1 [T0	1635	1643	6.497844	AGGTGG	0.19073	0.19127
cg1020029	FLJ44606	IRF-1 [T0	1855	1863	6.497844	AGGTGG	0.19073	0.19127
cg2709743	FLJ44606	XBP-1 [T	660	665	6.478682	GGGCAT	0.97656	0.97062
cg2709743	FLJ44606	XBP-1 [T	1787	1792	6.478682	GGGCAT	0.97656	0.97062
cg0230409	FLJ44606	XBP-1 [T	586	591	6.478682	GGGCAT	0.97656	0.97062
cg0230409	FLJ44606	XBP-1 [T	1713	1718	6.478682	GGGCAT	0.97656	0.97062
cg1020029	FLJ44606	XBP-1 [T	806	811	6.478682	GGGCAT	0.97656	0.97062
cg1020029	FLJ44606	XBP-1 [T	1933	1938	6.478682	GGGCAT	0.97656	0.97062
cg2709743	FLJ44606	c-Jun [T00	926	932	6.475265	CGCGTC	0.61035	0.60769
cg0230409	FLJ44606	c-Jun [T00	852	858	6.475265	CGCGTC	0.61035	0.60769
cg1020029	FLJ44606	c-Jun [T00	1072	1078	6.475265	CGCGTC	0.61035	0.60769
cg2709743	FLJ44606	GR-alpha [	1	5	6.263098	CCTCA	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	133	137	6.263098	TGAGG	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	161	165	6.263098	TAAGG	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	187	191	6.263098	TAAGG	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	281	285	6.263098	CCTTA	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	459	463	6.263098	TAAGG	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	977	981	6.263098	TAAGG	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	995	999	6.263098	CCTCA	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	1262	1266	6.263098	CCTCA	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	1286	1290	6.263098	TGAGG	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	1475	1479	6.263098	CCTTA	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	1773	1777	6.263098	TAAGG	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	1849	1853	6.263098	CCTTA	3.90625	3.91061
cg2709743	FLJ44606	GR-alpha [	1912	1916	6.263098	TGAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	59	63	6.263098	TGAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	87	91	6.263098	TAAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	113	117	6.263098	TAAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	207	211	6.263098	CCTTA	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	385	389	6.263098	TAAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	903	907	6.263098	TAAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	921	925	6.263098	CCTCA	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	1188	1192	6.263098	CCTCA	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	1212	1216	6.263098	TGAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	1401	1405	6.263098	CCTTA	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	1699	1703	6.263098	TAAGG	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	1775	1779	6.263098	CCTTA	3.90625	3.91061
cg0230409	FLJ44606	GR-alpha [	1838	1842	6.263098	TGAGG	3.90625	3.91061

cg1020029	FLJ44606	GR-alpha [	102	106	6.263098	CCTCA	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	147	151	6.263098	CCTCA	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	279	283	6.263098	TGAGG	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	307	311	6.263098	TAAGG	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	333	337	6.263098	TAAGG	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	427	431	6.263098	CCTTA	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	605	609	6.263098	TAAGG	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	1123	1127	6.263098	TAAGG	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	1141	1145	6.263098	CCTCA	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	1408	1412	6.263098	CCTCA	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	1432	1436	6.263098	TGAGG	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	1621	1625	6.263098	CCTTA	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	1919	1923	6.263098	TAAGG	3.90625	3.91061
cg1020029	FLJ44606	GR-alpha [	1995	1999	6.263098	CCTTA	3.90625	3.91061
cg2709743	FLJ44606	c-Ets-1 [T	1711	1717	6.167515	GTGGAA	0.36621	0.36731
cg0230409	FLJ44606	c-Ets-1 [T	1637	1643	6.167515	GTGGAA	0.36621	0.36731
cg1020029	FLJ44606	c-Ets-1 [T	1857	1863	6.167515	GTGGAA	0.36621	0.36731
cg2709743	FLJ44606	c-Jun [T00	372	378	6.152811	TTTGTCA	0.36621	0.37082
cg0230409	FLJ44606	c-Jun [T00	298	304	6.152811	TTTGTCA	0.36621	0.37082
cg1020029	FLJ44606	c-Jun [T00	518	524	6.152811	TTTGTCA	0.36621	0.37082
cg2709743	FLJ44606	GR-alpha [	300	304	6.055408	CCTAA	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	989	993	6.055408	CCTGA	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	1120	1124	6.055408	TCAGG	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	1159	1163	6.055408	CCTGA	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	1264	1268	6.055408	TCAGG	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	1462	1466	6.055408	TTAGG	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	1540	1544	6.055408	CCTGA	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	1761	1765	6.055408	TCAGG	3.90625	3.9065
cg2709743	FLJ44606	GR-alpha [	1879	1883	6.055408	TTAGG	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	226	230	6.055408	CCTAA	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	915	919	6.055408	CCTGA	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1046	1050	6.055408	TCAGG	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1085	1089	6.055408	CCTGA	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1190	1194	6.055408	TCAGG	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1388	1392	6.055408	TTAGG	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1466	1470	6.055408	CCTGA	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1687	1691	6.055408	TCAGG	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1805	1809	6.055408	TTAGG	3.90625	3.9065
cg0230409	FLJ44606	GR-alpha [	1994	1998	6.055408	CCTGA	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	446	450	6.055408	CCTAA	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	1135	1139	6.055408	CCTGA	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	1266	1270	6.055408	TCAGG	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	1305	1309	6.055408	CCTGA	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	1410	1414	6.055408	TCAGG	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	1608	1612	6.055408	TTAGG	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	1686	1690	6.055408	CCTGA	3.90625	3.9065
cg1020029	FLJ44606	GR-alpha [	1907	1911	6.055408	TCAGG	3.90625	3.9065
cg2709743	FLJ44606	C/EBPalph	424	430	5.996794	CATTGTT	0.97656	0.99

cg0230409	FLJ44606	C/EBPalph	350	356	5.996794	CATTGTT	0.97656	0.99
cg1020029	FLJ44606	C/EBPalph	570	576	5.996794	CATTGTT	0.97656	0.99
cg2709743	FLJ44606	RXR-alpha	432	438	5.937582	AGTACC(	0.73242	0.72249
cg0230409	FLJ44606	RXR-alpha	358	364	5.937582	AGTACC(	0.73242	0.72249
cg1020029	FLJ44606	RXR-alpha	578	584	5.937582	AGTACC(	0.73242	0.72249
cg2709743	FLJ44606	GCF [T00]	963	971	5.917256	CCTCGG(	0.64087	0.6219
cg0230409	FLJ44606	GCF [T00]	889	897	5.917256	CCTCGG(	0.64087	0.6219
cg1020029	FLJ44606	GCF [T00]	1109	1117	5.917256	CCTCGG(	0.64087	0.6219
cg2709743	FLJ44606	AR [T0004	1124	1132	5.8965	GTGGTG	0.24414	0.24229
cg0230409	FLJ44606	AR [T0004	1050	1058	5.8965	GTGGTG	0.24414	0.24229
cg1020029	FLJ44606	AR [T0004	1270	1278	5.8965	GTGGTG	0.24414	0.24229
cg2709743	FLJ44606	STAT4 [T(	1520	1525	5.882353	GGAAGG	0.48828	0.48408
cg2709743	FLJ44606	STAT4 [T(	1623	1628	5.882353	GGAAGG	0.48828	0.48408
cg2709743	FLJ44606	STAT4 [T(	1807	1812	5.882353	GGAAGG	0.48828	0.48408
cg2709743	FLJ44606	STAT4 [T(	1871	1876	5.882353	GGAAGG	0.48828	0.48408
cg0230409	FLJ44606	STAT4 [T(	1446	1451	5.882353	GGAAGG	0.48828	0.48408
cg0230409	FLJ44606	STAT4 [T(	1549	1554	5.882353	GGAAGG	0.48828	0.48408
cg0230409	FLJ44606	STAT4 [T(	1733	1738	5.882353	GGAAGG	0.48828	0.48408
cg0230409	FLJ44606	STAT4 [T(	1797	1802	5.882353	GGAAGG	0.48828	0.48408
cg1020029	FLJ44606	STAT4 [T(	1666	1671	5.882353	GGAAGG	0.48828	0.48408
cg1020029	FLJ44606	STAT4 [T(	1769	1774	5.882353	GGAAGG	0.48828	0.48408
cg1020029	FLJ44606	STAT4 [T(	1953	1958	5.882353	GGAAGG	0.48828	0.48408
cg2709743	FLJ44606	IRF-1 [T0(	1461	1469	5.823972	ATTAGG/	0.16785	0.16909
cg0230409	FLJ44606	IRF-1 [T0(	1387	1395	5.823972	ATTAGG/	0.16785	0.16909
cg1020029	FLJ44606	IRF-1 [T0(	1607	1615	5.823972	ATTAGG/	0.16785	0.16909
cg2709743	FLJ44606	c-Ets-1 [T(	778	784	5.814485	CTTCCCA	0.36621	0.36731
cg2709743	FLJ44606	c-Ets-1 [T(	1805	1811	5.814485	TGGGAA(	0.36621	0.36731
cg2709743	FLJ44606	c-Ets-1 [T(	1858	1864	5.814485	TGGGAA(	0.36621	0.36731
cg2709743	FLJ44606	c-Ets-1 [T(	1869	1875	5.814485	TGGGAA(	0.36621	0.36731
cg0230409	FLJ44606	c-Ets-1 [T(	704	710	5.814485	CTTCCCA	0.36621	0.36731
cg0230409	FLJ44606	c-Ets-1 [T(	1731	1737	5.814485	TGGGAA(	0.36621	0.36731
cg0230409	FLJ44606	c-Ets-1 [T(	1784	1790	5.814485	TGGGAA(	0.36621	0.36731
cg0230409	FLJ44606	c-Ets-1 [T(	1795	1801	5.814485	TGGGAA(	0.36621	0.36731
cg1020029	FLJ44606	c-Ets-1 [T(	924	930	5.814485	CTTCCCA	0.36621	0.36731
cg1020029	FLJ44606	c-Ets-1 [T(	1951	1957	5.814485	TGGGAA(	0.36621	0.36731
cg2709743	FLJ44606	VDR [T00	10	18	5.771401	GTTCAG(	0.42725	0.42999
cg1020029	FLJ44606	VDR [T00	156	164	5.771401	GTTCAG(	0.42725	0.42999
cg2709743	FLJ44606	c-Jun [T00	151	157	5.703976	GGGGTC.	0.48828	0.48665
cg2709743	FLJ44606	c-Jun [T00	1227	1233	5.703976	TGACCC(	0.48828	0.48665
cg0230409	FLJ44606	c-Jun [T00	77	83	5.703976	GGGGTC.	0.48828	0.48665
cg0230409	FLJ44606	c-Jun [T00	1153	1159	5.703976	TGACCC(	0.48828	0.48665
cg1020029	FLJ44606	c-Jun [T00	297	303	5.703976	GGGGTC.	0.48828	0.48665
cg1020029	FLJ44606	c-Jun [T00	1373	1379	5.703976	TGACCC(	0.48828	0.48665
cg2709743	FLJ44606	ENKTF-1	1194	1201	5.687009	CAAGGC(	0.73242	0.7249
cg0230409	FLJ44606	ENKTF-1	1120	1127	5.687009	CAAGGC(	0.73242	0.7249
cg1020029	FLJ44606	ENKTF-1	1340	1347	5.687009	CAAGGC(	0.73242	0.7249
cg2709743	FLJ44606	c-Ets-1 [T(	1518	1524	5.686398	AGGGAA	0.36621	0.3623
cg0230409	FLJ44606	c-Ets-1 [T(	1444	1450	5.686398	AGGGAA	0.36621	0.3623

cg1020029	FLJ44606	c-Ets-1 [T0	1664	1670	5.686398	AGGGAA	0.36621	0.3623
cg2709743	FLJ44606	AP-2alpha	1484	1489	5.568965	ATAGGC	0.48828	0.4878
cg2709743	FLJ44606	AP-2alpha	1884	1889	5.568965	ATAGGC	0.48828	0.4878
cg0230409	FLJ44606	AP-2alpha	1410	1415	5.568965	ATAGGC	0.48828	0.4878
cg0230409	FLJ44606	AP-2alpha	1810	1815	5.568965	ATAGGC	0.48828	0.4878
cg1020029	FLJ44606	AP-2alpha	1630	1635	5.568965	ATAGGC	0.48828	0.4878
cg2709743	FLJ44606	NFI/CTF [	1236	1243	5.558661	ATGTTTC	0.54932	0.55038
cg0230409	FLJ44606	NFI/CTF [	1162	1169	5.558661	ATGTTTC	0.54932	0.55038
cg1020029	FLJ44606	NFI/CTF [	1382	1389	5.558661	ATGTTTC	0.54932	0.55038
cg2709743	FLJ44606	c-Ets-1 [T0	1621	1627	5.558311	GGGGAA	0.36621	0.3623
cg2709743	FLJ44606	c-Ets-1 [T0	1700	1706	5.558311	GGGGAA	0.36621	0.3623
cg0230409	FLJ44606	c-Ets-1 [T0	1547	1553	5.558311	GGGGAA	0.36621	0.3623
cg0230409	FLJ44606	c-Ets-1 [T0	1626	1632	5.558311	GGGGAA	0.36621	0.3623
cg1020029	FLJ44606	c-Ets-1 [T0	1767	1773	5.558311	GGGGAA	0.36621	0.3623
cg1020029	FLJ44606	c-Ets-1 [T0	1846	1852	5.558311	GGGGAA	0.36621	0.3623
cg2709743	FLJ44606	Pax-5 [T00	1108	1114	5.544826	GGGCGT	0.73242	0.72046
cg2709743	FLJ44606	TFIID [T0	1878	1884	5.544826	TTTAGGA	0.73242	0.75085
cg0230409	FLJ44606	Pax-5 [T00	1034	1040	5.544826	GGGCGT	0.73242	0.72046
cg0230409	FLJ44606	TFIID [T0	1804	1810	5.544826	TTTAGGA	0.73242	0.75085
cg1020029	FLJ44606	Pax-5 [T00	1254	1260	5.544826	GGGCGT	0.73242	0.72046
cg0230409	FLJ44606	TCF-4 [T0	1932	1941	5.337909	TACTCAA	0.04959	0.04964
cg2709743	FLJ44606	RXR-alpha	333	339	5.271235	TCTACCC	0.61035	0.6044
cg0230409	FLJ44606	RXR-alpha	259	265	5.271235	TCTACCC	0.61035	0.6044
cg1020029	FLJ44606	RXR-alpha	479	485	5.271235	TCTACCC	0.61035	0.6044
cg2709743	FLJ44606	p53 [T006	1019	1025	5.133514	TCCGCCC	0.48828	0.47747
cg2709743	FLJ44606	p53 [T006	1039	1045	5.133514	TCCGCCC	0.48828	0.47747
cg2709743	FLJ44606	p53 [T006	1080	1086	5.133514	TCCGCCC	0.48828	0.47747
cg0230409	FLJ44606	p53 [T006	945	951	5.133514	TCCGCCC	0.48828	0.47747
cg0230409	FLJ44606	p53 [T006	965	971	5.133514	TCCGCCC	0.48828	0.47747
cg0230409	FLJ44606	p53 [T006	1006	1012	5.133514	TCCGCCC	0.48828	0.47747
cg1020029	FLJ44606	p53 [T006	1165	1171	5.133514	TCCGCCC	0.48828	0.47747
cg1020029	FLJ44606	p53 [T006	1185	1191	5.133514	TCCGCCC	0.48828	0.47747
cg1020029	FLJ44606	p53 [T006	1226	1232	5.133514	TCCGCCC	0.48828	0.47747
cg2709743	FLJ44606	AR [T0004	123	131	5.104816	TCTCTGT	0.11444	0.11247
cg0230409	FLJ44606	AR [T0004	49	57	5.104816	TCTCTGT	0.11444	0.11247
cg1020029	FLJ44606	AR [T0004	269	277	5.104816	TCTCTGT	0.11444	0.11247
cg2709743	FLJ44606	AP-2alpha	586	591	5.100982	AAAGGC	0.97656	0.97567
cg2709743	FLJ44606	AP-2alpha	1756	1761	5.100982	GCCTTT	0.97656	0.97567
cg0230409	FLJ44606	AP-2alpha	512	517	5.100982	AAAGGC	0.97656	0.97567
cg0230409	FLJ44606	AP-2alpha	1682	1687	5.100982	GCCTTT	0.97656	0.97567
cg1020029	FLJ44606	AP-2alpha	732	737	5.100982	AAAGGC	0.97656	0.97567
cg1020029	FLJ44606	AP-2alpha	1902	1907	5.100982	GCCTTT	0.97656	0.97567
cg2709743	FLJ44606	RXR-alpha	247	253	5.089356	ATCACCC	0.48828	0.484
cg0230409	FLJ44606	RXR-alpha	173	179	5.089356	ATCACCC	0.48828	0.484
cg1020029	FLJ44606	RXR-alpha	393	399	5.089356	ATCACCC	0.48828	0.484
cg2709743	FLJ44606	GR-beta [T	93	97	5.042296	GTATT	3.90625	3.95351
cg2709743	FLJ44606	GR-beta [T	175	179	5.042296	GGATT	3.90625	3.95351
cg2709743	FLJ44606	GR-beta [T	840	844	5.042296	GGATT	3.90625	3.95351

cg2709743	FLJ44606	GR-beta [T	1215	1219	5.042296	AATAC	3.90625	3.95351
cg2709743	FLJ44606	GR-beta [T	1813	1817	5.042296	GGATT	3.90625	3.95351
cg0230409	FLJ44606	GR-beta [T	19	23	5.042296	GTATT	3.90625	3.95351
cg0230409	FLJ44606	GR-beta [T	101	105	5.042296	GGATT	3.90625	3.95351
cg0230409	FLJ44606	GR-beta [T	766	770	5.042296	GGATT	3.90625	3.95351
cg0230409	FLJ44606	GR-beta [T	1141	1145	5.042296	AATAC	3.90625	3.95351
cg0230409	FLJ44606	GR-beta [T	1739	1743	5.042296	GGATT	3.90625	3.95351
cg0230409	FLJ44606	GR-beta [T	1930	1934	5.042296	AATAC	3.90625	3.95351
cg0230409	FLJ44606	GR-beta [T	1991	1995	5.042296	AATCC	3.90625	3.95351
cg1020029	FLJ44606	GR-beta [T	239	243	5.042296	GTATT	3.90625	3.95351
cg1020029	FLJ44606	GR-beta [T	321	325	5.042296	GGATT	3.90625	3.95351
cg1020029	FLJ44606	GR-beta [T	986	990	5.042296	GGATT	3.90625	3.95351
cg1020029	FLJ44606	GR-beta [T	1361	1365	5.042296	AATAC	3.90625	3.95351
cg1020029	FLJ44606	GR-beta [T	1959	1963	5.042296	GGATT	3.90625	3.95351
cg2709743	FLJ44606	E2F-1 [T0	1270	1277	5.042045	GCGGGA	0.18311	0.17901
cg2709743	FLJ44606	E2F-1 [T0	1425	1432	5.042045	CCTCCC	0.18311	0.17901
cg0230409	FLJ44606	E2F-1 [T0	1196	1203	5.042045	GCGGGA	0.18311	0.17901
cg0230409	FLJ44606	E2F-1 [T0	1351	1358	5.042045	CCTCCC	0.18311	0.17901
cg1020029	FLJ44606	E2F-1 [T0	1416	1423	5.042045	GCGGGA	0.18311	0.17901
cg1020029	FLJ44606	E2F-1 [T0	1571	1578	5.042045	CCTCCC	0.18311	0.17901
cg2709743	FLJ44606	C/EBPalph	1814	1820	5.024728	GATTGA	0.97656	0.99332
cg0230409	FLJ44606	C/EBPalph	1740	1746	5.024728	GATTGA	0.97656	0.99332
cg1020029	FLJ44606	C/EBPalph	1960	1966	5.024728	GATTGA	0.97656	0.99332
cg1020029	FLJ44606	IRF-1 [T0	1	9	4.968836	TTTCCC	0.1297	0.1302
cg2709743	FLJ44606	PXR-1:RX	1161	1168	4.90845	TGAACC	0.12207	0.12266
cg0230409	FLJ44606	PXR-1:RX	1087	1094	4.90845	TGAACC	0.12207	0.12266
cg1020029	FLJ44606	PXR-1:RX	1307	1314	4.90845	TGAACC	0.12207	0.12266
cg2709743	FLJ44606	XBP-1 [T0	28	33	4.894955	AGGCAT	0.97656	0.96979
cg1020029	FLJ44606	XBP-1 [T0	174	179	4.894955	AGGCAT	0.97656	0.96979
cg2709743	FLJ44606	AP-2alpha	299	304	4.890408	GCCTAA	0.97656	0.97567
cg0230409	FLJ44606	AP-2alpha	225	230	4.890408	GCCTAA	0.97656	0.97567
cg1020029	FLJ44606	AP-2alpha	445	450	4.890408	GCCTAA	0.97656	0.97567
cg2709743	FLJ44606	RXR-alpha	944	950	4.86724	GAGACC	0.48828	0.484
cg0230409	FLJ44606	RXR-alpha	870	876	4.86724	GAGACC	0.48828	0.484
cg1020029	FLJ44606	RXR-alpha	1090	1096	4.86724	GAGACC	0.48828	0.484
cg2709743	FLJ44606	NF-Y [T0	95	102	4.867193	ATTGGG	0.36621	0.36847
cg2709743	FLJ44606	NF-Y [T0	541	548	4.867193	ACCCCA	0.36621	0.36847
cg0230409	FLJ44606	NF-Y [T0	21	28	4.867193	ATTGGG	0.36621	0.36847
cg0230409	FLJ44606	NF-Y [T0	467	474	4.867193	ACCCCA	0.36621	0.36847
cg1020029	FLJ44606	NF-Y [T0	40	47	4.867193	ACCCCA	0.36621	0.36847
cg1020029	FLJ44606	NF-Y [T0	241	248	4.867193	ATTGGG	0.36621	0.36847
cg1020029	FLJ44606	NF-Y [T0	687	694	4.867193	ACCCCA	0.36621	0.36847
cg2709743	FLJ44606	GCF [T00	1151	1159	4.846987	TGGCCG	0.27466	0.26486
cg0230409	FLJ44606	GCF [T00	1077	1085	4.846987	TGGCCG	0.27466	0.26486
cg1020029	FLJ44606	GCF [T00	1297	1305	4.846987	TGGCCG	0.27466	0.26486
cg2709743	FLJ44606	HNF-3alph	579	586	4.842999	TATTTA	0.09155	0.09582
cg0230409	FLJ44606	HNF-3alph	505	512	4.842999	TATTTA	0.09155	0.09582
cg1020029	FLJ44606	HNF-3alph	725	732	4.842999	TATTTA	0.09155	0.09582

cg2709743	FLJ44606	p53 [T006	190	196	4.786849	GGGCAC	0.48828	0.47747
cg2709743	FLJ44606	p53 [T006	1032	1038	4.786849	GGGCAC	0.48828	0.47747
cg0230409	FLJ44606	p53 [T006	116	122	4.786849	GGGCAC	0.48828	0.47747
cg0230409	FLJ44606	p53 [T006	958	964	4.786849	GGGCAC	0.48828	0.47747
cg1020029	FLJ44606	p53 [T006	336	342	4.786849	GGGCAC	0.48828	0.47747
cg1020029	FLJ44606	p53 [T006	1178	1184	4.786849	GGGCAC	0.48828	0.47747
cg1020029	FLJ44606	C/EBPalph	63	69	4.776286	TATTGGT	0.97656	0.99332
cg2709743	FLJ44606	TFII-I [T0	77	82	4.756447	GGAAAT	2.92969	2.93695
cg2709743	FLJ44606	TFII-I [T0	99	104	4.756447	GGATAT	2.92969	2.93695
cg2709743	FLJ44606	TFII-I [T0	262	267	4.756447	CATTCC	2.92969	2.93695
cg2709743	FLJ44606	TFII-I [T0	1394	1399	4.756447	GGAATG	2.92969	2.93695
cg2709743	FLJ44606	TFII-I [T0	1465	1470	4.756447	GGAAAT	2.92969	2.93695
cg2709743	FLJ44606	TFII-I [T0	1695	1700	4.756447	GGAATG	2.92969	2.93695
cg2709743	FLJ44606	TFII-I [T0	1813	1818	4.756447	GGATTG	2.92969	2.93695
cg2709743	FLJ44606	TFII-I [T0	1928	1933	4.756447	CATTCC	2.92969	2.93695
cg2709743	FLJ44606	FOXP3 [T	2	7	4.756447	CTCAAC	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	257	262	4.756447	CAAAAC	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	352	357	4.756447	AAAAAC	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	392	397	4.756447	GTTGAG	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	554	559	4.756447	GTCAAC	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	691	696	4.756447	GTTGAG	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	699	704	4.756447	GTTTTC	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	719	724	4.756447	GTTTTC	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	1207	1212	4.756447	AAAAAC	2.92969	2.96063
cg2709743	FLJ44606	FOXP3 [T	1407	1412	4.756447	CAAAAC	2.92969	2.96063
cg0230409	FLJ44606	TFII-I [T0	3	8	4.756447	GGAAAT	2.92969	2.93695
cg0230409	FLJ44606	TFII-I [T0	25	30	4.756447	GGATAT	2.92969	2.93695
cg0230409	FLJ44606	TFII-I [T0	188	193	4.756447	CATTCC	2.92969	2.93695
cg0230409	FLJ44606	TFII-I [T0	1320	1325	4.756447	GGAATG	2.92969	2.93695
cg0230409	FLJ44606	TFII-I [T0	1391	1396	4.756447	GGAAAT	2.92969	2.93695
cg0230409	FLJ44606	TFII-I [T0	1621	1626	4.756447	GGAATG	2.92969	2.93695
cg0230409	FLJ44606	TFII-I [T0	1739	1744	4.756447	GGATTG	2.92969	2.93695
cg0230409	FLJ44606	TFII-I [T0	1854	1859	4.756447	CATTCC	2.92969	2.93695
cg0230409	FLJ44606	FOXP3 [T	183	188	4.756447	CAAAAC	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	278	283	4.756447	AAAAAC	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	318	323	4.756447	GTTGAG	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	480	485	4.756447	GTCAAC	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	617	622	4.756447	GTTGAG	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	625	630	4.756447	GTTTTC	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	645	650	4.756447	GTTTTC	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	1133	1138	4.756447	AAAAAC	2.92969	2.96063
cg0230409	FLJ44606	FOXP3 [T	1333	1338	4.756447	CAAAAC	2.92969	2.96063
cg1020029	FLJ44606	TFII-I [T0	223	228	4.756447	GGAAAT	2.92969	2.93695
cg1020029	FLJ44606	TFII-I [T0	245	250	4.756447	GGATAT	2.92969	2.93695
cg1020029	FLJ44606	TFII-I [T0	408	413	4.756447	CATTCC	2.92969	2.93695
cg1020029	FLJ44606	TFII-I [T0	1540	1545	4.756447	GGAATG	2.92969	2.93695
cg1020029	FLJ44606	TFII-I [T0	1611	1616	4.756447	GGAAAT	2.92969	2.93695
cg1020029	FLJ44606	TFII-I [T0	1841	1846	4.756447	GGAATG	2.92969	2.93695

cg1020029	FLJ44606	TFII-I [T0	1959	1964	4.756447	GGATTG	2.92969	2.93695
cg1020029	FLJ44606	FOXP3 [T	148	153	4.756447	CTCAAC	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	403	408	4.756447	CAAAAC	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	498	503	4.756447	AAAAAC	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	538	543	4.756447	GTTGAG	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	700	705	4.756447	GTCAAC	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	837	842	4.756447	GTTGAG	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	845	850	4.756447	GTTTTC	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	865	870	4.756447	GTTTTC	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	1353	1358	4.756447	AAAAAC	2.92969	2.96063
cg1020029	FLJ44606	FOXP3 [T	1553	1558	4.756447	CAAAAC	2.92969	2.96063
cg2709743	FLJ44606	c-Ets-1 [T	1218	1224	4.74411	ACGGAA	0.85449	0.85764
cg0230409	FLJ44606	c-Ets-1 [T	1144	1150	4.74411	ACGGAA	0.85449	0.85764
cg1020029	FLJ44606	c-Ets-1 [T	1364	1370	4.74411	ACGGAA	0.85449	0.85764
cg2709743	FLJ44606	VDR [T00	1157	1165	4.617121	CGCCTG	0.37384	0.37445
cg2709743	FLJ44606	VDR [T00	1375	1383	4.617121	TGGCTG	0.37384	0.37445
cg2709743	FLJ44606	VDR [T00	1813	1821	4.617121	GGATTG	0.37384	0.37445
cg0230409	FLJ44606	VDR [T00	1083	1091	4.617121	CGCCTG	0.37384	0.37445
cg0230409	FLJ44606	VDR [T00	1301	1309	4.617121	TGGCTG	0.37384	0.37445
cg0230409	FLJ44606	VDR [T00	1739	1747	4.617121	GGATTG	0.37384	0.37445
cg1020029	FLJ44606	VDR [T00	1303	1311	4.617121	CGCCTG	0.37384	0.37445
cg1020029	FLJ44606	VDR [T00	1521	1529	4.617121	TGGCTG	0.37384	0.37445
cg1020029	FLJ44606	VDR [T00	1959	1967	4.617121	GGATTG	0.37384	0.37445
cg2709743	FLJ44606	c-Ets-2 [T	1519	1527	4.589988	GGGAAG	0.06866	0.06881
cg0230409	FLJ44606	c-Ets-2 [T	1445	1453	4.589988	GGGAAG	0.06866	0.06881
cg1020029	FLJ44606	c-Ets-2 [T	1665	1673	4.589988	GGGAAG	0.06866	0.06881
cg2709743	FLJ44606	Sp1 [T007	1037	1046	4.572987	CTTCCG	0.08583	0.08339
cg0230409	FLJ44606	Sp1 [T007	963	972	4.572987	CTTCCG	0.08583	0.08339
cg1020029	FLJ44606	Sp1 [T007	1183	1192	4.572987	CTTCCG	0.08583	0.08339
cg2709743	FLJ44606	E2F-1 [T0	970	977	4.545253	GCGGGA	0.15259	0.14941
cg0230409	FLJ44606	E2F-1 [T0	896	903	4.545253	GCGGGA	0.15259	0.14941
cg1020029	FLJ44606	E2F-1 [T0	1116	1123	4.545253	GCGGGA	0.15259	0.14941
cg2709743	FLJ44606	Sp1 [T007	1017	1026	4.43736	CTTCCG	0.08583	0.08339
cg0230409	FLJ44606	Sp1 [T007	943	952	4.43736	CTTCCG	0.08583	0.08339
cg1020029	FLJ44606	Sp1 [T007	1163	1172	4.43736	CTTCCG	0.08583	0.08339
cg2709743	FLJ44606	RXR-alph	1652	1658	4.423008	GGGTTG	0.24414	0.24292
cg0230409	FLJ44606	RXR-alph	1578	1584	4.423008	GGGTTG	0.24414	0.24292
cg1020029	FLJ44606	RXR-alph	1798	1804	4.423008	GGGTTG	0.24414	0.24292
cg2709743	FLJ44606	AP-2alpha	161	166	4.422424	TAAGGC	0.97656	0.96979
cg2709743	FLJ44606	AP-2alpha	280	285	4.422424	GCCTTA	0.97656	0.96979
cg2709743	FLJ44606	AP-2alpha	459	464	4.422424	TAAGGC	0.97656	0.96979
cg0230409	FLJ44606	AP-2alpha	87	92	4.422424	TAAGGC	0.97656	0.96979
cg0230409	FLJ44606	AP-2alpha	206	211	4.422424	GCCTTA	0.97656	0.96979
cg0230409	FLJ44606	AP-2alpha	385	390	4.422424	TAAGGC	0.97656	0.96979
cg1020029	FLJ44606	AP-2alpha	307	312	4.422424	TAAGGC	0.97656	0.96979
cg1020029	FLJ44606	AP-2alpha	426	431	4.422424	GCCTTA	0.97656	0.96979
cg1020029	FLJ44606	AP-2alpha	605	610	4.422424	TAAGGC	0.97656	0.96979
cg2709743	FLJ44606	STAT4 [T	262	267	4.411765	CATTCC	1.95312	1.94235

cg2709743	FLJ44606	STAT4 [T	749	754	4.411765	GCTTCC	1.95312	1.94235
cg2709743	FLJ44606	STAT4 [T	1016	1021	4.411765	GCTTCC	1.95312	1.94235
cg2709743	FLJ44606	STAT4 [T	1394	1399	4.411765	GGAATG	1.95312	1.94235
cg2709743	FLJ44606	STAT4 [T	1663	1668	4.411765	GGAAGA	1.95312	1.94235
cg2709743	FLJ44606	STAT4 [T	1695	1700	4.411765	GGAATG	1.95312	1.94235
cg2709743	FLJ44606	STAT4 [T	1702	1707	4.411765	GGAAGA	1.95312	1.94235
cg2709743	FLJ44606	STAT4 [T	1915	1920	4.411765	GGAAGC	1.95312	1.94235
cg2709743	FLJ44606	STAT4 [T	1928	1933	4.411765	CATTCC	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	188	193	4.411765	CATTCC	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	675	680	4.411765	GCTTCC	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	942	947	4.411765	GCTTCC	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	1320	1325	4.411765	GGAATG	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	1589	1594	4.411765	GGAAGA	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	1621	1626	4.411765	GGAATG	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	1628	1633	4.411765	GGAAGA	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	1841	1846	4.411765	GGAAGC	1.95312	1.94235
cg0230409	FLJ44606	STAT4 [T	1854	1859	4.411765	CATTCC	1.95312	1.94235
cg1020029	FLJ44606	STAT4 [T	408	413	4.411765	CATTCC	1.95312	1.94235
cg1020029	FLJ44606	STAT4 [T	895	900	4.411765	GCTTCC	1.95312	1.94235
cg1020029	FLJ44606	STAT4 [T	1162	1167	4.411765	GCTTCC	1.95312	1.94235
cg1020029	FLJ44606	STAT4 [T	1540	1545	4.411765	GGAATG	1.95312	1.94235
cg1020029	FLJ44606	STAT4 [T	1809	1814	4.411765	GGAAGA	1.95312	1.94235
cg1020029	FLJ44606	STAT4 [T	1841	1846	4.411765	GGAATG	1.95312	1.94235
cg1020029	FLJ44606	STAT4 [T	1848	1853	4.411765	GGAAGA	1.95312	1.94235
cg2709743	FLJ44606	c-Ets-1 [T	1522	1528	4.411026	AAGGAA	0.85449	0.85764
cg0230409	FLJ44606	c-Ets-1 [T	1448	1454	4.411026	AAGGAA	0.85449	0.85764
cg1020029	FLJ44606	c-Ets-1 [T	1668	1674	4.411026	AAGGAA	0.85449	0.85764
cg2709743	FLJ44606	RAR-beta	906	915	4.307573	AGCGAA	0.14496	0.1447
cg0230409	FLJ44606	RAR-beta	832	841	4.307573	AGCGAA	0.14496	0.1447
cg1020029	FLJ44606	RAR-beta	1052	1061	4.307573	AGCGAA	0.14496	0.1447
cg2709743	FLJ44606	RAR-beta	1492	1501	4.289108	TGGGTTT	0.14496	0.1447
cg0230409	FLJ44606	RAR-beta	1418	1427	4.289108	TGGGTTT	0.14496	0.1447
cg1020029	FLJ44606	RAR-beta	1638	1647	4.289108	TGGGTTT	0.14496	0.1447
cg2709743	FLJ44606	c-Ets-1 [T	134	140	4.282938	GAGGAA	0.85449	0.85764
cg0230409	FLJ44606	c-Ets-1 [T	60	66	4.282938	GAGGAA	0.85449	0.85764
cg1020029	FLJ44606	c-Ets-1 [T	280	286	4.282938	GAGGAA	0.85449	0.85764
cg2709743	FLJ44606	RXR-alpha	1226	1232	4.24113	GTGACC	0.97656	0.9671
cg2709743	FLJ44606	RXR-alpha	1420	1426	4.24113	CGTACC	0.97656	0.9671
cg2709743	FLJ44606	RXR-alpha	1729	1735	4.24113	GGGTAA	0.97656	0.9671
cg0230409	FLJ44606	RXR-alpha	1152	1158	4.24113	GTGACC	0.97656	0.9671
cg0230409	FLJ44606	RXR-alpha	1346	1352	4.24113	CGTACC	0.97656	0.9671
cg0230409	FLJ44606	RXR-alpha	1655	1661	4.24113	GGGTAA	0.97656	0.9671
cg1020029	FLJ44606	RXR-alpha	1372	1378	4.24113	GTGACC	0.97656	0.9671
cg1020029	FLJ44606	RXR-alpha	1566	1572	4.24113	CGTACC	0.97656	0.9671
cg1020029	FLJ44606	RXR-alpha	1875	1881	4.24113	GGGTAA	0.97656	0.9671
cg2709743	FLJ44606	AR [T0004	1601	1609	4.241082	GGACAG	0.06866	0.06828
cg0230409	FLJ44606	AR [T0004	1527	1535	4.241082	GGACAG	0.06866	0.06828
cg1020029	FLJ44606	AR [T0004	1747	1755	4.241082	GGACAG	0.06866	0.06828

cg0230409	FLJ44606	C/EBPalph	1949	1955	4.235345	TATTGAT	0.48828	0.49358
cg2709743	FLJ44606	GR-beta [T	221	225	4.201913	CTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	225	229	4.201913	TTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	230	234	4.201913	AATAA	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	240	244	4.201913	AATAA	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	346	350	4.201913	TTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	369	373	4.201913	CTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	411	415	4.201913	TGATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	415	419	4.201913	TTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	457	461	4.201913	AATAA	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	578	582	4.201913	TTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	617	621	4.201913	TGATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	671	675	4.201913	AATCA	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	771	775	4.201913	TTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1253	1257	4.201913	AATAA	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1441	1445	4.201913	AATCG	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1477	1481	4.201913	TTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1483	1487	4.201913	AATAG	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1497	1501	4.201913	TTATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1822	1826	4.201913	TGATT	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1971	1975	4.201913	AATAA	7.8125	7.94607
cg2709743	FLJ44606	GR-beta [T	1992	1996	4.201913	AATAA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	147	151	4.201913	CTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	151	155	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	156	160	4.201913	AATAA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	166	170	4.201913	AATAA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	272	276	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	295	299	4.201913	CTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	337	341	4.201913	TGATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	341	345	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	383	387	4.201913	AATAA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	504	508	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	543	547	4.201913	TGATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	597	601	4.201913	AATCA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	697	701	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1179	1183	4.201913	AATAA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1367	1371	4.201913	AATCG	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1403	1407	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1409	1413	4.201913	AATAG	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1423	1427	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1748	1752	4.201913	TGATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1897	1901	4.201913	AATAA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1918	1922	4.201913	AATAA	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1948	1952	4.201913	TTATT	7.8125	7.94607
cg0230409	FLJ44606	GR-beta [T	1952	1956	4.201913	TGATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	139	143	4.201913	AATAG	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	367	371	4.201913	CTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	371	375	4.201913	TTATT	7.8125	7.94607

cg1020029	FLJ44606	GR-beta [T	376	380	4.201913	AATAA	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	386	390	4.201913	AATAA	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	492	496	4.201913	TTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	515	519	4.201913	CTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	557	561	4.201913	TGATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	561	565	4.201913	TTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	603	607	4.201913	AATAA	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	724	728	4.201913	TTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	763	767	4.201913	TGATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	817	821	4.201913	AATCA	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	917	921	4.201913	TTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	1399	1403	4.201913	AATAA	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	1587	1591	4.201913	AATCG	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	1623	1627	4.201913	TTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	1629	1633	4.201913	AATAG	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	1643	1647	4.201913	TTATT	7.8125	7.94607
cg1020029	FLJ44606	GR-beta [T	1968	1972	4.201913	TGATT	7.8125	7.94607
cg2709743	FLJ44606	NF-AT1 [T	1712	1721	4.134416	TGGAAA	0.08392	0.08485
cg0230409	FLJ44606	NF-AT1 [T	1638	1647	4.134416	TGGAAA	0.08392	0.08485
cg1020029	FLJ44606	NF-AT1 [T	1858	1867	4.134416	TGGAAA	0.08392	0.08485
cg2709743	FLJ44606	p53 [T006	1060	1066	4.125254	CCGGCC	0.73242	0.71379
cg2709743	FLJ44606	p53 [T006	1067	1073	4.125254	CAGGCC	0.73242	0.71379
cg0230409	FLJ44606	p53 [T006	986	992	4.125254	CCGGCC	0.73242	0.71379
cg0230409	FLJ44606	p53 [T006	993	999	4.125254	CAGGCC	0.73242	0.71379
cg1020029	FLJ44606	p53 [T006	1206	1212	4.125254	CCGGCC	0.73242	0.71379
cg1020029	FLJ44606	p53 [T006	1213	1219	4.125254	CAGGCC	0.73242	0.71379
cg1020029	FLJ44606	POU2F2 (	9	19	4.120113	TGTTTTA	0.01717	0.0178
cg2709743	FLJ44606	Pax-5 [T0	190	196	4.007279	GGGCAC	1.09863	1.07975
cg2709743	FLJ44606	Pax-5 [T0	493	499	4.007279	AGAGCC	1.09863	1.07975
cg2709743	FLJ44606	Pax-5 [T0	1032	1038	4.007279	GGGCAC	1.09863	1.07975
cg2709743	FLJ44606	Pax-5 [T0	1754	1760	4.007279	GGGCCT	1.09863	1.07975
cg2709743	FLJ44606	Pax-5 [T0	1787	1793	4.007279	GGGCAT	1.09863	1.07975
cg2709743	FLJ44606	TFIID [T0	224	230	4.007279	TTTATTA	1.09863	1.13456
cg2709743	FLJ44606	TFIID [T0	229	235	4.007279	TAATAA	1.09863	1.13456
cg2709743	FLJ44606	TFIID [T0	347	353	4.007279	TATTAA	1.09863	1.13456
cg2709743	FLJ44606	TFIID [T0	732	738	4.007279	TCTTAA	1.09863	1.13456
cg2709743	FLJ44606	TFIID [T0	814	820	4.007279	TTTATA	1.09863	1.13456
cg2709743	FLJ44606	TFIID [T0	1250	1256	4.007279	TTTAATA	1.09863	1.13456
cg2709743	FLJ44606	TFIID [T0	1344	1350	4.007279	TTTAATA	1.09863	1.13456
cg2709743	FLJ44606	TFIID [T0	1478	1484	4.007279	TATTAA	1.09863	1.13456
cg0230409	FLJ44606	Pax-5 [T0	116	122	4.007279	GGGCAC	1.09863	1.07975
cg0230409	FLJ44606	Pax-5 [T0	419	425	4.007279	AGAGCC	1.09863	1.07975
cg0230409	FLJ44606	Pax-5 [T0	958	964	4.007279	GGGCAC	1.09863	1.07975
cg0230409	FLJ44606	Pax-5 [T0	1680	1686	4.007279	GGGCCT	1.09863	1.07975
cg0230409	FLJ44606	Pax-5 [T0	1713	1719	4.007279	GGGCAT	1.09863	1.07975
cg0230409	FLJ44606	TFIID [T0	150	156	4.007279	TTTATTA	1.09863	1.13456
cg0230409	FLJ44606	TFIID [T0	155	161	4.007279	TAATAA	1.09863	1.13456
cg0230409	FLJ44606	TFIID [T0	273	279	4.007279	TATTAA	1.09863	1.13456

cg0230409	FLJ44606	TFIID [T0	658	664	4.007279	TCTTAA	1.09863	1.13456
cg0230409	FLJ44606	TFIID [T0	740	746	4.007279	TTTATAA	1.09863	1.13456
cg0230409	FLJ44606	TFIID [T0	1176	1182	4.007279	TTTAATA	1.09863	1.13456
cg0230409	FLJ44606	TFIID [T0	1270	1276	4.007279	TTTAATA	1.09863	1.13456
cg0230409	FLJ44606	TFIID [T0	1404	1410	4.007279	TATTAA	1.09863	1.13456
cg1020029	FLJ44606	Pax-5 [T0	336	342	4.007279	GGGCAC	1.09863	1.07975
cg1020029	FLJ44606	Pax-5 [T0	639	645	4.007279	AGAGCC	1.09863	1.07975
cg1020029	FLJ44606	Pax-5 [T0	1178	1184	4.007279	GGGCAC	1.09863	1.07975
cg1020029	FLJ44606	Pax-5 [T0	1900	1906	4.007279	GGGCCT	1.09863	1.07975
cg1020029	FLJ44606	Pax-5 [T0	1933	1939	4.007279	GGGCAT	1.09863	1.07975
cg1020029	FLJ44606	TFIID [T0	11	17	4.007279	TTTTAA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	89	95	4.007279	TTTATAA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	370	376	4.007279	TTTATTA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	375	381	4.007279	TAATAA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	493	499	4.007279	TATTAA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	878	884	4.007279	TCTTAA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	960	966	4.007279	TTTATAA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	1396	1402	4.007279	TTTAATA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	1490	1496	4.007279	TTTAATA	1.09863	1.13456
cg1020029	FLJ44606	TFIID [T0	1624	1630	4.007279	TATTAA	1.09863	1.13456
cg2709743	FLJ44606	AP-2alpha	26	31	3.970052	CAAGGC	0.97656	0.96469
cg2709743	FLJ44606	AP-2alpha	1194	1199	3.970052	CAAGGC	0.97656	0.96469
cg0230409	FLJ44606	AP-2alpha	1120	1125	3.970052	CAAGGC	0.97656	0.96469
cg1020029	FLJ44606	AP-2alpha	172	177	3.970052	CAAGGC	0.97656	0.96469
cg1020029	FLJ44606	AP-2alpha	1340	1345	3.970052	CAAGGC	0.97656	0.96469
cg2709743	FLJ44606	NF-AT1 [	1465	1473	3.917696	GGAAAT	0.07629	0.07734
cg0230409	FLJ44606	NF-AT1 [	1391	1399	3.917696	GGAAAT	0.07629	0.07734
cg1020029	FLJ44606	NF-AT1 [	1611	1619	3.917696	GGAAAT	0.07629	0.07734
cg2709743	FLJ44606	NFI/CTF [	336	343	3.793671	ACCCTTC	0.18311	0.18109
cg0230409	FLJ44606	NFI/CTF [	262	269	3.793671	ACCCTTC	0.18311	0.18109
cg1020029	FLJ44606	NFI/CTF [	482	489	3.793671	ACCCTTC	0.18311	0.18109
cg2709743	FLJ44606	E2F-1 [T0	1661	1668	3.784875	GCGGAA	0.15259	0.15068
cg0230409	FLJ44606	E2F-1 [T0	1587	1594	3.784875	GCGGAA	0.15259	0.15068
cg1020029	FLJ44606	E2F-1 [T0	1807	1814	3.784875	GCGGAA	0.15259	0.15068
cg2709743	FLJ44606	GR [T050	257	263	3.763516	CAAAAC	0.73242	0.74251
cg2709743	FLJ44606	GR [T050	1407	1413	3.763516	CAAAAC	0.73242	0.74251
cg0230409	FLJ44606	GR [T050	183	189	3.763516	CAAAAC	0.73242	0.74251
cg0230409	FLJ44606	GR [T050	1333	1339	3.763516	CAAAAC	0.73242	0.74251
cg1020029	FLJ44606	GR [T050	403	409	3.763516	CAAAAC	0.73242	0.74251
cg1020029	FLJ44606	GR [T050	1553	1559	3.763516	CAAAAC	0.73242	0.74251
cg2709743	FLJ44606	p53 [T006	1573	1579	3.750231	GGGCTG	0.73242	0.71379
cg0230409	FLJ44606	p53 [T006	1499	1505	3.750231	GGGCTG	0.73242	0.71379
cg1020029	FLJ44606	p53 [T006	1719	1725	3.750231	GGGCTG	0.73242	0.71379
cg2709743	FLJ44606	NF-AT2 [	1465	1474	3.689016	GGAAAT	0.03433	0.03499
cg0230409	FLJ44606	NF-AT2 [	1391	1400	3.689016	GGAAAT	0.03433	0.03499
cg1020029	FLJ44606	NF-AT2 [	1611	1620	3.689016	GGAAAT	0.03433	0.03499
cg2709743	FLJ44606	Sp1 [T007	1078	1087	3.623596	CTTCCGC	0.07439	0.07186
cg0230409	FLJ44606	Sp1 [T007	1004	1013	3.623596	CTTCCGC	0.07439	0.07186

cg1020029	FLJ44606	Sp1 [T007	1224	1233	3.623596	CTTCCG	0.07439	0.07186
cg2709743	FLJ44606	p53 [T006	1787	1793	3.516613	GGGCAT	0.73242	0.7189
cg0230409	FLJ44606	p53 [T006	1713	1719	3.516613	GGGCAT	0.73242	0.7189
cg1020029	FLJ44606	p53 [T006	1933	1939	3.516613	GGGCAT	0.73242	0.7189
cg2709743	FLJ44606	HNF-3alph	1211	1218	3.500065	ACAAAA	0.27466	0.28532
cg0230409	FLJ44606	HNF-3alph	1137	1144	3.500065	ACAAAA	0.27466	0.28532
cg1020029	FLJ44606	HNF-3alph	1357	1364	3.500065	ACAAAA	0.27466	0.28532
cg2709743	FLJ44606	c-Myb [T0	1409	1416	3.438142	AAACTG	0.12207	0.12203
cg0230409	FLJ44606	c-Myb [T0	1335	1342	3.438142	AAACTG	0.12207	0.12203
cg1020029	FLJ44606	c-Myb [T0	1555	1562	3.438142	AAACTG	0.12207	0.12203
cg2709743	FLJ44606	RXR-alpha	958	964	3.392904	CTCACC	1.09863	1.08572
cg2709743	FLJ44606	RXR-alpha	981	987	3.392904	GGAACC	1.09863	1.08572
cg2709743	FLJ44606	RXR-alpha	1045	1051	3.392904	CGCACC	1.09863	1.08572
cg2709743	FLJ44606	RXR-alpha	1843	1849	3.392904	AGGACC	1.09863	1.08572
cg0230409	FLJ44606	RXR-alpha	884	890	3.392904	CTCACC	1.09863	1.08572
cg0230409	FLJ44606	RXR-alpha	907	913	3.392904	GGAACC	1.09863	1.08572
cg0230409	FLJ44606	RXR-alpha	971	977	3.392904	CGCACC	1.09863	1.08572
cg0230409	FLJ44606	RXR-alpha	1769	1775	3.392904	AGGACC	1.09863	1.08572
cg1020029	FLJ44606	RXR-alpha	1104	1110	3.392904	CTCACC	1.09863	1.08572
cg1020029	FLJ44606	RXR-alpha	1127	1133	3.392904	GGAACC	1.09863	1.08572
cg1020029	FLJ44606	RXR-alpha	1191	1197	3.392904	CGCACC	1.09863	1.08572
cg1020029	FLJ44606	RXR-alpha	1989	1995	3.392904	AGGACC	1.09863	1.08572
cg2709743	FLJ44606	p53 [T006	759	765	3.375208	CCCGCC	0.73242	0.7189
cg2709743	FLJ44606	p53 [T006	1588	1594	3.375208	GGGCGT	0.73242	0.7189
cg0230409	FLJ44606	p53 [T006	685	691	3.375208	CCCGCC	0.73242	0.7189
cg0230409	FLJ44606	p53 [T006	1514	1520	3.375208	GGGCGT	0.73242	0.7189
cg1020029	FLJ44606	p53 [T006	905	911	3.375208	CCCGCC	0.73242	0.7189
cg1020029	FLJ44606	p53 [T006	1734	1740	3.375208	GGGCGT	0.73242	0.7189
cg2709743	FLJ44606	GR-beta [T	145	149	3.361531	AATCT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	199	203	3.361531	AATAT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	385	389	3.361531	AATAT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	573	577	3.361531	AATAT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	574	578	3.361531	ATATT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	819	823	3.361531	AATCT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	1347	1351	3.361531	AATAT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	1348	1352	3.361531	ATATT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	1459	1463	3.361531	ATATT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	1526	1530	3.361531	AATAT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	71	75	3.361531	AATCT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	125	129	3.361531	AATAT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	311	315	3.361531	AATAT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	499	503	3.361531	AATAT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	500	504	3.361531	ATATT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	745	749	3.361531	AATCT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	1273	1277	3.361531	AATAT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	1274	1278	3.361531	ATATT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	1385	1389	3.361531	ATATT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	1452	1456	3.361531	AATAT	3.90625	3.99611

cg1020029	FLJ44606	GR-beta [T	16	20	3.361531	AATCT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	61	65	3.361531	AATAT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	62	66	3.361531	ATATT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	108	112	3.361531	AATAT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	291	295	3.361531	AATCT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	345	349	3.361531	AATAT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	531	535	3.361531	AATAT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	719	723	3.361531	AATAT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	720	724	3.361531	ATATT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	965	969	3.361531	AATCT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	1493	1497	3.361531	AATAT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	1494	1498	3.361531	ATATT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	1605	1609	3.361531	ATATT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	1672	1676	3.361531	AATAT	3.90625	3.99611
cg0230409	FLJ44606	T3R-beta1	1959	1967	3.351341	TCACCA	0.27466	0.2755
cg2709743	FLJ44606	GATA-2 [	787	795	3.333333	GCGCTA	0.30518	0.30786
cg0230409	FLJ44606	GATA-2 [	713	721	3.333333	GCGCTA	0.30518	0.30786
cg1020029	FLJ44606	GATA-2 [	933	941	3.333333	GCGCTA	0.30518	0.30786
cg0230409	FLJ44606	PR B [T00	1943	1949	3.29756	AACATT	0.24414	0.25122
cg0230409	FLJ44606	PR A [T01	1943	1949	3.29756	AACATT	0.24414	0.25122
cg2709743	FLJ44606	c-Ets-2 [T	131	139	3.2883	CTTGAG	0.18311	0.18304
cg2709743	FLJ44606	c-Ets-2 [T	1910	1918	3.2883	GGTGAG	0.18311	0.18304
cg0230409	FLJ44606	c-Ets-2 [T	57	65	3.2883	CTTGAG	0.18311	0.18304
cg0230409	FLJ44606	c-Ets-2 [T	1836	1844	3.2883	GGTGAG	0.18311	0.18304
cg1020029	FLJ44606	c-Ets-2 [T	277	285	3.2883	CTTGAG	0.18311	0.18304
cg2709743	FLJ44606	E2F-1 [T0	899	906	3.288084	GCGGCA	0.15259	0.14974
cg0230409	FLJ44606	E2F-1 [T0	825	832	3.288084	GCGGCA	0.15259	0.14974
cg1020029	FLJ44606	E2F-1 [T0	1045	1052	3.288084	GCGGCA	0.15259	0.14974
cg2709743	FLJ44606	Elk-1 [T00	1911	1919	3.247448	GTGAGG	0.07629	0.07656
cg0230409	FLJ44606	Elk-1 [T00	1837	1845	3.247448	GTGAGG	0.07629	0.07656
cg2709743	FLJ44606	RAR-beta	645	654	3.244529	ATTAAA	0.12207	0.12169
cg0230409	FLJ44606	RAR-beta	571	580	3.244529	ATTAAA	0.12207	0.12169
cg1020029	FLJ44606	RAR-beta	791	800	3.244529	ATTAAA	0.12207	0.12169
cg2709743	FLJ44606	c-Ets-1 [T	1017	1023	3.231072	CTTCCG	0.24414	0.23981
cg2709743	FLJ44606	c-Ets-1 [T	1037	1043	3.231072	CTTCCG	0.24414	0.23981
cg2709743	FLJ44606	c-Ets-1 [T	1078	1084	3.231072	CTTCCG	0.24414	0.23981
cg2709743	FLJ44606	c-Ets-1 [T	1661	1667	3.231072	GCGGAA	0.24414	0.23981
cg0230409	FLJ44606	c-Ets-1 [T	943	949	3.231072	CTTCCG	0.24414	0.23981
cg0230409	FLJ44606	c-Ets-1 [T	963	969	3.231072	CTTCCG	0.24414	0.23981
cg0230409	FLJ44606	c-Ets-1 [T	1004	1010	3.231072	CTTCCG	0.24414	0.23981
cg0230409	FLJ44606	c-Ets-1 [T	1587	1593	3.231072	GCGGAA	0.24414	0.23981
cg1020029	FLJ44606	c-Ets-1 [T	1163	1169	3.231072	CTTCCG	0.24414	0.23981
cg1020029	FLJ44606	c-Ets-1 [T	1183	1189	3.231072	CTTCCG	0.24414	0.23981
cg1020029	FLJ44606	c-Ets-1 [T	1224	1230	3.231072	CTTCCG	0.24414	0.23981
cg1020029	FLJ44606	c-Ets-1 [T	1807	1813	3.231072	GCGGAA	0.24414	0.23981
cg2709743	FLJ44606	AP-2alpha	937	942	3.229049	AGAGGC	0.48828	0.48238
cg2709743	FLJ44606	AP-2alpha	1010	1015	3.229049	GCCTCT	0.48828	0.48238
cg2709743	FLJ44606	AP-2alpha	1257	1262	3.229049	AGAGGC	0.48828	0.48238

cg0230409	FLJ44606	AP-2alpha	863	868	3.229049	AGAGGC	0.48828	0.48238
cg0230409	FLJ44606	AP-2alpha	936	941	3.229049	GCCTCT	0.48828	0.48238
cg0230409	FLJ44606	AP-2alpha	1183	1188	3.229049	AGAGGC	0.48828	0.48238
cg1020029	FLJ44606	AP-2alpha	1083	1088	3.229049	AGAGGC	0.48828	0.48238
cg1020029	FLJ44606	AP-2alpha	1156	1161	3.229049	GCCTCT	0.48828	0.48238
cg1020029	FLJ44606	AP-2alpha	1403	1408	3.229049	AGAGGC	0.48828	0.48238
cg2709743	FLJ44606	RAR-beta	1874	1883	3.226064	AGGGTT	0.12207	0.12169
cg0230409	FLJ44606	RAR-beta	1800	1809	3.226064	AGGGTT	0.12207	0.12169
cg2709743	FLJ44606	TCF-4E [T	1512	1518	3.151193	CTTTGC	0.24414	0.24672
cg0230409	FLJ44606	TCF-4E [T	1438	1444	3.151193	CTTTGC	0.24414	0.24672
cg1020029	FLJ44606	TCF-4E [T	1658	1664	3.151193	CTTTGC	0.24414	0.24672
cg2709743	FLJ44606	IRF-1 [T0	1216	1224	3.145547	ATACGG	0.07629	0.07756
cg0230409	FLJ44606	IRF-1 [T0	1142	1150	3.145547	ATACGG	0.07629	0.07756
cg1020029	FLJ44606	IRF-1 [T0	1362	1370	3.145547	ATACGG	0.07629	0.07756
cg2709743	FLJ44606	Elk-1 [T00	750	758	3.121991	CTTCCTT	0.07629	0.07656
cg0230409	FLJ44606	Elk-1 [T00	676	684	3.121991	CTTCCTT	0.07629	0.07656
cg1020029	FLJ44606	Elk-1 [T00	896	904	3.121991	CTTCCTT	0.07629	0.07656
cg2709743	FLJ44606	C/EBPalph	1823	1829	3.014837	GATTGC	0.48828	0.4911
cg0230409	FLJ44606	C/EBPalph	1749	1755	3.014837	GATTGC	0.48828	0.4911
cg0230409	FLJ44606	C/EBPalph	1953	1959	3.014837	GATTGC	0.48828	0.4911
cg1020029	FLJ44606	C/EBPalph	1969	1975	3.014837	GATTGC	0.48828	0.4911
cg2709743	FLJ44606	C/EBPalph	16	22	2.981957	CATTGT	0.48828	0.4911
cg2709743	FLJ44606	C/EBPalph	307	313	2.981957	CACAAT	0.48828	0.4911
cg2709743	FLJ44606	C/EBPalph	507	513	2.981957	CACAAT	0.48828	0.4911
cg0230409	FLJ44606	C/EBPalph	233	239	2.981957	CACAAT	0.48828	0.4911
cg0230409	FLJ44606	C/EBPalph	433	439	2.981957	CACAAT	0.48828	0.4911
cg1020029	FLJ44606	C/EBPalph	42	48	2.981957	CCCAAT	0.48828	0.4911
cg1020029	FLJ44606	C/EBPalph	162	168	2.981957	CATTGT	0.48828	0.4911
cg1020029	FLJ44606	C/EBPalph	453	459	2.981957	CACAAT	0.48828	0.4911
cg1020029	FLJ44606	C/EBPalph	653	659	2.981957	CACAAT	0.48828	0.4911
cg2709743	FLJ44606	c-Ets-2 [T	751	759	2.945838	TTCCTTT	0.06104	0.06231
cg0230409	FLJ44606	c-Ets-2 [T	677	685	2.945838	TTCCTTT	0.06104	0.06231
cg1020029	FLJ44606	c-Ets-2 [T	897	905	2.945838	TTCCTTT	0.06104	0.06231
cg2709743	FLJ44606	STAT4 [T	512	517	2.941176	TGTTCC	2.92969	2.929
cg2709743	FLJ44606	STAT4 [T	777	782	2.941176	ACTTCC	2.92969	2.929
cg2709743	FLJ44606	STAT4 [T	981	986	2.941176	GGAACC	2.92969	2.929
cg2709743	FLJ44606	STAT4 [T	1036	1041	2.941176	ACTTCC	2.92969	2.929
cg2709743	FLJ44606	STAT4 [T	1077	1082	2.941176	ACTTCC	2.92969	2.929
cg2709743	FLJ44606	STAT4 [T	1243	1248	2.941176	GGAACC	2.92969	2.929
cg2709743	FLJ44606	STAT4 [T	1524	1529	2.941176	GGAATA	2.92969	2.929
cg2709743	FLJ44606	STAT4 [T	1860	1865	2.941176	GGAAGT	2.92969	2.929
cg0230409	FLJ44606	STAT4 [T	438	443	2.941176	TGTTCC	2.92969	2.929
cg0230409	FLJ44606	STAT4 [T	703	708	2.941176	ACTTCC	2.92969	2.929
cg0230409	FLJ44606	STAT4 [T	907	912	2.941176	GGAACC	2.92969	2.929
cg0230409	FLJ44606	STAT4 [T	962	967	2.941176	ACTTCC	2.92969	2.929
cg0230409	FLJ44606	STAT4 [T	1003	1008	2.941176	ACTTCC	2.92969	2.929
cg0230409	FLJ44606	STAT4 [T	1169	1174	2.941176	GGAACC	2.92969	2.929
cg0230409	FLJ44606	STAT4 [T	1450	1455	2.941176	GGAATA	2.92969	2.929

cg0230409	FLJ44606	STAT4 [T	1786	1791	2.941176	GGAAGT	2.92969	2.929
cg1020029	FLJ44606	STAT4 [T	658	663	2.941176	TGTTCC	2.92969	2.929
cg1020029	FLJ44606	STAT4 [T	923	928	2.941176	ACTTCC	2.92969	2.929
cg1020029	FLJ44606	STAT4 [T	1127	1132	2.941176	GGAACC	2.92969	2.929
cg1020029	FLJ44606	STAT4 [T	1182	1187	2.941176	ACTTCC	2.92969	2.929
cg1020029	FLJ44606	STAT4 [T	1223	1228	2.941176	ACTTCC	2.92969	2.929
cg1020029	FLJ44606	STAT4 [T	1389	1394	2.941176	GGAACC	2.92969	2.929
cg1020029	FLJ44606	STAT4 [T	1670	1675	2.941176	GGAATA	2.92969	2.929
cg2709743	FLJ44606	p53 [T006	660	666	2.813291	GGGCAT	0.48828	0.47786
cg2709743	FLJ44606	p53 [T006	890	896	2.813291	GGGCAG	0.48828	0.47786
cg0230409	FLJ44606	p53 [T006	586	592	2.813291	GGGCAT	0.48828	0.47786
cg0230409	FLJ44606	p53 [T006	816	822	2.813291	GGGCAG	0.48828	0.47786
cg1020029	FLJ44606	p53 [T006	806	812	2.813291	GGGCAT	0.48828	0.47786
cg1020029	FLJ44606	p53 [T006	1036	1042	2.813291	GGGCAG	0.48828	0.47786
cg2709743	FLJ44606	AhR:Arnt	1086	1095	2.810335	CCACGC	0.01717	0.01648
cg0230409	FLJ44606	AhR:Arnt	1012	1021	2.810335	CCACGC	0.01717	0.01648
cg1020029	FLJ44606	AhR:Arnt	1232	1241	2.810335	CCACGC	0.01717	0.01648
cg2709743	FLJ44606	PR B [T00	260	266	2.80933	AACATT	0.73242	0.74818
cg2709743	FLJ44606	PR B [T00	424	430	2.80933	CATTGT	0.73242	0.74818
cg2709743	FLJ44606	PR B [T00	509	515	2.80933	CAATGT	0.73242	0.74818
cg2709743	FLJ44606	PR A [T01	260	266	2.80933	AACATT	0.73242	0.74818
cg2709743	FLJ44606	PR A [T01	424	430	2.80933	CATTGT	0.73242	0.74818
cg2709743	FLJ44606	PR A [T01	509	515	2.80933	CAATGT	0.73242	0.74818
cg0230409	FLJ44606	PR B [T00	186	192	2.80933	AACATT	0.73242	0.74818
cg0230409	FLJ44606	PR B [T00	350	356	2.80933	CATTGT	0.73242	0.74818
cg0230409	FLJ44606	PR B [T00	435	441	2.80933	CAATGT	0.73242	0.74818
cg0230409	FLJ44606	PR A [T01	186	192	2.80933	AACATT	0.73242	0.74818
cg0230409	FLJ44606	PR A [T01	350	356	2.80933	CATTGT	0.73242	0.74818
cg0230409	FLJ44606	PR A [T01	435	441	2.80933	CAATGT	0.73242	0.74818
cg1020029	FLJ44606	PR B [T00	406	412	2.80933	AACATT	0.73242	0.74818
cg1020029	FLJ44606	PR B [T00	570	576	2.80933	CATTGT	0.73242	0.74818
cg1020029	FLJ44606	PR B [T00	655	661	2.80933	CAATGT	0.73242	0.74818
cg1020029	FLJ44606	PR A [T01	406	412	2.80933	AACATT	0.73242	0.74818
cg1020029	FLJ44606	PR A [T01	570	576	2.80933	CATTGT	0.73242	0.74818
cg1020029	FLJ44606	PR A [T01	655	661	2.80933	CAATGT	0.73242	0.74818
cg2709743	FLJ44606	RXR-alph	1594	1600	2.726556	GGGTTG	0.85449	0.84796
cg0230409	FLJ44606	RXR-alph	1520	1526	2.726556	GGGTTG	0.85449	0.84796
cg1020029	FLJ44606	RXR-alph	1740	1746	2.726556	GGGTTG	0.85449	0.84796
cg2709743	FLJ44606	NF-Y [T0	452	459	2.673185	TGCCCA	0.21362	0.21485
cg0230409	FLJ44606	NF-Y [T0	378	385	2.673185	TGCCCA	0.21362	0.21485
cg1020029	FLJ44606	NF-Y [T0	598	605	2.673185	TGCCCA	0.21362	0.21485
cg2709743	FLJ44606	Sp1 [T007	757	766	2.656136	TTCCCG	0.04005	0.03892
cg0230409	FLJ44606	Sp1 [T007	683	692	2.656136	TTCCCG	0.04005	0.03892
cg1020029	FLJ44606	Sp1 [T007	903	912	2.656136	TTCCCG	0.04005	0.03892
cg2709743	FLJ44606	AP-2alpha	994	999	2.550491	GCCTCA	0.48828	0.48266
cg2709743	FLJ44606	AP-2alpha	1261	1266	2.550491	GCCTCA	0.48828	0.48266
cg2709743	FLJ44606	AP-2alpha	1286	1291	2.550491	TGAGGC	0.48828	0.48266
cg0230409	FLJ44606	AP-2alpha	920	925	2.550491	GCCTCA	0.48828	0.48266

cg0230409	FLJ44606	AP-2alpha	1187	1192	2.550491	GCCTCA	0.48828	0.48266
cg0230409	FLJ44606	AP-2alpha	1212	1217	2.550491	TGAGGC	0.48828	0.48266
cg1020029	FLJ44606	AP-2alpha	1140	1145	2.550491	GCCTCA	0.48828	0.48266
cg1020029	FLJ44606	AP-2alpha	1407	1412	2.550491	GCCTCA	0.48828	0.48266
cg1020029	FLJ44606	AP-2alpha	1432	1437	2.550491	TGAGGC	0.48828	0.48266
cg2709743	FLJ44606	RXR-alph	538	544	2.544678	TTCACC	0.85449	0.84796
cg0230409	FLJ44606	RXR-alph	464	470	2.544678	TTCACC	0.85449	0.84796
cg1020029	FLJ44606	RXR-alph	37	43	2.544678	TGCACC	0.85449	0.84796
cg1020029	FLJ44606	RXR-alph	684	690	2.544678	TTCACC	0.85449	0.84796
cg2709743	FLJ44606	ENKTF-1	913	920	2.511511	CCCCGC	0.12207	0.11894
cg2709743	FLJ44606	ENKTF-1	1000	1007	2.511511	CGCCGC	0.12207	0.11894
cg0230409	FLJ44606	ENKTF-1	839	846	2.511511	CCCCGC	0.12207	0.11894
cg0230409	FLJ44606	ENKTF-1	926	933	2.511511	CGCCGC	0.12207	0.11894
cg1020029	FLJ44606	ENKTF-1	1059	1066	2.511511	CCCCGC	0.12207	0.11894
cg1020029	FLJ44606	ENKTF-1	1146	1153	2.511511	CGCCGC	0.12207	0.11894
cg2709743	FLJ44606	PXR-1:RX	831	838	2.454225	GTAGTT	0.12207	0.12266
cg0230409	FLJ44606	PXR-1:RX	757	764	2.454225	GTAGTT	0.12207	0.12266
cg1020029	FLJ44606	PXR-1:RX	977	984	2.454225	GTAGTT	0.12207	0.12266
cg1020029	FLJ44606	NF-Y [T0	64	71	2.420868	ATTGGT	0.21362	0.21485
cg2709743	FLJ44606	IRF-1 [T0	1830	1838	2.418514	TTTCCC	0.02289	0.02311
cg0230409	FLJ44606	IRF-1 [T0	1756	1764	2.418514	TTTCCC	0.02289	0.02311
cg1020029	FLJ44606	IRF-1 [T0	1976	1984	2.418514	TTTCCC	0.02289	0.02311
cg2709743	FLJ44606	C/EBPalp	543	549	2.371703	CCCAAT	0.48828	0.49114
cg0230409	FLJ44606	C/EBPalp	469	475	2.371703	CCCAAT	0.48828	0.49114
cg1020029	FLJ44606	C/EBPalp	689	695	2.371703	CCCAAT	0.48828	0.49114
cg2709743	FLJ44606	c-Jun [T00	1182	1188	2.345465	TGACAC	0.48828	0.48929
cg0230409	FLJ44606	c-Jun [T00	1108	1114	2.345465	TGACAC	0.48828	0.48929
cg1020029	FLJ44606	c-Jun [T00	1328	1334	2.345465	TGACAC	0.48828	0.48929
cg2709743	FLJ44606	GCF [T00	920	928	2.339499	AGCCTG	0.06104	0.05925
cg0230409	FLJ44606	GCF [T00	846	854	2.339499	AGCCTG	0.06104	0.05925
cg1020029	FLJ44606	GCF [T00	1066	1074	2.339499	AGCCTG	0.06104	0.05925
cg2709743	FLJ44606	RXR-alph	1627	1633	2.322562	GGGTCT	0.85449	0.84796
cg0230409	FLJ44606	RXR-alph	1553	1559	2.322562	GGGTCT	0.85449	0.84796
cg1020029	FLJ44606	RXR-alph	1773	1779	2.322562	GGGTCT	0.85449	0.84796
cg2709743	FLJ44606	T3R-beta1	1906	1914	2.259951	GGGAGG	0.03052	0.03041
cg0230409	FLJ44606	T3R-beta1	1832	1840	2.259951	GGGAGG	0.03052	0.03041
cg2709743	FLJ44606	GATA-1 [	881	886	2.176375	TATCCA	3.90625	3.92756
cg2709743	FLJ44606	GATA-1 [	1881	1886	2.176375	AGGATA	3.90625	3.92756
cg2709743	FLJ44606	GATA-1 [	1987	1992	2.176375	TGGATA	3.90625	3.92756
cg0230409	FLJ44606	GATA-1 [	807	812	2.176375	TATCCA	3.90625	3.92756
cg0230409	FLJ44606	GATA-1 [	1807	1812	2.176375	AGGATA	3.90625	3.92756
cg0230409	FLJ44606	GATA-1 [	1913	1918	2.176375	TGGATA	3.90625	3.92756
cg1020029	FLJ44606	GATA-1 [	1027	1032	2.176375	TATCCA	3.90625	3.92756
cg2709743	FLJ44606	GATA-1 [	98	103	2.001358	GGGATA	3.90625	3.92756
cg2709743	FLJ44606	GATA-1 [	1471	1476	2.001358	TATCCC	3.90625	3.92756
cg0230409	FLJ44606	GATA-1 [	24	29	2.001358	GGGATA	3.90625	3.92756
cg0230409	FLJ44606	GATA-1 [	1397	1402	2.001358	TATCCC	3.90625	3.92756
cg1020029	FLJ44606	GATA-1 [	244	249	2.001358	GGGATA	3.90625	3.92756

cg1020029	FLJ44606	GATA-1 [	1617	1622	2.001358	TATCCC	3.90625	3.92756
cg2709743	FLJ44606	p53 [T006	450	456	1.970013	TTTGCCC	0.36621	0.36261
cg0230409	FLJ44606	p53 [T006	376	382	1.970013	TTTGCCC	0.36621	0.36261
cg1020029	FLJ44606	p53 [T006	596	602	1.970013	TTTGCCC	0.36621	0.36261
cg2709743	FLJ44606	AP-2alpha	1357	1362	1.871933	GCCTCC	0.97656	0.95407
cg0230409	FLJ44606	AP-2alpha	1283	1288	1.871933	GCCTCC	0.97656	0.95407
cg1020029	FLJ44606	AP-2alpha	1503	1508	1.871933	GCCTCC	0.97656	0.95407
cg2709743	FLJ44606	TBP [T007	814	823	1.871542	TTTATA	0.18311	0.18942
cg0230409	FLJ44606	TBP [T007	740	749	1.871542	TTTATA	0.18311	0.18942
cg0230409	FLJ44606	TBP [T007	1970	1979	1.871542	TTTATAC	0.18311	0.18942
cg1020029	FLJ44606	TBP [T007	89	98	1.871542	TTTATA	0.18311	0.18942
cg1020029	FLJ44606	TBP [T007	960	969	1.871542	TTTATA	0.18311	0.18942
cg2709743	FLJ44606	C/EBPalph	138	144	1.830762	AATTGA	0.48828	0.49438
cg0230409	FLJ44606	C/EBPalph	64	70	1.830762	AATTGA	0.48828	0.49438
cg1020029	FLJ44606	C/EBPalph	284	290	1.830762	AATTGA	0.48828	0.49438
cg2709743	FLJ44606	FOXP3 [T	1654	1659	1.824994	GTTGTA	0.48828	0.49451
cg0230409	FLJ44606	FOXP3 [T	1580	1585	1.824994	GTTGTA	0.48828	0.49451
cg1020029	FLJ44606	FOXP3 [T	1800	1805	1.824994	GTTGTA	0.48828	0.49451
cg2709743	FLJ44606	c-Ets-1 [T	1463	1469	1.769212	TAGGAA	0.12207	0.12414
cg0230409	FLJ44606	c-Ets-1 [T	1389	1395	1.769212	TAGGAA	0.12207	0.12414
cg1020029	FLJ44606	c-Ets-1 [T	1609	1615	1.769212	TAGGAA	0.12207	0.12414
cg2709743	FLJ44606	C/EBPalph	94	100	1.761449	TATTGG	0.48828	0.49438
cg2709743	FLJ44606	C/EBPalph	454	460	1.761449	CCCAAT	0.48828	0.49438
cg0230409	FLJ44606	C/EBPalph	20	26	1.761449	TATTGG	0.48828	0.49438
cg0230409	FLJ44606	C/EBPalph	380	386	1.761449	CCCAAT	0.48828	0.49438
cg1020029	FLJ44606	C/EBPalph	240	246	1.761449	TATTGG	0.48828	0.49438
cg1020029	FLJ44606	C/EBPalph	600	606	1.761449	CCCAAT	0.48828	0.49438
cg2709743	FLJ44606	GR-beta [T	15	19	1.680765	GCATT	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	70	74	1.680765	AATTC	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	80	84	1.680765	AATGC	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	137	141	1.680765	GAATT	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	638	642	1.680765	GAATT	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	639	643	1.680765	AATTC	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	865	869	1.680765	AATTC	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	1396	1400	1.680765	AATGC	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	1789	1793	1.680765	GCATT	3.90625	3.94936
cg2709743	FLJ44606	GR-beta [T	1927	1931	1.680765	GCATT	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	6	10	1.680765	AATGC	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	63	67	1.680765	GAATT	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	564	568	1.680765	GAATT	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	565	569	1.680765	AATTC	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	791	795	1.680765	AATTC	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	1322	1326	1.680765	AATGC	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	1715	1719	1.680765	GCATT	3.90625	3.94936
cg0230409	FLJ44606	GR-beta [T	1853	1857	1.680765	GCATT	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	35	39	1.680765	AATGC	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	84	88	1.680765	GCATT	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	161	165	1.680765	GCATT	3.90625	3.94936

cg1020029	FLJ44606	GR-beta [T	216	220	1.680765	AATTC	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	226	230	1.680765	AATGC	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	283	287	1.680765	GAATT	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	784	788	1.680765	GAATT	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	785	789	1.680765	AATTC	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	1011	1015	1.680765	AATTC	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	1542	1546	1.680765	AATGC	3.90625	3.94936
cg1020029	FLJ44606	GR-beta [T	1935	1939	1.680765	GCATT	3.90625	3.94936
cg2709743	FLJ44606	C/EBPbeta	25	28	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	96	99	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	149	152	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	252	255	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	340	343	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	455	458	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	544	547	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	610	613	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	827	830	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	884	887	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1005	1008	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1193	1196	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1199	1202	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1240	1243	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1277	1280	1.639871	CCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1374	1377	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1570	1573	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1597	1600	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1857	1860	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	22	25	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	75	78	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	178	181	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	266	269	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	381	384	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	470	473	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	536	539	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	753	756	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	810	813	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	931	934	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1119	1122	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1125	1128	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1166	1169	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1203	1206	1.639871	CCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1300	1303	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1496	1499	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1523	1526	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1783	1786	1.639871	TTGG	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1962	1965	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	43	46	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	58	61	1.639871	CCAA	15.625	15.72563

cg1020029	FLJ44606	C/EBPbeta	65	68	1.639871	TTGG	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	115	118	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	171	174	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	242	245	1.639871	TTGG	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	295	298	1.639871	TTGG	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	398	401	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	486	489	1.639871	TTGG	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	601	604	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	690	693	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	756	759	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	973	976	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1030	1033	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1151	1154	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1339	1342	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1345	1348	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1386	1389	1.639871	TTGG	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1423	1426	1.639871	CCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1520	1523	1.639871	TTGG	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1716	1719	1.639871	TTGG	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1743	1746	1.639871	TTGG	15.625	15.72563
cg2709743	FLJ44606	XBP-1 [T	311	316	1.583727	ATGACA	0.97656	0.98146
cg0230409	FLJ44606	XBP-1 [T	237	242	1.583727	ATGACA	0.97656	0.98146
cg1020029	FLJ44606	XBP-1 [T	111	116	1.583727	ATGACC	0.97656	0.98146
cg1020029	FLJ44606	XBP-1 [T	457	462	1.583727	ATGACA	0.97656	0.98146
cg2709743	FLJ44606	Pax-5 [T0	759	765	1.537547	CCCGCC	0.73242	0.71311
cg2709743	FLJ44606	Pax-5 [T0	1588	1594	1.537547	GGGCGT	0.73242	0.71311
cg0230409	FLJ44606	Pax-5 [T0	685	691	1.537547	CCCGCC	0.73242	0.71311
cg0230409	FLJ44606	Pax-5 [T0	1514	1520	1.537547	GGGCGT	0.73242	0.71311
cg1020029	FLJ44606	Pax-5 [T0	905	911	1.537547	CCCGCC	0.73242	0.71311
cg1020029	FLJ44606	Pax-5 [T0	1734	1740	1.537547	GGGCGT	0.73242	0.71311
cg2709743	FLJ44606	STAT4 [T	136	141	1.470588	GGAATT	1.95312	1.96333
cg2709743	FLJ44606	STAT4 [T	755	760	1.470588	TTTTCC	1.95312	1.96333
cg2709743	FLJ44606	STAT4 [T	865	870	1.470588	AATTCC	1.95312	1.96333
cg2709743	FLJ44606	STAT4 [T	1220	1225	1.470588	GGAAAA	1.95312	1.96333
cg2709743	FLJ44606	STAT4 [T	1713	1718	1.470588	GGAAAC	1.95312	1.96333
cg2709743	FLJ44606	STAT4 [T	1829	1834	1.470588	TTTTCC	1.95312	1.96333
cg0230409	FLJ44606	STAT4 [T	62	67	1.470588	GGAATT	1.95312	1.96333
cg0230409	FLJ44606	STAT4 [T	681	686	1.470588	TTTTCC	1.95312	1.96333
cg0230409	FLJ44606	STAT4 [T	791	796	1.470588	AATTCC	1.95312	1.96333
cg0230409	FLJ44606	STAT4 [T	1146	1151	1.470588	GGAAAA	1.95312	1.96333
cg0230409	FLJ44606	STAT4 [T	1639	1644	1.470588	GGAAAC	1.95312	1.96333
cg0230409	FLJ44606	STAT4 [T	1755	1760	1.470588	TTTTCC	1.95312	1.96333
cg1020029	FLJ44606	STAT4 [T	0	5	1.470588	TTTTCC	1.95312	1.96333
cg1020029	FLJ44606	STAT4 [T	282	287	1.470588	GGAATT	1.95312	1.96333
cg1020029	FLJ44606	STAT4 [T	901	906	1.470588	TTTTCC	1.95312	1.96333
cg1020029	FLJ44606	STAT4 [T	1011	1016	1.470588	AATTCC	1.95312	1.96333
cg1020029	FLJ44606	STAT4 [T	1366	1371	1.470588	GGAAAA	1.95312	1.96333
cg1020029	FLJ44606	STAT4 [T	1859	1864	1.470588	GGAAAC	1.95312	1.96333

cg1020029	FLJ44606	STAT4 [T	1975	1980	1.470588	TTTTCC	1.95312	1.96333
cg2709743	FLJ44606	C/EBPbeta	3	6	1.366559	TCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	132	135	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	140	143	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	155	158	1.366559	TCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	393	396	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	530	533	1.366559	TCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	555	558	1.366559	TCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	568	571	1.366559	TCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	642	645	1.366559	TCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	692	695	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1144	1147	1.366559	TCAA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1285	1288	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1556	1559	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1816	1819	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	C/EBPbeta	1953	1956	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	58	61	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	66	69	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	81	84	1.366559	TCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	319	322	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	456	459	1.366559	TCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	481	484	1.366559	TCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	494	497	1.366559	TCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	568	571	1.366559	TCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	618	621	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1070	1073	1.366559	TCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1211	1214	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1482	1485	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1742	1745	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1879	1882	1.366559	TTGA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1935	1938	1.366559	TCAA	15.625	15.72563
cg0230409	FLJ44606	C/EBPbeta	1951	1954	1.366559	TTGA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	149	152	1.366559	TCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	278	281	1.366559	TTGA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	286	289	1.366559	TTGA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	301	304	1.366559	TCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	539	542	1.366559	TTGA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	676	679	1.366559	TCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	701	704	1.366559	TCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	714	717	1.366559	TCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	788	791	1.366559	TCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	838	841	1.366559	TTGA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1290	1293	1.366559	TCAA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1431	1434	1.366559	TTGA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1702	1705	1.366559	TTGA	15.625	15.72563
cg1020029	FLJ44606	C/EBPbeta	1962	1965	1.366559	TTGA	15.625	15.72563
cg2709743	FLJ44606	AP-2alpha	1717	1722	1.357116	ACAGGC	0.48828	0.48203
cg0230409	FLJ44606	AP-2alpha	1643	1648	1.357116	ACAGGC	0.48828	0.48203

cg1020029	FLJ44606	AP-2alpha	1863	1868	1.357116	ACAGGC	0.48828	0.48203
cg2709743	FLJ44606	GCF [T00	1022	1030	1.26923	GCCCTG(	0.03052	0.02943
cg0230409	FLJ44606	GCF [T00	948	956	1.26923	GCCCTG(	0.03052	0.02943
cg1020029	FLJ44606	GCF [T00	1168	1176	1.26923	GCCCTG(	0.03052	0.02943
cg2709743	FLJ44606	PEA3 [T0(	1638	1646	1.194633	AGGATG	0.06866	0.06895
cg0230409	FLJ44606	PEA3 [T0(	1564	1572	1.194633	AGGATG	0.06866	0.06895
cg1020029	FLJ44606	PEA3 [T0(	1784	1792	1.194633	AGGATG	0.06866	0.06895
cg2709743	FLJ44606	GCF [T00	968	976	1.070269	GCGCGG	0.18311	0.17647
cg0230409	FLJ44606	GCF [T00	894	902	1.070269	GCGCGG	0.18311	0.17647
cg1020029	FLJ44606	GCF [T00	1114	1122	1.070269	GCGCGG	0.18311	0.17647
cg2709743	FLJ44606	TBP [T007	197	206	0.935771	AAAATA	0.12207	0.12628
cg0230409	FLJ44606	TBP [T007	123	132	0.935771	AAAATA	0.12207	0.12628
cg1020029	FLJ44606	TBP [T007	343	352	0.935771	AAAATA	0.12207	0.12628
cg2709743	FLJ44606	GATA-1 [	791	796	0.863549	TATCAC	1.95312	1.98662
cg0230409	FLJ44606	GATA-1 [	717	722	0.863549	TATCAC	1.95312	1.98662
cg1020029	FLJ44606	GATA-1 [	937	942	0.863549	TATCAC	1.95312	1.98662
cg2709743	FLJ44606	RXR-alpha	152	158	0.848226	GGGTCA	0.48828	0.48333
cg2709743	FLJ44606	RXR-alpha	908	914	0.848226	CGAACC	0.48828	0.48333
cg0230409	FLJ44606	RXR-alpha	78	84	0.848226	GGGTCA	0.48828	0.48333
cg0230409	FLJ44606	RXR-alpha	834	840	0.848226	CGAACC	0.48828	0.48333
cg1020029	FLJ44606	RXR-alpha	298	304	0.848226	GGGTCA	0.48828	0.48333
cg1020029	FLJ44606	RXR-alpha	1054	1060	0.848226	CGAACC	0.48828	0.48333
cg2709743	FLJ44606	GR-beta [	69	73	0.840383	TAATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	138	142	0.840383	AATTG	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	310	314	0.840383	AATGA	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	423	427	0.840383	TCATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	545	549	0.840383	CAATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	546	550	0.840383	AATTA	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	643	647	0.840383	CAATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	644	648	0.840383	AATTA	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	767	771	0.840383	TCATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	859	863	0.840383	TAATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	860	864	0.840383	AATTA	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	887	891	0.840383	AATGG	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1247	1251	0.840383	CCATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1305	1309	0.840383	CCATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1329	1333	0.840383	CCATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1341	1345	0.840383	TAATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1468	1472	0.840383	AATTA	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1697	1701	0.840383	AATGG	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1956	1960	0.840383	AATGG	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1974	1978	0.840383	AATGA	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1982	1986	0.840383	AATGA	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1994	1998	0.840383	TAATT	7.8125	7.94706
cg2709743	FLJ44606	GR-beta [	1995	1999	0.840383	AATTA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [	64	68	0.840383	AATTG	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [	236	240	0.840383	AATGA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [	349	353	0.840383	TCATT	7.8125	7.94706

cg0230409	FLJ44606	GR-beta [T	471	475	0.840383	CAATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	472	476	0.840383	AATTA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	569	573	0.840383	CAATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	570	574	0.840383	AATTA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	693	697	0.840383	TCATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	785	789	0.840383	TAATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	786	790	0.840383	AATTA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	813	817	0.840383	AATGG	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1173	1177	0.840383	CCATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1231	1235	0.840383	CCATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1255	1259	0.840383	CCATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1267	1271	0.840383	TAATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1394	1398	0.840383	AATTA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1623	1627	0.840383	AATGG	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1882	1886	0.840383	AATGG	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1900	1904	0.840383	AATGA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1908	1912	0.840383	AATGA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1920	1924	0.840383	TAATT	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1921	1925	0.840383	AATTA	7.8125	7.94706
cg0230409	FLJ44606	GR-beta [T	1977	1981	0.840383	TCATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	24	28	0.840383	TAATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	25	29	0.840383	AATTA	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	118	122	0.840383	AATGA	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	215	219	0.840383	TAATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	284	288	0.840383	AATTG	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	456	460	0.840383	AATGA	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	569	573	0.840383	TCATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	691	695	0.840383	CAATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	692	696	0.840383	AATTA	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	789	793	0.840383	CAATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	790	794	0.840383	AATTA	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	913	917	0.840383	TCATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1005	1009	0.840383	TAATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1006	1010	0.840383	AATTA	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1033	1037	0.840383	AATGG	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1393	1397	0.840383	CCATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1451	1455	0.840383	CCATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1475	1479	0.840383	CCATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1487	1491	0.840383	TAATT	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1614	1618	0.840383	AATTA	7.8125	7.94706
cg1020029	FLJ44606	GR-beta [T	1843	1847	0.840383	AATGG	7.8125	7.94706
cg2709743	FLJ44606	PXR-1:RX	1379	1386	0.818075	TGAACT	0.12207	0.12266
cg0230409	FLJ44606	PXR-1:RX	1305	1312	0.818075	TGAACT	0.12207	0.12266
cg1020029	FLJ44606	PXR-1:RX	1525	1532	0.818075	TGAACT	0.12207	0.12266
cg2709743	FLJ44606	AP-2alpha	1158	1163	0.678558	GCCTGA	0.48828	0.48199
cg0230409	FLJ44606	AP-2alpha	1084	1089	0.678558	GCCTGA	0.48828	0.48199
cg1020029	FLJ44606	AP-2alpha	1304	1309	0.678558	GCCTGA	0.48828	0.48199
cg2709743	FLJ44606	RXR-alph	647	653	0.62611	TAAACC	0.12207	0.12313

cg2709743	FLJ44606	RXR-alpha	1493	1499	0.62611	GGGTTT	0.12207	0.12313
cg2709743	FLJ44606	RXR-alpha	1875	1881	0.62611	GGGTTT	0.12207	0.12313
cg0230409	FLJ44606	RXR-alpha	573	579	0.62611	TAAACC	0.12207	0.12313
cg0230409	FLJ44606	RXR-alpha	1419	1425	0.62611	GGGTTT	0.12207	0.12313
cg0230409	FLJ44606	RXR-alpha	1801	1807	0.62611	GGGTTT	0.12207	0.12313
cg1020029	FLJ44606	RXR-alpha	793	799	0.62611	TAAACC	0.12207	0.12313
cg1020029	FLJ44606	RXR-alpha	1639	1645	0.62611	GGGTTT	0.12207	0.12313
cg2709743	FLJ44606	c-Ets-1 [T	750	756	0.256174	CTTCCTT	0.24414	0.24569
cg0230409	FLJ44606	c-Ets-1 [T	676	682	0.256174	CTTCCTT	0.24414	0.24569
cg1020029	FLJ44606	c-Ets-1 [T	896	902	0.256174	CTTCCTT	0.24414	0.24569
cg2709743	FLJ44606	AP-2alpha	1053	1058	0.226186	CCAGGC	0.97656	0.95305
cg2709743	FLJ44606	AP-2alpha	1066	1071	0.226186	CCAGGC	0.97656	0.95305
cg0230409	FLJ44606	AP-2alpha	979	984	0.226186	CCAGGC	0.97656	0.95305
cg0230409	FLJ44606	AP-2alpha	992	997	0.226186	CCAGGC	0.97656	0.95305
cg1020029	FLJ44606	AP-2alpha	1199	1204	0.226186	CCAGGC	0.97656	0.95305
cg1020029	FLJ44606	AP-2alpha	1212	1217	0.226186	CCAGGC	0.97656	0.95305
cg2709743	FLJ44606	GR-alpha [	439	443	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	467	471	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	526	530	0.207689	CCTTT	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	534	538	0.207689	CCTTT	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	550	554	0.207689	AAAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	586	590	0.207689	AAAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	753	757	0.207689	CCTTT	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	937	941	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1011	1015	0.207689	CCTCT	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1165	1169	0.207689	CCTTT	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1257	1261	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1560	1564	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1691	1695	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1707	1711	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1726	1730	0.207689	AGAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1757	1761	0.207689	CCTTT	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1841	1845	0.207689	AAAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	365	369	0.207689	AGAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	393	397	0.207689	AGAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	452	456	0.207689	CCTTT	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	460	464	0.207689	CCTTT	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	476	480	0.207689	AAAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	512	516	0.207689	AAAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	679	683	0.207689	CCTTT	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	863	867	0.207689	AGAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	937	941	0.207689	CCTCT	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1091	1095	0.207689	CCTTT	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1183	1187	0.207689	AGAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1486	1490	0.207689	AGAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1617	1621	0.207689	AGAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1633	1637	0.207689	AGAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1652	1656	0.207689	AGAGG	7.8125	7.81264

cg0230409	FLJ44606	GR-alpha [	1683	1687	0.207689	CCTTT	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1767	1771	0.207689	AAAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	134	138	0.207689	CCTCT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	585	589	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	613	617	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	672	676	0.207689	CCTTT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	680	684	0.207689	CCTTT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	696	700	0.207689	AAAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	732	736	0.207689	AAAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	899	903	0.207689	CCTTT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1083	1087	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1157	1161	0.207689	CCTCT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1311	1315	0.207689	CCTTT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1403	1407	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1706	1710	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1837	1841	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1853	1857	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1872	1876	0.207689	AGAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1903	1907	0.207689	CCTTT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1987	1991	0.207689	AAAGG	7.8125	7.81264
cg2709743	FLJ44606	HNF-1A [	1339	1346	0.143882	GTTAAT	0.24414	0.25261
cg0230409	FLJ44606	HNF-1A [	1265	1272	0.143882	GTTAAT	0.24414	0.25261
cg1020029	FLJ44606	HNF-1A [	1485	1492	0.143882	GTTAAT	0.24414	0.25261
cg2709743	FLJ44606	c-Ets-1 [T	1913	1919	0.128087	GAGGAA	0.24414	0.2429
cg0230409	FLJ44606	c-Ets-1 [T	1839	1845	0.128087	GAGGAA	0.24414	0.2429
cg2709743	FLJ44606	PXR-1:RX	1817	1824	0.123583	TGAACT	0.12207	0.12407
cg0230409	FLJ44606	PXR-1:RX	1743	1750	0.123583	TGAACT	0.12207	0.12407
cg1020029	FLJ44606	PXR-1:RX	1963	1970	0.123583	TGAACT	0.12207	0.12407
cg2709743	FLJ44606	GATA-1 [	1116	1121	0.105011	TATCTC	0.97656	0.98738
cg0230409	FLJ44606	GATA-1 [	1042	1047	0.105011	TATCTC	0.97656	0.98738
cg1020029	FLJ44606	GATA-1 [	1262	1267	0.105011	TATCTC	0.97656	0.98738
cg2709743	FLJ44606	GR-alpha [	267	271	0	CCTGT	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1484	1488	0	ATAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1717	1721	0	ACAGG	7.8125	7.81264
cg2709743	FLJ44606	GR-alpha [	1884	1888	0	ATAGG	7.8125	7.81264
cg2709743	FLJ44606	AP-2alpha	921	926	0	GCCTGC	0.97656	0.95305
cg2709743	FLJ44606	AP-2alpha	1613	1618	0	GCAGGC	0.97656	0.95305
cg2709743	FLJ44606	XBP-1 [T	765	770	0	CGTCAT	0.97656	0.98127
cg2709743	FLJ44606	Pax-5 [T0	1060	1066	0	CCGGCC	1.09863	1.06846
cg2709743	FLJ44606	Pax-5 [T0	1067	1073	0	CAGGCC	1.09863	1.06846
cg2709743	FLJ44606	Pax-5 [T0	1573	1579	0	GGGCTG	1.09863	1.06846
cg2709743	FLJ44606	E2F-1 [T0	756	763	0	TTTCCCC	0.03052	0.03017
cg2709743	FLJ44606	TFII-I [T0	126	131	0	CTGTCC	1.46484	1.45997
cg2709743	FLJ44606	TFII-I [T0	880	885	0	CTATCC	1.46484	1.45997
cg2709743	FLJ44606	TFII-I [T0	1601	1606	0	GGACAG	1.46484	1.45997
cg2709743	FLJ44606	TFII-I [T0	1882	1887	0	GGATAG	1.46484	1.45997
cg2709743	FLJ44606	STAT4 [T	77	82	0	GGAAAT	0.48828	0.49387
cg2709743	FLJ44606	STAT4 [T	1465	1470	0	GGAAAT	0.48828	0.49387

cg2709743	FLJ44606	YY1 [T00	120	123	0	CCAT	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	166	169	0	CCAT	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	173	176	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	560	563	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	838	841	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	846	849	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	888	891	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1247	1250	0	CCAT	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1305	1308	0	CCAT	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1329	1332	0	CCAT	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1390	1393	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1489	1492	0	CCAT	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1491	1494	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1650	1653	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1678	1681	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1698	1701	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1747	1750	0	CCAT	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1868	1871	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1957	1960	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	YY1 [T00	1986	1989	0	ATGG	7.8125	7.81711
cg2709743	FLJ44606	GCF [T00	1027	1035	0	GCGCCG	0.09155	0.08765
cg2709743	FLJ44606	GCF [T00	1057	1065	0	GCGCCG	0.09155	0.08765
cg2709743	FLJ44606	ER-alpha [	153	157	0	GGTCA	1.95312	1.9404
cg2709743	FLJ44606	ER-alpha [	553	557	0	GGTCA	1.95312	1.9404
cg2709743	FLJ44606	ER-alpha [	1227	1231	0	TGACC	1.95312	1.9404
cg2709743	FLJ44606	GATA-1 [	387	392	0	TATCTG	0.97656	0.98738
cg2709743	FLJ44606	GATA-1 [	1456	1461	0	CAGATA	0.97656	0.98738
cg2709743	FLJ44606	C/EBPbeta	8	11	0	TTGT	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	18	21	0	TTGT	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	53	56	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	58	61	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	235	238	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	256	259	0	GCAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	295	298	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	308	311	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	373	376	0	TTGT	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	426	429	0	TTGT	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	451	454	0	TTGC	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	508	511	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1188	1191	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1211	1214	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1406	1409	0	GCAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1431	1434	0	GCAA	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1514	1517	0	TTGC	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1655	1658	0	TTGT	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1767	1770	0	TTGT	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1825	1828	0	TTGC	15.625	15.71349
cg2709743	FLJ44606	C/EBPbeta	1888	1891	0	GCAA	15.625	15.71349

cg2709743	FLJ44606	C/EBPbeta	1899	1902	0	ACAA	15.625	15.71349
cg2709743	FLJ44606	TFIID [T0	182	188	0	TTTTTTA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	183	189	0	TTTTTAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	330	336	0	TTTTCTA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	349	355	0	TTAAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	350	356	0	TAAAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	568	574	0	TCAAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	581	587	0	TTTAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	582	588	0	TTAAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	734	740	0	TTAAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	735	741	0	TAAAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	1205	1211	0	TAAAAA	1.09863	1.13474
cg2709743	FLJ44606	TFIID [T0	1282	1288	0	TTTTTGA	1.09863	1.13474
cg2709743	FLJ44606	GR-beta [T	60	64	0	AATGT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	261	265	0	ACATT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	314	318	0	ACATT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	398	402	0	AATGT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	510	514	0	AATGT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	864	868	0	AAATT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	1342	1346	0	AATTT	3.90625	3.99611
cg2709743	FLJ44606	GR-beta [T	1467	1471	0	AAATT	3.90625	3.99611
cg2709743	FLJ44606	STAT1beta	73	82	0	TCTGGG	0.01717	0.01735
cg2709743	FLJ44606	PR B [T00	288	294	0	AACAGT	0.36621	0.36944
cg2709743	FLJ44606	PR A [T01	288	294	0	AACAGT	0.36621	0.36944
cg2709743	FLJ44606	GR [T050	569	575	0	CAAAAA	0.36621	0.37562
cg2709743	FLJ44606	GR [T050	1281	1287	0	CTTTTTG	0.36621	0.37562
cg2709743	FLJ44606	HNF-1A [	1307	1314	0	ATTTTAA	0.24414	0.25261
cg2709743	FLJ44606	IRF-2 [T01	380	385	0	AAGTGA	0.48828	0.49387
cg2709743	FLJ44606	IRF-2 [T01	1224	1229	0	AAGTGA	0.48828	0.49387
cg0230409	FLJ44606	GR-alpha [	193	197	0	CCTGT	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1410	1414	0	ATAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1643	1647	0	ACAGG	7.8125	7.81264
cg0230409	FLJ44606	GR-alpha [	1810	1814	0	ATAGG	7.8125	7.81264
cg0230409	FLJ44606	AP-2alpha	847	852	0	GCCTGC	0.97656	0.95305
cg0230409	FLJ44606	AP-2alpha	1539	1544	0	GCAGGC	0.97656	0.95305
cg0230409	FLJ44606	XBP-1 [T0	691	696	0	CGTCAT	0.97656	0.98127
cg0230409	FLJ44606	Pax-5 [T0	986	992	0	CCGGCC	1.09863	1.06846
cg0230409	FLJ44606	Pax-5 [T0	993	999	0	CAGGCC	1.09863	1.06846
cg0230409	FLJ44606	Pax-5 [T0	1499	1505	0	GGGCTG	1.09863	1.06846
cg0230409	FLJ44606	E2F-1 [T0	682	689	0	TTTCCC	0.03052	0.03017
cg0230409	FLJ44606	TFII-I [T0	52	57	0	CTGTCC	1.46484	1.45997
cg0230409	FLJ44606	TFII-I [T0	806	811	0	CTATCC	1.46484	1.45997
cg0230409	FLJ44606	TFII-I [T0	1527	1532	0	GGACAG	1.46484	1.45997
cg0230409	FLJ44606	TFII-I [T0	1808	1813	0	GGATAG	1.46484	1.45997
cg0230409	FLJ44606	STAT4 [T	3	8	0	GGAAAT	0.48828	0.49387
cg0230409	FLJ44606	STAT4 [T	1391	1396	0	GGAAAT	0.48828	0.49387
cg0230409	FLJ44606	YY1 [T00	46	49	0	CCAT	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	92	95	0	CCAT	7.8125	7.81711

cg0230409	FLJ44606	YY1 [T00	99	102	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	486	489	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	764	767	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	772	775	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	814	817	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1173	1176	0	CCAT	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1231	1234	0	CCAT	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1255	1258	0	CCAT	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1316	1319	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1415	1418	0	CCAT	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1417	1420	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1576	1579	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1604	1607	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1624	1627	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1673	1676	0	CCAT	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1794	1797	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1883	1886	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	YY1 [T00	1912	1915	0	ATGG	7.8125	7.81711
cg0230409	FLJ44606	GCF [T00	953	961	0	GCGCCG	0.09155	0.08765
cg0230409	FLJ44606	GCF [T00	983	991	0	GCGCCG	0.09155	0.08765
cg0230409	FLJ44606	ER-alpha [	79	83	0	GGTCA	1.95312	1.9404
cg0230409	FLJ44606	ER-alpha [	479	483	0	GGTCA	1.95312	1.9404
cg0230409	FLJ44606	ER-alpha [	1153	1157	0	TGACC	1.95312	1.9404
cg0230409	FLJ44606	GATA-1 [	313	318	0	TATCTG	0.97656	0.98738
cg0230409	FLJ44606	GATA-1 [	1382	1387	0	CAGATA	0.97656	0.98738
cg0230409	FLJ44606	C/EBPbeta	161	164	0	ACAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	182	185	0	GCAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	221	224	0	ACAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	234	237	0	ACAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	299	302	0	TTGT	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	352	355	0	TTGT	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	377	380	0	TTGC	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	434	437	0	ACAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1114	1117	0	ACAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1137	1140	0	ACAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1332	1335	0	GCAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1357	1360	0	GCAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1440	1443	0	TTGC	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1581	1584	0	TTGT	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1693	1696	0	TTGT	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1751	1754	0	TTGC	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1814	1817	0	GCAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1825	1828	0	ACAA	15.625	15.71349
cg0230409	FLJ44606	C/EBPbeta	1955	1958	0	TTGC	15.625	15.71349
cg0230409	FLJ44606	TFIID [T0	108	114	0	TTTTTTA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	109	115	0	TTTTTAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	256	262	0	TTTTCTA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	275	281	0	TTAAAA	1.09863	1.13474

cg0230409	FLJ44606	TFIID [T0	276	282	0	TAAAAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	494	500	0	TCAAAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	507	513	0	TTTAAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	508	514	0	TTAAAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	660	666	0	TTAAAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	661	667	0	TAAAAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	1131	1137	0	TAAAAA	1.09863	1.13474
cg0230409	FLJ44606	TFIID [T0	1208	1214	0	TTTTTGA	1.09863	1.13474
cg0230409	FLJ44606	GR-beta [T	187	191	0	ACATT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	240	244	0	ACATT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	324	328	0	AATGT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	436	440	0	AATGT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	790	794	0	AAATT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	1268	1272	0	AATTT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	1393	1397	0	AAATT	3.90625	3.99611
cg0230409	FLJ44606	GR-beta [T	1944	1948	0	ACATT	3.90625	3.99611
cg0230409	FLJ44606	PR B [T00	214	220	0	AACAGT	0.36621	0.36944
cg0230409	FLJ44606	PR A [T01	214	220	0	AACAGT	0.36621	0.36944
cg0230409	FLJ44606	GR [T0507	495	501	0	CAAAAA	0.36621	0.37562
cg0230409	FLJ44606	GR [T0507	1207	1213	0	CTTTTTG	0.36621	0.37562
cg0230409	FLJ44606	HNF-1A [	1233	1240	0	ATTTTA	0.24414	0.25261
cg0230409	FLJ44606	IRF-2 [T01	306	311	0	AAGTGA	0.48828	0.49387
cg0230409	FLJ44606	IRF-2 [T01	1150	1155	0	AAGTGA	0.48828	0.49387
cg1020029	FLJ44606	GR-alpha [	30	34	0	CCTAT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	413	417	0	CCTGT	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1630	1634	0	ATAGG	7.8125	7.81264
cg1020029	FLJ44606	GR-alpha [	1863	1867	0	ACAGG	7.8125	7.81264
cg1020029	FLJ44606	AP-2alpha	1067	1072	0	GCCTGC	0.97656	0.95305
cg1020029	FLJ44606	AP-2alpha	1759	1764	0	GCAGGC	0.97656	0.95305
cg1020029	FLJ44606	XBP-1 [T0	911	916	0	CGTCAT	0.97656	0.98127
cg1020029	FLJ44606	Pax-5 [T0	1206	1212	0	CCGGCC	1.09863	1.06846
cg1020029	FLJ44606	Pax-5 [T0	1213	1219	0	CAGGCC	1.09863	1.06846
cg1020029	FLJ44606	Pax-5 [T0	1719	1725	0	GGGCTG	1.09863	1.06846
cg1020029	FLJ44606	E2F-1 [T0	902	909	0	TTTCCC	0.03052	0.03017
cg1020029	FLJ44606	TFII-I [T0	272	277	0	CTGTCC	1.46484	1.45997
cg1020029	FLJ44606	TFII-I [T0	1026	1031	0	CTATCC	1.46484	1.45997
cg1020029	FLJ44606	TFII-I [T0	1747	1752	0	GGACAG	1.46484	1.45997
cg1020029	FLJ44606	STAT4 [T	223	228	0	GGAAAT	0.48828	0.49387
cg1020029	FLJ44606	STAT4 [T	1611	1616	0	GGAAAT	0.48828	0.49387
cg1020029	FLJ44606	YY1 [T00	266	269	0	CCAT	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	312	315	0	CCAT	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	319	322	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	706	709	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	984	987	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	992	995	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1034	1037	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1393	1396	0	CCAT	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1451	1454	0	CCAT	7.8125	7.81711

cg1020029	FLJ44606	YY1 [T00	1475	1478	0	CCAT	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1536	1539	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1635	1638	0	CCAT	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1637	1640	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1796	1799	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1824	1827	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1844	1847	0	ATGG	7.8125	7.81711
cg1020029	FLJ44606	YY1 [T00	1893	1896	0	CCAT	7.8125	7.81711
cg1020029	FLJ44606	GCF [T00	1173	1181	0	GCGCCG	0.09155	0.08765
cg1020029	FLJ44606	GCF [T00	1203	1211	0	GCGCCG	0.09155	0.08765
cg1020029	FLJ44606	ER-alpha [	112	116	0	TGACC	1.95312	1.9404
cg1020029	FLJ44606	ER-alpha [	299	303	0	GGTCA	1.95312	1.9404
cg1020029	FLJ44606	ER-alpha [	699	703	0	GGTCA	1.95312	1.9404
cg1020029	FLJ44606	ER-alpha [	1373	1377	0	TGACC	1.95312	1.9404
cg1020029	FLJ44606	GATA-1 [	533	538	0	TATCTG	0.97656	0.98738
cg1020029	FLJ44606	GATA-1 [	1602	1607	0	CAGATA	0.97656	0.98738
cg1020029	FLJ44606	C/EBPbeta	154	157	0	TTGT	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	164	167	0	TTGT	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	199	202	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	204	207	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	381	384	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	402	405	0	GCAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	441	444	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	454	457	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	519	522	0	TTGT	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	572	575	0	TTGT	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	597	600	0	TTGC	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	654	657	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1334	1337	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1357	1360	0	ACAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1552	1555	0	GCAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1577	1580	0	GCAA	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1660	1663	0	TTGC	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1801	1804	0	TTGT	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1913	1916	0	TTGT	15.625	15.71349
cg1020029	FLJ44606	C/EBPbeta	1971	1974	0	TTGC	15.625	15.71349
cg1020029	FLJ44606	TFIID [T0	88	94	0	TTTTATA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	328	334	0	TTTTTTA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	329	335	0	TTTTTAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	476	482	0	TTTTCTA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	495	501	0	TTAAAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	496	502	0	TAAAAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	714	720	0	TCAAAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	727	733	0	TTTAAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	728	734	0	TTAAAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	880	886	0	TTAAAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	881	887	0	TAAAAA	1.09863	1.13474
cg1020029	FLJ44606	TFIID [T0	1351	1357	0	TAAAAA	1.09863	1.13474

cg1020029	FLJ44606	TFIID [T0	1428	1434	0	TTTTTGA	1.09863	1.13474
cg1020029	FLJ44606	GR-beta [T	45	49	0	AATGT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	206	210	0	AATGT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	407	411	0	ACATT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	460	464	0	ACATT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	544	548	0	AATGT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	656	660	0	AATGT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	1010	1014	0	AAATT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	1488	1492	0	AATTT	3.90625	3.99611
cg1020029	FLJ44606	GR-beta [T	1613	1617	0	AAATT	3.90625	3.99611
cg1020029	FLJ44606	STAT1beta	219	228	0	TCTGGGA	0.01717	0.01735
cg1020029	FLJ44606	PR B [T00	434	440	0	AACAGT	0.36621	0.36944
cg1020029	FLJ44606	PR A [T01	434	440	0	AACAGT	0.36621	0.36944
cg1020029	FLJ44606	GR [T0507	715	721	0	CAAAAA	0.36621	0.37562
cg1020029	FLJ44606	GR [T0507	1427	1433	0	CTTTTTG	0.36621	0.37562
cg1020029	FLJ44606	HNF-1A [T	1453	1460	0	ATTTTAA	0.24414	0.25261
cg1020029	FLJ44606	IRF-2 [T01	526	531	0	AAGTGA	0.48828	0.49387
cg1020029	FLJ44606	IRF-2 [T01	1370	1375	0	AAGTGA	0.48828	0.49387
cg0541306	GALNTL2	c-Myb [T0	706	713	9.815171	ACAAGT	0.36621	0.3712
cg0541306	GALNTL2	XBP-1 [T0	131	136	9.789909	ATGTCT	1.95312	1.95208
cg0541306	GALNTL2	XBP-1 [T0	220	225	9.789909	ATGGCT	1.95312	1.95208
cg0541306	GALNTL2	XBP-1 [T0	1054	1059	9.789909	AGCCAT	1.95312	1.95208
cg0541306	GALNTL2	XBP-1 [T0	1595	1600	9.789909	ATGTCT	1.95312	1.95208
cg0541306	GALNTL2	NF-1 [T00	222	229	9.761671	GGCTCCA	0.24414	0.24405
cg0541306	GALNTL2	PR B [T00	582	588	9.743489	TGGTGTT	1.09863	1.10292
cg0541306	GALNTL2	PR B [T00	1133	1139	9.743489	AACACA	1.09863	1.10292
cg0541306	GALNTL2	PR B [T00	1267	1273	9.743489	CTGTGTT	1.09863	1.10292
cg0541306	GALNTL2	PR A [T01	582	588	9.743489	TGGTGTT	1.09863	1.10292
cg0541306	GALNTL2	PR A [T01	1133	1139	9.743489	AACACA	1.09863	1.10292
cg0541306	GALNTL2	PR A [T01	1267	1273	9.743489	CTGTGTT	1.09863	1.10292
cg0541306	GALNTL2	c-Myb [T0	1605	1612	9.729271	TTCAGTT	0.36621	0.37054
cg0541306	GALNTL2	LEF-1 [T0	1551	1558	9.72404	CTTTGCC	0.21362	0.2139
cg0541306	GALNTL2	GATA-3 [T	1408	1419	9.719337	CGAGATA	0.01597	0.01612
cg0541306	GALNTL2	c-Jun [T00	102	108	9.717135	TGACCTC	0.73242	0.73031
cg0541306	GALNTL2	c-Ets-1 [T0	1684	1690	9.713162	ATTCCCC	0.36621	0.36441
cg0541306	GALNTL2	NF-AT1 [T	945	953	9.691726	GGAAAC	0.16785	0.1682
cg0541306	GALNTL2	NF-AT1 [T	1849	1857	9.691726	TAGGTTT	0.16785	0.1682
cg0541306	GALNTL2	RAR-beta	787	796	9.641259	CCCCAAC	0.21362	0.21243
cg0541306	GALNTL2	RAR-beta	1375	1384	9.641259	GGGGTTT	0.21362	0.21243
cg0541306	GALNTL2	Elk-1 [T00	989	997	9.62002	GGAGGG	0.07629	0.07577
cg0541306	GALNTL2	Pax-5 [T0	889	895	9.552105	GGGCGC	1.46484	1.43083
cg0541306	GALNTL2	TFIID [T0	1552	1558	9.552105	TTTGCCA	1.46484	1.48472
cg0541306	GALNTL2	TFIID [T0	1630	1636	9.552105	TTTCCCA	1.46484	1.48472
cg0541306	GALNTL2	EBF [T054	1082	1092	9.522901	TTCACAC	0.06866	0.06676
cg0541306	GALNTL2	NF-1 [T00	82	89	9.513281	TTGGGTT	0.73242	0.73053
cg0541306	GALNTL2	NF-1 [T00	319	326	9.513281	CAAGCCA	0.73242	0.73053
cg0541306	GALNTL2	NF-1 [T00	804	811	9.513281	TTGGGGT	0.73242	0.73053
cg0541306	GALNTL2	TFII-I [T0	14	19	9.512894	GGATGG	7.32422	7.29728

cg0541306	GALNTL2	TFII-I [T0	33	38	9.512894	GGACAC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	390	395	9.512894	GGATGG	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	538	543	9.512894	GTGTCC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	623	628	9.512894	GGATTT	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	925	930	9.512894	GTATCC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	945	950	9.512894	GGAAAC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1073	1078	9.512894	TTTTCC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1106	1111	9.512894	GGAAAA	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1213	1218	9.512894	TTATCC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1230	1235	9.512894	GGACAC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1383	1388	9.512894	GGACAC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1507	1512	9.512894	AAGTCC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1713	1718	9.512894	GTGTCC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1852	1857	9.512894	GTTTCC	7.32422	7.29728
cg0541306	GALNTL2	TFII-I [T0	1896	1901	9.512894	TTATCC	7.32422	7.29728
cg0541306	GALNTL2	FOXP3 [T	368	373	9.512894	GAGAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	575	580	9.512894	GTTGGT	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	683	688	9.512894	ACCAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	702	707	9.512894	GAGAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	788	793	9.512894	CCCAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1130	1135	9.512894	GTAAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1189	1194	9.512894	CAGAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1271	1276	9.512894	GTTGGC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1574	1579	9.512894	GTTGGC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1763	1768	9.512894	CAGAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1799	1804	9.512894	GTTATG	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1816	1821	9.512894	ATAAAC	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1846	1851	9.512894	GTTTAG	7.32422	7.35678
cg0541306	GALNTL2	FOXP3 [T	1895	1900	9.512894	GTTATC	7.32422	7.35678
cg0541306	GALNTL2	TCF-4E [T	1308	1314	9.453578	TCCAAA	0.48828	0.49215
cg0541306	GALNTL2	TCF-4E [T	1345	1351	9.453578	CTCAAA	0.48828	0.49215
cg0541306	GALNTL2	NFI/CTF [	78	85	9.352332	GTCTTT	0.54932	0.54821
cg0541306	GALNTL2	NFI/CTF [	323	330	9.352332	CCAAGG	0.54932	0.54821
cg0541306	GALNTL2	NFI/CTF [	1309	1316	9.352332	CCAAAG	0.54932	0.54821
cg0541306	GALNTL2	c-Ets-1 [T	586	592	9.276861	GTTCCC	0.36621	0.36441
cg0541306	GALNTL2	SRY [T00	1306	1314	9.264664	AGTCCA	0.12207	0.12265
cg0541306	GALNTL2	NF-AT1 [	1925	1933	9.18189	GGAAAG	0.22888	0.22959
cg0541306	GALNTL2	USF2 [T0	1686	1695	9.056375	TCCCCA	0.1545	0.15287
cg0541306	GALNTL2	HNF-1C [	670	678	9.032578	GTTAAT	0.12207	0.12495
cg0541306	GALNTL2	c-Jun [T00	1674	1680	9.013496	CATGTC	0.61035	0.61059
cg0541306	GALNTL2	PXR-1:RX	748	755	8.998824	TGAACA	0.24414	0.2439
cg0541306	GALNTL2	PXR-1:RX	1538	1545	8.998824	GATGTT	0.24414	0.2439
cg0541306	GALNTL2	NF-AT2 [	1595	1604	8.984657	ATGTCT	0.05341	0.05386
cg0541306	GALNTL2	LEF-1 [T0	80	87	8.973041	CTTTGG	0.54932	0.55326
cg0541306	GALNTL2	GR [T050	1310	1316	8.971049	CAAAGC	0.61035	0.61632
cg0541306	GALNTL2	GR [T050	1738	1744	8.971049	GGCTTT	0.61035	0.61632
cg0541306	GALNTL2	c-Myb [T0	1448	1455	8.947824	AGAAGT	0.39673	0.40028
cg0541306	GALNTL2	T3R-beta1	1424	1432	8.924046	TCACCG	0.2594	0.25766

cg0541306	GALNTL2	c-Ets-2 [T(	940	948	8.912323	CTTTAGC	0.27466	0.27495
cg0541306	GALNTL2	c-Ets-2 [T(	1489	1497	8.912323	TTCCTGC	0.27466	0.27495
cg0541306	GALNTL2	c-Ets-2 [T(	1920	1928	8.912323	GCTCAG(	0.27466	0.27495
cg0541306	GALNTL2	GATA-2 ['	922	930	8.888889	TCAGTA'	0.22888	0.22993
cg0541306	GALNTL2	PR B [T00	935	941	8.827054	AACAGC'	0.36621	0.36944
cg0541306	GALNTL2	PR B [T00	1192	1198	8.827054	AACAGC'	0.36621	0.36944
cg0541306	GALNTL2	PR A [T01	935	941	8.827054	AACAGC'	0.36621	0.36944
cg0541306	GALNTL2	PR A [T01	1192	1198	8.827054	AACAGC'	0.36621	0.36944
cg0541306	GALNTL2	NFI/CTF [	1517	1524	8.814757	TCACTTC	0.48828	0.48804
cg0541306	GALNTL2	c-Jun [T00	678	684	8.807683	TGACAA(	0.61035	0.61059
cg0541306	GALNTL2	E2F-1 [T0	1930	1937	8.76494	GCGGAG	0.27466	0.26875
cg0541306	GALNTL2	XBP-1 [T(	1353	1358	8.75604	ATGAAC	2.92969	2.9674
cg0541306	GALNTL2	STAT1bet:	1073	1082	8.695301	TTTTCCA	0.22316	0.22446
cg0541306	GALNTL2	STAT1bet:	1102	1111	8.695301	TGCAGG.	0.22316	0.22446
cg0541306	GALNTL2	IRF-1 [T0(	473	481	8.661524	TTTCCTC	0.20599	0.20664
cg0541306	GALNTL2	PPAR-alpl	1638	1648	8.543553	CTCTGG(	0.02003	0.01963
cg0541306	GALNTL2	HNF-3alpl	1415	1422	8.343064	GTAAAA'	0.27466	0.28528
cg0541306	GALNTL2	c-Ets-2 [T(	1101	1109	8.339336	CTGCAG(	0.13733	0.13681
cg0541306	GALNTL2	PR B [T00	203	209	8.338824	CCCTGTT	1.09863	1.10009
cg0541306	GALNTL2	PR B [T00	666	672	8.338824	CCCTGTT	1.09863	1.10009
cg0541306	GALNTL2	PR B [T00	834	840	8.338824	AACAGG	1.09863	1.10009
cg0541306	GALNTL2	PR A [T01	203	209	8.338824	CCCTGTT	1.09863	1.10009
cg0541306	GALNTL2	PR A [T01	666	672	8.338824	CCCTGTT	1.09863	1.10009
cg0541306	GALNTL2	PR A [T01	834	840	8.338824	AACAGG	1.09863	1.10009
cg0541306	GALNTL2	ATF3 [T01	407	414	8.313799	TGACGT(	0.27466	0.27431
cg0541306	GALNTL2	PXR-1:RX	252	259	8.304332	AGTGTT(	0.12207	0.12266
cg0541306	GALNTL2	GR-alpha [	22	26	8.281568	CAAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	158	162	8.281568	GGAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	194	198	8.281568	GGAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	243	247	8.281568	CCTCC	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	324	328	8.281568	CAAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	341	345	8.281568	CCTCC	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	385	389	8.281568	GAAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	402	406	8.281568	CCTTG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	451	455	8.281568	CCTCC	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	476	480	8.281568	CCTCC	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	638	642	8.281568	GGAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	726	730	8.281568	CCTTC	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	768	772	8.281568	GAAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	894	898	8.281568	CCTCC	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	980	984	8.281568	CAAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	985	989	8.281568	GGAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	989	993	8.281568	GGAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	1316	1320	8.281568	CCTTG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	1362	1366	8.281568	GGAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	1527	1531	8.281568	CCTTG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	1603	1607	8.281568	CCTTC	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	1726	1730	8.281568	CCTTC	7.8125	7.72956

cg0541306	GALNTL2	GR-alpha [	1877	1881	8.281568	GAAGG	7.8125	7.72956
cg0541306	GALNTL2	GR-alpha [	1963	1967	8.281568	CAAGG	7.8125	7.72956
cg0541306	GALNTL2	NF-AT2 [T	1069	1078	8.245775	GCATTTT	0.08965	0.09068
cg0541306	GALNTL2	c-Ets-1 [T0	212	218	8.244941	GTGGAA	0.24414	0.2425
cg0541306	GALNTL2	IRF-1 [T0	941	949	8.242487	TTTAGGA	0.25177	0.25263
cg0541306	GALNTL2	c-Jun [T00	1363	1369	8.242207	GAGGTC	0.48828	0.49076
cg0541306	GALNTL2	NFI/CTF [	1571	1578	8.241664	TTGGTTC	0.18311	0.1823
cg0541306	GALNTL2	ENKTF-1	972	979	8.19852	TGGCCA	0.73242	0.71737
cg0541306	GALNTL2	LEF-1 [T0	1344	1351	8.117221	ACTCAA	0.12207	0.1241
cg0541306	GALNTL2	GR-alpha [	105	109	8.073878	CCTGC	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	168	172	8.073878	GCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	189	193	8.073878	CCTGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	307	311	8.073878	CCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	373	377	8.073878	CCTGC	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	531	535	8.073878	CCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	548	552	8.073878	CCTAG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	563	567	8.073878	CCTGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	568	572	8.073878	CCTAG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	620	624	8.073878	CTAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	950	954	8.073878	CCTGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	975	979	8.073878	CCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1014	1018	8.073878	CCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1094	1098	8.073878	CCTGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1103	1107	8.073878	GCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1185	1189	8.073878	CCTGC	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1227	1231	8.073878	CCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1239	1243	8.073878	CCTGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1293	1297	8.073878	CCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1491	1495	8.073878	CCTGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1512	1516	8.073878	CCTAG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1612	1616	8.073878	CCTGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1665	1669	8.073878	CCTGC	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1669	1673	8.073878	CCAGG	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1692	1696	8.073878	CCTGC	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1717	1721	8.073878	CCTAC	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1755	1759	8.073878	CCTAC	7.8125	7.72238
cg0541306	GALNTL2	GR-alpha [	1914	1918	8.073878	GTAGG	7.8125	7.72238
cg0541306	GALNTL2	Pax-5 [T0	25	31	8.014558	GGGCAT	2.19727	2.14502
cg0541306	GALNTL2	Pax-5 [T0	860	866	8.014558	GGGCTG	2.19727	2.14502
cg0541306	GALNTL2	Pax-5 [T0	1288	1294	8.014558	TAAGCC	2.19727	2.14502
cg0541306	GALNTL2	Pax-5 [T0	1918	1924	8.014558	GGGCTC	2.19727	2.14502
cg0541306	GALNTL2	Pax-5 [T0	1981	1987	8.014558	GGGCAG	2.19727	2.14502
cg0541306	GALNTL2	TFIID [T0	904	910	8.014558	TTTGATA	2.19727	2.24348
cg0541306	GALNTL2	TFIID [T0	943	949	8.014558	TAGGAA	2.19727	2.24348
cg0541306	GALNTL2	TFIID [T0	1074	1080	8.014558	TTTCCAA	2.19727	2.24348
cg0541306	GALNTL2	c-Jun [T00	1513	1519	7.937147	CTAGTCA	0.48828	0.49076
cg0541306	GALNTL2	c-Ets-2 [T0	697	705	7.84116	TTCCTGA	0.32043	0.32298
cg0541306	GALNTL2	c-Myb [T0	642	649	7.825375	GAACTT	0.21362	0.21454

cg0541306	GALNTL2	c-Myb [T0	1077	1084	7.825375	CCAAGT	0.21362	0.21454
cg0541306	GALNTL2	IRF-1 [T0	1102	1110	7.82345	TGCAGG	0.25177	0.25263
cg0541306	GALNTL2	c-Ets-2 [T	1325	1333	7.76635	TTCCTGT	0.32043	0.32298
cg0541306	GALNTL2	c-Myb [T0	571	578	7.662426	AGAAGT	0.42725	0.43114
cg0541306	GALNTL2	p53 [T006	1524	1530	7.641867	GGGCCT	0.73242	0.7186
cg0541306	GALNTL2	p53 [T006	1642	1648	7.641867	GGGCCT	0.73242	0.7186
cg0541306	GALNTL2	ELF-1 [T0	693	705	7.62178	ACACTT	0.00846	0.00852
cg0541306	GALNTL2	LEF-1 [T0	1307	1314	7.6105	GTCCAA	0.21362	0.21302
cg0541306	GALNTL2	NFI/CTF [	1063	1070	7.587343	CCAAAT	0.36621	0.36674
cg0541306	GALNTL2	GATA-3 [	864	875	7.563095	TGAGAT	0.0056	0.00566
cg0541306	GALNTL2	c-Jun [T00	407	413	7.538568	TGACGT	0.48828	0.48775
cg0541306	GALNTL2	GR [T050	737	743	7.527031	CAAATA	1.83105	1.86007
cg0541306	GALNTL2	GR [T050	832	838	7.527031	CAAACA	1.83105	1.86007
cg0541306	GALNTL2	GR [T050	1885	1891	7.527031	CATTTC	1.83105	1.86007
cg0541306	GALNTL2	p53 [T006	1835	1841	7.47855	GGGCTA	0.73242	0.7186
cg0541306	GALNTL2	RAR-beta:	1918	1929	7.477995	GGGCTC	0.02861	0.02796
cg0541306	GALNTL2	IRF-1 [T0	1921	1929	7.477948	CTCAGG	0.14496	0.14449
cg0541306	GALNTL2	C/EBPalph	632	638	7.465744	TGCAAT	0.48828	0.49653
cg0541306	GALNTL2	C/EBPalph	1027	1033	7.465744	TGCAAT	0.48828	0.49653
cg0541306	GALNTL2	p53 [T006	889	895	7.458735	GGGCGC	0.73242	0.7186
cg0541306	GALNTL2	NF-1 [T00	1897	1904	7.445595	TATCCC	0.24414	0.24565
cg0541306	GALNTL2	PEA3 [T0	1057	1065	7.421728	CATCAT	0.34332	0.34161
cg0541306	GALNTL2	PEA3 [T0	1259	1267	7.421728	CAACAT	0.34332	0.34161
cg0541306	GALNTL2	LEF-1 [T0	376	383	7.396545	GCACAA	0.21362	0.21302
cg0541306	GALNTL2	p53 [T006	1311	1317	7.266844	AAAGCC	0.73242	0.7186
cg0541306	GALNTL2	p53 [T006	1708	1714	7.266844	GGGCTG	0.73242	0.7186
cg0541306	GALNTL2	c-Ets-1 [T	1630	1636	7.199436	TTTCCCA	0.73242	0.73099
cg0541306	GALNTL2	SRY [T00	375	383	7.175614	TGCACA	0.30518	0.30739
cg0541306	GALNTL2	XBP-1 [T	4	9	7.172312	ATGAGG	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	234	239	7.172312	CTTCAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	503	508	7.172312	CTTCAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1039	1044	7.172312	ACTCAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1057	1062	7.172312	CATCAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1457	1462	7.172312	CCTCAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1536	1541	7.172312	ATGATG	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1566	1571	7.172312	CCTCAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1591	1596	7.172312	ATGAAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1680	1685	7.172312	ATTCAT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1791	1796	7.172312	ATGATT	2.92969	2.97018
cg0541306	GALNTL2	XBP-1 [T	1882	1887	7.172312	CTTCAT	2.92969	2.97018
cg0541306	GALNTL2	AR [T000	410	418	7.15496	CGTCTGT	0.23651	0.23551
cg0541306	GALNTL2	NF-AT1 [	1106	1114	7.095752	GGAAAA	0.15259	0.1548
cg0541306	GALNTL2	AR [T000	33	41	7.049779	GGACAC	0.23651	0.23551
cg0541306	GALNTL2	NFI/CTF [	789	796	7.014249	CCAACC	0.73242	0.73214
cg0541306	GALNTL2	AR [T000	1812	1820	6.976688	GGACAT	0.23651	0.23551
cg0541306	GALNTL2	IRF-1 [T0	1630	1638	6.968314	TTTCCCA	0.1297	0.13036
cg0541306	GALNTL2	RXR-alph	70	76	6.967687	ACCACC	0.36621	0.36214
cg0541306	GALNTL2	NF-1 [T00	646	653	6.948522	TTGGCT	0.48828	0.4856

cg0541306	GALNTL2	NF-1 [T00	785	792	6.948522	AGCCCC	0.48828	0.4856
cg0541306	GALNTL2	NF-1 [T00	1521	1528	6.948522	TTGGGG	0.48828	0.4856
cg0541306	GALNTL2	c-Ets-1 [T	1853	1859	6.943262	TTTCCCC	0.73242	0.73099
cg0541306	GALNTL2	ENKTF-1	1014	1021	6.942764	CCAGGC	1.46484	1.44228
cg0541306	GALNTL2	ENKTF-1	1551	1558	6.942764	CTTTGCC	1.46484	1.44228
cg0541306	GALNTL2	VDR [T00	255	263	6.925682	GTTCAG	0.42725	0.43062
cg0541306	GALNTL2	VDR [T00	1960	1968	6.925682	GTTCAA	0.42725	0.43062
cg0541306	GALNTL2	STAT1bet	1599	1608	6.908963	CTTTCCT	0.103	0.10372
cg0541306	GALNTL2	PEA3 [T0	503	511	6.824411	CTTCATC	0.22888	0.22933
cg0541306	GALNTL2	AR [T000	1325	1333	6.817719	TTCCTGT	0.23651	0.23551
cg0541306	GALNTL2	p53 [T006	1918	1924	6.778774	GGGCTC	1.09863	1.07125
cg0541306	GALNTL2	c-Ets-2 [T	1610	1618	6.769996	TTCCTGC	0.03052	0.03102
cg0541306	GALNTL2	AR [T000	196	204	6.723093	AGGCTG	0.19836	0.19597
cg0541306	GALNTL2	c-Ets-2 [T	906	914	6.695187	TGATAG	0.09155	0.09289
cg0541306	GALNTL2	PXR-1:RX	1957	1964	6.668182	TGTGTTC	0.24414	0.24672
cg0541306	GALNTL2	TFII-I [T0	1162	1167	6.581441	GGAGTG	0.97656	0.97366
cg0541306	GALNTL2	FOXP3 [T	1438	1443	6.581441	GTTGAA	0.97656	0.99397
cg0541306	GALNTL2	RXR-alph	778	784	6.563693	AATACC	0.24414	0.2434
cg0541306	GALNTL2	PXR-1:RX	733	740	6.5446	TGAACA	0.24414	0.24672
cg0541306	GALNTL2	PXR-1:RX	1354	1361	6.5446	TGAACA	0.24414	0.24672
cg0541306	GALNTL2	XBP-1 [T	25	30	6.478682	GGGCAT	0.97656	0.97062
cg0541306	GALNTL2	XBP-1 [T	304	309	6.478682	ATGCCA	0.97656	0.97062
cg0541306	GALNTL2	XBP-1 [T	393	398	6.478682	TGGCAT	0.97656	0.97062
cg0541306	GALNTL2	XBP-1 [T	1620	1625	6.478682	ATGCCA	0.97656	0.97062
cg0541306	GALNTL2	c-Fos [T00	1033	1042	6.448203	GCTGTG	0.04578	0.04589
cg0541306	GALNTL2	c-Ets-1 [T	1074	1080	6.423689	TTTCCA	0.48828	0.48798
cg0541306	GALNTL2	TCF-4E [T	1356	1362	6.302385	AACAAA	0.61035	0.61344
cg0541306	GALNTL2	TCF-4E [T	1551	1557	6.302385	CTTTGCC	0.61035	0.61344
cg0541306	GALNTL2	GR-alpha [	5	9	6.263098	TGAGG	3.90625	3.91061
cg0541306	GALNTL2	GR-alpha [	518	522	6.263098	TAAGG	3.90625	3.91061
cg0541306	GALNTL2	GR-alpha [	523	527	6.263098	CCTCA	3.90625	3.91061
cg0541306	GALNTL2	GR-alpha [	556	560	6.263098	CCTCA	3.90625	3.91061
cg0541306	GALNTL2	GR-alpha [	1457	1461	6.263098	CCTCA	3.90625	3.91061
cg0541306	GALNTL2	GR-alpha [	1566	1570	6.263098	CCTCA	3.90625	3.91061
cg0541306	GALNTL2	GR-alpha [	1645	1649	6.263098	CCTTA	3.90625	3.91061
cg0541306	GALNTL2	NF-AT1 [	1596	1604	6.253078	TGTCTTT	0.03815	0.03835
cg0541306	GALNTL2	C/EBPalp	745	751	6.245236	TATTGA	0.97656	0.99
cg0541306	GALNTL2	c-Myb [T0	685	692	6.157321	CAACTT	0.21362	0.21535
cg0541306	GALNTL2	RXR-alph	1717	1723	6.119461	CCTACC	0.73242	0.72249
cg0541306	GALNTL2	RXR-alph	1912	1918	6.119461	GGGTAG	0.73242	0.72249
cg0541306	GALNTL2	c-Fos [T00	262	271	6.103724	CCAGTG	0.09155	0.09126
cg0541306	GALNTL2	HNF-1B [	1463	1471	6.086797	TATTTA	0.09918	0.10196
cg0541306	GALNTL2	IRF-1 [T0	1074	1082	6.078807	TTTCCA	0.16785	0.16909
cg0541306	GALNTL2	GR-alpha [	208	212	6.055408	TTAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	333	337	6.055408	CCTGA	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	558	562	6.055408	TCAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	699	703	6.055408	CCTGA	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	857	861	6.055408	TCAGG	3.90625	3.9065

cg0541306	GALNTL2	GR-alpha [	942	946	6.055408	TTAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1202	1206	6.055408	TTAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1280	1284	6.055408	TTAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1367	1371	6.055408	TCAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1729	1733	6.055408	TCAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1831	1835	6.055408	TTAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1848	1852	6.055408	TTAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1858	1862	6.055408	CCTAA	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1870	1874	6.055408	CCTGA	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1922	1926	6.055408	TCAGG	3.90625	3.9065
cg0541306	GALNTL2	GR-alpha [	1944	1948	6.055408	CCTGA	3.90625	3.9065
cg0541306	GALNTL2	C/EBPalph	1569	1575	5.996794	CATTGG	0.97656	0.99
cg0541306	GALNTL2	PXR-1:RX	335	342	5.850108	TGAACC	0.06104	0.06035
cg0541306	GALNTL2	RBP-Jkapp	585	596	5.820496	TGTTCCC	0.00572	0.00572
cg0541306	GALNTL2	PU.1 [T02	693	705	5.775822	ACACTT	0.00432	0.00433
cg0541306	GALNTL2	VDR [T00	292	300	5.771401	GTTCAG	0.42725	0.42999
cg0541306	GALNTL2	VDR [T00	331	339	5.771401	CCCCTG	0.42725	0.42999
cg0541306	GALNTL2	VDR [T00	710	718	5.771401	GTTCAG	0.42725	0.42999
cg0541306	GALNTL2	VDR [T00	1541	1549	5.771401	GTTCAA	0.42725	0.42999
cg0541306	GALNTL2	IRF-1 [T0	1853	1861	5.770812	TTTCCCC	0.16785	0.16909
cg0541306	GALNTL2	HNF-1C [	1462	1470	5.695506	TTATTTA	0.07629	0.07817
cg0541306	GALNTL2	ENKTF-1	565	572	5.687009	TGGCCT	0.73242	0.7249
cg0541306	GALNTL2	ENKTF-1	647	654	5.687009	TGGCTCT	0.73242	0.7249
cg0541306	GALNTL2	ENKTF-1	1051	1058	5.687009	CAGAGC	0.73242	0.7249
cg0541306	GALNTL2	ENKTF-1	1576	1583	5.687009	TGGCTC	0.73242	0.7249
cg0541306	GALNTL2	ENKTF-1	1737	1744	5.687009	TGGCTTT	0.73242	0.7249
cg0541306	GALNTL2	c-Ets-1 [T	991	997	5.686398	AGGGAA	0.36621	0.3623
cg0541306	GALNTL2	AR [T000	1230	1238	5.644986	GGACAC	0.05341	0.05229
cg0541306	GALNTL2	c-Jun [T00	998	1004	5.590308	AGCGTC	0.48828	0.48665
cg0541306	GALNTL2	AP-2alpha	238	243	5.568965	ATAGGC	0.48828	0.4878
cg0541306	GALNTL2	AP-2alpha	876	881	5.568965	GCCTAT	0.48828	0.4878
cg0541306	GALNTL2	NFI/CTF [	361	368	5.558661	GAGTTT	0.54932	0.55038
cg0541306	GALNTL2	NFI/CTF [	800	807	5.558661	AAGCTT	0.54932	0.55038
cg0541306	GALNTL2	Pax-5 [T0	1835	1841	5.544826	GGGCTA	0.73242	0.72046
cg0541306	GALNTL2	TFIID [T0	941	947	5.544826	TTTAGG	0.73242	0.75085
cg0541306	GALNTL2	TFIID [T0	1465	1471	5.544826	TTTAAC	0.73242	0.75085
cg0541306	GALNTL2	p53 [T006	860	866	5.508538	GGGCTG	0.61035	0.59991
cg0541306	GALNTL2	p53 [T006	1288	1294	5.508538	TAAGCC	0.61035	0.59991
cg0541306	GALNTL2	C/EBPalph	1582	1588	5.455853	AGCAAT	0.73242	0.74391
cg0541306	GALNTL2	RAR-beta	333	342	5.389083	CCTGAA	0.15259	0.15189
cg0541306	GALNTL2	C/EBPalph	604	610	5.38654	ACCAAT	0.73242	0.74391
cg0541306	GALNTL2	IRF-1 [T0	1600	1608	5.309227	TTTCCTT	0.22888	0.23087
cg0541306	GALNTL2	RXR-alpha	1371	1377	5.271235	GGGTGG	0.61035	0.6044
cg0541306	GALNTL2	RXR-alpha	1721	1727	5.271235	CCCACC	0.61035	0.6044
cg0541306	GALNTL2	GR [T050	78	84	5.207533	GTCTTTC	0.24414	0.24606
cg0541306	GALNTL2	GR [T050	1377	1383	5.207533	GGTTTTC	0.24414	0.24606
cg0541306	GALNTL2	c-Myb [T0	912	919	5.137438	GAACTG	0.30518	0.30568
cg0541306	GALNTL2	NF-AT1 [	1070	1078	5.125037	CATTTTT	0.05341	0.05402

cg0541306	GALNTL2	AP-2alpha	1549	1554	5.100982	GCCTTT	0.97656	0.97567
cg0541306	GALNTL2	USF2 [T0	1659	1668	5.052423	GTGACA	0.103	0.10178
cg0541306	GALNTL2	AP-1 [T00	266	274	5.043062	TGACTC	0.12207	0.12162
cg0541306	GALNTL2	AP-1 [T00	916	924	5.043062	TGGGAG	0.12207	0.12162
cg0541306	GALNTL2	GR-beta [T	623	627	5.042296	GGATT	3.90625	3.95351
cg0541306	GALNTL2	GR-beta [T	657	661	5.042296	GGATT	3.90625	3.95351
cg0541306	GALNTL2	GR-beta [T	778	782	5.042296	AATAC	3.90625	3.95351
cg0541306	GALNTL2	GR-beta [T	1224	1228	5.042296	AATCC	3.90625	3.95351
cg0541306	GALNTL2	GR-beta [T	1284	1288	5.042296	GGATT	3.90625	3.95351
cg0541306	GALNTL2	EBF [T05	1236	1246	5.026987	ACCCCT	0.02289	0.02224
cg0541306	GALNTL2	C/EBPalph	1221	1227	5.024728	TTCAAT	0.97656	0.99332
cg0541306	GALNTL2	c-Jun [T00	1660	1666	5.000337	TGACAC	0.61035	0.61057
cg0541306	GALNTL2	c-Myb [T0	113	120	4.974489	CAACTG	0.30518	0.30568
cg0541306	GALNTL2	PXR-1:RX	16	23	4.90845	ATGGTT	0.12207	0.12266
cg0541306	GALNTL2	XBP-1 [T	1671	1676	4.894955	AGGCAT	0.97656	0.96979
cg0541306	GALNTL2	XBP-1 [T	1941	1946	4.894955	ATGCCT	0.97656	0.96979
cg0541306	GALNTL2	XBP-1 [T	1952	1957	4.894955	AGGCAT	0.97656	0.96979
cg0541306	GALNTL2	AR [T000	535	543	4.890444	GCTGTG	0.11444	0.11247
cg0541306	GALNTL2	AR [T000	1710	1718	4.890444	GCTGTG	0.11444	0.11247
cg0541306	GALNTL2	AP-2alpha	1202	1207	4.890408	TTAGGC	0.97656	0.97567
cg0541306	GALNTL2	C/EBPalph	1468	1474	4.776286	AACAAT	0.97656	0.99332
cg0541306	GALNTL2	TFII-I [T0	1223	1228	4.756447	CAATCC	2.92969	2.93695
cg0541306	GALNTL2	TFII-I [T0	1429	1434	4.756447	GGATAT	2.92969	2.93695
cg0541306	GALNTL2	TFII-I [T0	1683	1688	4.756447	CATTCC	2.92969	2.93695
cg0541306	GALNTL2	TFII-I [T0	1812	1817	4.756447	GGACAT	2.92969	2.93695
cg0541306	GALNTL2	FOXP3 [T	111	116	4.756447	ATCAAC	2.92969	2.96063
cg0541306	GALNTL2	FOXP3 [T	932	937	4.756447	CAAAAC	2.92969	2.96063
cg0541306	GALNTL2	FOXP3 [T	1257	1262	4.756447	ATCAAC	2.92969	2.96063
cg0541306	GALNTL2	FOXP3 [T	1297	1302	4.756447	GTTGAT	2.92969	2.96063
cg0541306	GALNTL2	FOXP3 [T	1378	1383	4.756447	GTTTTG	2.92969	2.96063
cg0541306	GALNTL2	FOXP3 [T	1474	1479	4.756447	AAAAAC	2.92969	2.96063
cg0541306	GALNTL2	PPAR-alph	538	548	4.727619	GTGTCC	0.03242	0.03183
cg0541306	GALNTL2	VDR [T00	19	27	4.617121	GTTCAA	0.37384	0.37445
cg0541306	GALNTL2	VDR [T00	729	737	4.617121	TCAGTG	0.37384	0.37445
cg0541306	GALNTL2	VDR [T00	744	752	4.617121	CTATTG	0.37384	0.37445
cg0541306	GALNTL2	c-Ets-2 [T	724	732	4.589988	TTCCTTC	0.06866	0.06881
cg0541306	GALNTL2	c-Ets-2 [T	1601	1609	4.589988	TTCCTTC	0.06866	0.06881
cg0541306	GALNTL2	MAZ [T00	984	996	4.524062	GGGAGG	0.00188	0.00184
cg0541306	GALNTL2	AP-2alpha	567	572	4.438035	GCCTAG	0.97656	0.96979
cg0541306	GALNTL2	AP-2alpha	518	523	4.422424	TAAGGC	0.97656	0.96979
cg0541306	GALNTL2	AP-2alpha	1644	1649	4.422424	GCCTTA	0.97656	0.96979
cg0541306	GALNTL2	STAT4 [T	722	727	4.411765	TCTTCC	1.95312	1.94235
cg0541306	GALNTL2	STAT4 [T	993	998	4.411765	GGAAGA	1.95312	1.94235
cg0541306	GALNTL2	STAT4 [T	1487	1492	4.411765	TCTTCC	1.95312	1.94235
cg0541306	GALNTL2	STAT4 [T	1683	1688	4.411765	CATTCC	1.95312	1.94235
cg0541306	GALNTL2	HOXD9 [T	1471	1480	4.321431	AATAAA	0.03433	0.03596
cg0541306	GALNTL2	HOXD10 [	1471	1480	4.321431	AATAAA	0.03433	0.03596
cg0541306	GALNTL2	C/EBPalph	775	781	4.235345	AGCAAT	0.48828	0.49358

cg0541306	GALNTL	GR-beta [T	445	449	4.201913	AATCA	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	739	743	4.201913	AATAG	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	744	748	4.201913	CTATT	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	901	905	4.201913	TGATT	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1299	1303	4.201913	TGATT	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1462	1466	4.201913	TTATT	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1471	1475	4.201913	AATAA	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1743	1747	4.201913	TGATT	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1787	1791	4.201913	AATAA	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1792	1796	4.201913	TGATT	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1808	1812	4.201913	AATAG	7.8125	7.94607
cg0541306	GALNTL	GR-beta [T	1828	1832	4.201913	CTATT	7.8125	7.94607
cg0541306	GALNTL	NF-1 [T00	1575	1582	4.135372	TTGGCT	0.24414	0.24154
cg0541306	GALNTL	TCF-4 [T0	1343	1352	4.102712	CACTCA	0.01144	0.01138
cg0541306	GALNTL	PXR-1:RX	289	296	4.090374	CTGGTT	0.12207	0.12119
cg0541306	GALNTL	SRY [T00	1740	1748	4.087393	CTTTGA	0.12207	0.12407
cg0541306	GALNTL	RXR-alph	1114	1120	4.019014	GGGTGT	0.97656	0.9671
cg0541306	GALNTL	RXR-alph	1233	1239	4.019014	CACACC	0.97656	0.9671
cg0541306	GALNTL	Pax-5 [T0	1311	1317	4.007279	AAAGCC	1.09863	1.07975
cg0541306	GALNTL	Pax-5 [T0	1524	1530	4.007279	GGGCCT	1.09863	1.07975
cg0541306	GALNTL	Pax-5 [T0	1642	1648	4.007279	GGGCCT	1.09863	1.07975
cg0541306	GALNTL	Pax-5 [T0	1708	1714	4.007279	GGGCTG	1.09863	1.07975
cg0541306	GALNTL	TFIID [T0	1413	1419	4.007279	TAGTAA	1.09863	1.13456
cg0541306	GALNTL	TFIID [T0	1533	1539	4.007279	TTTATG	1.09863	1.13456
cg0541306	GALNTL	TFIID [T0	1805	1811	4.007279	TTTAAT	1.09863	1.13456
cg0541306	GALNTL	MAZ [T00	980	992	3.973255	CAAGGG	0.00587	0.00576
cg0541306	GALNTL	AP-2alpha	1526	1531	3.970052	GCCTTG	0.97656	0.96469
cg0541306	GALNTL	AP-2alpha	1963	1968	3.970052	CAAGGC	0.97656	0.96469
cg0541306	GALNTL	c-Ets-1 [T	909	915	3.846637	TAGGAA	0.24414	0.24526
cg0541306	GALNTL	AR [T000	1383	1391	3.814754	GGACAC	0.06866	0.06828
cg0541306	GALNTL	NFI/CTF [	1314	1321	3.793671	GCCCTT	0.18311	0.18109
cg0541306	GALNTL	GR [T050	379	385	3.763516	CAAAGA	0.73242	0.74251
cg0541306	GALNTL	GR [T050	932	938	3.763516	CAAAAC	0.73242	0.74251
cg0541306	GALNTL	p53 [T006	466	472	3.750231	CCAGCC	0.73242	0.71379
cg0541306	GALNTL	p53 [T006	543	549	3.750231	CCAGCC	0.73242	0.71379
cg0541306	GALNTL	p53 [T006	783	789	3.750231	CCAGCC	0.73242	0.71379
cg0541306	GALNTL	p53 [T006	1242	1248	3.750231	GGGCTG	0.73242	0.71379
cg0541306	GALNTL	p53 [T006	1623	1629	3.750231	CCAGCC	0.73242	0.71379
cg0541306	GALNTL	AP-2alpha	1877	1882	3.743866	GAAGGC	0.48828	0.48238
cg0541306	GALNTL	PEA3 [T0	1350	1358	3.710864	AGGATG	0.09155	0.09258
cg0541306	GALNTL	PEA3 [T0	1756	1764	3.710864	CTACAT	0.09155	0.09258
cg0541306	GALNTL	c-Ets-1 [T	639	645	3.590463	GAGGAA	0.61035	0.60765
cg0541306	GALNTL	VDR [T00	1081	1089	3.462841	GTTCAC	0.21362	0.21341
cg0541306	GALNTL	VDR [T00	1350	1358	3.462841	AGGATG	0.21362	0.21341
cg0541306	GALNTL	c-Ets-1 [T	1324	1330	3.462376	GTTCCT	0.61035	0.60765
cg0541306	GALNTL	c-Ets-1 [T	1609	1615	3.462376	GTTCCT	0.61035	0.60765
cg0541306	GALNTL	RXR-alph	84	90	3.392904	GGGTTA	1.09863	1.08572
cg0541306	GALNTL	Elk-1 [T00	696	704	3.381796	CTTCCT	0.04578	0.04588

cg0541306	GALNTL2	GR-beta [T	673	677	3.361531	AATCT	3.90625	3.99611
cg0541306	GALNTL2	GR-beta [T	1210	1214	3.361531	AGATT	3.90625	3.99611
cg0541306	GALNTL2	GR-beta [T	1419	1423	3.361531	AATAT	3.90625	3.99611
cg0541306	GALNTL2	GR-beta [T	1420	1424	3.361531	ATATT	3.90625	3.99611
cg0541306	GALNTL2	GR-beta [T	1431	1435	3.361531	ATATT	3.90625	3.99611
cg0541306	GALNTL2	AP-2alpha	42	47	3.229049	AGAGGC	0.48828	0.48238
cg0541306	GALNTL2	AP-2alpha	1652	1657	3.229049	AGAGGC	0.48828	0.48238
cg0541306	GALNTL2	AP-2alpha	1950	1955	3.229049	AGAGGC	0.48828	0.48238
cg0541306	GALNTL2	RXR-alpha	1376	1382	3.170788	GGGTTTT	0.24414	0.24522
cg0541306	GALNTL2	TCF-4E [T	1740	1746	3.151193	CTTTGAT	0.24414	0.24672
cg0541306	GALNTL2	TFIID [T0	125	131	3.075094	TTTTGCA	0.12207	0.12409
cg0541306	GALNTL2	STAT4 [T	472	477	2.941176	CTTTCC	2.92969	2.929
cg0541306	GALNTL2	STAT4 [T	585	590	2.941176	TGTTCC	2.92969	2.929
cg0541306	GALNTL2	STAT4 [T	695	700	2.941176	ACTTCC	2.92969	2.929
cg0541306	GALNTL2	STAT4 [T	1323	1328	2.941176	TGTTCC	2.92969	2.929
cg0541306	GALNTL2	STAT4 [T	1599	1604	2.941176	CTTTCC	2.92969	2.929
cg0541306	GALNTL2	STAT4 [T	1629	1634	2.941176	CTTTCC	2.92969	2.929
cg0541306	GALNTL2	STAT4 [T	1925	1930	2.941176	GGAAAG	2.92969	2.929
cg0541306	GALNTL2	p53 [T006	1981	1987	2.813291	GGGCAG	0.48828	0.47786
cg0541306	GALNTL2	PR B [T00	1468	1474	2.80933	AACAAT	0.73242	0.74818
cg0541306	GALNTL2	PR A [T01	1468	1474	2.80933	AACAAT	0.73242	0.74818
cg0541306	GALNTL2	RXR-alpha	789	795	2.726556	CCAACC	0.85449	0.84796
cg0541306	GALNTL2	c-Ets-2 [T	636	644	2.715313	ATGGAG	0.07629	0.07593
cg0541306	GALNTL2	c-Jun [T00	266	272	2.654872	TGACTC	0.48828	0.48929
cg0541306	GALNTL2	c-Jun [T00	918	924	2.654872	GGAGTC	0.48828	0.48929
cg0541306	GALNTL2	AP-2alpha	522	527	2.550491	GCCTCA	0.48828	0.48266
cg0541306	GALNTL2	AP-2alpha	555	560	2.550491	GCCTCA	0.48828	0.48266
cg0541306	GALNTL2	AP-2alpha	1456	1461	2.550491	GCCTCA	0.48828	0.48266
cg0541306	GALNTL2	AP-2alpha	1565	1570	2.550491	GCCTCA	0.48828	0.48266
cg0541306	GALNTL2	RXR-alpha	807	813	2.544678	GGGTGC	0.85449	0.84796
cg0541306	GALNTL2	RAR-beta:	330	341	2.492665	TCCCCTC	0.00215	0.00209
cg0541306	GALNTL2	NF-Y [T0	602	609	2.420868	CCACCA	0.21362	0.21485
cg0541306	GALNTL2	c-Jun [T00	1394	1400	2.345465	TGACAC	0.48828	0.48929
cg0541306	GALNTL2	Elk-1 [T00	1488	1496	2.299314	CTTCCTC	0.09155	0.09114
cg0541306	GALNTL2	GATA-2 [	866	874	2.222222	AGATAG	0.22888	0.23091
cg0541306	GALNTL2	GATA-1 [	926	931	2.001358	TATCCC	3.90625	3.92756
cg0541306	GALNTL2	GATA-1 [	1214	1219	2.001358	TATCCC	3.90625	3.92756
cg0541306	GALNTL2	GATA-1 [	1897	1902	2.001358	TATCCC	3.90625	3.92756
cg0541306	GALNTL2	GATA-1 [	879	884	1.896347	TATCCG	3.90625	3.92756
cg0541306	GALNTL2	GATA-1 [	1428	1433	1.896347	CGGATA	3.90625	3.92756
cg0541306	GALNTL2	ATF-2 [T0	406	415	1.87457	GTGACG	0.01144	0.01128
cg0541306	GALNTL2	AP-2alpha	194	199	1.871933	GGAGGC	0.97656	0.95407
cg0541306	GALNTL2	AP-2alpha	242	247	1.871933	GCCTCC	0.97656	0.95407
cg0541306	GALNTL2	AP-2alpha	450	455	1.871933	GCCTCC	0.97656	0.95407
cg0541306	GALNTL2	AP-2alpha	893	898	1.871933	GCCTCC	0.97656	0.95407
cg0541306	GALNTL2	TFII-I [T0	40	45	1.824994	GGAGAG	0.48828	0.48408
cg0541306	GALNTL2	c-Ets-1 [T	943	949	1.769212	TAGGAA	0.12207	0.12414
cg0541306	GALNTL2	p53 [T006	25	31	1.758307	GGGCAT	0.36621	0.36261

cg0541306	GALNTL2	GR-beta [T	1030	1034	1.680765	AATGC	3.90625	3.94936
cg0541306	GALNTL2	GR-beta [T	1066	1070	1.680765	AATGC	3.90625	3.94936
cg0541306	GALNTL2	GR-beta [T	1069	1073	1.680765	GCATT	3.90625	3.94936
cg0541306	GALNTL2	GR-beta [T	1585	1589	1.680765	AATGC	3.90625	3.94936
cg0541306	GALNTL2	c-Ets-2 [T	474	482	1.64415	TTCCTCC	0.04578	0.04579
cg0541306	GALNTL2	c-Ets-1 [T	1600	1606	1.641124	TTTCCTT	0.36621	0.36952
cg0541306	GALNTL2	C/EBPbeta	61	64	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	82	85	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	226	229	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	323	326	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	365	368	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	576	579	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	590	593	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	605	608	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	646	649	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	684	687	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	789	792	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	795	798	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	804	807	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	931	934	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1063	1066	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1077	1080	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1160	1163	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1272	1275	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1309	1312	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1318	1321	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1381	1384	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1521	1524	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1571	1574	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1575	1578	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1736	1739	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1796	1799	1.639871	TTGG	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1901	1904	1.639871	CCAA	15.625	15.72563
cg0541306	GALNTL2	XBP-1 [T	101	106	1.583727	ATGACC	0.97656	0.98146
cg0541306	GALNTL2	XBP-1 [T	430	435	1.583727	ATGACA	0.97656	0.98146
cg0541306	GALNTL2	XBP-1 [T	1676	1681	1.583727	TGTCAT	0.97656	0.98146
cg0541306	GALNTL2	TFIID [T0	1073	1079	1.537547	TTTTCCA	0.73242	0.75096
cg0541306	GALNTL2	TFIID [T0	1379	1385	1.537547	TTTTGGA	0.73242	0.75096
cg0541306	GALNTL2	c-Ets-1 [T	473	479	1.513038	TTTCCTC	0.36621	0.36952
cg0541306	GALNTL2	STAT4 [T	214	219	1.470588	GGAACT	1.95312	1.96333
cg0541306	GALNTL2	STAT4 [T	641	646	1.470588	GGAACT	1.95312	1.96333
cg0541306	GALNTL2	STAT4 [T	911	916	1.470588	GGAACT	1.95312	1.96333
cg0541306	GALNTL2	STAT4 [T	945	950	1.470588	GGAAAC	1.95312	1.96333
cg0541306	GALNTL2	STAT4 [T	1073	1078	1.470588	TTTTCC	1.95312	1.96333
cg0541306	GALNTL2	STAT4 [T	1106	1111	1.470588	GGAAAA	1.95312	1.96333
cg0541306	GALNTL2	STAT4 [T	1608	1613	1.470588	AGTTCC	1.95312	1.96333
cg0541306	GALNTL2	STAT4 [T	1852	1857	1.470588	GTTTCC	1.95312	1.96333
cg0541306	GALNTL2	TCF-4 [T0	1739	1748	1.461318	GCTTTGA	0.04578	0.04635

cg0541306	GALNTL2	PR B [T00	251	257	1.404665	CAGTGTT	0.36621	0.37023
cg0541306	GALNTL2	PR A [T01	251	257	1.404665	CAGTGTT	0.36621	0.37023
cg0541306	GALNTL2	c-Ets-1 [T0	1104	1110	1.384951	CAGGAA	0.36621	0.36952
cg0541306	GALNTL2	c-Ets-1 [T0	1923	1929	1.384951	CAGGAA	0.36621	0.36952
cg0541306	GALNTL2	NF-AT1 [T	1070	1079	1.378139	CATTTTT	0.01907	0.0194
cg0541306	GALNTL2	C/EBPbeta	21	24	1.366559	TCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	112	115	1.366559	TCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	151	154	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	677	680	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	747	750	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	905	908	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1222	1225	1.366559	TCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1258	1261	1.366559	TCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1298	1301	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1303	1306	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1346	1349	1.366559	TCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1389	1392	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1439	1442	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1543	1546	1.366559	TCAA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1742	1745	1.366559	TTGA	15.625	15.72563
cg0541306	GALNTL2	C/EBPbeta	1962	1965	1.366559	TCAA	15.625	15.72563
cg0541306	GALNTL2	LEF-1 [T0	1740	1747	1.362541	CTTTGAT	0.09155	0.09326
cg0541306	GALNTL2	AP-2alpha	281	286	1.357116	GCCTGT	0.48828	0.48203
cg0541306	GALNTL2	AP-2alpha	433	438	1.357116	ACAGGC	0.48828	0.48203
cg0541306	GALNTL2	AP-2alpha	611	616	1.357116	ACAGGC	0.48828	0.48203
cg0541306	GALNTL2	AP-2alpha	835	840	1.357116	ACAGGC	0.48828	0.48203
cg0541306	GALNTL2	NF-Y [T0	1570	1577	1.285795	ATTGGTT	0.18311	0.18459
cg0541306	GALNTL2	CREB [T0	407	415	1.140913	TGACGTC	0.05341	0.05293
cg0541306	GALNTL2	GATA-1 [	110	115	1.038567	TATCAA	1.95312	1.98662
cg0541306	GALNTL2	GATA-1 [	905	910	1.038567	TTGATA	1.95312	1.98662
cg0541306	GALNTL2	GATA-1 [	1256	1261	1.038567	TATCAA	1.95312	1.98662
cg0541306	GALNTL2	SRY [T00	1354	1362	0.999172	TGAACA	0.06104	0.06205
cg0541306	GALNTL2	E2F-1 [T0	1329	1336	0.993583	TGTCCCC	0.03052	0.02978
cg0541306	GALNTL2	Elk-1 [T00	723	731	0.957025	CTTCCTT	0.03052	0.03057
cg0541306	GALNTL2	GR-beta [T	3	7	0.840383	AATGA	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	429	433	0.840383	AATGA	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	509	513	0.840383	CCATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	606	610	0.840383	CAATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	607	611	0.840383	AATTA	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	635	639	0.840383	AATGG	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1041	1045	0.840383	TCATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1277	1281	0.840383	TAATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1278	1282	0.840383	AATTA	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1459	1463	0.840383	TCATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1568	1572	0.840383	TCATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1678	1682	0.840383	TCATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1682	1686	0.840383	TCATT	7.8125	7.94706
cg0541306	GALNTL2	GR-beta [T	1790	1794	0.840383	AATGA	7.8125	7.94706

cg0541306	GALNTL2	GR-beta [T	1884	1888	0.840383	TCATT	7.8125	7.94706
cg0541306	GALNTL2	PXR-1:RX	707	714	0.818075	CAAGTT	0.12207	0.12266
cg0541306	GALNTL2	PXR-1:RX	1078	1085	0.818075	CAAGTT	0.12207	0.12266
cg0541306	GALNTL2	GATA-1 [	756	761	0.758539	TATCAG	1.95312	1.98662
cg0541306	GALNTL2	AP-2alpha	558	563	0.678558	TCAGGC	0.48828	0.48199
cg0541306	GALNTL2	AP-2alpha	1943	1948	0.678558	GCCTGA	0.48828	0.48199
cg0541306	GALNTL2	LEF-1 [T0	1355	1362	0.641865	GAACAA	0.06104	0.06131
cg0541306	GALNTL2	HNF-1A [	670	677	0.431647	GTTAAT	0.24414	0.24974
cg0541306	GALNTL2	c-Fos [T00	919	928	0.424029	GAGTCA	0.01144	0.01141
cg0541306	GALNTL2	AP-1 [T00	1037	1045	0.348957	TGACTC	0.09155	0.09215
cg0541306	GALNTL2	GATA-1 [	592	597	0.280028	AAGATA	0.97656	0.99875
cg0541306	GALNTL2	GATA-1 [	1170	1175	0.280028	AAGATA	0.97656	0.99875
cg0541306	GALNTL2	GATA-1 [	1839	1844	0.280028	TATCTT	0.97656	0.99875
cg0541306	GALNTL2	c-Ets-1 [T	723	729	0.256174	CTTCCTT	0.24414	0.24569
cg0541306	GALNTL2	AP-2alpha	188	193	0.226186	GCCTGG	0.97656	0.95305
cg0541306	GALNTL2	AP-2alpha	531	536	0.226186	CCAGGC	0.97656	0.95305
cg0541306	GALNTL2	AP-2alpha	562	567	0.226186	GCCTGG	0.97656	0.95305
cg0541306	GALNTL2	AP-2alpha	975	980	0.226186	CCAGGC	0.97656	0.95305
cg0541306	GALNTL2	AP-2alpha	1014	1019	0.226186	CCAGGC	0.97656	0.95305
cg0541306	GALNTL2	AP-2alpha	1669	1674	0.226186	CCAGGC	0.97656	0.95305
cg0541306	GALNTL2	GR-alpha [	42	46	0.207689	AGAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	296	300	0.207689	AGAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	471	475	0.207689	CCTTT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	961	965	0.207689	CCTTT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1111	1115	0.207689	AGAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1151	1155	0.207689	CCTCT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1218	1222	0.207689	CCTTT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1251	1255	0.207689	AAAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1348	1352	0.207689	AAAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1359	1363	0.207689	AAAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1498	1502	0.207689	CCTCT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1550	1554	0.207689	CCTTT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1628	1632	0.207689	CCTTT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1637	1641	0.207689	CCTCT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1652	1656	0.207689	AGAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1950	1954	0.207689	AGAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1974	1978	0.207689	CCTCT	7.8125	7.81264
cg0541306	GALNTL2	HNF-1A [	1463	1470	0.143882	TATTTA	0.24414	0.25261
cg0541306	GALNTL2	GATA-1 [	865	870	0.105011	GAGATA	0.97656	0.98738
cg0541306	GALNTL2	GATA-1 [	1409	1414	0.105011	GAGATA	0.97656	0.98738
cg0541306	GALNTL2	GR-alpha [	204	208	0	CCTGT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	238	242	0	ATAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	282	286	0	CCTGT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	433	437	0	ACAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	611	615	0	ACAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	667	671	0	CCTGT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	835	839	0	ACAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	877	881	0	CCTAT	7.8125	7.81264

cg0541306	GALNTL2	GR-alpha [	908	912	0	ATAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1085	1089	0	ACAGG	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1266	1270	0	CCTGT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1327	1331	0	CCTGT	7.8125	7.81264
cg0541306	GALNTL2	GR-alpha [	1809	1813	0	ATAGG	7.8125	7.81264
cg0541306	GALNTL2	AP-2alpha	1184	1189	0	GCCTGC	0.97656	0.95305
cg0541306	GALNTL2	RXR-alpha	335	341	0	TGAACC	0.24414	0.2444
cg0541306	GALNTL2	Pax-5 [T0	466	472	0	CCAGCC	1.09863	1.06846
cg0541306	GALNTL2	Pax-5 [T0	543	549	0	CCAGCC	1.09863	1.06846
cg0541306	GALNTL2	Pax-5 [T0	783	789	0	CCAGCC	1.09863	1.06846
cg0541306	GALNTL2	Pax-5 [T0	1242	1248	0	GGGCTG	1.09863	1.06846
cg0541306	GALNTL2	Pax-5 [T0	1623	1629	0	CCAGCC	1.09863	1.06846
cg0541306	GALNTL2	TFII-I [T0	199	204	0	CTGTCC	1.46484	1.45997
cg0541306	GALNTL2	TFII-I [T0	413	418	0	CTGTCC	1.46484	1.45997
cg0541306	GALNTL2	TFII-I [T0	472	477	0	CTTTCC	1.46484	1.45997
cg0541306	GALNTL2	TFII-I [T0	878	883	0	CTATCC	1.46484	1.45997
cg0541306	GALNTL2	TFII-I [T0	1328	1333	0	CTGTCC	1.46484	1.45997
cg0541306	GALNTL2	TFII-I [T0	1599	1604	0	CTTTCC	1.46484	1.45997
cg0541306	GALNTL2	TFII-I [T0	1629	1634	0	CTTTCC	1.46484	1.45997
cg0541306	GALNTL2	TFII-I [T0	1925	1930	0	GGAAAG	1.46484	1.45997
cg0541306	GALNTL2	c-Ets-1 [T	696	702	0	CTTCCTC	0.24414	0.2429
cg0541306	GALNTL2	c-Ets-1 [T	1488	1494	0	CTTCCTC	0.24414	0.2429
cg0541306	GALNTL2	YY1 [T00	16	19	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	31	34	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	156	159	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	220	223	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	392	395	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	423	426	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	480	483	0	CCAT	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	509	512	0	CCAT	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	581	584	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	636	639	0	ATGG	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	1019	1022	0	CCAT	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	1056	1059	0	CCAT	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	1556	1559	0	CCAT	7.8125	7.81711
cg0541306	GALNTL2	YY1 [T00	1823	1826	0	CCAT	7.8125	7.81711
cg0541306	GALNTL2	ER-alpha [	102	106	0	TGACC	1.95312	1.9404
cg0541306	GALNTL2	ER-alpha [	248	252	0	GGTCA	1.95312	1.9404
cg0541306	GALNTL2	ER-alpha [	1365	1369	0	GGTCA	1.95312	1.9404
cg0541306	GALNTL2	C/EBPbeta	127	130	0	TTGC	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	318	321	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	378	381	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	404	407	0	TTGT	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	489	492	0	TTGT	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	495	498	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	615	618	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	631	634	0	TTGC	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	633	636	0	GCAA	15.625	15.71349

cg0541306	GALNTL2	C/EBPbeta	680	683	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	706	709	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	736	739	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	751	754	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	776	779	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	827	830	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	831	834	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	979	982	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1028	1031	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1136	1139	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1322	1325	0	TTGT	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1357	1360	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1402	1405	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1469	1472	0	ACAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1529	1532	0	TTGC	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1553	1556	0	TTGC	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1583	1586	0	GCAA	15.625	15.71349
cg0541306	GALNTL2	C/EBPbeta	1889	1892	0	TTGC	15.625	15.71349
cg0541306	GALNTL2	c-Jun [T00	1037	1043	0	TGACTC	0.12207	0.12266
cg0541306	GALNTL2	FOXP3 [T	679	684	0	GACAAC	1.46484	1.47315
cg0541306	GALNTL2	FOXP3 [T	750	755	0	AACAAC	1.46484	1.47315
cg0541306	GALNTL2	FOXP3 [T	1321	1326	0	GTTGTT	1.46484	1.47315
cg0541306	GALNTL2	GR-beta [T	1482	1486	0	ACATT	3.90625	3.99611
cg0541306	GALNTL2	GR-beta [T	1594	1598	0	AATGT	3.90625	3.99611
cg0541306	GALNTL2	GR [T050	123	129	0	CTTTTTG	0.36621	0.37562
cg0541306	GALNTL2	IRF-2 [T01	120	125	0	TCACTT	0.48828	0.49387
cg0541306	GALNTL2	IRF-2 [T01	348	353	0	AAGTGA	0.48828	0.49387
cg0541306	GALNTL2	IRF-2 [T01	1517	1522	0	TCACTT	0.48828	0.49387
cg0541306	GALNTL2	TBP [T007	1170	1179	0	AAGATA	0.03052	0.03159
cg0932411	GEMIN8	HNF-1C [	1274	1282	9.996165	ATGCAT	0.10681	0.10839
cg0932411	GEMIN8	c-Ets-1 [T	1470	1476	9.969337	TGGGAA	0.24414	0.2459
cg0932411	GEMIN8	STAT5A [	1463	1475	9.952027	TACTTTC	0.01878	0.01918
cg0932411	GEMIN8	HNF-1B [	1660	1668	9.892991	ATATTA	0.12207	0.12399
cg0932411	GEMIN8	E2F [T002	34	43	9.822406	AGGCGC	0.06866	0.06777
cg0932411	GEMIN8	XBP-1 [T	43	48	9.789909	ATGTCT	1.95312	1.95208
cg0932411	GEMIN8	XBP-1 [T	145	150	9.789909	AGACAT	1.95312	1.95208
cg0932411	GEMIN8	XBP-1 [T	896	901	9.789909	ATGGCT	1.95312	1.95208
cg0932411	GEMIN8	XBP-1 [T	1575	1580	9.789909	ATGGCT	1.95312	1.95208
cg0932411	GEMIN8	NF-1 [T00	1396	1403	9.761671	AGAACC	0.24414	0.24405
cg0932411	GEMIN8	PR B [T00	235	241	9.743489	AACACG	1.09863	1.10292
cg0932411	GEMIN8	PR B [T00	1170	1176	9.743489	AACACC	1.09863	1.10292
cg0932411	GEMIN8	PR A [T01	235	241	9.743489	AACACG	1.09863	1.10292
cg0932411	GEMIN8	PR A [T01	1170	1176	9.743489	AACACC	1.09863	1.10292
cg0932411	GEMIN8	AhR:Arnt	756	765	9.738501	CGTGGC	0.17929	0.17456
cg0932411	GEMIN8	EBF [T05	652	662	9.652631	CGCGCA	0.06866	0.06676
cg0932411	GEMIN8	RAR-beta	1027	1036	9.641259	CGGGTT	0.21362	0.21243
cg0932411	GEMIN8	HNF-1C [	424	432	9.639597	ACAATT	0.19836	0.20229
cg0932411	GEMIN8	RAR-beta	107	116	9.622793	AAGAAA	0.21362	0.21243

cg0932411	GEMIN8	Pax-5 [T0	205	211	9.552105	GGGCAA	1.46484	1.43083
cg0932411	GEMIN8	Pax-5 [T0	558	564	9.552105	GGGCGT	1.46484	1.43083
cg0932411	GEMIN8	Pax-5 [T0	880	886	9.552105	GGGCGG	1.46484	1.43083
cg0932411	GEMIN8	Pax-5 [T0	1743	1749	9.552105	GTGGCC	1.46484	1.43083
cg0932411	GEMIN8	TFIID [T0	1825	1831	9.552105	TGAGAA	1.46484	1.48472
cg0932411	GEMIN8	NF-1 [T00	647	654	9.535536	TTGGCC	0.73242	0.73053
cg0932411	GEMIN8	NF-1 [T00	1560	1567	9.535536	ATGCCC	0.73242	0.73053
cg0932411	GEMIN8	E2F-1 [T0	820	827	9.529774	GCGGTG	0.15259	0.14917
cg0932411	GEMIN8	E2F-1 [T0	1018	1025	9.529774	TGCACC	0.15259	0.14917
cg0932411	GEMIN8	HNF-1B [	1233	1241	9.522068	TTTGTA	0.09155	0.09374
cg0932411	GEMIN8	TFII-I [T0	201	206	9.512894	GGATGG	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	210	215	9.512894	AAATCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	332	337	9.512894	GGATGG	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	589	594	9.512894	GGAAAC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	599	604	9.512894	CCGTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	667	672	9.512894	TTTTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	779	784	9.512894	AAGTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	894	899	9.512894	GGATGG	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	980	985	9.512894	GGACGG	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1030	1035	9.512894	GTTTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1049	1054	9.512894	TTGTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1073	1078	9.512894	TTTTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1077	1082	9.512894	CCTTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1156	1161	9.512894	TTGTCC	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1472	1477	9.512894	GGAATT	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1486	1491	9.512894	GGAAAA	7.32422	7.29728
cg0932411	GEMIN8	TFII-I [T0	1547	1552	9.512894	GGAAAA	7.32422	7.29728
cg0932411	GEMIN8	FOXP3 [T	25	30	9.512894	ATAAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	52	57	9.512894	GATAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	244	249	9.512894	GTTCTC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	502	507	9.512894	AGCAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	646	651	9.512894	GTTGGC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	716	721	9.512894	GTTGCC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	1277	1282	9.512894	CATAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	1395	1400	9.512894	AAGAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	1406	1411	9.512894	ATAAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	1513	1518	9.512894	GTTTAT	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	1563	1568	9.512894	CCCAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	1751	1756	9.512894	GAGAAC	7.32422	7.35678
cg0932411	GEMIN8	FOXP3 [T	1864	1869	9.512894	GATAAC	7.32422	7.35678
cg0932411	GEMIN8	LEF-1 [T0	582	589	9.313676	CCCCAA	0.21362	0.2139
cg0932411	GEMIN8	c-Myb [T0	280	287	9.29064	AAACTA	0.36621	0.37054
cg0932411	GEMIN8	c-Ets-1 [T	1479	1485	9.19359	ATTCCA	0.85449	0.85523
cg0932411	GEMIN8	HNF-1C [	1665	1673	9.170047	AACTTT	0.12207	0.12495
cg0932411	GEMIN8	E2F-1 [T0	647	654	9.140572	TTGGCC	0.27466	0.26875
cg0932411	GEMIN8	COUP-TF	68	80	9.093379	AGCTGA	0.01878	0.01865
cg0932411	GEMIN8	c-Myb [T0	1204	1211	9.024874	CTCAGT	0.39673	0.40028
cg0932411	GEMIN8	c-Jun [T00	1602	1608	9.013496	TGACGT	0.61035	0.61059

cg0932411	GEMIN8	NF-AT2 [	1486	1495	8.984657	GGAAAA	0.05341	0.05386
cg0932411	GEMIN8	GR [T050	64	70	8.971049	CAAAAG	0.61035	0.61632
cg0932411	GEMIN8	GR [T050	208	214	8.971049	CAAAAT	0.61035	0.61632
cg0932411	GEMIN8	GR [T050	1810	1816	8.971049	GATTTT	0.61035	0.61632
cg0932411	GEMIN8	c-Ets-2 [T	441	449	8.912323	ATTTAG	0.27466	0.27495
cg0932411	GEMIN8	c-Ets-2 [T	1623	1631	8.912323	TTCCTG	0.27466	0.27495
cg0932411	GEMIN8	p53 [T006	294	300	8.912104	AGGGCC	0.12207	0.11837
cg0932411	GEMIN8	p53 [T006	550	556	8.912104	AGGGCC	0.12207	0.11837
cg0932411	GEMIN8	Elk-1 [T00	740	748	8.897321	CTTCCG	0.24414	0.24034
cg0932411	GEMIN8	PR B [T00	1491	1497	8.827054	AACAGG	0.36621	0.36944
cg0932411	GEMIN8	PR A [T01	1491	1497	8.827054	AACAGG	0.36621	0.36944
cg0932411	GEMIN8	NFI/CTF [	1584	1591	8.814757	TCAATT	0.48828	0.48804
cg0932411	GEMIN8	NF-AT1 [	1051	1059	8.769753	GTCCTT	0.22888	0.22959
cg0932411	GEMIN8	XBP-1 [T	319	324	8.75604	TTTCAT	2.92969	2.9674
cg0932411	GEMIN8	XBP-1 [T	450	455	8.75604	TCTCAT	2.92969	2.9674
cg0932411	GEMIN8	XBP-1 [T	497	502	8.75604	ATGAGA	2.92969	2.9674
cg0932411	GEMIN8	XBP-1 [T	1259	1264	8.75604	TCTCAT	2.92969	2.9674
cg0932411	GEMIN8	XBP-1 [T	1433	1438	8.75604	TATCAT	2.92969	2.9674
cg0932411	GEMIN8	XBP-1 [T	1824	1829	8.75604	ATGAGA	2.92969	2.9674
cg0932411	GEMIN8	RXR-alpha	859	865	8.664139	GCTACC	0.12207	0.12014
cg0932411	GEMIN8	NF-AT1 [	1070	1078	8.532897	TCGTTT	0.10681	0.10725
cg0932411	GEMIN8	AP-1 [T00	1578	1586	8.513775	GCTAAG	0.03052	0.03084
cg0932411	GEMIN8	HNF-3alp	1456	1463	8.343064	TATTTA	0.27466	0.28528
cg0932411	GEMIN8	HNF-3alp	1642	1649	8.343064	TTAAAA	0.27466	0.28528
cg0932411	GEMIN8	HNF-3alp	1838	1845	8.343064	GTAAAA	0.27466	0.28528
cg0932411	GEMIN8	PR B [T00	712	718	8.338824	GGCTGT	1.09863	1.10009
cg0932411	GEMIN8	PR B [T00	1114	1120	8.338824	TTCTGT	1.09863	1.10009
cg0932411	GEMIN8	PR B [T00	1367	1373	8.338824	CCCTGT	1.09863	1.10009
cg0932411	GEMIN8	PR A [T01	712	718	8.338824	GGCTGT	1.09863	1.10009
cg0932411	GEMIN8	PR A [T01	1114	1120	8.338824	TTCTGT	1.09863	1.10009
cg0932411	GEMIN8	PR A [T01	1367	1373	8.338824	CCCTGT	1.09863	1.10009
cg0932411	GEMIN8	IRF-1 [T0	1055	1063	8.316022	TTTCCT	0.20599	0.20664
cg0932411	GEMIN8	ATF3 [T0	509	516	8.313799	TGACGT	0.27466	0.27431
cg0932411	GEMIN8	ATF3 [T0	798	805	8.313799	GGACGT	0.27466	0.27431
cg0932411	GEMIN8	ATF3 [T0	1428	1435	8.313799	TGACAT	0.27466	0.27431
cg0932411	GEMIN8	GR-alpha	17	21	8.281568	CAAGG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	74	78	8.281568	CCTCC	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	151	155	8.281568	CCTTC	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	459	463	8.281568	CCTCC	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	521	525	8.281568	CCTCG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	571	575	8.281568	CCTCC	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	614	618	8.281568	CCTCG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	671	675	8.281568	CCTTG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	702	706	8.281568	CGAGG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	706	710	8.281568	GGAGG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	833	837	8.281568	GGAGG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	1077	1081	8.281568	CCTTC	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha	1082	1086	8.281568	CCTTG	7.8125	7.72956

cg0932411	GEMIN8	GR-alpha [	1250	1254	8.281568	CCTCG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha [	1483	1487	8.281568	CAAGG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha [	1568	1572	8.281568	CAAGG	7.8125	7.72956
cg0932411	GEMIN8	GR-alpha [	1878	1882	8.281568	GAAGG	7.8125	7.72956
cg0932411	GEMIN8	GCF [T00	624	632	8.256755	GCGCAG	0.09155	0.09002
cg0932411	GEMIN8	HNF-1B [	1125	1133	8.255112	TTCTTA	0.11444	0.11669
cg0932411	GEMIN8	c-Jun [T00	71	77	8.242207	TGACCT	0.48828	0.49076
cg0932411	GEMIN8	p53 [T006	295	301	8.208781	GGGCCC	0.48828	0.47377
cg0932411	GEMIN8	p53 [T006	337	343	8.208781	GGGGCC	0.48828	0.47377
cg0932411	GEMIN8	ENKTF-1	648	655	8.19852	TGGCCG	0.73242	0.71737
cg0932411	GEMIN8	ENKTF-1	897	904	8.19852	TGGCTG	0.73242	0.71737
cg0932411	GEMIN8	ENKTF-1	956	963	8.19852	TGGCGG	0.73242	0.71737
cg0932411	GEMIN8	HNF-1C [	1659	1667	8.131138	AATATT	0.19836	0.20224
cg0932411	GEMIN8	c-Jun [T00	1607	1613	8.128539	TGACAT	0.48828	0.49076
cg0932411	GEMIN8	NF-AT1 [	1547	1555	8.12076	GGAAAA	0.1297	0.12988
cg0932411	GEMIN8	LEF-1 [T0	1180	1187	8.117221	CTTTGA	0.12207	0.1241
cg0932411	GEMIN8	IRF-1 [T0	1031	1039	8.078284	TTTCCA	0.25177	0.25263
cg0932411	GEMIN8	GR-alpha [	32	36	8.073878	GTAGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	77	81	8.073878	CCTGC	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	142	146	8.073878	CCTAG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	170	174	8.073878	CCTGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	223	227	8.073878	CCTAC	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	265	269	8.073878	CCTGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	292	296	8.073878	CCAGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	432	436	8.073878	CCTGC	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	548	552	8.073878	CCAGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	639	643	8.073878	CCTGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	655	659	8.073878	GCAGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	662	666	8.073878	CCTAG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	816	820	8.073878	GCAGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	848	852	8.073878	CCTGC	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	885	889	8.073878	GCAGG	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	1363	1367	8.073878	CCTGC	7.8125	7.72238
cg0932411	GEMIN8	GR-alpha [	1625	1629	8.073878	CCTGG	7.8125	7.72238
cg0932411	GEMIN8	Pax-5 [T0	6	12	8.014558	GGGCAG	2.19727	2.14502
cg0932411	GEMIN8	Pax-5 [T0	268	274	8.014558	GGGCAG	2.19727	2.14502
cg0932411	GEMIN8	Pax-5 [T0	295	301	8.014558	GGGCCC	2.19727	2.14502
cg0932411	GEMIN8	Pax-5 [T0	337	343	8.014558	GGGGCC	2.19727	2.14502
cg0932411	GEMIN8	Pax-5 [T0	456	462	8.014558	GGGCCT	2.19727	2.14502
cg0932411	GEMIN8	Pax-5 [T0	659	665	8.014558	GGGCCT	2.19727	2.14502
cg0932411	GEMIN8	Pax-5 [T0	960	966	8.014558	GGGCAC	2.19727	2.14502
cg0932411	GEMIN8	TFIID [T0	1124	1130	8.014558	TTTCTTA	2.19727	2.24348
cg0932411	GEMIN8	TFIID [T0	1147	1153	8.014558	TTTCTTA	2.19727	2.24348
cg0932411	GEMIN8	TFIID [T0	1181	1187	8.014558	TTTGAA	2.19727	2.24348
cg0932411	GEMIN8	TFIID [T0	1233	1239	8.014558	TTTGTA	2.19727	2.24348
cg0932411	GEMIN8	TFIID [T0	1336	1342	8.014558	TTTGTA	2.19727	2.24348
cg0932411	GEMIN8	TFIID [T0	1545	1551	8.014558	TTGGAA	2.19727	2.24348
cg0932411	GEMIN8	TFIID [T0	1670	1676	8.014558	TAACAA	2.19727	2.24348

cg0932411	GEMIN8	C/EBPalph	1726	1732	8.006685	CATTGT	0.24414	0.24674
cg0932411	GEMIN8	c-Myb [T0	54	61	8.005241	TAACTC	0.21362	0.21454
cg0932411	GEMIN8	ATF-1 [T0	1599	1609	7.870358	TAATGA	0.07153	0.07147
cg0932411	GEMIN8	RXR-alpha	904	910	7.815913	GGGTGG	0.24414	0.24104
cg0932411	GEMIN8	GATA-2 [	135	143	7.777778	GCAATA	0.30518	0.30758
cg0932411	GEMIN8	GATA-2 [	189	197	7.777778	AGATAC	0.30518	0.30758
cg0932411	GEMIN8	c-Myb [T0	1774	1781	7.739476	GAACTG	0.42725	0.43114
cg0932411	GEMIN8	p53 [T006	18	24	7.641867	AAGGCC	0.73242	0.7186
cg0932411	GEMIN8	AR [T000	1153	1161	7.623968	AATTTGT	0.25177	0.25079
cg0932411	GEMIN8	NFI/CTF [	63	70	7.587343	CCAAAA	0.36621	0.36674
cg0932411	GEMIN8	c-Jun [T00	509	515	7.538568	TGACGT	0.48828	0.48775
cg0932411	GEMIN8	c-Jun [T00	799	805	7.538568	GACGTC	0.48828	0.48775
cg0932411	GEMIN8	GR [T050	471	477	7.527031	CCTTTTC	1.83105	1.86007
cg0932411	GEMIN8	GR [T050	1333	1339	7.527031	ATGTTTC	1.83105	1.86007
cg0932411	GEMIN8	GR [T050	1673	1679	7.527031	CAAATA	1.83105	1.86007
cg0932411	GEMIN8	RAR-beta	588	597	7.47824	AGGAAA	0.24414	0.24343
cg0932411	GEMIN8	C/EBPalph	434	440	7.465744	TGCAAT	0.48828	0.49653
cg0932411	GEMIN8	C/EBPalph	1303	1309	7.465744	CATTGC	0.48828	0.49653
cg0932411	GEMIN8	C/EBPalph	1973	1979	7.465744	CATTGC	0.48828	0.49653
cg0932411	GEMIN8	RAR-beta	1191	1200	7.459774	GATTAA	0.24414	0.24343
cg0932411	GEMIN8	C/EBPalph	1543	1549	7.396431	AATTGG	0.48828	0.49653
cg0932411	GEMIN8	C/EBPalph	1760	1766	7.396431	AATTGT	0.48828	0.49653
cg0932411	GEMIN8	E2F-1 [T0	882	889	7.336545	GCGGCA	0.45776	0.44878
cg0932411	GEMIN8	SRY [T00	1180	1188	7.175614	CTTTGA	0.30518	0.30739
cg0932411	GEMIN8	XBP-1 [T	438	443	7.172312	ATGATT	2.92969	2.97018
cg0932411	GEMIN8	p53 [T006	1743	1749	7.150251	GTGGCC	1.09863	1.07125
cg0932411	GEMIN8	p53 [T006	173	179	7.103527	GGGCGA	1.09863	1.07125
cg0932411	GEMIN8	NF-AT1 [	664	672	7.095752	TAGTTTT	0.15259	0.1548
cg0932411	GEMIN8	Pax-5 [T0	173	179	7.082373	GGGCGA	0.12207	0.12014
cg0932411	GEMIN8	HNF-3alph	1677	1684	7.000129	TATTTAC	0.82397	0.84946
cg0932411	GEMIN8	HNF-3alph	1810	1817	7.000129	GATTTC	0.82397	0.84946
cg0932411	GEMIN8	RXR-alpha	1590	1596	6.967687	GGGTGG	0.36621	0.36214
cg0932411	GEMIN8	ENKTF-1	34	41	6.942764	AGGCGC	1.46484	1.44228
cg0932411	GEMIN8	ENKTF-1	287	294	6.942764	CGATGC	1.46484	1.44228
cg0932411	GEMIN8	ENKTF-1	1576	1583	6.942764	TGGCTA	1.46484	1.44228
cg0932411	GEMIN8	p53 [T006	456	462	6.938545	GGGCCT	1.09863	1.07125
cg0932411	GEMIN8	p53 [T006	642	648	6.891821	GGGCGT	1.09863	1.07125
cg0932411	GEMIN8	p53 [T006	1021	1027	6.891821	ACCGCC	1.09863	1.07125
cg0932411	GEMIN8	EBF [T05	1745	1755	6.87365	GGCCCT	0.03052	0.02964
cg0932411	GEMIN8	HOXD9 [	1978	1987	6.852796	CATTTCT	0.07629	0.0789
cg0932411	GEMIN8	HOXD10 [	1978	1987	6.852796	CATTTCT	0.07629	0.0789
cg0932411	GEMIN8	C/EBPalph	1984	1990	6.786177	TATTGT	0.73242	0.74337
cg0932411	GEMIN8	AR [T000	1046	1054	6.760234	TTTTTGT	0.23651	0.23551
cg0932411	GEMIN8	ATF3 [T01	1602	1609	6.744803	TGACGT	0.27466	0.27656
cg0932411	GEMIN8	Elk-1 [T00	773	781	6.732355	CGCCGG	0.06104	0.05967
cg0932411	GEMIN8	c-Ets-1 [T	748	754	6.693449	GCGGAA	0.48828	0.48798
cg0932411	GEMIN8	Elk-1 [T00	836	844	6.598007	GGCCGG	0.06104	0.05967
cg0932411	GEMIN8	TFII-I [T0	578	583	6.581441	CACTCC	0.97656	0.97366

cg0932411	GEMIN8	TFII-I [T0	689	694	6.581441	GGAGTG	0.97656	0.97366
cg0932411	GEMIN8	FOXP3 [T	1133	1138	6.581441	TAAAAC	0.97656	0.99397
cg0932411	GEMIN8	FOXP3 [T	1140	1145	6.581441	GTTTTA	0.97656	0.99397
cg0932411	GEMIN8	FOXP3 [T	1167	1172	6.581441	TAAAAC	0.97656	0.99397
cg0932411	GEMIN8	PPAR-alp	403	413	6.51544	CTCTGG	0.03719	0.03639
cg0932411	GEMIN8	XBP-1 [T	289	294	6.478682	ATGCCA	0.97656	0.97062
cg0932411	GEMIN8	XBP-1 [T	1560	1565	6.478682	ATGCCC	0.97656	0.97062
cg0932411	GEMIN8	XBP-1 [T	1966	1971	6.478682	TGGCAT	0.97656	0.97062
cg0932411	GEMIN8	E2F-1 [T0	939	946	6.47044	GCGGGG	0.12207	0.12031
cg0932411	GEMIN8	c-Ets-1 [T	1545	1551	6.423689	TTGGAA	0.48828	0.48798
cg0932411	GEMIN8	p53 [T006	723	729	6.400205	GGGCGA	0.48828	0.47541
cg0932411	GEMIN8	TCF-4E [T	1180	1186	6.302385	CTTTGA	0.61035	0.61344
cg0932411	GEMIN8	GR-alpha [	231	235	6.263098	CCTTA	3.90625	3.91061
cg0932411	GEMIN8	GR-alpha [	575	579	6.263098	CCTCA	3.90625	3.91061
cg0932411	GEMIN8	GR-alpha [	1005	1009	6.263098	TAAGG	3.90625	3.91061
cg0932411	GEMIN8	GR-alpha [	1058	1062	6.263098	CCTCA	3.90625	3.91061
cg0932411	GEMIN8	GR-alpha [	1790	1794	6.263098	TAAGG	3.90625	3.91061
cg0932411	GEMIN8	GR-alpha [	1846	1850	6.263098	CCTCA	3.90625	3.91061
cg0932411	GEMIN8	GR-alpha [	1888	1892	6.263098	TGAGG	3.90625	3.91061
cg0932411	GEMIN8	p53 [T006	558	564	6.188498	GGGCGT	0.61035	0.594
cg0932411	GEMIN8	p53 [T006	880	886	6.188498	GGGCGG	0.61035	0.594
cg0932411	GEMIN8	RXR-alph	1008	1014	6.119461	GGGTCG	0.73242	0.72249
cg0932411	GEMIN8	GCF [T00	528	536	6.116216	TCTCTG	0.64087	0.6219
cg0932411	GEMIN8	GR-alpha [	443	447	6.055408	TTAGG	3.90625	3.9065
cg0932411	GEMIN8	GR-alpha [	1282	1286	6.055408	CCTAA	3.90625	3.9065
cg0932411	GEMIN8	GR-alpha [	1296	1300	6.055408	CCTGA	3.90625	3.9065
cg0932411	GEMIN8	GR-alpha [	1555	1559	6.055408	CCTAA	3.90625	3.9065
cg0932411	GEMIN8	GR-alpha [	1748	1752	6.055408	CCTGA	3.90625	3.9065
cg0932411	GEMIN8	GR-alpha [	1756	1760	6.055408	CCTGA	3.90625	3.9065
cg0932411	GEMIN8	c-Ets-1 [T	1031	1037	6.039428	TTTCCA	0.36621	0.36731
cg0932411	GEMIN8	C/EBPalp	322	328	5.996794	CATTGG	0.97656	0.99
cg0932411	GEMIN8	RXR-alph	250	256	5.937582	GGCACC	0.73242	0.72249
cg0932411	GEMIN8	RXR-alph	961	967	5.937582	GGCACC	0.73242	0.72249
cg0932411	GEMIN8	p53 [T006	659	665	5.883561	GGGCCT	0.61035	0.594
cg0932411	GEMIN8	STAT4 [T	1077	1082	5.882353	CCTTCC	0.48828	0.48408
cg0932411	GEMIN8	AR [T000	163	171	5.859358	TGGCTG	0.24414	0.24229
cg0932411	GEMIN8	C/EBPalp	1445	1451	5.850545	GGCAAT	0.97656	0.99
cg0932411	GEMIN8	C/EBPalp	1583	1589	5.850545	GTCAAT	0.97656	0.99
cg0932411	GEMIN8	VDR [T00	1769	1777	5.771401	AGTCTG	0.42725	0.42999
cg0932411	GEMIN8	NF-kappa	776	786	5.762942	CGGAAG	0.04053	0.03971
cg0932411	GEMIN8	RXR-alph	1170	1176	5.715466	AACACC	0.61035	0.6044
cg0932411	GEMIN8	HNF-1C [	1892	1900	5.695506	GTTAAA	0.07629	0.07817
cg0932411	GEMIN8	ENKTF-1	1744	1751	5.687009	TGGCCC	0.73242	0.7249
cg0932411	GEMIN8	c-Ets-1 [T	1078	1084	5.686398	CTTCCC	0.36621	0.3623
cg0932411	GEMIN8	NF-AT1 [	1486	1494	5.604085	GGAAAA	0.03815	0.03856
cg0932411	GEMIN8	NFI/CTF [	1245	1252	5.558661	CCAAGC	0.54932	0.55038
cg0932411	GEMIN8	NFI/CTF [	1400	1407	5.558661	CCAAGC	0.54932	0.55038
cg0932411	GEMIN8	c-Ets-1 [T	1240	1246	5.558311	CTTCCC	0.36621	0.3623

cg0932411	GEMIN8	Pax-5 [T0	133	139	5.544826	GGGCAA	0.73242	0.72046
cg0932411	GEMIN8	Pax-5 [T0	642	648	5.544826	GGGCGT	0.73242	0.72046
cg0932411	GEMIN8	Pax-5 [T0	1021	1027	5.544826	ACCGCC	0.73242	0.72046
cg0932411	GEMIN8	Pax-5 [T0	1444	1450	5.544826	GGGCAA	0.73242	0.72046
cg0932411	GEMIN8	TFIID [T0	442	448	5.544826	TTTAGG	0.73242	0.75085
cg0932411	GEMIN8	TFIID [T0	1668	1674	5.544826	TTTAAC	0.73242	0.75085
cg0932411	GEMIN8	NF-AT1 [	1027	1036	5.512555	CGGGTT	0.05913	0.05965
cg0932411	GEMIN8	HNF-1A [	1369	1376	5.466509	CTGTTA	0.24414	0.2469
cg0932411	GEMIN8	ATF [T00	1598	1609	5.46568	TTAATG	0.02575	0.02579
cg0932411	GEMIN8	p53 [T006	338	344	5.39549	GGGCCC	0.61035	0.59991
cg0932411	GEMIN8	p53 [T006	551	557	5.39549	GGGCCC	0.61035	0.59991
cg0932411	GEMIN8	C/EBPalp	1409	1415	5.38654	AACAAT	0.73242	0.74391
cg0932411	GEMIN8	AP-1 [T00	1381	1389	5.321703	CAAGAG	0.09155	0.09214
cg0932411	GEMIN8	IRF-1 [T0	1074	1082	5.309227	TTTCCTT	0.22888	0.23087
cg0932411	GEMIN8	ETF [T002	551	561	5.246906	GGGCCC	0.02861	0.02737
cg0932411	GEMIN8	C/EBPalp	134	140	5.240291	GGCAAT	0.97656	0.99332
cg0932411	GEMIN8	GR [T050	1178	1184	5.207533	GTCTTT	0.24414	0.24606
cg0932411	GEMIN8	c-Jun [T00	607	613	5.193102	GAAGTC	0.61035	0.61057
cg0932411	GEMIN8	AP-2alpha	1037	1042	5.100982	GCCTTT	0.97656	0.97567
cg0932411	GEMIN8	AP-2alpha	1097	1102	5.100982	GCCTTT	0.97656	0.97567
cg0932411	GEMIN8	HNF-1B [	1891	1899	5.055806	GGTTAA	0.04578	0.04699
cg0932411	GEMIN8	USF2 [T0	259	268	5.052423	GAATCA	0.103	0.10178
cg0932411	GEMIN8	GR-beta [	211	215	5.042296	AATCC	3.90625	3.95351
cg0932411	GEMIN8	GR-beta [	483	487	5.042296	GGATT	3.90625	3.95351
cg0932411	GEMIN8	GR-beta [	1359	1363	5.042296	AATAC	3.90625	3.95351
cg0932411	GEMIN8	GR-beta [	1461	1465	5.042296	AATAC	3.90625	3.95351
cg0932411	GEMIN8	GR-beta [	1595	1599	5.042296	GTATT	3.90625	3.95351
cg0932411	GEMIN8	GR-beta [	1617	1621	5.042296	GTATT	3.90625	3.95351
cg0932411	GEMIN8	GR-beta [	1705	1709	5.042296	GTATT	3.90625	3.95351
cg0932411	GEMIN8	GR-beta [	1842	1846	5.042296	AATAC	3.90625	3.95351
cg0932411	GEMIN8	E2F-1 [T0	480	487	5.042045	GCGGGA	0.18311	0.17901
cg0932411	GEMIN8	NFI/CTF [	584	591	5.021086	CCAAAG	0.24414	0.24103
cg0932411	GEMIN8	HNF-1A [	230	237	4.972635	ACCTTA	0.36621	0.37179
cg0932411	GEMIN8	IRF-1 [T0	668	676	4.963725	TTTCCTT	0.1297	0.1302
cg0932411	GEMIN8	IRF-1 [T0	1482	1490	4.963725	CCAAGG	0.1297	0.1302
cg0932411	GEMIN8	XBP-1 [T	1687	1692	4.894955	ATGCCG	0.97656	0.96979
cg0932411	GEMIN8	c-Jun [T00	1428	1434	4.883696	TGACAT	0.61035	0.61057
cg0932411	GEMIN8	GCF [T00	648	656	4.846987	TGGCCG	0.27466	0.26486
cg0932411	GEMIN8	GCF [T00	765	773	4.846987	GCGCGG	0.27466	0.26486
cg0932411	GEMIN8	GCF [T00	1718	1726	4.846987	GCGCTG	0.27466	0.26486
cg0932411	GEMIN8	HNF-3alp	1951	1958	4.842999	TTAAAA	0.09155	0.09582
cg0932411	GEMIN8	p53 [T006	942	948	4.786849	GGGCAC	0.48828	0.47747
cg0932411	GEMIN8	TFII-I [T0	138	143	4.756447	ATATCC	2.92969	2.93695
cg0932411	GEMIN8	TFII-I [T0	196	201	4.756447	GGACTG	2.92969	2.93695
cg0932411	GEMIN8	TFII-I [T0	408	413	4.756447	GGACTG	2.92969	2.93695
cg0932411	GEMIN8	TFII-I [T0	950	955	4.756447	GGACTG	2.92969	2.93695
cg0932411	GEMIN8	TFII-I [T0	1571	1576	4.756447	GGAAAT	2.92969	2.93695
cg0932411	GEMIN8	FOXP3 [T	278	283	4.756447	AAAAAC	2.92969	2.96063

cg0932411	GEMIN8	FOXP3 [T	666	671	4.756447	GTTTTC	2.92969	2.96063
cg0932411	GEMIN8	FOXP3 [T	1072	1077	4.756447	GTTTTC	2.92969	2.96063
cg0932411	GEMIN8	FOXP3 [T	1118	1123	4.756447	GTTTTC	2.92969	2.96063
cg0932411	GEMIN8	FOXP3 [T	1315	1320	4.756447	CAAAAC	2.92969	2.96063
cg0932411	GEMIN8	FOXP3 [T	1488	1493	4.756447	AAAAAC	2.92969	2.96063
cg0932411	GEMIN8	PPAR-alph	1439	1449	4.727619	TTCTGG	0.03242	0.03183
cg0932411	GEMIN8	HNF-1A [	1125	1132	4.684871	TTCTTA	0.12207	0.12485
cg0932411	GEMIN8	HNF-1A [	1371	1378	4.684871	GTTAAC	0.12207	0.12485
cg0932411	GEMIN8	c-Ets-1 [T	729	735	4.654478	CTGGAA	0.85449	0.85764
cg0932411	GEMIN8	p53 [T006	620	626	4.645444	GGGCGC	0.24414	0.23584
cg0932411	GEMIN8	c-Ets-2 [T	1075	1083	4.589988	TTCCTT	0.06866	0.06881
cg0932411	GEMIN8	c-Ets-1 [T	444	450	4.539113	TAGGAA	0.85449	0.85764
cg0932411	GEMIN8	T3R-beta1	611	619	4.481316	TCACCT	0.27466	0.27551
cg0932411	GEMIN8	IRF-1 [T0	1543	1551	4.462268	AATTGG	0.05341	0.05405
cg0932411	GEMIN8	AP-2alpha	661	666	4.438035	GCCTAG	0.97656	0.96979
cg0932411	GEMIN8	STAT4 [T	380	385	4.411765	GGAAGC	1.95312	1.94235
cg0932411	GEMIN8	STAT4 [T	731	736	4.411765	GGAAGC	1.95312	1.94235
cg0932411	GEMIN8	STAT4 [T	739	744	4.411765	GCTTCC	1.95312	1.94235
cg0932411	GEMIN8	STAT4 [T	840	845	4.411765	GGAAGC	1.95312	1.94235
cg0932411	GEMIN8	STAT4 [T	1107	1112	4.411765	TCTTCC	1.95312	1.94235
cg0932411	GEMIN8	AR [T000	1718	1726	4.241082	GCGCTG	0.06866	0.06828
cg0932411	GEMIN8	C/EBPalph	1356	1362	4.235345	AGCAAT	0.48828	0.49358
cg0932411	GEMIN8	AP-2alpha	32	37	4.211849	GTAGGC	0.97656	0.96469
cg0932411	GEMIN8	GR-beta [	183	187	4.201913	CTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	260	264	4.201913	AATCA	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	303	307	4.201913	CTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	316	320	4.201913	TGATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	374	378	4.201913	TGATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	439	443	4.201913	TGATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	854	858	4.201913	AATCG	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1187	1191	4.201913	AATAG	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1477	1481	4.201913	TTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1515	1519	4.201913	TTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1526	1530	4.201913	TTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1620	1624	4.201913	TTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1884	1888	4.201913	CTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1927	1931	4.201913	TTATT	7.8125	7.94607
cg0932411	GEMIN8	GR-beta [	1983	1987	4.201913	CTATT	7.8125	7.94607
cg0932411	GEMIN8	NF-Y [T0	1544	1551	4.186615	ATTGGA	0.18311	0.1853
cg0932411	GEMIN8	ATF-2 [T0	1601	1610	4.17677	ATGACG	0.03433	0.03472
cg0932411	GEMIN8	c-Ets-1 [T	1622	1628	4.154851	ATTCCT	0.24414	0.24526
cg0932411	GEMIN8	NF-AT1 [	1546	1555	4.134416	TGGAAA	0.08392	0.08485
cg0932411	GEMIN8	p53 [T006	462	468	4.125254	CCGGCC	0.73242	0.71379
cg0932411	GEMIN8	p53 [T006	912	918	4.125254	GGGCCG	0.73242	0.71379
cg0932411	GEMIN8	c-Ets-2 [T	669	677	4.091811	TTCCTT	0.16022	0.16243
cg0932411	GEMIN8	c-Ets-2 [T	1481	1489	4.091811	TCCAAG	0.16022	0.16243
cg0932411	GEMIN8	c-Ets-2 [T	1566	1574	4.091811	AACAAG	0.16022	0.16243
cg0932411	GEMIN8	p53 [T006	960	966	4.083527	GGGCAC	0.73242	0.71379

cg0932411	GEMIN8	RXR-alpha	109	115	4.019014	GAAACC	0.97656	0.9671
cg0932411	GEMIN8	RXR-alpha	590	596	4.019014	GAAACC	0.97656	0.9671
cg0932411	GEMIN8	RXR-alpha	1028	1034	4.019014	GGGTTT	0.97656	0.9671
cg0932411	GEMIN8	c-Ets-2 [T	584	592	4.017001	CCAAAG	0.16022	0.16243
cg0932411	GEMIN8	c-Ets-2 [T	1109	1117	4.017001	TTCCTTT	0.16022	0.16243
cg0932411	GEMIN8	STAT1bet	1567	1576	4.01053	ACAAGG	0.03433	0.03457
cg0932411	GEMIN8	Pax-5 [T0	18	24	4.007279	AAGGCC	1.09863	1.07975
cg0932411	GEMIN8	Pax-5 [T0	294	300	4.007279	AGGGCC	1.09863	1.07975
cg0932411	GEMIN8	Pax-5 [T0	550	556	4.007279	AGGGCC	1.09863	1.07975
cg0932411	GEMIN8	Pax-5 [T0	942	948	4.007279	GGGCAC	1.09863	1.07975
cg0932411	GEMIN8	Pax-5 [T0	1559	1565	4.007279	AATGCC	1.09863	1.07975
cg0932411	GEMIN8	TFIID [T0	356	362	4.007279	TCTTAA	1.09863	1.13456
cg0932411	GEMIN8	TFIID [T0	1458	1464	4.007279	TTTAAT	1.09863	1.13456
cg0932411	GEMIN8	TFIID [T0	1514	1520	4.007279	TTTATTA	1.09863	1.13456
cg0932411	GEMIN8	TFIID [T0	1529	1535	4.007279	TTTTAA	1.09863	1.13456
cg0932411	GEMIN8	TFIID [T0	1926	1932	4.007279	TTTATTA	1.09863	1.13456
cg0932411	GEMIN8	c-Myb [T0	1237	1244	3.973336	TAACTT	0.09155	0.09154
cg0932411	GEMIN8	AP-2alpha	17	22	3.970052	CAAGGC	0.97656	0.96469
cg0932411	GEMIN8	NF-Y [T0	1587	1594	3.95898	ATTGGG	0.18311	0.1853
cg0932411	GEMIN8	AhR:Arnt	885	894	3.888628	GCAGGC	0.02289	0.02208
cg0932411	GEMIN8	PPAR-alph	1156	1166	3.872523	TTGTCC	0.02575	0.02522
cg0932411	GEMIN8	GR [T050	1315	1321	3.763516	CAAAAC	0.73242	0.74251
cg0932411	GEMIN8	HNF-1C [	1386	1394	3.755157	GTCATT	0.04578	0.04699
cg0932411	GEMIN8	TBP [T00	1856	1865	3.743085	TTTATA	0.03052	0.03162
cg0932411	GEMIN8	p53 [T006	133	139	3.728319	GGGCAA	0.73242	0.7189
cg0932411	GEMIN8	p53 [T006	1444	1450	3.728319	GGGCAA	0.73242	0.7189
cg0932411	GEMIN8	Sp1 [T007	879	888	3.623596	GGGGCG	0.07439	0.07186
cg0932411	GEMIN8	HNF-1B [	1387	1395	3.610263	TCATTA	0.04578	0.0471
cg0932411	GEMIN8	RXR-alpha	975	981	3.574782	GGGTCG	1.09863	1.08572
cg0932411	GEMIN8	p53 [T006	1559	1565	3.516613	AATGCC	0.73242	0.7189
cg0932411	GEMIN8	HNF-3alph	1539	1546	3.500065	TGAAAA	0.27466	0.28532
cg0932411	GEMIN8	c-Ets-1 [T	378	384	3.487246	TCGGAA	0.61035	0.60765
cg0932411	GEMIN8	Sp1 [T007	1019	1028	3.454722	GCACCG	0.07439	0.07186
cg0932411	GEMIN8	RXR-alpha	1793	1799	3.392904	GGGTAA	1.09863	1.08572
cg0932411	GEMIN8	p53 [T006	937	943	3.375208	GGGCGG	0.73242	0.7189
cg0932411	GEMIN8	GR-beta [	137	141	3.361531	AATAT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	310	314	3.361531	AGATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	448	452	3.361531	AATCT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1190	1194	3.361531	AGATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1330	1334	3.361531	AATAT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1455	1459	3.361531	ATATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1659	1663	3.361531	AATAT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1660	1664	3.361531	ATATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1675	1679	3.361531	AATAT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1676	1680	3.361531	ATATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [	1809	1813	3.361531	AGATT	3.90625	3.99611
cg0932411	GEMIN8	IRF-1 [T0	585	593	3.347186	CAAAGG	0.06866	0.06927
cg0932411	GEMIN8	T3R-beta1	262	270	3.332047	TCACCT	0.27466	0.2755

cg0932411	GEMIN8	PR B [T00	1409	1415	3.29756	AACAAT	0.24414	0.25122
cg0932411	GEMIN8	PR B [T00	1946	1952	3.29756	AACATT	0.24414	0.25122
cg0932411	GEMIN8	PR A [T01	1409	1415	3.29756	AACAAT	0.24414	0.25122
cg0932411	GEMIN8	PR A [T01	1946	1952	3.29756	AACATT	0.24414	0.25122
cg0932411	GEMIN8	c-Ets-2 [T	1056	1064	3.2883	TTCCTC	0.18311	0.18304
cg0932411	GEMIN8	E2F-1 [T0	748	755	3.288084	GCGGAA	0.15259	0.14974
cg0932411	GEMIN8	c-Jun [T00	1383	1389	3.244843	AGAGTC	0.24414	0.24403
cg0932411	GEMIN8	AP-2alpha	401	406	3.229049	GCCTCT	0.48828	0.48238
cg0932411	GEMIN8	c-Ets-1 [T	740	746	3.102985	CTTCCG	0.24414	0.23981
cg0932411	GEMIN8	c-Ets-1 [T	775	781	3.102985	CCGGAA	0.24414	0.23981
cg0932411	GEMIN8	c-Ets-1 [T	838	844	3.102985	CCGGAA	0.24414	0.23981
cg0932411	GEMIN8	USF1 [T0	750	759	3.033037	GGAACA	0.06294	0.06201
cg0932411	GEMIN8	Elk-1 [T00	1108	1116	2.987643	CTTCCT	0.07629	0.07656
cg0932411	GEMIN8	STAT4 [T	446	451	2.941176	GGAATC	2.92969	2.929
cg0932411	GEMIN8	STAT4 [T	750	755	2.941176	GGAACA	2.92969	2.929
cg0932411	GEMIN8	STAT4 [T	777	782	2.941176	GGAAGT	2.92969	2.929
cg0932411	GEMIN8	STAT4 [T	1054	1059	2.941176	CTTTCC	2.92969	2.929
cg0932411	GEMIN8	STAT4 [T	1239	1244	2.941176	ACTTCC	2.92969	2.929
cg0932411	GEMIN8	STAT4 [T	1478	1483	2.941176	TATTCC	2.92969	2.929
cg0932411	GEMIN8	STAT4 [T	1621	1626	2.941176	TATTCC	2.92969	2.929
cg0932411	GEMIN8	IRF-1 [T0	1567	1575	2.890712	ACAAGG	0.07629	0.07756
cg0932411	GEMIN8	USF1 [T0	754	763	2.862167	CACGTG	0.06294	0.06201
cg0932411	GEMIN8	p53 [T006	268	274	2.813291	GGGCAG	0.48828	0.47786
cg0932411	GEMIN8	NF-1 [T00	324	331	2.813149	TTGGTC	0.24414	0.24101
cg0932411	GEMIN8	PR B [T00	1318	1324	2.80933	AACATT	0.73242	0.74818
cg0932411	GEMIN8	PR B [T00	1374	1380	2.80933	AACATT	0.73242	0.74818
cg0932411	GEMIN8	PR A [T01	1318	1324	2.80933	AACATT	0.73242	0.74818
cg0932411	GEMIN8	PR A [T01	1374	1380	2.80933	AACATT	0.73242	0.74818
cg0932411	GEMIN8	CREB [T0	1602	1610	2.664517	TGACGT	0.06104	0.06135
cg0932411	GEMIN8	PPAR-alp	945	955	2.642917	CACTGG	0.00858	0.00847
cg0932411	GEMIN8	TCF-4 [T0	1179	1188	2.632973	TCTTTG	0.03433	0.03506
cg0932411	GEMIN8	c-Jun [T00	1580	1586	2.538231	TAAGTC	0.48828	0.48929
cg0932411	GEMIN8	c-Fos [T00	1384	1393	2.521126	GAGTCA	0.03052	0.03034
cg0932411	GEMIN8	ENKTF-1	907	914	2.511511	TGGCGG	0.12207	0.11894
cg0932411	GEMIN8	C/EBPalp	423	429	2.371703	CACAAT	0.48828	0.49114
cg0932411	GEMIN8	C/EBPalp	1586	1592	2.371703	AATTGG	0.48828	0.49114
cg0932411	GEMIN8	GCF [T00	653	661	2.339499	GCGCAG	0.06104	0.05925
cg0932411	GEMIN8	T3R-beta1	220	228	2.240658	TCACCT	0.15259	0.15262
cg0932411	GEMIN8	GATA-2 [	1002	1010	2.222222	AGATAA	0.22888	0.23091
cg0932411	GEMIN8	GATA-2 [	1911	1919	2.222222	TCTTTA	0.22888	0.23091
cg0932411	GEMIN8	GATA-1 [	139	144	2.176375	TATCCT	3.90625	3.92756
cg0932411	GEMIN8	GCF [T00	963	971	2.140539	CACCCG	0.09155	0.08882
cg0932411	GEMIN8	AP-2alpha	1249	1254	2.098119	GCCTCG	0.97656	0.95407
cg0932411	GEMIN8	NF-1 [T00	1697	1704	2.067686	TGTGCC	0.12207	0.12133
cg0932411	GEMIN8	p53 [T006	205	211	1.970013	GGGCAA	0.36621	0.36261
cg0932411	GEMIN8	ATF-2 [T0	508	517	1.87457	GTGACG	0.01144	0.01128
cg0932411	GEMIN8	ATF-2 [T0	797	806	1.87457	CGGACG	0.01144	0.01128
cg0932411	GEMIN8	AP-2alpha	458	463	1.871933	GCCTCC	0.97656	0.95407

cg0932411	GEMIN8	AP-2alpha	706	711	1.871933	GGAGGC	0.97656	0.95407
cg0932411	GEMIN8	AP-2alpha	833	838	1.871933	GGAGGC	0.97656	0.95407
cg0932411	GEMIN8	C/EBPalpl	1847	1853	1.830762	CTCAATT	0.48828	0.49438
cg0932411	GEMIN8	TFII-I [T0	675	680	1.824994	GGAGAG	0.48828	0.48408
cg0932411	GEMIN8	TFII-I [T0	920	925	1.824994	GGAGAG	0.48828	0.48408
cg0932411	GEMIN8	p53 [T006	6	12	1.758307	GGGCAG	0.36621	0.36261
cg0932411	GEMIN8	GR-beta [T	116	120	1.680765	GAATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	216	220	1.680765	GAATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	217	221	1.680765	AATTC	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	352	356	1.680765	GAATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	353	357	1.680765	AATTC	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1285	1289	1.680765	AATGC	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1302	1306	1.680765	GCATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1473	1477	1.680765	GAATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1523	1527	1.680765	GAATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1559	1563	1.680765	AATGC	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1639	1643	1.680765	GAATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1759	1763	1.680765	GAATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1972	1976	1.680765	GCATT	3.90625	3.94936
cg0932411	GEMIN8	GR-beta [T	1977	1981	1.680765	GCATT	3.90625	3.94936
cg0932411	GEMIN8	c-Ets-1 [T	587	593	1.641124	AAGGAA	0.36621	0.36952
cg0932411	GEMIN8	c-Ets-1 [T	668	674	1.641124	TTTCCTT	0.36621	0.36952
cg0932411	GEMIN8	c-Ets-1 [T	1074	1080	1.641124	TTTCCTT	0.36621	0.36952
cg0932411	GEMIN8	c-Ets-1 [T	1484	1490	1.641124	AAGGAA	0.36621	0.36952
cg0932411	GEMIN8	c-Ets-1 [T	1569	1575	1.641124	AAGGAA	0.36621	0.36952
cg0932411	GEMIN8	C/EBPbeta	63	66	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	324	327	1.639871	TTGG	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	515	518	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	584	587	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	647	650	1.639871	TTGG	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	673	676	1.639871	TTGG	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1245	1248	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1400	1403	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1482	1485	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1545	1548	1.639871	TTGG	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1564	1567	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1588	1591	1.639871	TTGG	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1701	1704	1.639871	CCAA	15.625	15.72563
cg0932411	GEMIN8	Pax-5 [T0	620	626	1.537547	GGGCGC	0.73242	0.71311
cg0932411	GEMIN8	Pax-5 [T0	937	943	1.537547	GGGCGG	0.73242	0.71311
cg0932411	GEMIN8	TFIID [T0	1546	1552	1.537547	TGGAAA	0.73242	0.75096
cg0932411	GEMIN8	TFIID [T0	1812	1818	1.537547	TTTTGA	0.73242	0.75096
cg0932411	GEMIN8	TFIID [T0	1837	1843	1.537547	TGTAAA	0.73242	0.75096
cg0932411	GEMIN8	c-Ets-1 [T	1055	1061	1.513038	TTTCCTC	0.36621	0.36952
cg0932411	GEMIN8	STAT4 [T	589	594	1.470588	GGAAAC	1.95312	1.96333
cg0932411	GEMIN8	STAT4 [T	667	672	1.470588	TTTTCC	1.95312	1.96333
cg0932411	GEMIN8	STAT4 [T	1030	1035	1.470588	GTTTCC	1.95312	1.96333
cg0932411	GEMIN8	STAT4 [T	1073	1078	1.470588	TTTTCC	1.95312	1.96333

cg0932411	GEMIN8	STAT4 [T	1472	1477	1.470588	GGAATT	1.95312	1.96333
cg0932411	GEMIN8	STAT4 [T	1486	1491	1.470588	GGAAAA	1.95312	1.96333
cg0932411	GEMIN8	STAT4 [T	1547	1552	1.470588	GGAAAA	1.95312	1.96333
cg0932411	GEMIN8	C/EBPbeta	48	51	1.366559	TCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	122	125	1.366559	TTGA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	154	157	1.366559	TCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1182	1185	1.366559	TTGA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1210	1213	1.366559	TTGA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1584	1587	1.366559	TCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1814	1817	1.366559	TTGA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1848	1851	1.366559	TCAA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1887	1890	1.366559	TTGA	15.625	15.72563
cg0932411	GEMIN8	C/EBPbeta	1907	1910	1.366559	TTGA	15.625	15.72563
cg0932411	GEMIN8	HNF-3alpł	1527	1534	1.342935	TATTTTA	0.03052	0.03194
cg0932411	GEMIN8	ENKTF-1	758	765	1.255756	TGGCGT	0.24414	0.23904
cg0932411	GEMIN8	ENKTF-1	763	770	1.255756	TGGCGC	0.24414	0.23904
cg0932411	GEMIN8	C/EBPalpł	1885	1891	1.220508	TATTGA	0.24414	0.247
cg0932411	GEMIN8	PEA3 [T0	145	153	1.194633	AGACAT	0.06866	0.06895
cg0932411	GEMIN8	GCF [T00	772	780	1.070269	GCGCCG	0.18311	0.17647
cg0932411	GEMIN8	GCF [T00	874	882	1.070269	GCGCCG	0.18311	0.17647
cg0932411	GEMIN8	GCF [T00	968	976	1.070269	GCGCCG	0.18311	0.17647
cg0932411	GEMIN8	HNF-1A [	1038	1045	1.069403	CCTTTA	0.48828	0.49664
cg0932411	GEMIN8	GATA-1 [	1433	1438	1.038567	TATCAT	1.95312	1.98662
cg0932411	GEMIN8	CREB [T0	509	517	1.027269	TGACGT	0.05341	0.05293
cg0932411	GEMIN8	Sp1 [T007	936	945	0.949391	CGGGCG	0.01335	0.01279
cg0932411	GEMIN8	HNF-1A [	425	432	0.925521	CAATTA	0.48828	0.49664
cg0932411	GEMIN8	CREB [T0	797	805	0.91273	CGGACG	0.05341	0.05293
cg0932411	GEMIN8	GATA-1 [	1862	1867	0.863549	GTGATA	1.95312	1.98662
cg0932411	GEMIN8	GR-beta [	321	325	0.840383	TCATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	425	429	0.840383	CAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	426	430	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	437	441	0.840383	AATGA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	492	496	0.840383	TAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	493	497	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1152	1156	0.840383	TAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1340	1344	0.840383	TAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1341	1345	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1387	1391	0.840383	TCATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1411	1415	0.840383	CAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1412	1416	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1435	1439	0.840383	TCATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1447	1451	0.840383	CAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1448	1452	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1524	1528	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1543	1547	0.840383	AATTG	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1574	1578	0.840383	AATGG	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1585	1589	0.840383	CAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [	1586	1590	0.840383	AATTG	7.8125	7.94706

cg0932411	GEMIN8	GR-beta [T	1600	1604	0.840383	AATGA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1640	1644	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1646	1650	0.840383	AATGG	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1725	1729	0.840383	CCATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1760	1764	0.840383	AATTG	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1798	1802	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1823	1827	0.840383	AATGA	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1849	1853	0.840383	CAATT	7.8125	7.94706
cg0932411	GEMIN8	GR-beta [T	1955	1959	0.840383	AATTA	7.8125	7.94706
cg0932411	GEMIN8	NF-Y [T0	323	330	0.680578	ATTGGT	0.09155	0.09259
cg0932411	GEMIN8	AP-2alpha	1295	1300	0.678558	GCCTGA	0.48828	0.48199
cg0932411	GEMIN8	PR B [T00	1136	1142	0.48823	AACAGT	0.12207	0.12407
cg0932411	GEMIN8	PR A [T01	1136	1142	0.48823	AACAGT	0.12207	0.12407
cg0932411	GEMIN8	HNF-1A [	1190	1197	0.431647	AGATTA	0.24414	0.24974
cg0932411	GEMIN8	HNF-1A [	86	93	0.287765	GTTAAA	0.24414	0.24974
cg0932411	GEMIN8	HNF-1A [	1387	1394	0.287765	TCATTA	0.24414	0.24974
cg0932411	GEMIN8	HNF-1A [	1666	1673	0.287765	ACTTTA	0.24414	0.24974
cg0932411	GEMIN8	HNF-1A [	1892	1899	0.287765	GTTAAA	0.24414	0.24974
cg0932411	GEMIN8	GATA-1 [	50	55	0.280028	AAGATA	0.97656	0.99875
cg0932411	GEMIN8	GATA-1 [	488	493	0.280028	AAGATA	0.97656	0.99875
cg0932411	GEMIN8	GATA-1 [	1269	1274	0.280028	AAGATA	0.97656	0.99875
cg0932411	GEMIN8	GATA-1 [	1915	1920	0.280028	TATCTT	0.97656	0.99875
cg0932411	GEMIN8	c-Ets-1 [T	1108	1114	0.256174	CTTCCTT	0.24414	0.24569
cg0932411	GEMIN8	GR-alpha [	82	86	0.207689	AGAGG	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	130	134	0.207689	AGAGG	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	402	406	0.207689	CCTCT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	418	422	0.207689	CCTCT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	471	475	0.207689	CCTTT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	586	590	0.207689	AAAGG	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	683	687	0.207689	AGAGG	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	922	926	0.207689	AGAGG	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	1038	1042	0.207689	CCTTT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	1053	1057	0.207689	CCTTT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	1098	1102	0.207689	CCTTT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	1111	1115	0.207689	CCTTT	7.8125	7.81264
cg0932411	GEMIN8	PXR-1:RX	1773	1780	0.123583	TGAACT	0.12207	0.12407
cg0932411	GEMIN8	GATA-1 [	1001	1006	0.105011	GAGATA	0.97656	0.98738
cg0932411	GEMIN8	GATA-1 [	1779	1784	0.105011	GAGATA	0.97656	0.98738
cg0932411	GEMIN8	GR-alpha [	788	792	0	CCTGT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	1368	1372	0	CCTGT	7.8125	7.81264
cg0932411	GEMIN8	GR-alpha [	1492	1496	0	ACAGG	7.8125	7.81264
cg0932411	GEMIN8	AP-2alpha	816	821	0	GCAGGC	0.97656	0.95305
cg0932411	GEMIN8	AP-2alpha	847	852	0	GCCTGC	0.97656	0.95305
cg0932411	GEMIN8	AP-2alpha	885	890	0	GCAGGC	0.97656	0.95305
cg0932411	GEMIN8	XBP-1 [T	1385	1390	0	AGTCAT	0.97656	0.98127
cg0932411	GEMIN8	XBP-1 [T	1601	1606	0	ATGACG	0.97656	0.98127
cg0932411	GEMIN8	RXR-alph	1193	1199	0	TTAACC	0.24414	0.2444
cg0932411	GEMIN8	Pax-5 [T0	338	344	0	GGGCCC	1.09863	1.06846

cg0932411	GEMIN8	Pax-5 [T0	462	468	0	CCGGCC	1.09863	1.06846
cg0932411	GEMIN8	Pax-5 [T0	551	557	0	GGGCCC	1.09863	1.06846
cg0932411	GEMIN8	Pax-5 [T0	912	918	0	GGGCCG	1.09863	1.06846
cg0932411	GEMIN8	Pax-5 [T0	1363	1369	0	CCTGCC	1.09863	1.06846
cg0932411	GEMIN8	p53 [T006	1363	1369	0	CCTGCC	0.36621	0.35912
cg0932411	GEMIN8	TFII-I [T0	166	171	0	CTGTCC	1.46484	1.45997
cg0932411	GEMIN8	TFII-I [T0	1054	1059	0	CTTTCC	1.46484	1.45997
cg0932411	GEMIN8	TFII-I [T0	1721	1726	0	CTGTCC	1.46484	1.45997
cg0932411	GEMIN8	STAT4 [T	1571	1576	0	GGAAAT	0.48828	0.49387
cg0932411	GEMIN8	YY1 [T00	23	26	0	CCAT	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	203	206	0	ATGG	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	334	337	0	ATGG	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	454	457	0	ATGG	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	896	899	0	ATGG	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	1349	1352	0	CCAT	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	1453	1456	0	CCAT	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	1575	1578	0	ATGG	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	1647	1650	0	ATGG	7.8125	7.81711
cg0932411	GEMIN8	YY1 [T00	1725	1728	0	CCAT	7.8125	7.81711
cg0932411	GEMIN8	ER-alpha [	71	75	0	TGACC	1.95312	1.9404
cg0932411	GEMIN8	GATA-1 [	188	193	0	CAGATA	0.97656	0.98738
cg0932411	GEMIN8	GATA-1 [	1504	1509	0	CAGATA	0.97656	0.98738
cg0932411	GEMIN8	C/EBPbeta	16	19	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	94	97	0	GCAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	135	138	0	GCAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	207	210	0	GCAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	424	427	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	435	438	0	GCAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	475	478	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	503	506	0	GCAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	631	634	0	TTGC	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	717	720	0	TTGC	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1049	1052	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1084	1087	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1156	1159	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1234	1237	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1305	1308	0	TTGC	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1314	1317	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1337	1340	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1357	1360	0	GCAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1380	1383	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1393	1396	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1410	1413	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1446	1449	0	GCAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1567	1570	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1672	1675	0	ACAA	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1728	1731	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1762	1765	0	TTGT	15.625	15.71349

cg0932411	GEMIN8	C/EBPbeta	1975	1978	0	TTGC	15.625	15.71349
cg0932411	GEMIN8	C/EBPbeta	1986	1989	0	TTGT	15.625	15.71349
cg0932411	GEMIN8	TFIID [T0	119	125	0	TTTTTGA	1.09863	1.13474
cg0932411	GEMIN8	TFIID [T0	275	281	0	TTTAAA	1.09863	1.13474
cg0932411	GEMIN8	TFIID [T0	276	282	0	TTAAAA	1.09863	1.13474
cg0932411	GEMIN8	TFIID [T0	1182	1188	0	TTGAAA	1.09863	1.13474
cg0932411	GEMIN8	TFIID [T0	1530	1536	0	TTTAAA	1.09863	1.13474
cg0932411	GEMIN8	TFIID [T0	1531	1537	0	TTAAAA	1.09863	1.13474
cg0932411	GEMIN8	TFIID [T0	1950	1956	0	TTTAAA	1.09863	1.13474
cg0932411	GEMIN8	GR-beta [T	117	121	0	AATTT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1153	1157	0	AATTT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1319	1323	0	ACATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1375	1379	0	ACATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1474	1478	0	AATTT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1542	1546	0	AAATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1609	1613	0	ACATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1797	1801	0	AAATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1835	1839	0	AATGT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1850	1854	0	AATTT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1903	1907	0	AAATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1904	1908	0	AATTT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1947	1951	0	ACATT	3.90625	3.99611
cg0932411	GEMIN8	GR-beta [T	1954	1958	0	AAATT	3.90625	3.99611
cg0932411	GEMIN8	GR [T050	118	124	0	ATTTTTC	0.36621	0.37562
cg0932411	GEMIN8	GR [T050	1045	1051	0	CTTTTTG	0.36621	0.37562
cg0932411	GEMIN8	HNF-3alph	1183	1190	0	TGAAAA	0.09155	0.09511
cg0932411	GEMIN8	HNF-1A [	1660	1667	0	ATATTA	0.24414	0.25261
cg0932411	GEMIN8	IRF-2 [T0	1536	1541	0	AAGTGA	0.48828	0.49387
cg0932411	GEMIN8	c-Myc [T0	754	759	0	CACGTG	0.48828	0.48199
cg2521727	GNG4	RAR-beta:	428	439	9.97066	GGGCTC	0.06974	0.07677
cg0457660	GNG4	c-Ets-1 [T	867	873	9.969337	ATTCCC	0.24414	0.23698
cg0457660	GNG4	c-Ets-1 [T	1926	1932	9.969337	TGGGAA	0.24414	0.23698
cg2521727	GNG4	STAT5A [	1010	1022	9.952027	TTCAAA	0.01878	0.01703
cg0457660	GNG4	LEF-1 [T0	1799	1806	9.937995	CTTTGG	0.12207	0.1238
cg2521727	GNG4	PEA3 [T0	1951	1959	9.937959	TGGATG	0.18311	0.18382
cg0457660	GNG4	PEA3 [T0	442	450	9.937959	TCCCAT	0.18311	0.18382
cg2521727	GNG4	ELF-1 [T0	48	60	9.87459	ATACTT	0.00727	0.00709
cg0457660	GNG4	c-Ets-1 [T	703	709	9.841249	AGGGAA	0.24414	0.23698
cg2521727	GNG4	COUP-TF	105	117	9.828903	TGGGAG	0.02503	0.02544
cg0457660	GNG4	STAT1bet	334	343	9.807397	GTTTCC	0.14877	0.14533
cg0457660	GNG4	STAT1bet	1786	1795	9.807397	GTTTCC	0.14877	0.14533
cg2521727	GNG4	XBP-1 [T	266	271	9.789909	ATGGCT	1.95312	1.94901
cg2521727	GNG4	XBP-1 [T	868	873	9.789909	AGACAT	1.95312	1.94901
cg2521727	GNG4	XBP-1 [T	910	915	9.789909	ATGGCT	1.95312	1.94901
cg2521727	GNG4	XBP-1 [T	1146	1151	9.789909	ATGTCT	1.95312	1.94901
cg2521727	GNG4	XBP-1 [T	1164	1169	9.789909	CGCCAT	1.95312	1.94901
cg2521727	GNG4	XBP-1 [T	1510	1515	9.789909	ATGGCG	1.95312	1.94901
cg0457660	GNG4	XBP-1 [T	323	328	9.789909	AGCCAT	1.95312	1.94901

cg0457660	GNG4	XBP-1 [T	1676	1681	9.789909	ATGTCT	1.95312	1.94901
cg0457660	GNG4	XBP-1 [T	1931	1936	9.789909	ATGTCT	1.95312	1.94901
cg0457660	GNG4	Elk-1 [T00	887	895	9.754368	TGAGGG	0.10681	0.11027
cg2521727	GNG4	PR B [T00	743	749	9.743489	TTGTGTT	1.09863	1.0981
cg2521727	GNG4	PR A [T01	743	749	9.743489	TTGTGTT	1.09863	1.0981
cg0457660	GNG4	PR B [T00	964	970	9.743489	AACACA	1.09863	1.0981
cg0457660	GNG4	PR B [T00	1939	1945	9.743489	AACACA	1.09863	1.0981
cg0457660	GNG4	PR A [T01	964	970	9.743489	AACACA	1.09863	1.0981
cg0457660	GNG4	PR A [T01	1939	1945	9.743489	AACACA	1.09863	1.0981
cg0457660	GNG4	c-Myb [T0	1541	1548	9.729271	TAACTG	0.36621	0.34746
cg0457660	GNG4	LEF-1 [T0	1023	1030	9.72404	CTTTGC	0.21362	0.21229
cg0457660	GNG4	c-Jun [T00	396	402	9.717135	CAGGTC	0.73242	0.7366
cg0457660	GNG4	RAR-beta	331	340	9.641259	GGGGTT	0.21362	0.22369
cg0457660	GNG4	HNF-1C [	1651	1659	9.639597	AGAATT	0.19836	0.18179
cg0457660	GNG4	NF-AT2 [	1811	1820	9.5654	TACCATT	0.04578	0.04451
cg2521727	GNG4	TFIID [T0	456	462	9.552105	TCCCAA	1.46484	1.37777
cg2521727	GNG4	TFIID [T0	506	512	9.552105	TTTCTCA	1.46484	1.37777
cg2521727	GNG4	TFIID [T0	1858	1864	9.552105	TCCCAA	1.46484	1.37777
cg2521727	GNG4	Pax-5 [T0	1637	1643	9.552105	GTTGCC	1.46484	1.61918
cg2521727	GNG4	Pax-5 [T0	1804	1810	9.552105	GTTGCC	1.46484	1.61918
cg0457660	GNG4	TFIID [T0	1389	1395	9.552105	TCCCAA	1.46484	1.37777
cg0457660	GNG4	TFIID [T0	1444	1450	9.552105	TTTGAC	1.46484	1.37777
cg0457660	GNG4	Pax-5 [T0	36	42	9.552105	GGGCAA	1.46484	1.61918
cg0457660	GNG4	Pax-5 [T0	249	255	9.552105	GGGCAA	1.46484	1.61918
cg0457660	GNG4	Pax-5 [T0	1622	1628	9.552105	GGGCAA	1.46484	1.61918
cg0457660	GNG4	NF-1 [T00	1114	1121	9.535536	GTGGCC	0.73242	0.74634
cg2521727	GNG4	HNF-1B [	762	770	9.522068	TTTGTA	0.09155	0.08192
cg2521727	GNG4	FOXP3 [T	20	25	9.512894	GTTCTC	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	224	229	9.512894	GTTCTT	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	366	371	9.512894	GTTATT	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	497	502	9.512894	GCCAAC	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	604	609	9.512894	GTTCTG	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	623	628	9.512894	ACCAAC	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	1041	1046	9.512894	AAGAAC	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	1120	1125	9.512894	GTTATT	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	1152	1157	9.512894	GTTGCT	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	1490	1495	9.512894	CAGAAC	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	1570	1575	9.512894	GTTATT	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	1637	1642	9.512894	GTTGCC	7.32422	7.22156
cg2521727	GNG4	FOXP3 [T	1804	1809	9.512894	GTTGCC	7.32422	7.22156
cg2521727	GNG4	TFII-I [T0	195	200	9.512894	TTTTCC	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	318	323	9.512894	CCTTCC	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	630	635	9.512894	GGAAAA	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1035	1040	9.512894	GGAAGG	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1070	1075	9.512894	GGACAC	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1241	1246	9.512894	GGATAC	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1253	1258	9.512894	GGAAAA	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1344	1349	9.512894	TTGTCC	7.32422	7.44385

cg2521727	GNG4	TFII-I [T0	1387	1392	9.512894	GGATGG	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1403	1408	9.512894	GGATAA	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1952	1957	9.512894	GGATGG	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1961	1966	9.512894	AAGTCC	7.32422	7.44385
cg2521727	GNG4	TFII-I [T0	1972	1977	9.512894	GGATAA	7.32422	7.44385
cg0457660	GNG4	FOXP3 [T	37	42	9.512894	GGCAAC	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	182	187	9.512894	GTTTAT	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	242	247	9.512894	GTTCTT	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	342	347	9.512894	CAGAAC	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	525	530	9.512894	GTTGCT	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	629	634	9.512894	GAGAAC	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	813	818	9.512894	AGCAAC	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	961	966	9.512894	AATAAC	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	1794	1799	9.512894	GTTGCC	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	1844	1849	9.512894	GTTATT	7.32422	7.22156
cg0457660	GNG4	FOXP3 [T	1904	1909	9.512894	GTTGCT	7.32422	7.22156
cg0457660	GNG4	TFII-I [T0	152	157	9.512894	TTTTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	159	164	9.512894	GTTTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	334	339	9.512894	GTTTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	436	441	9.512894	GGACAC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	444	449	9.512894	CCATCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	539	544	9.512894	TTTTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	594	599	9.512894	CCATCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	1120	1125	9.512894	AATTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	1436	1441	9.512894	AATTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	1505	1510	9.512894	GGAAAA	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	1524	1529	9.512894	TTTTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	1786	1791	9.512894	GTTTCC	7.32422	7.44385
cg0457660	GNG4	TFII-I [T0	1958	1963	9.512894	GGAACG	7.32422	7.44385
cg0457660	GNG4	c-Jun [T00	737	743	9.511322	TGACCA	0.73242	0.7366
cg0457660	GNG4	TCF-4E [	399	405	9.453578	GTCAAA	0.48828	0.46934
cg0457660	GNG4	TCF-4E [	1480	1486	9.453578	TACAAA	0.48828	0.46934
cg2521727	GNG4	c-Jun [T00	1058	1064	9.442241	GCTGTC	0.73242	0.7366
cg2521727	GNG4	c-Jun [T00	1299	1305	9.442241	TGACAG	0.73242	0.7366
cg0457660	GNG4	c-Jun [T00	1561	1567	9.442241	GCTGTC	0.73242	0.7366
cg2521727	GNG4	c-Jun [T00	872	878	9.397655	ATTGTC	0.73242	0.7366
cg2521727	GNG4	c-Ets-1 [T	823	829	9.276861	TGGGAA	0.36621	0.37402
cg0457660	GNG4	SRY [T00	397	405	9.264664	AGGTCA	0.12207	0.11857
cg0457660	GNG4	NF-kappa	1926	1937	9.230305	TGGGAA	0.01872	0.01973
cg0457660	GNG4	NF-AT1 [	299	307	9.18189	TCCCTT	0.22888	0.22581
cg0457660	GNG4	NF-AT1 [	156	164	9.158155	CCTGTT	0.22888	0.22581
cg0457660	GNG4	c-Ets-1 [T	297	303	9.148774	GTTCCC	0.85449	0.84987
cg2521727	GNG4	PXR-1:RX	155	162	9.122407	TGAACA	0.24414	0.24356
cg2521727	GNG4	STAT5A [	552	564	9.080962	CTCCCA	0.02816	0.02551
cg2521727	GNG4	HNF-1B [	26	34	9.080623	AGTTAA	0.08392	0.07596
cg0457660	GNG4	c-Ets-1 [T	1437	1443	9.065503	ATTCCA	0.85449	0.84987
cg0457660	GNG4	AhR [T01	1179	1189	9.058053	AGTGGC	0.03242	0.03333
cg2521727	GNG4	USF2 [T0	1741	1750	9.056375	CAGGTG	0.1545	0.16206

cg0457660	GNG4	c-Ets-1 [T	1965	1971	9.020687	GGGGAA	0.85449	0.84987
cg0457660	GNG4	NF-AT2 [	727	736	9.016873	GGATCT	0.05341	0.05145
cg2521727	GNG4	c-Jun [T00	187	193	9.013496	TGACAT	0.61035	0.60549
cg0457660	GNG4	c-Jun [T00	1446	1452	9.013496	TGACAT	0.61035	0.60549
cg0457660	GNG4	MEF-2A [	1297	1307	9.003254	TATTTTT	0.07343	0.06466
cg2521727	GNG4	PXR-1:RX	1329	1336	8.998824	GTTGTT	0.24414	0.24356
cg2521727	GNG4	LEF-1 [T0	456	463	8.973041	TCCCAA	0.54932	0.53171
cg2521727	GNG4	LEF-1 [T0	1858	1865	8.973041	TCCCAA	0.54932	0.53171
cg0457660	GNG4	LEF-1 [T0	1389	1396	8.973041	TCCCAA	0.54932	0.53171
cg2521727	GNG4	GR [T050	930	936	8.971049	CAAAAG	0.61035	0.5928
cg0457660	GNG4	GR [T050	401	407	8.971049	CAAAGC	0.61035	0.5928
cg0457660	GNG4	GR [T050	1556	1562	8.971049	CAAAAG	0.61035	0.5928
cg0457660	GNG4	EBF [T05	30	40	8.948874	CACCCT	0.01526	0.01642
cg2521727	GNG4	c-Myb [T0	1492	1499	8.947824	GAACTT	0.39673	0.37851
cg2521727	GNG4	c-Myb [T0	1791	1798	8.947824	AGAAGT	0.39673	0.37851
cg0457660	GNG4	c-Ets-1 [T	664	670	8.937416	ATTCCA	0.85449	0.84987
cg2521727	GNG4	c-Ets-2 [T	320	328	8.912323	TTCCTG	0.27466	0.27171
cg0457660	GNG4	c-Ets-2 [T	712	720	8.912323	TTCCTG	0.27466	0.27171
cg0457660	GNG4	c-Ets-2 [T	733	741	8.912323	TTCCTG	0.27466	0.27171
cg0457660	GNG4	c-Ets-2 [T	1644	1652	8.912323	TTCCTG	0.27466	0.27171
cg2521727	GNG4	c-Myb [T0	362	369	8.872587	GCTAGT	0.39673	0.37851
cg0457660	GNG4	HOXD9 [	1861	1870	8.847863	TAGTGC	0.04578	0.03831
cg0457660	GNG4	HOXD10 [	1861	1870	8.847863	TAGTGC	0.04578	0.03831
cg2521727	GNG4	PR B [T00	1084	1090	8.827054	ATCTGT	0.36621	0.35051
cg2521727	GNG4	PR A [T01	1084	1090	8.827054	ATCTGT	0.36621	0.35051
cg2521727	GNG4	NFI/CTF [	32	39	8.814757	CCAAAA	0.48828	0.48845
cg0457660	GNG4	c-Ets-1 [T	1569	1575	8.809329	ATTCCA	0.85449	0.84987
cg2521727	GNG4	c-Jun [T00	840	846	8.807683	TGACGA	0.61035	0.60549
cg0457660	GNG4	NF-AT2 [	148	157	8.794303	CACCTT	0.05341	0.05145
cg2521727	GNG4	NF-1 [T00	454	461	8.790071	CCTCCC	0.24414	0.24339
cg2521727	GNG4	NF-1 [T00	1856	1863	8.790071	CCTCCC	0.24414	0.24339
cg0457660	GNG4	NF-1 [T00	1387	1394	8.790071	CCTCCC	0.24414	0.24339
cg2521727	GNG4	LEF-1 [T0	741	748	8.759086	CTTTGT	0.54932	0.53171
cg0457660	GNG4	LEF-1 [T0	1479	1486	8.759086	TTACAA	0.54932	0.53171
cg2521727	GNG4	XBP-1 [T	480	485	8.75604	ATGAGC	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	508	513	8.75604	TCTCAT	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	547	552	8.75604	ATGAGC	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	969	974	8.75604	TTTCAT	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	993	998	8.75604	ATGAAA	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	1080	1085	8.75604	GATCAT	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	1332	1337	8.75604	GTTCAT	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	1497	1502	8.75604	TCTCAT	2.92969	2.75329
cg2521727	GNG4	XBP-1 [T	1628	1633	8.75604	TCTCAT	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T	80	85	8.75604	ATGAGA	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T	85	90	8.75604	ATGATC	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T	849	854	8.75604	TTTCAT	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T	1091	1096	8.75604	GATCAT	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T	1450	1455	8.75604	ATGATA	2.92969	2.75329

cg0457660	GNG4	XBP-1 [T0	1510	1515	8.75604	ATGATA	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T0	1531	1536	8.75604	TTTCAT	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T0	1730	1735	8.75604	TCTCAT	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T0	1735	1740	8.75604	TTTCAT	2.92969	2.75329
cg0457660	GNG4	XBP-1 [T0	1750	1755	8.75604	ATGAGA	2.92969	2.75329
cg0457660	GNG4	RAR-beta	115	124	8.541284	AGGGTT	0.26703	0.27434
cg0457660	GNG4	p53 [T006	601	607	8.537081	GGGCTC	0.12207	0.13169
cg0457660	GNG4	NF-AT1 [	1505	1513	8.532897	GGAAAA	0.10681	0.10494
cg0457660	GNG4	HNF-1B [	1606	1614	8.482557	TCTATA	0.11444	0.10456
cg0457660	GNG4	LEF-1 [T0	1084	1091	8.457856	CTTCAA	0.15259	0.154
cg2521727	GNG4	c-Ets-1 [T	1088	1094	8.373028	GTTCCA	0.24414	0.23702
cg0457660	GNG4	LEF-1 [T0	249	256	8.361499	GGGCAA	0.15259	0.154
cg2521727	GNG4	HNF-3alph	1597	1604	8.343064	AATTTA	0.27466	0.23078
cg0457660	GNG4	HNF-3alph	752	759	8.343064	TTTAAA	0.27466	0.23078
cg2521727	GNG4	c-Ets-2 [T	781	789	8.339336	TTCCTG	0.13733	0.13927
cg2521727	GNG4	PR B [T00	72	78	8.338824	AACAGC	1.09863	1.09384
cg2521727	GNG4	PR B [T00	157	163	8.338824	AACAGC	1.09863	1.09384
cg2521727	GNG4	PR B [T00	592	598	8.338824	AACAGA	1.09863	1.09384
cg2521727	GNG4	PR B [T00	1148	1154	8.338824	GTCTGT	1.09863	1.09384
cg2521727	GNG4	PR B [T00	1633	1639	8.338824	TTCTGT	1.09863	1.09384
cg2521727	GNG4	PR A [T01	72	78	8.338824	AACAGC	1.09863	1.09384
cg2521727	GNG4	PR A [T01	157	163	8.338824	AACAGC	1.09863	1.09384
cg2521727	GNG4	PR A [T01	592	598	8.338824	AACAGA	1.09863	1.09384
cg2521727	GNG4	PR A [T01	1148	1154	8.338824	GTCTGT	1.09863	1.09384
cg2521727	GNG4	PR A [T01	1633	1639	8.338824	TTCTGT	1.09863	1.09384
cg0457660	GNG4	PR B [T00	40	46	8.338824	AACAGA	1.09863	1.09384
cg0457660	GNG4	PR B [T00	52	58	8.338824	CTCTGT	1.09863	1.09384
cg0457660	GNG4	PR B [T00	155	161	8.338824	TCCTGT	1.09863	1.09384
cg0457660	GNG4	PR B [T00	1670	1676	8.338824	AACAGG	1.09863	1.09384
cg0457660	GNG4	PR B [T00	1875	1881	8.338824	AACAGG	1.09863	1.09384
cg0457660	GNG4	PR A [T01	40	46	8.338824	AACAGA	1.09863	1.09384
cg0457660	GNG4	PR A [T01	52	58	8.338824	CTCTGT	1.09863	1.09384
cg0457660	GNG4	PR A [T01	155	161	8.338824	TCCTGT	1.09863	1.09384
cg0457660	GNG4	PR A [T01	1670	1676	8.338824	AACAGG	1.09863	1.09384
cg0457660	GNG4	PR A [T01	1875	1881	8.338824	AACAGG	1.09863	1.09384
cg2521727	GNG4	ATF3 [T0	1272	1279	8.313799	TGACGC	0.27466	0.27379
cg0457660	GNG4	PXR-1:RX	1885	1892	8.304332	TGAACA	0.12207	0.11843
cg2521727	GNG4	GR-alpha [	54	58	8.281568	CCTTC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	97	101	8.281568	GGAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	107	111	8.281568	GGAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	134	138	8.281568	GGAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	176	180	8.281568	CAAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	199	203	8.281568	CCTTC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	289	293	8.281568	CCTCC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	308	312	8.281568	CCTCC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	315	319	8.281568	CCTCC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	318	322	8.281568	CCTTC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	454	458	8.281568	CCTCC	7.8125	8.20394

cg2521727	GNG4	GR-alpha [	651	655	8.281568	GGAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	728	732	8.281568	CAAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1036	1040	8.281568	GAAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1054	1058	8.281568	GAAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1130	1134	8.281568	CCTTG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1474	1478	8.281568	CCTTC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1532	1536	8.281568	CCTCC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1556	1560	8.281568	GGAGG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1682	1686	8.281568	CCTTG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1826	1830	8.281568	CCTTG	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1843	1847	8.281568	CCTCC	7.8125	8.20394
cg2521727	GNG4	GR-alpha [	1856	1860	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	131	135	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	479	483	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	678	682	8.281568	CCTTG	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	698	702	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	719	723	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	774	778	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	842	846	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1007	1011	8.281568	GGAGG	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1014	1018	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1083	1087	8.281568	CCTTC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1211	1215	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1387	1391	8.281568	CCTCC	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1618	1622	8.281568	CCTCG	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1696	1700	8.281568	CAAGG	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1782	1786	8.281568	GAAGG	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1790	1794	8.281568	CCTTG	7.8125	8.20394
cg0457660	GNG4	GR-alpha [	1993	1997	8.281568	CAAGG	7.8125	8.20394
cg2521727	GNG4	c-Ets-1 [T	1409	1415	8.244941	GTTCCA	0.24414	0.2494
cg2521727	GNG4	c-Jun [T00	108	114	8.242207	GAGGTC	0.48828	0.47447
cg0457660	GNG4	c-Jun [T00	695	701	8.242207	TGACCT	0.48828	0.47447
cg0457660	GNG4	c-Jun [T00	716	722	8.242207	TGACCT	0.48828	0.47447
cg0457660	GNG4	c-Jun [T00	1360	1366	8.242207	TGACCT	0.48828	0.47447
cg0457660	GNG4	c-Jun [T00	1975	1981	8.242207	TGACCT	0.48828	0.47447
cg2521727	GNG4	NFI/CTF [	1965	1972	8.241664	CCAACC	0.18311	0.1922
cg2521727	GNG4	NF-AT2 [	191	200	8.21356	ATGTTT	0.08965	0.08482
cg0457660	GNG4	p53 [T006	235	241	8.208781	GGGGCC	0.48828	0.55336
cg2521727	GNG4	ENKTF-1	493	500	8.19852	CCCGGC	0.73242	0.80254
cg2521727	GNG4	ENKTF-1	1511	1518	8.19852	TGGCGG	0.73242	0.80254
cg0457660	GNG4	ENKTF-1	316	323	8.19852	TCTCGC	0.73242	0.80254
cg0457660	GNG4	ENKTF-1	1028	1035	8.19852	CCTGGC	0.73242	0.80254
cg2521727	GNG4	NF-1 [T00	1828	1835	8.191058	TTGGCC	0.24414	0.24485
cg2521727	GNG4	SRY [T00	1008	1016	8.174786	TATTCA	0.15259	0.14791
cg2521727	GNG4	SRY [T00	1096	1104	8.174786	CATTCA	0.15259	0.14791
cg0457660	GNG4	SRY [T00	1083	1091	8.174786	CCTTCA	0.15259	0.14791
cg0457660	GNG4	NF-AT1 [	1521	1529	8.12076	GAGTTT	0.1297	0.12846
cg2521727	GNG4	LEF-1 [T0	1009	1016	8.117221	ATTCAA	0.12207	0.11275

cg2521727	GNG4	LEF-1 [T0	1097	1104	8.117221	ATTCAA	0.12207	0.11275
cg0457660	GNG4	c-Ets-1 [T	1684	1690	8.116854	GTTCCAC	0.24414	0.2494
cg0457660	GNG4	c-Ets-1 [T	1956	1962	8.116854	CTGGAA	0.24414	0.2494
cg0457660	GNG4	HNF-4alph	1482	1494	8.080203	CAAAGT	0.01502	0.01404
cg2521727	GNG4	VDR [T00	1332	1340	8.079962	GTTCATC	0.24414	0.22992
cg0457660	GNG4	VDR [T00	225	233	8.079962	ATTCTGA	0.24414	0.22992
cg2521727	GNG4	IRF-1 [T0	1226	1234	8.078284	GCCTGG	0.25177	0.2462
cg2521727	GNG4	IRF-1 [T0	1247	1255	8.078284	TTTCCAC	0.25177	0.2462
cg2521727	GNG4	GR-alpha	93	97	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	103	107	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	170	174	8.073878	GCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	240	244	8.073878	CCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	273	277	8.073878	CCTGC	7.8125	8.20289
cg2521727	GNG4	GR-alpha	292	296	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	311	315	8.073878	CCTGC	7.8125	8.20289
cg2521727	GNG4	GR-alpha	425	429	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	449	453	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	534	538	8.073878	CCTAG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	535	539	8.073878	CTAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	669	673	8.073878	CCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	783	787	8.073878	CCTGC	7.8125	8.20289
cg2521727	GNG4	GR-alpha	857	861	8.073878	CCTAG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1227	1231	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1250	1254	8.073878	CCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1305	1309	8.073878	CCTGC	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1318	1322	8.073878	CCTGC	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1378	1382	8.073878	GCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1399	1403	8.073878	GCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1422	1426	8.073878	CCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1552	1556	8.073878	CCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1691	1695	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1809	1813	8.073878	CCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1917	1921	8.073878	CCAGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1927	1931	8.073878	CCTGG	7.8125	8.20289
cg2521727	GNG4	GR-alpha	1969	1973	8.073878	CCAGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	33	37	8.073878	CCTGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	113	117	8.073878	CCAGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	201	205	8.073878	CCTGC	7.8125	8.20289
cg0457660	GNG4	GR-alpha	356	360	8.073878	CCTGC	7.8125	8.20289
cg0457660	GNG4	GR-alpha	378	382	8.073878	CCTGC	7.8125	8.20289
cg0457660	GNG4	GR-alpha	564	568	8.073878	GCAGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	598	602	8.073878	CCTGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	701	705	8.073878	CCAGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	830	834	8.073878	GTAGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	1028	1032	8.073878	CCTGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	1165	1169	8.073878	CCAGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	1214	1218	8.073878	CCTGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha	1233	1237	8.073878	CCTGC	7.8125	8.20289

cg0457660	GNG4	GR-alpha [	1340	1344	8.073878	CCAGG	7.8125	8.20289
cg0457660	GNG4	GR-alpha [	1578	1582	8.073878	CCTAG	7.8125	8.20289
cg0457660	GNG4	GR-alpha [	1986	1990	8.073878	GTAGG	7.8125	8.20289
cg0457660	GNG4	HNF-1C [	1605	1613	8.067744	TTCTAT	0.19836	0.18126
cg2521727	GNG4	TFIID [T0	566	572	8.014558	TTAGAA	2.19727	1.99811
cg2521727	GNG4	TFIID [T0	642	648	8.014558	TTTCAG	2.19727	1.99811
cg2521727	GNG4	TFIID [T0	762	768	8.014558	TTTGTA	2.19727	1.99811
cg2521727	GNG4	TFIID [T0	920	926	8.014558	TCTGAA	2.19727	1.99811
cg2521727	GNG4	TFIID [T0	1616	1622	8.014558	TTTGAG	2.19727	1.99811
cg2521727	GNG4	Pax-5 [T0	295	301	8.014558	GGGCTC	2.19727	2.42766
cg2521727	GNG4	Pax-5 [T0	428	434	8.014558	GGGCTC	2.19727	2.42766
cg2521727	GNG4	Pax-5 [T0	1453	1459	8.014558	TCTGCC	2.19727	2.42766
cg2521727	GNG4	Pax-5 [T0	1694	1700	8.014558	GGGCTC	2.19727	2.42766
cg2521727	GNG4	Pax-5 [T0	1755	1761	8.014558	TGTGCC	2.19727	2.42766
cg0457660	GNG4	TFIID [T0	876	882	8.014558	TTGCAA	2.19727	1.99811
cg0457660	GNG4	TFIID [T0	1139	1145	8.014558	TTTGAG	2.19727	1.99811
cg0457660	GNG4	TFIID [T0	1349	1355	8.014558	TCTCAA	2.19727	1.99811
cg0457660	GNG4	TFIID [T0	1479	1485	8.014558	TTACAA	2.19727	1.99811
cg0457660	GNG4	TFIID [T0	1660	1666	8.014558	TTTGTTA	2.19727	1.99811
cg0457660	GNG4	TFIID [T0	1869	1875	8.014558	TTTGCA	2.19727	1.99811
cg0457660	GNG4	TFIID [T0	1870	1876	8.014558	TTGCAA	2.19727	1.99811
cg0457660	GNG4	Pax-5 [T0	145	151	8.014558	GGGCAC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	235	241	8.014558	GGGGCC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	373	379	8.014558	GCAGCC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	386	392	8.014558	TGGGCC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	387	393	8.014558	GGGCCC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	785	791	8.014558	GCAGCC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	1239	1245	8.014558	TCAGCC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	1335	1341	8.014558	GGTGCC	2.19727	2.42766
cg0457660	GNG4	Pax-5 [T0	1414	1420	8.014558	TGAGCC	2.19727	2.42766
cg2521727	GNG4	c-Ets-2 [T	855	863	7.84116	TTCCTAC	0.32043	0.30792
cg2521727	GNG4	c-Ets-2 [T	1248	1256	7.84116	TTCCAGC	0.32043	0.30792
cg2521727	GNG4	IRF-1 [T0	1249	1257	7.82345	TCCAGG	0.25177	0.2462
cg0457660	GNG4	IRF-1 [T0	711	719	7.82345	TTTCCTC	0.25177	0.2462
cg0457660	GNG4	IRF-1 [T0	732	740	7.82345	TTTCCTC	0.25177	0.2462
cg2521727	GNG4	T3R-beta1	1933	1941	7.813363	GGTGGG	0.27466	0.28753
cg0457660	GNG4	GATA-2 [	1451	1459	7.777778	TGATAT	0.30518	0.29346
cg0457660	GNG4	T3R-beta1	1161	1169	7.774776	TCACCC	0.27466	0.28753
cg2521727	GNG4	c-Myb [T0	23	30	7.739476	CTCAGT	0.42725	0.40917
cg0457660	GNG4	HNF-1B [	1662	1670	7.737819	TGTTAA	0.09155	0.08229
cg0457660	GNG4	IRF-1 [T0	540	548	7.732782	TTTCCAC	0.14496	0.14723
cg0457660	GNG4	LEF-1 [T0	398	405	7.719635	GGTCAA	0.21362	0.21504
cg0457660	GNG4	EBF [T05	515	525	7.659914	TCCTCAC	0.01144	0.0122
cg0457660	GNG4	NFI/CTF [	381	388	7.587343	GCTCTTC	0.36621	0.36269
cg2521727	GNG4	GR [T050	33	39	7.527031	CAAAAG	1.83105	1.71535
cg2521727	GNG4	GR [T050	70	76	7.527031	CAAACA	1.83105	1.71535
cg2521727	GNG4	GR [T050	543	549	7.527031	CAAAAT	1.83105	1.71535
cg2521727	GNG4	GR [T050	590	596	7.527031	CAAACA	1.83105	1.71535

cg2521727	GNG4	GR [T050	709	715	7.527031	TTATTT	1.83105	1.71535
cg2521727	GNG4	GR [T050	759	765	7.527031	CCTTTT	1.83105	1.71535
cg0457660	GNG4	GR [T050	140	146	7.527031	CAAAAG	1.83105	1.71535
cg0457660	GNG4	GR [T050	252	258	7.527031	CAAAGC	1.83105	1.71535
cg0457660	GNG4	GR [T050	938	944	7.527031	CAAAAT	1.83105	1.71535
cg0457660	GNG4	GR [T050	1441	1447	7.527031	CATTTT	1.83105	1.71535
cg0457660	GNG4	GR [T050	1515	1521	7.527031	AATTTT	1.83105	1.71535
cg0457660	GNG4	GR [T050	1721	1727	7.527031	AATTTT	1.83105	1.71535
cg0457660	GNG4	GR [T050	1845	1851	7.527031	TTATTT	1.83105	1.71535
cg0457660	GNG4	GR [T050	1866	1872	7.527031	CTATTT	1.83105	1.71535
cg0457660	GNG4	GR [T050	1873	1879	7.527031	CAAACA	1.83105	1.71535
cg2521727	GNG4	RBP-Jkapp	1417	1428	7.483495	TCTTCC	0.02337	0.02319
cg2521727	GNG4	RAR-beta:	1694	1705	7.477995	GGGCTC	0.02861	0.03163
cg2521727	GNG4	PEA3 [T0	13	21	7.421728	TGGATG	0.34332	0.35389
cg2521727	GNG4	PEA3 [T0	658	666	7.421728	TGGATG	0.34332	0.35389
cg0457660	GNG4	AR [T000	686	694	7.406474	CAGCTG	0.25177	0.2544
cg2521727	GNG4	LEF-1 [T0	518	525	7.396545	GTGCAA	0.21362	0.21504
cg2521727	GNG4	PPAR-alph	1730	1740	7.370536	TGCTGG	0.04482	0.04884
cg2521727	GNG4	PXR-1:RX	724	731	7.362674	TGAACA	0.24414	0.24326
cg2521727	GNG4	HNF-1B [	896	904	7.353754	TAAGTA	0.09155	0.08229
cg2521727	GNG4	HNF-1C [	895	903	7.313515	TTAAGT	0.08392	0.07663
cg0457660	GNG4	HOXD9 [	530	539	7.270719	TTTTTAT	0.06866	0.05771
cg0457660	GNG4	HOXD9 [	961	970	7.270719	AATAAC	0.06866	0.05771
cg0457660	GNG4	HOXD10 [	530	539	7.270719	TTTTTAT	0.06866	0.05771
cg0457660	GNG4	HOXD10 [	961	970	7.270719	AATAAC	0.06866	0.05771
cg2521727	GNG4	p53 [T006	123	129	7.266844	GGGCTG	0.73242	0.79826
cg2521727	GNG4	p53 [T006	158	164	7.266844	ACAGCC	0.73242	0.79826
cg0457660	GNG4	p53 [T006	575	581	7.266844	GGGCTG	0.73242	0.79826
cg2521727	GNG4	NF-AT1 [	1576	1584	7.211175	TCTCTTT	0.15259	0.14325
cg2521727	GNG4	SRY [T00	721	729	7.175614	CTTTGA	0.30518	0.29547
cg2521727	GNG4	SRY [T00	741	749	7.175614	CTTTGT	0.30518	0.29547
cg2521727	GNG4	XBP-1 [T	16	21	7.172312	ATGAGT	2.92969	2.7512
cg2521727	GNG4	XBP-1 [T	262	267	7.172312	CATCAT	2.92969	2.7512
cg2521727	GNG4	XBP-1 [T	561	566	7.172312	ATGAAT	2.92969	2.7512
cg2521727	GNG4	XBP-1 [T	661	666	7.172312	ATGAGG	2.92969	2.7512
cg2521727	GNG4	XBP-1 [T	1213	1218	7.172312	ACTCAT	2.92969	2.7512
cg2521727	GNG4	XBP-1 [T	1294	1299	7.172312	ATGAGT	2.92969	2.7512
cg2521727	GNG4	XBP-1 [T	1371	1376	7.172312	ATGAAT	2.92969	2.7512
cg2521727	GNG4	XBP-1 [T	1664	1669	7.172312	AATCAT	2.92969	2.7512
cg0457660	GNG4	XBP-1 [T	793	798	7.172312	CCTCAT	2.92969	2.7512
cg0457660	GNG4	XBP-1 [T	796	801	7.172312	CATCAT	2.92969	2.7512
cg0457660	GNG4	XBP-1 [T	897	902	7.172312	ATGATT	2.92969	2.7512
cg0457660	GNG4	XBP-1 [T	1598	1603	7.172312	ATGAAT	2.92969	2.7512
cg0457660	GNG4	XBP-1 [T	1631	1636	7.172312	ATTCAT	2.92969	2.7512
cg0457660	GNG4	p53 [T006	386	392	7.153797	TGGGCC	1.09863	1.22478
cg0457660	GNG4	p53 [T006	387	393	7.153797	GGGCCC	1.09863	1.22478
cg0457660	GNG4	c-Myb [T0	133	140	7.127234	TCCAGT	0.18311	0.17765
cg0457660	GNG4	c-Myb [T0	1838	1845	7.127234	TAACTG	0.18311	0.17765

cg2521727	GNG4	Ik-1 [T027	97	109	7.122895	GGAGGG	0.01064	0.01145
cg2521727	GNG4	Ik-1 [T027	324	336	7.122895	TGAGGA	0.01064	0.01145
cg2521727	GNG4	Ik-1 [T027	1517	1529	7.122895	GACAGT	0.01064	0.01145
cg0457660	GNG4	Ik-1 [T027	1823	1835	7.122895	TCCCAG	0.01064	0.01145
cg0457660	GNG4	c-Ets-1 [T	160	166	7.071349	TTTCCCT	0.73242	0.73732
cg0457660	GNG4	IRF-1 [T0	1501	1509	7.044985	TAGAGG	0.1297	0.12685
cg0457660	GNG4	IRF-1 [T0	1816	1824	7.044985	TTTCCTC	0.1297	0.12685
cg0457660	GNG4	IRF-1 [T0	303	311	7.041849	TTTCCCC	0.1297	0.12685
cg2521727	GNG4	C/EBPalph	871	877	7.00174	CATTGT	0.73242	0.68282
cg2521727	GNG4	HNF-3alph	568	575	7.000129	AGAAAA	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	638	645	7.000129	TATTTT	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	691	698	7.000129	TATTTCT	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	710	717	7.000129	TATTTGT	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	1015	1022	7.000129	AGAAAA	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	1229	1236	7.000129	TGGAAA	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	1602	1609	7.000129	AAAAAA	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	1612	1619	7.000129	TATTTT	0.82397	0.71909
cg2521727	GNG4	HNF-3alph	1775	1782	7.000129	AATTTTT	0.82397	0.71909
cg0457660	GNG4	HNF-3alph	536	543	7.000129	TATTTT	0.82397	0.71909
cg0457660	GNG4	HNF-3alph	902	909	7.000129	TATTTCT	0.82397	0.71909
cg0457660	GNG4	HNF-3alph	951	958	7.000129	TAAAAA	0.82397	0.71909
cg0457660	GNG4	HNF-3alph	1441	1448	7.000129	CATTTC	0.82397	0.71909
cg0457660	GNG4	HNF-3alph	1601	1608	7.000129	AATTTC	0.82397	0.71909
cg0457660	GNG4	HNF-3alph	1634	1641	7.000129	CATTTTT	0.82397	0.71909
cg0457660	GNG4	HNF-3alph	1867	1874	7.000129	TATTTGC	0.82397	0.71909
cg0457660	GNG4	AR [T000	944	952	6.976688	GGACAT	0.23651	0.23986
cg2521727	GNG4	NF-1 [T00	1425	1432	6.948522	GGAGCC	0.48828	0.50205
cg0457660	GNG4	NF-1 [T00	1801	1808	6.948522	TTGGCTC	0.48828	0.50205
cg0457660	GNG4	c-Ets-1 [T	303	309	6.943262	TTTCCCC	0.73242	0.73732
cg0457660	GNG4	ENKTF-1	14	21	6.942764	TCGCGC	1.46484	1.56616
cg0457660	GNG4	ENKTF-1	360	367	6.942764	CACGGC	1.46484	1.56616
cg0457660	GNG4	ENKTF-1	1181	1188	6.942764	TGGCGT	1.46484	1.56616
cg0457660	GNG4	ENKTF-1	1852	1859	6.942764	CTTGGC	1.46484	1.56616
cg0457660	GNG4	AhR:Arnt	1277	1286	6.928166	CCACGC	0.0515	0.0599
cg2521727	GNG4	VDR [T00	1681	1689	6.925682	GCCTTG	0.42725	0.41
cg0457660	GNG4	VDR [T00	1881	1889	6.925682	CTCCTG	0.42725	0.41
cg0457660	GNG4	VDR [T00	1990	1998	6.925682	GTTCAA	0.42725	0.41
cg0457660	GNG4	STAT1bet	159	168	6.908963	GTTTCCC	0.103	0.09938
cg0457660	GNG4	C/EBPalph	221	227	6.85549	TGCAAT	0.73242	0.68282
cg0457660	GNG4	C/EBPalph	1718	1724	6.85549	TGCAAT	0.73242	0.68282
cg0457660	GNG4	C/EBPalph	1914	1920	6.85549	AATTGC	0.73242	0.68282
cg2521727	GNG4	E2F-1 [T0	255	262	6.839754	GCGGCA	0.30518	0.33862
cg2521727	GNG4	HNF-1B [	1119	1127	6.831535	GGTTAT	0.07629	0.07044
cg0457660	GNG4	PEA3 [T0	592	600	6.824411	CTCCATC	0.22888	0.22744
cg0457660	GNG4	NF-AT1 [	728	736	6.799037	GATCTTT	0.15259	0.14325
cg2521727	GNG4	c-Jun [T00	232	238	6.787369	TCTGTCA	0.73242	0.73062
cg2521727	GNG4	c-Jun [T00	1487	1493	6.787369	TGACAG	0.73242	0.73062
cg0457660	GNG4	NFI/CTF [	484	491	6.786076	CCAATC	0.73242	0.74795

cg0457660	GNG4	NFI/CTF [	1849	1856	6.786076	TTGCTTC	0.73242	0.74795
cg2521727	GNG4	p53 [T006	295	301	6.778774	GGGCTC	1.09863	1.22478
cg2521727	GNG4	p53 [T006	428	434	6.778774	GGGCTC	1.09863	1.22478
cg2521727	GNG4	p53 [T006	1694	1700	6.778774	GGGCTC	1.09863	1.22478
cg0457660	GNG4	p53 [T006	1414	1420	6.778774	TGAGCC	1.09863	1.22478
cg2521727	GNG4	LEF-1 [T0	721	728	6.75468	CTTTGA	0.06104	0.05927
cg2521727	GNG4	NF-1 [T00	494	501	6.722386	CCGGCC	0.24414	0.2565
cg0457660	GNG4	NF-1 [T00	1853	1860	6.722386	TTGGCC	0.24414	0.2565
cg0457660	GNG4	c-Myb [T0	521	528	6.719843	GGGAGT	0.30518	0.30272
cg0457660	GNG4	c-Ets-2 [T	154	162	6.695187	TTCCTGT	0.09155	0.08559
cg0457660	GNG4	c-Ets-2 [T	1745	1753	6.695187	TTCCTAT	0.09155	0.08559
cg2521727	GNG4	HNF-1C [	1120	1128	6.678556	GTTATTC	0.05341	0.04756
cg2521727	GNG4	c-Jun [T00	300	306	6.668031	CAAGTC	0.61035	0.6179
cg2521727	GNG4	GATA-2 [	1322	1330	6.666667	CGATAT	0.24414	0.2357
cg0457660	GNG4	GATA-2 [	1155	1163	6.666667	GCTGTA	0.24414	0.2357
cg2521727	GNG4	RelA [T00	438	448	6.604033	GATCTTC	0.01001	0.01051
cg2521727	GNG4	AR [T000	1341	1349	6.603347	GACTTG	0.19836	0.20813
cg0457660	GNG4	HNF-1C [	1536	1544	6.596946	TTTTTTA	0.05341	0.04756
cg0457660	GNG4	HNF-1C [	1663	1671	6.596946	GTTAAA	0.05341	0.04756
cg2521727	GNG4	FOXP3 [T	747	752	6.581441	GTTTTA	0.97656	0.904
cg2521727	GNG4	FOXP3 [T	1288	1293	6.581441	GTTTTA	0.97656	0.904
cg2521727	GNG4	TFII-I [T0	609	614	6.581441	GGAGAT	0.97656	0.9991
cg2521727	GNG4	TFII-I [T0	654	659	6.581441	GGAGTG	0.97656	0.9991
cg2521727	GNG4	TFII-I [T0	1649	1654	6.581441	GGAGTG	0.97656	0.9991
cg0457660	GNG4	TFII-I [T0	25	30	6.581441	CACTCC	0.97656	0.9991
cg0457660	GNG4	TFII-I [T0	191	196	6.581441	GGAGAT	0.97656	0.9991
cg0457660	GNG4	TFII-I [T0	439	444	6.581441	CACTCC	0.97656	0.9991
cg0457660	GNG4	TFII-I [T0	616	621	6.581441	CACTCC	0.97656	0.9991
cg0457660	GNG4	TFII-I [T0	668	673	6.581441	CACTCC	0.97656	0.9991
cg0457660	GNG4	TFII-I [T0	1172	1177	6.581441	GGAGTG	0.97656	0.9991
cg0457660	GNG4	AR [T000	472	480	6.566205	TGCCTG	0.19836	0.20813
cg0457660	GNG4	p53 [T006	373	379	6.563521	GCAGCC	0.48828	0.54643
cg0457660	GNG4	p53 [T006	785	791	6.563521	GCAGCC	0.48828	0.54643
cg0457660	GNG4	NF-AT2 [	1782	1791	6.521557	GAAGGT	0.01907	0.01803
cg2521727	GNG4	XBP-1 [T	355	360	6.478682	ATGCCC	0.97656	0.99906
cg2521727	GNG4	XBP-1 [T	1748	1753	6.478682	ATGCCA	0.97656	0.99906
cg0457660	GNG4	XBP-1 [T	612	617	6.478682	ATGCCA	0.97656	0.99906
cg2521727	GNG4	c-Jun [T00	956	962	6.462218	GTAGTC	0.61035	0.6179
cg0457660	GNG4	RAR-beta	1322	1331	6.415195	GGGGTT	0.18311	0.1857
cg0457660	GNG4	RAR-beta	294	303	6.39673	AGGGTT	0.18311	0.1857
cg0457660	GNG4	C/EBPalpl	1117	1123	6.391486	GCCAAT	0.48828	0.47407
cg0457660	GNG4	C/EBPalpl	1433	1439	6.391486	GCCAAT	0.48828	0.47407
cg2521727	GNG4	TCF-4E [T	721	727	6.302385	CTTTGA	0.61035	0.59686
cg2521727	GNG4	TCF-4E [T	884	890	6.302385	CTTTGTT	0.61035	0.59686
cg2521727	GNG4	TCF-4E [T	1010	1016	6.302385	TTCAAA	0.61035	0.59686
cg2521727	GNG4	TCF-4E [T	1098	1104	6.302385	TTCAAA	0.61035	0.59686
cg2521727	GNG4	TCF-4E [T	1800	1806	6.302385	CTTTGTT	0.61035	0.59686
cg0457660	GNG4	TCF-4E [T	250	256	6.302385	GGCAAA	0.61035	0.59686

cg0457660	GNG4	TCF-4E [T	1023	1029	6.302385	CTTTGCC	0.61035	0.59686
cg0457660	GNG4	TCF-4E [T	1085	1091	6.302385	TTCAAA(	0.61035	0.59686
cg0457660	GNG4	TCF-4E [T	1659	1665	6.302385	CTTTGTT	0.61035	0.59686
cg0457660	GNG4	TCF-4E [T	1680	1686	6.302385	CTTTGTT	0.61035	0.59686
cg0457660	GNG4	c-Ets-1 [T(	335	341	6.295602	TTTCCAT	0.48828	0.48842
cg0457660	GNG4	c-Ets-1 [T(	1525	1531	6.295602	TTTCCAT	0.48828	0.48842
cg2521727	GNG4	GR-alpha [	67	71	6.263098	CCTCA	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	280	284	6.263098	CCTTA	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	324	328	6.263098	TGAGG	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	579	583	6.263098	CCTTA	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	662	666	6.263098	TGAGG	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	816	820	6.263098	CCTCA	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	1714	1718	6.263098	CCTCA	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	1818	1822	6.263098	CCTCA	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	1850	1854	6.263098	CCTCA	3.90625	3.89624
cg2521727	GNG4	GR-alpha [	1975	1979	6.263098	TAAGG	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	415	419	6.263098	TAAGG	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	516	520	6.263098	CCTCA	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	793	797	6.263098	CCTCA	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	887	891	6.263098	TGAGG	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	1237	1241	6.263098	CCTCA	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	1363	1367	6.263098	CCTCA	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	1381	1385	6.263098	CCTCA	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	1831	1835	6.263098	CCTCA	3.90625	3.89624
cg0457660	GNG4	GR-alpha [	1978	1982	6.263098	CCTCA	3.90625	3.89624
cg0457660	GNG4	C/EBPalpl	1460	1466	6.245236	TTCAATA	0.97656	0.91422
cg2521727	GNG4	PEA3 [T0(	990	998	6.227095	TGGATGA	0.03815	0.03662
cg0457660	GNG4	NF-AT2 [T	535	544	6.184331	ATATTTT	0.04196	0.03934
cg2521727	GNG4	c-Ets-1 [T(	1580	1586	6.167515	TTTCCAC	0.36621	0.36174
cg0457660	GNG4	RXR-alpha	828	834	6.119461	GGGTAG(	0.73242	0.78318
cg2521727	GNG4	GR-alpha [	322	326	6.055408	CCTGA	3.90625	3.89835
cg2521727	GNG4	GR-alpha [	407	411	6.055408	TTAGG	3.90625	3.89835
cg2521727	GNG4	GR-alpha [	1349	1353	6.055408	CCTGA	3.90625	3.89835
cg2521727	GNG4	GR-alpha [	1480	1484	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	164	168	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	395	399	6.055408	TCAGG	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	518	522	6.055408	TCAGG	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	693	697	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	714	718	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	735	739	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	1058	1062	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	1358	1362	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	1646	1650	6.055408	CCTGA	3.90625	3.89835
cg0457660	GNG4	GR-alpha [	1883	1887	6.055408	CCTGA	3.90625	3.89835
cg2521727	GNG4	c-Ets-1 [T(	628	634	6.039428	CTGGAA	0.36621	0.36174
cg2521727	GNG4	c-Ets-1 [T(	1228	1234	6.039428	CTGGAA	0.36621	0.36174
cg2521727	GNG4	c-Ets-1 [T(	1247	1253	6.039428	TTTCCAC	0.36621	0.36174
cg0457660	GNG4	c-Ets-1 [T(	540	546	6.039428	TTTCCAC	0.36621	0.36174

cg0457660	GNG4	NF-kappa	1965	1975	6.017416	GGGGAA	0.04053	0.04443
cg2521727	GNG4	RXR-alpha	1061	1067	5.937582	GTCACC	0.73242	0.78318
cg0457660	GNG4	RXR-alpha	769	775	5.937582	GGGTGC	0.73242	0.78318
cg2521727	GNG4	HOXD9 [T	691	700	5.898575	TATTTCT	0.05722	0.04686
cg2521727	GNG4	HOXD10 [	691	700	5.898575	TATTTCT	0.05722	0.04686
cg0457660	GNG4	HOXD9 [T	902	911	5.898575	TATTTCT	0.05722	0.04686
cg0457660	GNG4	HOXD10 [	902	911	5.898575	TATTTCT	0.05722	0.04686
cg2521727	GNG4	STAT4 [T	318	323	5.882353	CCTTCC	0.48828	0.51201
cg2521727	GNG4	STAT4 [T	1035	1040	5.882353	GGAAGG	0.48828	0.51201
cg2521727	GNG4	c-Myb [T0	625	632	5.841835	CAACTG	0.21362	0.2053
cg2521727	GNG4	c-Ets-1 [T	146	152	5.814485	CTTCCC	0.36621	0.36174
cg2521727	GNG4	c-Ets-1 [T	441	447	5.814485	CTTCCC	0.36621	0.36174
cg2521727	GNG4	c-Ets-1 [T	1418	1424	5.814485	CTTCCC	0.36621	0.36174
cg2521727	GNG4	c-Ets-1 [T	1525	1531	5.814485	TGGGAA	0.36621	0.36174
cg2521727	GNG4	STAT1bet	1226	1235	5.796867	GCCTGG	0.1545	0.14881
cg2521727	GNG4	STAT1bet	1249	1258	5.796867	TCCAGG	0.1545	0.14881
cg2521727	GNG4	c-Jun [T00	718	724	5.783074	TGACTT	0.36621	0.34478
cg0457660	GNG4	c-Jun [T00	1949	1955	5.783074	TGACTT	0.36621	0.34478
cg2521727	GNG4	C/EBPalph	1185	1191	5.781231	TATTGG	0.97656	0.91422
cg2521727	GNG4	VDR [T00	720	728	5.771401	ACTTTG	0.42725	0.41266
cg0457660	GNG4	VDR [T00	137	145	5.771401	GTTCAA	0.42725	0.41266
cg2521727	GNG4	ENKTF-1	1161	1168	5.687009	GTACGC	0.73242	0.76357
cg2521727	GNG4	ENKTF-1	1461	1468	5.687009	CTGTGC	0.73242	0.76357
cg2521727	GNG4	ENKTF-1	1562	1569	5.687009	TGGCTC	0.73242	0.76357
cg0457660	GNG4	ENKTF-1	401	408	5.687009	CAAAGC	0.73242	0.76357
cg2521727	GNG4	c-Ets-1 [T	755	761	5.686398	CTTCCCT	0.36621	0.38732
cg0457660	GNG4	c-Ets-1 [T	889	895	5.686398	AGGGAA	0.36621	0.38732
cg2521727	GNG4	c-Fos [T00	1921	1930	5.679695	GAGTCA	0.04578	0.04712
cg2521727	GNG4	HNF-1A [	25	32	5.610392	CAGTTA	0.24414	0.23087
cg2521727	GNG4	NF-AT1 [	192	200	5.604085	TGTTTTT	0.03815	0.03643
cg2521727	GNG4	NF-AT1 [	1253	1261	5.604085	GGAAAA	0.03815	0.03643
cg2521727	GNG4	T3R-beta1	1924	1932	5.591999	TCACCT	0.21362	0.21789
cg0457660	GNG4	T3R-beta1	746	754	5.591999	TCACCTT	0.21362	0.21789
cg2521727	GNG4	AP-2alpha	1876	1881	5.568965	ATAGGC	0.48828	0.48642
cg2521727	GNG4	AP-2alpha	1899	1904	5.568965	GCCTAT	0.48828	0.48642
cg0457660	GNG4	IRF-1 [T0	335	343	5.564062	TTTCCAT	0.22888	0.21959
cg2521727	GNG4	T3R-beta1	1062	1070	5.553412	TCACCC	0.21362	0.21789
cg0457660	GNG4	TFIID [T0	927	933	5.544826	TACTAA	0.73242	0.65314
cg0457660	GNG4	TFIID [T0	1309	1315	5.544826	TTTAGTA	0.73242	0.65314
cg0457660	GNG4	TFIID [T0	1662	1668	5.544826	TGTTAA	0.73242	0.65314
cg0457660	GNG4	TFIID [T0	1909	1915	5.544826	TGGTAA	0.73242	0.65314
cg0457660	GNG4	p53 [T006	1239	1245	5.508538	TCAGCC	0.61035	0.65765
cg0457660	GNG4	p53 [T006	236	242	5.39549	GGGCCC	0.61035	0.65765
cg0457660	GNG4	NF-AT1 [	1812	1820	5.354841	ACCATT	0.03815	0.03643
cg0457660	GNG4	TCF-4 [T0	397	406	5.337909	AGGTCA	0.04959	0.04908
cg0457660	GNG4	PPAR-alph	231	241	5.285833	AACTGG	0.03529	0.03856
cg0457660	GNG4	HOXD9 [T	69	78	5.275652	AATAAA	0.04578	0.03952
cg0457660	GNG4	HOXD10 [	69	78	5.275652	AATAAA	0.04578	0.03952

cg2521727	GNG4	RXR-alpha	444	450	5.271235	CCCACC(	0.61035	0.65415
cg0457660	GNG4	RXR-alpha	1373	1379	5.271235	CCCACC(	0.61035	0.65415
cg2521727	GNG4	C/EBPalph	4	10	5.240291	GGCAAT.	0.97656	0.90302
cg2521727	GNG4	GR [T050'	521	527	5.207533	CAAAGA	0.24414	0.24013
cg2521727	GNG4	GR [T050'	829	835	5.207533	CAAAAC	0.24414	0.24013
cg0457660	GNG4	GR [T050'	1678	1684	5.207533	GTCTTTC	0.24414	0.24013
cg0457660	GNG4	GR [T050'	1699	1705	5.207533	GGTTTTC	0.24414	0.24013
cg0457660	GNG4	c-Jun [T00	457	463	5.193102	TGACTTC	0.61035	0.60573
cg0457660	GNG4	c-Myb [T0	230	237	5.137438	GAACTG(	0.30518	0.30087
cg0457660	GNG4	c-Myb [T0	307	314	5.137438	CCCAGT	0.30518	0.30087
cg0457660	GNG4	NF-AT1 [1	536	544	5.125037	TATTTTT	0.05341	0.05073
cg2521727	GNG4	HNF-1A [	27	34	5.116518	GTTAAC(	0.36621	0.34064
cg0457660	GNG4	HNF-1A [	1704	1711	5.116518	TGCTTA/	0.36621	0.34064
cg2521727	GNG4	AP-2alpha	882	887	5.100982	GCCTTT	0.97656	0.97517
cg0457660	GNG4	AP-2alpha	1021	1026	5.100982	GCCTTT	0.97656	0.97517
cg0457660	GNG4	AP-2alpha	1468	1473	5.100982	AAAGGC	0.97656	0.97517
cg0457660	GNG4	AP-2alpha	1797	1802	5.100982	GCCTTT	0.97656	0.97517
cg2521727	GNG4	RXR-alpha	1468	1474	5.089356	AGCACC(	0.48828	0.51407
cg0457660	GNG4	RXR-alpha	1160	1166	5.089356	ATCACC(	0.48828	0.51407
cg2521727	GNG4	USF2 [T0(	1474	1483	5.052423	CCTTCAC	0.103	0.10797
cg0457660	GNG4	USF2 [T0(	1041	1050	5.052423	CAGGTG.	0.103	0.10797
cg2521727	GNG4	GR-beta [1	7	11	5.042296	AATAC	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	47	51	5.042296	AATAC	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	334	338	5.042296	GGATT	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	469	473	5.042296	GGATT	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	530	534	5.042296	AATAC	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	637	641	5.042296	GTATT	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	686	690	5.042296	AATCC	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	1840	1844	5.042296	AATCC	3.90625	3.7093
cg2521727	GNG4	GR-beta [1	1871	1875	5.042296	GGATT	3.90625	3.7093
cg0457660	GNG4	GR-beta [1	486	490	5.042296	AATCC	3.90625	3.7093
cg0457660	GNG4	GR-beta [1	865	869	5.042296	GTATT	3.90625	3.7093
cg0457660	GNG4	GR-beta [1	1258	1262	5.042296	GGATT	3.90625	3.7093
cg0457660	GNG4	GR-beta [1	1296	1300	5.042296	GTATT	3.90625	3.7093
cg2521727	GNG4	C/EBPalph	1661	1667	5.024728	TGCAAT(	0.97656	0.90302
cg2521727	GNG4	C/EBPalph	1837	1843	5.024728	TGCAAT(	0.97656	0.90302
cg0457660	GNG4	C/EBPalph	1403	1409	5.024728	GATTGC/	0.97656	0.90302
cg0457660	GNG4	HNF-1B [	1537	1545	4.953067	TTTTTAA	0.04578	0.0409
cg2521727	GNG4	c-Ets-1 [T(	1172	1178	4.910652	ATGGAA	0.48828	0.48026
cg2521727	GNG4	XBP-1 [T(	476	481	4.894955	AGGCAT	0.97656	0.99839
cg2521727	GNG4	XBP-1 [T(	813	818	4.894955	ATGCCT	0.97656	0.99839
cg2521727	GNG4	XBP-1 [T(	1878	1883	4.894955	AGGCAT	0.97656	0.99839
cg0457660	GNG4	XBP-1 [T(	1055	1060	4.894955	ATGCCT	0.97656	0.99839
cg2521727	GNG4	AP-2alpha	407	412	4.890408	TTAGGC	0.97656	0.97517
cg2521727	GNG4	IRF-1 [T0(	1580	1588	4.881305	TTTCCAC	0.1297	0.12724
cg2521727	GNG4	RXR-alpha	390	396	4.86724	GGGTCT(	0.48828	0.51407
cg2521727	GNG4	RXR-alpha	1625	1631	4.86724	GGGTCT(	0.48828	0.51407
cg2521727	GNG4	C/EBPalph	1019	1025	4.845599	AATTGC	0.97656	0.90302

cg0457660	GNG4	C/EBPalph	1224	1230	4.845599	AGCAAT	0.97656	0.90302
cg2521727	GNG4	HNF-3alph	368	375	4.842999	TATTTA	0.09155	0.07438
cg2521727	GNG4	HNF-3alph	1593	1600	4.842999	TTAAAA	0.09155	0.07438
cg2521727	GNG4	HNF-3alph	1771	1778	4.842999	TTAAAA	0.09155	0.07438
cg2521727	GNG4	NF-AT1 [	1229	1238	4.823485	TGGAAA	0.07629	0.07281
cg2521727	GNG4	NF-AT1 [	1243	1252	4.823485	ATACTT	0.07629	0.07281
cg2521727	GNG4	NF-AT1 [	1576	1585	4.823485	TCTCTTT	0.07629	0.07281
cg0457660	GNG4	NF-AT1 [	331	340	4.823485	GGGGTT	0.07629	0.07281
cg2521727	GNG4	AP-1 [T00	1918	1926	4.815705	CAGGAG	0.12207	0.12309
cg0457660	GNG4	C/EBPalph	1454	1460	4.776286	TATTGT	0.97656	0.90302
cg2521727	GNG4	FOXP3 [T	185	190	4.756447	GTTGAC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	193	198	4.756447	GTTTTT	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	235	240	4.756447	GTCAAC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	732	737	4.756447	GTTTTT	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	790	795	4.756447	CAAAAC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	829	834	4.756447	CAAAAC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	888	893	4.756447	GTTGAG	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	925	930	4.756447	AAAAAC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	950	955	4.756447	AAAAAC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	967	972	4.756447	GTTTTC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	1255	1260	4.756447	AAAAAC	2.92969	2.82
cg2521727	GNG4	FOXP3 [T	1912	1917	4.756447	CTCAAC	2.92969	2.82
cg2521727	GNG4	TFII-I [T0	853	858	4.756447	CATTCC	2.92969	2.89715
cg2521727	GNG4	TFII-I [T0	1230	1235	4.756447	GGAAAT	2.92969	2.89715
cg2521727	GNG4	TFII-I [T0	1839	1844	4.756447	CAATCC	2.92969	2.89715
cg0457660	GNG4	FOXP3 [T	421	426	4.756447	GAAAAC	2.92969	2.82
cg0457660	GNG4	FOXP3 [T	548	553	4.756447	GTTTTT	2.92969	2.82
cg0457660	GNG4	FOXP3 [T	969	974	4.756447	AAAAAC	2.92969	2.82
cg0457660	GNG4	FOXP3 [T	1382	1387	4.756447	CTCAAC	2.92969	2.82
cg0457660	GNG4	FOXP3 [T	1398	1403	4.756447	GTTGAG	2.92969	2.82
cg0457660	GNG4	FOXP3 [T	1523	1528	4.756447	GTTTTC	2.92969	2.82
cg0457660	GNG4	FOXP3 [T	1667	1672	4.756447	AAAAAC	2.92969	2.82
cg0457660	GNG4	FOXP3 [T	1700	1705	4.756447	GTTTTG	2.92969	2.82
cg0457660	GNG4	TFII-I [T0	485	490	4.756447	CAATCC	2.92969	2.89715
cg0457660	GNG4	TFII-I [T0	944	949	4.756447	GGACAT	2.92969	2.89715
cg0457660	GNG4	TFII-I [T0	1078	1083	4.756447	CAGTCC	2.92969	2.89715
cg0457660	GNG4	TFII-I [T0	1614	1619	4.756447	CATTCC	2.92969	2.89715
cg0457660	GNG4	TFII-I [T0	1642	1647	4.756447	CATTCC	2.92969	2.89715
cg0457660	GNG4	TFII-I [T0	1815	1820	4.756447	ATTTCC	2.92969	2.89715
cg0457660	GNG4	TFII-I [T0	1928	1933	4.756447	GGAATG	2.92969	2.89715
cg2521727	GNG4	c-Myb [T0	766	773	4.754782	TAACTG	0.30518	0.30087
cg0457660	GNG4	c-Myb [T0	1495	1502	4.754782	GACAGT	0.30518	0.30087
cg2521727	GNG4	Ik-1 [T027	1725	1737	4.748597	CAAGCT	0.00313	0.00339
cg0457660	GNG4	Ik-1 [T027	1248	1260	4.748597	CGAGTA	0.00313	0.00339
cg2521727	GNG4	VDR [T00	151	159	4.617121	CAGCTG	0.37384	0.36855
cg2521727	GNG4	VDR [T00	1795	1803	4.617121	GTTCAC	0.37384	0.36855
cg2521727	GNG4	c-Ets-2 [T	1034	1042	4.589988	AGGAAG	0.06866	0.06805
cg2521727	GNG4	NF-AT2 [	630	639	4.586038	GGAAAA	0.04196	0.03925

cg0457660	GNG4	NF-AT1 [T	1783	1791	4.566689	AAGGTTT	0.06866	0.06549
cg2521727	GNG4	c-Ets-1 [T(	854	860	4.539113	ATTCCTA	0.85449	0.8381
cg0457660	GNG4	T3R-beta1	649	657	4.481316	GTCTGGT	0.27466	0.27245
cg2521727	GNG4	NF-AT2 [T	1242	1251	4.460114	GATACTT	0.04196	0.03925
cg0457660	GNG4	T3R-beta1	1328	1336	4.442729	TCACCAT	0.27466	0.27245
cg2521727	GNG4	AP-2alpha	535	540	4.438035	CTAGGC	0.97656	0.99839
cg0457660	GNG4	RXR-alpha	28	34	4.423008	TCCACC(	0.24414	0.25781
cg2521727	GNG4	AP-2alpha	279	284	4.422424	GCCTTA	0.97656	0.99839
cg2521727	GNG4	AP-2alpha	578	583	4.422424	GCCTTA	0.97656	0.99839
cg2521727	GNG4	AP-2alpha	1975	1980	4.422424	TAAGGC	0.97656	0.99839
cg2521727	GNG4	STAT4 [T(	145	150	4.411765	GCTTCC	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	440	445	4.411765	TCTTCC	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	754	759	4.411765	TCTTCC	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	779	784	4.411765	TCTTCC	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	853	858	4.411765	CATTCC	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	1039	1044	4.411765	GGAAGA	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	1174	1179	4.411765	GGAAGA	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	1417	1422	4.411765	TCTTCC	1.95312	1.99838
cg2521727	GNG4	STAT4 [T(	1527	1532	4.411765	GGAAGC	1.95312	1.99838
cg0457660	GNG4	STAT4 [T(	637	642	4.411765	TCTTCC	1.95312	1.99838
cg0457660	GNG4	STAT4 [T(	891	896	4.411765	GGAAGA	1.95312	1.99838
cg0457660	GNG4	STAT4 [T(	1614	1619	4.411765	CATTCC	1.95312	1.99838
cg0457660	GNG4	STAT4 [T(	1642	1647	4.411765	CATTCC	1.95312	1.99838
cg0457660	GNG4	STAT4 [T(	1743	1748	4.411765	GCTTCC	1.95312	1.99838
cg0457660	GNG4	STAT4 [T(	1928	1933	4.411765	GGAATG	1.95312	1.99838
cg0457660	GNG4	STAT4 [T(	1958	1963	4.411765	GGAACG	1.95312	1.99838
cg0457660	GNG4	c-Ets-1 [T(	1121	1127	4.411026	ATTCCTT	0.85449	0.8381
cg2521727	GNG4	HOXD9 [T	367	376	4.321431	TTATTTT	0.03433	0.02831
cg2521727	GNG4	HOXD10 [	367	376	4.321431	TTATTTT	0.03433	0.02831
cg2521727	GNG4	PEA3 [T0(	302	310	4.30818	AGTCAT(	0.13733	0.13607
cg0457660	GNG4	c-Ets-1 [T(	1615	1621	4.282938	ATTCCTC	0.85449	0.8381
cg0457660	GNG4	RXR-alpha	1369	1375	4.24113	GTGACC(	0.97656	1.02803
cg2521727	GNG4	GR-beta [T	367	371	4.201913	TTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	372	376	4.201913	TTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	690	694	4.201913	CTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	696	700	4.201913	CTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	709	713	4.201913	TTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	795	799	4.201913	CGATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	916	920	4.201913	CGATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1007	1011	4.201913	CTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1121	1125	4.201913	TTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1233	1237	4.201913	AATAA	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1571	1575	4.201913	TTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1588	1592	4.201913	TTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1611	1615	4.201913	TTATT	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1664	1668	4.201913	AATCA	7.8125	7.23274
cg2521727	GNG4	GR-beta [T	1901	1905	4.201913	CTATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	69	73	4.201913	AATAA	7.8125	7.23274

cg0457660	GNG4	GR-beta [T	413	417	4.201913	AATAA	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	504	508	4.201913	TGATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	662	666	4.201913	CTATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	898	902	4.201913	TGATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	901	905	4.201913	TTATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	907	911	4.201913	CTATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	919	923	4.201913	TGATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	955	959	4.201913	AATCA	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	961	965	4.201913	AATAA	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	1463	1467	4.201913	AATAG	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	1473	1477	4.201913	CTATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	1585	1589	4.201913	TTATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	1845	1849	4.201913	TTATT	7.8125	7.23274
cg0457660	GNG4	GR-beta [T	1866	1870	4.201913	CTATT	7.8125	7.23274
cg0457660	GNG4	NF-Y [T0	481	488	4.186615	TCCCCA	0.18311	0.17499
cg0457660	GNG4	c-Ets-1 [T	1643	1649	4.154851	ATTCCTC	0.24414	0.23719
cg2521727	GNG4	NF-1 [T00	785	792	4.135372	TGCCCCA	0.24414	0.25714
cg0457660	GNG4	NF-1 [T00	246	253	4.135372	TTGGGG	0.24414	0.25714
cg0457660	GNG4	NF-1 [T00	1191	1198	4.135372	TTGGCTC	0.24414	0.25714
cg2521727	GNG4	p53 [T006	100	106	4.125254	GGGCCTC	0.73242	0.82434
cg2521727	GNG4	POU2F2 (	562	572	4.120113	TGAATTA	0.01717	0.01453
cg0457660	GNG4	c-Ets-2 [T	1788	1796	4.091811	TTCCTTC	0.16022	0.15061
cg0457660	GNG4	SRY [T00	1478	1486	4.087393	TTTACAA	0.12207	0.11312
cg0457660	GNG4	p53 [T006	145	151	4.083527	GGGCAC	0.73242	0.82434
cg0457660	GNG4	p53 [T006	1335	1341	4.083527	GGTGCCC	0.73242	0.82434
cg0457660	GNG4	RelA [T00	1925	1935	4.075851	GTGGGA	0.00811	0.0081
cg2521727	GNG4	IRF-1 [T0	626	634	4.043231	AACTGG	0.1297	0.12468
cg0457660	GNG4	IRF-1 [T0	160	168	4.035054	TTTCCCT	0.1297	0.12468
cg0457660	GNG4	RXR-alpha	116	122	4.019014	GGGTTTC	0.97656	1.02803
cg0457660	GNG4	RXR-alpha	126	132	4.019014	CACACCC	0.97656	1.02803
cg0457660	GNG4	RXR-alpha	332	338	4.019014	GGGTTTC	0.97656	1.02803
cg0457660	GNG4	RXR-alpha	1323	1329	4.019014	GGGTTTC	0.97656	1.02803
cg0457660	GNG4	c-Ets-2 [T	639	647	4.017001	TTCCTTT	0.16022	0.15061
cg2521727	GNG4	TFIID [T0	212	218	4.007279	TTTAAGA	1.09863	0.94722
cg2521727	GNG4	TFIID [T0	700	706	4.007279	TTTTAAA	1.09863	0.94722
cg2521727	GNG4	TFIID [T0	1025	1031	4.007279	TTTTAAA	1.09863	0.94722
cg2521727	GNG4	TFIID [T0	1591	1597	4.007279	TTTTAAA	1.09863	0.94722
cg2521727	GNG4	TFIID [T0	1769	1775	4.007279	TTTTAAA	1.09863	0.94722
cg2521727	GNG4	Pax-5 [T0	123	129	4.007279	GGGCTG	1.09863	1.18533
cg2521727	GNG4	Pax-5 [T0	158	164	4.007279	ACAGCC	1.09863	1.18533
cg0457660	GNG4	TFIID [T0	751	757	4.007279	TTTTAAA	1.09863	0.94722
cg0457660	GNG4	TFIID [T0	1478	1484	4.007279	TTTACAA	1.09863	0.94722
cg0457660	GNG4	Pax-5 [T0	575	581	4.007279	GGGCTG	1.09863	1.18533
cg0457660	GNG4	Pax-5 [T0	601	607	4.007279	GGGCTCT	1.09863	1.18533
cg2521727	GNG4	AP-2alpha	176	181	3.970052	CAAGGC	0.97656	1.02535
cg2521727	GNG4	AP-2alpha	1681	1686	3.970052	GCCTTG	0.97656	1.02535
cg0457660	GNG4	Elk-1 [T00	1744	1752	3.944668	CTTCCTA	0.09155	0.08816
cg2521727	GNG4	NFI/CTF [	1824	1831	3.793671	ACCCTTC	0.18311	0.19063

cg0457660	GNG4	NFI/CTF [	1797	1804	3.793671	GCCTTTC	0.18311	0.19063
cg0457660	GNG4	IRF-1 [T0	153	161	3.788396	TTTCCTC	0.1297	0.12468
cg2521727	GNG4	GR [T050	739	745	3.763516	CTCTTTC	0.73242	0.6946
cg2521727	GNG4	GR [T050	790	796	3.763516	CAAAAC	0.73242	0.6946
cg2521727	GNG4	GR [T050	1012	1018	3.763516	CAAAGA	0.73242	0.6946
cg0457660	GNG4	GR [T050	1087	1093	3.763516	CAAAGA	0.73242	0.6946
cg0457660	GNG4	GR [T050	1778	1784	3.763516	CAAAGA	0.73242	0.6946
cg0457660	GNG4	p53 [T006	585	591	3.750231	GGGCTT	0.73242	0.82434
cg2521727	GNG4	AP-2alpha	1054	1059	3.743866	GAAGGC	0.48828	0.5124
cg0457660	GNG4	MEF-2A [	62	72	3.681692	AGAAAA	0.00191	0.0016
cg0457660	GNG4	c-Ets-1 [T	311	317	3.590463	GTTCCTC	0.61035	0.61936
cg2521727	GNG4	c-Ets-2 [T	52	60	3.518824	TTCCTTC	0.18311	0.18314
cg2521727	GNG4	c-Ets-2 [T	197	205	3.518824	TTCCTTC	0.18311	0.18314
cg2521727	GNG4	HNF-3alph	373	380	3.500065	TATTTT	0.27466	0.23175
cg2521727	GNG4	HNF-3alph	703	710	3.500065	TAAAAA	0.27466	0.23175
cg2521727	GNG4	HNF-3alph	1201	1208	3.500065	AAAAAA	0.27466	0.23175
cg2521727	GNG4	HNF-3alph	1606	1613	3.500065	AATTTT	0.27466	0.23175
cg2521727	GNG4	HNF-3alph	1766	1773	3.500065	AATTTT	0.27466	0.23175
cg0457660	GNG4	HNF-3alph	65	72	3.500065	AAAAAA	0.27466	0.23175
cg0457660	GNG4	HNF-3alph	1297	1304	3.500065	TATTTT	0.27466	0.23175
cg0457660	GNG4	HNF-3alph	1515	1522	3.500065	AATTTC	0.27466	0.23175
cg2521727	GNG4	NF-Y [T0	1186	1193	3.490142	ATTGGC	0.48828	0.48427
cg0457660	GNG4	NF-Y [T0	1431	1438	3.490142	CTGCCA	0.48828	0.48427
cg0457660	GNG4	NF-AT1 [	149	157	3.407861	ACCTTTT	0.03052	0.02886
cg0457660	GNG4	RXR-alpha	295	301	3.392904	GGGTTC	1.09863	1.1653
cg0457660	GNG4	RXR-alpha	1010	1016	3.392904	GGGTCC	1.09863	1.1653
cg2521727	GNG4	Elk-1 [T00	319	327	3.381796	CTTCCTC	0.04578	0.04517
cg0457660	GNG4	p53 [T006	1278	1284	3.375208	CACGCC	0.73242	0.80362
cg2521727	GNG4	GR-beta [	400	404	3.361531	AGATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	862	866	3.361531	AATAT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	863	867	3.361531	ATATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	892	896	3.361531	AGATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	978	982	3.361531	AGATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	1048	1052	3.361531	AATCT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	1184	1188	3.361531	ATATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	1205	1209	3.361531	AATAT	3.90625	3.51525
cg2521727	GNG4	GR-beta [	1236	1240	3.361531	AATCT	3.90625	3.51525
cg0457660	GNG4	GR-beta [	193	197	3.361531	AGATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [	535	539	3.361531	ATATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [	707	711	3.361531	AATCT	3.90625	3.51525
cg0457660	GNG4	GR-beta [	1402	1406	3.361531	AGATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [	1453	1457	3.361531	ATATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [	1567	1571	3.361531	ATATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [	1753	1757	3.361531	AGATT	3.90625	3.51525
cg2521727	GNG4	T3R-beta1	1477	1485	3.351341	TCACCTC	0.27466	0.27326
cg0457660	GNG4	T3R-beta1	1039	1047	3.351341	TACAGG	0.27466	0.27326
cg0457660	GNG4	c-Ets-2 [T	1616	1624	3.2883	TTCCTCC	0.18311	0.18314
cg0457660	GNG4	PXR-1:RX	1987	1994	3.2723	TAGGTTC	0.12207	0.11883

cg2521727	GNG4	AP-2alpha	1719	1724	3.229049	GCCTCT	0.48828	0.5124
cg2521727	GNG4	AP-2alpha	1831	1836	3.229049	GCCTCT	0.48828	0.5124
cg0457660	GNG4	AP-2alpha	50	55	3.229049	GCCTCT	0.48828	0.5124
cg2521727	GNG4	TCF-4E [T	519	525	3.151193	TGCAAA	0.24414	0.23169
cg0457660	GNG4	TCF-4E [T	1776	1782	3.151193	ATCAAA	0.24414	0.23169
cg0457660	GNG4	SRY [T00	1774	1782	3.088221	AGATCA	0.06104	0.05645
cg2521727	GNG4	TFIID [T0	541	547	3.075094	TGCAAA	0.12207	0.11309
cg0457660	GNG4	TFIID [T0	877	883	3.075094	TGCAAA	0.12207	0.11309
cg0457660	GNG4	c-Jun [T00	1370	1376	3.049104	TGACCC	0.24414	0.2435
cg2521727	GNG4	p53 [T006	1755	1761	3.028543	TGTGCC	0.48828	0.53227
cg2521727	GNG4	p53 [T006	1637	1643	3.024997	GTTGCC	0.48828	0.53227
cg2521727	GNG4	p53 [T006	1804	1810	3.024997	GTTGCC	0.48828	0.53227
cg0457660	GNG4	p53 [T006	36	42	3.024997	GGGCAA	0.48828	0.53227
cg2521727	GNG4	C/EBPalph	401	407	3.014837	GATTGC	0.48828	0.47526
cg0457660	GNG4	Elk-1 [T00	638	646	2.987643	CTTCCTT	0.07629	0.07518
cg2521727	GNG4	c-Myb [T0	1275	1282	2.984694	CGCAGT	0.03052	0.03199
cg0457660	GNG4	C/EBPalph	977	983	2.981957	CACAAT	0.48828	0.47526
cg0457660	GNG4	C/EBPalph	1711	1717	2.981957	CATTGT	0.48828	0.47526
cg0457660	GNG4	c-Ets-2 [T	1122	1130	2.945838	TTCCTTT	0.06104	0.05567
cg2521727	GNG4	STAT4 [T	50	55	2.941176	ACTTCC	2.92969	2.92382
cg2521727	GNG4	STAT4 [T	825	830	2.941176	GGAACA	2.92969	2.92382
cg2521727	GNG4	STAT4 [T	1087	1092	2.941176	TGTTCC	2.92969	2.92382
cg2521727	GNG4	STAT4 [T	1246	1251	2.941176	CTTTCC	2.92969	2.92382
cg2521727	GNG4	STAT4 [T	1579	1584	2.941176	CTTTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	296	301	2.941176	GGTTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	302	307	2.941176	CTTTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	663	668	2.941176	TATTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	705	710	2.941176	GGAATC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	710	715	2.941176	CTTTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	731	736	2.941176	CTTTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	866	871	2.941176	TATTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	1568	1573	2.941176	TATTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	1683	1688	2.941176	TGTTCC	2.92969	2.92382
cg0457660	GNG4	STAT4 [T	1967	1972	2.941176	GGAACC	2.92969	2.92382
cg2521727	GNG4	STAT1bet	1246	1255	2.898434	CTTTCCA	0.0515	0.04956
cg2521727	GNG4	IRF-1 [T0	196	204	2.890712	TTTCCTT	0.07629	0.07093
cg0457660	GNG4	IRF-1 [T0	1787	1795	2.890712	TTTCCTT	0.07629	0.07093
cg2521727	GNG4	TCF-4 [T0	1008	1017	2.859093	TATTCA	0.03433	0.03101
cg0457660	GNG4	TCF-4 [T0	1774	1783	2.859093	AGATCA	0.03433	0.03101
cg0457660	GNG4	NF-1 [T00	385	392	2.813149	TTGGGC	0.24414	0.2566
cg0457660	GNG4	PR B [T00	345	351	2.80933	AACATT	0.73242	0.66711
cg0457660	GNG4	PR B [T00	979	985	2.80933	CAATGT	0.73242	0.66711
cg0457660	GNG4	PR B [T00	1454	1460	2.80933	TATTGTT	0.73242	0.66711
cg0457660	GNG4	PR B [T00	1709	1715	2.80933	AACATT	0.73242	0.66711
cg0457660	GNG4	PR A [T01	345	351	2.80933	AACATT	0.73242	0.66711
cg0457660	GNG4	PR A [T01	979	985	2.80933	CAATGT	0.73242	0.66711
cg0457660	GNG4	PR A [T01	1454	1460	2.80933	TATTGTT	0.73242	0.66711
cg0457660	GNG4	PR A [T01	1709	1715	2.80933	AACATT	0.73242	0.66711

cg2521727	GNG4	NF-AT1 [	629	638	2.756277	TGGAAA	0.05913	0.05541
cg0457660	GNG4	NF-AT1 [	536	545	2.756277	TATTTTT	0.05913	0.05541
cg2521727	GNG4	c-Jun [T00	1920	1926	2.654872	GGAGTC	0.48828	0.48077
cg2521727	GNG4	NF-AT1 [	1243	1251	2.619709	ATACTTT	0.09155	0.08666
cg2521727	GNG4	PXR-1:RX	1685	1692	2.577808	TGAACT	0.12207	0.11843
cg2521727	GNG4	AP-2alpha	815	820	2.550491	GCCTCA	0.48828	0.51216
cg2521727	GNG4	AP-2alpha	1713	1718	2.550491	GCCTCA	0.48828	0.51216
cg2521727	GNG4	AP-2alpha	1817	1822	2.550491	GCCTCA	0.48828	0.51216
cg0457660	GNG4	AP-2alpha	1236	1241	2.550491	GCCTCA	0.48828	0.51216
cg0457660	GNG4	AP-2alpha	1380	1385	2.550491	GCCTCA	0.48828	0.51216
cg0457660	GNG4	TCF-4 [T0	1083	1092	2.548903	CCTTCA	0.03433	0.03112
cg2521727	GNG4	RXR-alph	248	254	2.544678	GGGTGC	0.85449	0.89683
cg2521727	GNG4	RXR-alph	489	495	2.544678	TGCACC	0.85449	0.89683
cg2521727	GNG4	RXR-alph	1936	1942	2.544678	GGGTGA	0.85449	0.89683
cg0457660	GNG4	RXR-alph	1217	1223	2.544678	GGGTGC	0.85449	0.89683
cg2521727	GNG4	PXR-1:RX	1792	1799	2.454225	GAAGTT	0.12207	0.11843
cg2521727	GNG4	Ik-1 [T027	459	471	2.374299	CAAAGT	0.00063	0.00068
cg2521727	GNG4	Ik-1 [T027	1861	1873	2.374299	CAAAGT	0.00063	0.00068
cg2521727	GNG4	c-Jun [T00	1272	1278	2.345465	TGACGC	0.48828	0.48077
cg2521727	GNG4	LEF-1 [T0	884	891	2.345041	CTTTGTT	0.09155	0.09076
cg2521727	GNG4	LEF-1 [T0	1800	1807	2.345041	CTTTGTT	0.09155	0.09076
cg2521727	GNG4	Elk-1 [T00	1031	1039	2.299314	AAGAGG	0.09155	0.09306
cg2521727	GNG4	T3R-beta1	112	120	2.240658	TCACCA	0.15259	0.15303
cg2521727	GNG4	GATA-2 [	1972	1980	2.222222	GGATAA	0.22888	0.21978
cg0457660	GNG4	T3R-beta1	451	459	2.221365	CACAGG	0.15259	0.15303
cg2521727	GNG4	GATA-1 [	1240	1245	2.176375	TGGATA	3.90625	3.79558
cg2521727	GNG4	GATA-1 [	1971	1976	2.176375	AGGATA	3.90625	3.79558
cg2521727	GNG4	RAR-beta	1819	1828	2.16302	CTCAAA	0.07629	0.07711
cg2521727	GNG4	TCF-4 [T0	720	729	2.160205	ACTTTG	0.04196	0.03736
cg0457660	GNG4	c-Ets-2 [	312	320	2.142327	TTCCTCT	0.16785	0.16456
cg0457660	GNG4	c-Ets-2 [	1817	1825	2.142327	TTCCTCT	0.16785	0.16456
cg0457660	GNG4	RAR-beta	179	188	2.126088	AGGGTT	0.07629	0.07711
cg2521727	GNG4	NF-1 [T00	847	854	2.067686	TTGGCA	0.12207	0.12476
cg2521727	GNG4	NF-AT2 [	1230	1239	2.029228	GGAAAT	0.01526	0.01375
cg0457660	GNG4	LEF-1 [T0	1659	1666	2.004405	CTTTGTT	0.18311	0.17215
cg2521727	GNG4	GATA-1 [	1321	1326	2.001358	GCGATA	3.90625	3.79558
cg2521727	GNG4	GATA-1 [	1402	1407	2.001358	GGGATA	3.90625	3.79558
cg2521727	GNG4	SRY [T00	884	892	1.998343	CTTTGTT	0.03052	0.02861
cg0457660	GNG4	p53 [T006	249	255	1.970013	GGGCAA	0.36621	0.38097
cg0457660	GNG4	p53 [T006	1622	1628	1.970013	GGGCAA	0.36621	0.38097
cg2521727	GNG4	NF-AT1 [	1230	1238	1.94698	GGAAAT	0.06866	0.0623
cg0457660	GNG4	PR B [T00	1394	1400	1.892895	AAGTGT	0.12207	0.1127
cg0457660	GNG4	PR A [T01	1394	1400	1.892895	AAGTGT	0.12207	0.1127
cg2521727	GNG4	AP-2alpha	134	139	1.871933	GGAGGC	0.97656	1.07805
cg2521727	GNG4	AP-2alpha	314	319	1.871933	GCCTCC	0.97656	1.07805
cg2521727	GNG4	AP-2alpha	453	458	1.871933	GCCTCC	0.97656	1.07805
cg2521727	GNG4	AP-2alpha	1531	1536	1.871933	GCCTCC	0.97656	1.07805
cg2521727	GNG4	AP-2alpha	1556	1561	1.871933	GGAGGC	0.97656	1.07805

cg2521727	GNG4	AP-2alpha	1855	1860	1.871933	GCCTCC	0.97656	1.07805
cg0457660	GNG4	AP-2alpha	773	778	1.871933	GCCTCC	0.97656	1.07805
cg0457660	GNG4	AP-2alpha	1210	1215	1.871933	GCCTCC	0.97656	1.07805
cg0457660	GNG4	TFII-I [T0	104	109	1.824994	CTCTCC	0.48828	0.51201
cg0457660	GNG4	TFII-I [T0	109	114	1.824994	CTCTCC	0.48828	0.51201
cg0457660	GNG4	TFII-I [T0	567	572	1.824994	GGAGAG	0.48828	0.51201
cg0457660	GNG4	TFII-I [T0	604	609	1.824994	CTCTCC	0.48828	0.51201
cg0457660	GNG4	TFII-I [T0	1820	1825	1.824994	CTCTCC	0.48828	0.51201
cg0457660	GNG4	C/EBPalph	958	964	1.761449	CACAAT	0.48828	0.46352
cg2521727	GNG4	p53 [T006	1453	1459	1.758307	TCTGCCC	0.36621	0.38097
cg2521727	GNG4	GR-beta [T	563	567	1.680765	GAATT	3.90625	3.70067
cg2521727	GNG4	GR-beta [T	572	576	1.680765	AATTC	3.90625	3.70067
cg2521727	GNG4	GR-beta [T	801	805	1.680765	GAATT	3.90625	3.70067
cg2521727	GNG4	GR-beta [T	812	816	1.680765	AATGC	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	224	228	1.680765	AATTC	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	756	760	1.680765	AATTC	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	988	992	1.680765	AATGC	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	1120	1124	1.680765	AATTC	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	1227	1231	1.680765	AATTC	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	1436	1440	1.680765	AATTC	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	1582	1586	1.680765	GCATT	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	1600	1604	1.680765	GAATT	3.90625	3.70067
cg0457660	GNG4	GR-beta [T	1652	1656	1.680765	GAATT	3.90625	3.70067
cg2521727	GNG4	c-Ets-1 [T	196	202	1.641124	TTTCCTT	0.36621	0.35197
cg0457660	GNG4	c-Ets-1 [T	1787	1793	1.641124	TTTCCTT	0.36621	0.35197
cg2521727	GNG4	C/EBPbeta	32	35	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	419	422	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	458	461	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	498	501	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	624	627	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	789	792	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	834	837	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	847	850	1.639871	TTGG	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1187	1190	1.639871	TTGG	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1429	1432	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1828	1831	1.639871	TTGG	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1860	1863	1.639871	CCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1965	1968	1.639871	CCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	189	192	1.639871	TTGG	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	246	249	1.639871	TTGG	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	385	388	1.639871	TTGG	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	484	487	1.639871	CCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1118	1121	1.639871	CCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1191	1194	1.639871	TTGG	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1391	1394	1.639871	CCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1434	1437	1.639871	CCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1801	1804	1.639871	TTGG	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1853	1856	1.639871	TTGG	15.625	15.23827

cg2521727	GNG4	XBP-1 [T	874	879	1.583727	TGTCAT	0.97656	0.94995
cg2521727	GNG4	XBP-1 [T	1444	1449	1.583727	ATGACA	0.97656	0.94995
cg2521727	GNG4	XBP-1 [T	1486	1491	1.583727	ATGACA	0.97656	0.94995
cg0457660	GNG4	XBP-1 [T	1563	1568	1.583727	TGTCAT	0.97656	0.94995
cg2521727	GNG4	TFIID [T0	377	383	1.537547	TTTTGTA	0.73242	0.65627
cg2521727	GNG4	TFIID [T0	629	635	1.537547	TGGAAA	0.73242	0.65627
cg2521727	GNG4	TFIID [T0	640	646	1.537547	TTTTTCA	0.73242	0.65627
cg2521727	GNG4	TFIID [T0	761	767	1.537547	TTTTGTA	0.73242	0.65627
cg2521727	GNG4	TFIID [T0	922	928	1.537547	TGAAAA	0.73242	0.65627
cg2521727	GNG4	TFIID [T0	1197	1203	1.537547	TGAAAA	0.73242	0.65627
cg2521727	GNG4	TFIID [T0	1779	1785	1.537547	TTTTGTA	0.73242	0.65627
cg2521727	GNG4	Pax-5 [T0	173	179	1.537547	GGGCAA	0.73242	0.83087
cg0457660	GNG4	TFIID [T0	138	144	1.537547	TTCAAA	0.73242	0.65627
cg0457660	GNG4	TFIID [T0	539	545	1.537547	TTTTCCA	0.73242	0.65627
cg0457660	GNG4	TFIID [T0	1292	1298	1.537547	TTTTGTA	0.73242	0.65627
cg0457660	GNG4	TFIID [T0	1477	1483	1.537547	TTTTACA	0.73242	0.65627
cg0457660	GNG4	TFIID [T0	1524	1530	1.537547	TTTTCCA	0.73242	0.65627
cg0457660	GNG4	TFIID [T0	1637	1643	1.537547	TTTTACA	0.73242	0.65627
cg0457660	GNG4	Pax-5 [T0	1278	1284	1.537547	CACGCC	0.73242	0.83087
cg0457660	GNG4	IRF-1 [T0	1525	1533	1.529008	TTTCCAT	0.04578	0.04268
cg0457660	GNG4	c-Ets-1 [T	1503	1509	1.513038	GAGGAA	0.36621	0.35197
cg0457660	GNG4	c-Ets-1 [T	1816	1822	1.513038	TTTCCTC	0.36621	0.35197
cg2521727	GNG4	RXR-alph	1821	1827	1.474336	CAAACC	0.48828	0.52093
cg2521727	GNG4	STAT4 [T	195	200	1.470588	TTTTCC	1.95312	1.90161
cg2521727	GNG4	STAT4 [T	630	635	1.470588	GGAAAA	1.95312	1.90161
cg2521727	GNG4	STAT4 [T	1253	1258	1.470588	GGAAAA	1.95312	1.90161
cg2521727	GNG4	STAT4 [T	1408	1413	1.470588	AGTTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	152	157	1.470588	TTTTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	159	164	1.470588	GTTTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	310	315	1.470588	AGTTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	334	339	1.470588	GTTTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	539	544	1.470588	TTTTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	1120	1125	1.470588	AATTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	1436	1441	1.470588	AATTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	1505	1510	1.470588	GGAAAA	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	1524	1529	1.470588	TTTTCC	1.95312	1.90161
cg0457660	GNG4	STAT4 [T	1786	1791	1.470588	GTTTCC	1.95312	1.90161
cg0457660	GNG4	GR [T050	548	554	1.444018	GTTTTTC	0.12207	0.11476
cg0457660	GNG4	GR [T050	968	974	1.444018	CAAAAA	0.12207	0.11476
cg2521727	GNG4	NF-AT1 [	630	638	1.437145	GGAAAA	0.00763	0.00705
cg0457660	GNG4	PR B [T00	1887	1893	1.404665	AACACT	0.36621	0.35143
cg0457660	GNG4	PR A [T01	1887	1893	1.404665	AACACT	0.36621	0.35143
cg0457660	GNG4	AR [T000	436	444	1.403904	GGACAC	0.09155	0.09239
cg2521727	GNG4	c-Ets-1 [T	1251	1257	1.384951	CAGGAA	0.36621	0.35197
cg0457660	GNG4	c-Ets-1 [T	153	159	1.384951	TTTCCTC	0.36621	0.35197
cg0457660	GNG4	c-Ets-1 [T	711	717	1.384951	TTTCCTC	0.36621	0.35197
cg0457660	GNG4	c-Ets-1 [T	732	738	1.384951	TTTCCTC	0.36621	0.35197
cg0457660	GNG4	NF-AT1 [	1521	1530	1.378139	GAGTTT	0.01907	0.01758

cg2521727	GNG4	C/EBPbeta	69	72	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	186	189	1.366559	TTGA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	236	239	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	299	302	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	432	435	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	723	726	1.366559	TTGA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	889	892	1.366559	TTGA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1011	1014	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1052	1055	1.366559	TTGA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1099	1102	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1157	1160	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1617	1620	1.366559	TTGA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1684	1687	1.366559	TTGA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1698	1701	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1724	1727	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1820	1823	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	C/EBPbeta	1913	1916	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	59	62	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	139	142	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	400	403	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1086	1089	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1140	1143	1.366559	TTGA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1351	1354	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1365	1368	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1383	1386	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1399	1402	1.366559	TTGA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1445	1448	1.366559	TTGA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1461	1464	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1519	1522	1.366559	TTGA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1589	1592	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1695	1698	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1777	1780	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1980	1983	1.366559	TCAA	15.625	15.23827
cg0457660	GNG4	C/EBPbeta	1992	1995	1.366559	TCAA	15.625	15.23827
cg2521727	GNG4	AP-2alpha	339	344	1.357116	ACAGGC	0.48828	0.51319
cg2521727	GNG4	AP-2alpha	474	479	1.357116	ACAGGC	0.48828	0.51319
cg2521727	GNG4	AP-2alpha	1138	1143	1.357116	ACAGGC	0.48828	0.51319
cg0457660	GNG4	AP-2alpha	473	478	1.357116	GCCTGT	0.48828	0.51319
cg0457660	GNG4	AP-2alpha	1876	1881	1.357116	ACAGGC	0.48828	0.51319
cg2521727	GNG4	HNF-3alph	1589	1596	1.342935	TATTTTA	0.03052	0.02477
cg0457660	GNG4	p53 [T006	1422	1428	1.270236	CGTGCC	0.12207	0.13816
cg0457660	GNG4	ENKTF-1	775	782	1.255756	CTCCGC	0.24414	0.27027
cg2521727	GNG4	HNF-1A [	617	624	1.213286	GGTTTA	0.48828	0.45029
cg0457660	GNG4	PEA3 [T0	1673	1681	1.194633	AGGATG	0.06866	0.06787
cg2521727	GNG4	c-Ets-2 [T	1030	1038	1.071163	AAAGAG	0.06104	0.0583
cg0457660	GNG4	c-Ets-2 [T	1500	1508	1.071163	TTAGAG	0.06104	0.0583
cg0457660	GNG4	NF-Y [T0	1115	1122	1.069274	TGGCCA	0.12207	0.11765
cg2521727	GNG4	USF2 [T0	1921	1930	1.048473	GAGTCA	0.01717	0.01798

cg0457660	GNG4	GATA-1 [	1450	1455	1.038567	ATGATA	1.95312	1.80234
cg0457660	GNG4	GATA-1 [	1510	1515	1.038567	ATGATA	1.95312	1.80234
cg0457660	GNG4	GATA-1 [	1693	1698	1.038567	TATCAA	1.95312	1.80234
cg2521727	GNG4	SRY [T00	1800	1808	0.999172	CTTTGT	0.06104	0.0571
cg0457660	GNG4	SRY [T00	1659	1667	0.999172	CTTTGT	0.06104	0.0571
cg2521727	GNG4	E2F-1 [T0	1513	1520	0.993583	GCGGGA	0.03052	0.03367
cg2521727	GNG4	Elk-1 [T00	51	59	0.957025	CTTCCT	0.03052	0.03046
cg0457660	GNG4	PXR-1:RX	134	141	0.941658	CCAGTT	0.12207	0.11843
cg0457660	GNG4	PXR-1:RX	229	236	0.941658	TGAACT	0.12207	0.11843
cg0457660	GNG4	TBP [T00	532	541	0.935771	TTTATA	0.12207	0.10448
cg0457660	GNG4	HNF-1A [	1652	1659	0.925521	GAATTA	0.48828	0.45029
cg0457660	GNG4	GATA-1 [	1159	1164	0.863549	TATCAC	1.95312	1.80234
cg2521727	GNG4	GR-beta [	546	550	0.840383	AATGA	7.8125	7.2174
cg2521727	GNG4	GR-beta [	560	564	0.840383	AATGA	7.8125	7.2174
cg2521727	GNG4	GR-beta [	564	568	0.840383	AATTA	7.8125	7.2174
cg2521727	GNG4	GR-beta [	707	711	0.840383	AATTA	7.8125	7.2174
cg2521727	GNG4	GR-beta [	802	806	0.840383	AATTA	7.8125	7.2174
cg2521727	GNG4	GR-beta [	909	913	0.840383	AATGG	7.8125	7.2174
cg2521727	GNG4	GR-beta [	971	975	0.840383	TCATT	7.8125	7.2174
cg2521727	GNG4	GR-beta [	1019	1023	0.840383	AATTG	7.8125	7.2174
cg2521727	GNG4	GR-beta [	1215	1219	0.840383	TCATT	7.8125	7.2174
cg2521727	GNG4	GR-beta [	1293	1297	0.840383	AATGA	7.8125	7.2174
cg2521727	GNG4	GR-beta [	1374	1378	0.840383	AATGG	7.8125	7.2174
cg2521727	GNG4	GR-beta [	1485	1489	0.840383	AATGA	7.8125	7.2174
cg2521727	GNG4	GR-beta [	1630	1634	0.840383	TCATT	7.8125	7.2174
cg2521727	GNG4	GR-beta [	1765	1769	0.840383	TAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	79	83	0.840383	AATGA	7.8125	7.2174
cg0457660	GNG4	GR-beta [	223	227	0.840383	CAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	896	900	0.840383	AATGA	7.8125	7.2174
cg0457660	GNG4	GR-beta [	941	945	0.840383	AATGG	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1119	1123	0.840383	CAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1226	1230	0.840383	CAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1288	1292	0.840383	TAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1435	1439	0.840383	CAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1440	1444	0.840383	CCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1509	1513	0.840383	AATGA	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1514	1518	0.840383	TAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1528	1532	0.840383	CCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1533	1537	0.840383	TCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1597	1601	0.840383	AATGA	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1613	1617	0.840383	CCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1629	1633	0.840383	CCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1633	1637	0.840383	TCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1653	1657	0.840383	AATTA	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1720	1724	0.840383	CAATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1732	1736	0.840383	TCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1737	1741	0.840383	TCATT	7.8125	7.2174
cg0457660	GNG4	GR-beta [	1813	1817	0.840383	CCATT	7.8125	7.2174

cg0457660	GNG4	GR-beta [T	1914	1918	0.840383	AATTG	7.8125	7.2174
cg2521727	GNG4	Elk-1 [T00	1035	1043	0.822677	GGAAGG	0.03052	0.03046
cg0457660	GNG4	NF-AT2 [T	706	715	0.771098	GAATCT	0.00763	0.00693
cg0457660	GNG4	AP-2alpha	1057	1062	0.678558	GCCTGA	0.48828	0.51196
cg2521727	GNG4	AR [T000	1070	1078	0.649362	GGACAC	0.01526	0.01599
cg0457660	GNG4	NF-AT1 [T	707	715	0.648993	AATCTT	0.02289	0.02115
cg0457660	GNG4	LEF-1 [T0	1680	1687	0.641865	CTTTGTT	0.06104	0.05974
cg0457660	GNG4	RXR-alpha	180	186	0.62611	GGGTTT	0.12207	0.11915
cg0457660	GNG4	C/EBPalph	483	489	0.540941	CCCAAT	0.24414	0.24432
cg0457660	GNG4	USF2 [T0	453	462	0.524236	CAGGTG	0.01144	0.01199
cg0457660	GNG4	c-Ets-1 [T	1744	1750	0.384261	CTTCCT	0.24414	0.23743
cg2521727	GNG4	GATA-1 [	36	41	0.280028	AAGATA	0.97656	0.8795
cg0457660	GNG4	GATA-1 [	185	190	0.280028	TATCTT	0.97656	0.8795
cg0457660	GNG4	GATA-1 [	911	916	0.280028	TATCTA	0.97656	0.8795
cg2521727	GNG4	c-Ets-1 [T	51	57	0.256174	CTTCCTT	0.24414	0.23743
cg2521727	GNG4	c-Ets-1 [T	1037	1043	0.256174	AAGGAA	0.24414	0.23743
cg0457660	GNG4	c-Ets-1 [T	638	644	0.256174	CTTCCTT	0.24414	0.23743
cg2521727	GNG4	AP-2alpha	92	97	0.226186	GCCTGG	0.97656	1.07867
cg2521727	GNG4	AP-2alpha	102	107	0.226186	GCCTGG	0.97656	1.07867
cg2521727	GNG4	AP-2alpha	240	245	0.226186	CCAGGC	0.97656	1.07867
cg2521727	GNG4	AP-2alpha	1226	1231	0.226186	GCCTGG	0.97656	1.07867
cg2521727	GNG4	AP-2alpha	1809	1814	0.226186	CCAGGC	0.97656	1.07867
cg0457660	GNG4	AP-2alpha	1027	1032	0.226186	GCCTGG	0.97656	1.07867
cg0457660	GNG4	AP-2alpha	1165	1170	0.226186	CCAGGC	0.97656	1.07867
cg0457660	GNG4	AP-2alpha	1340	1345	0.226186	CCAGGC	0.97656	1.07867
cg2521727	GNG4	TCF-4 [T0	1096	1105	0.22612	CATTCA	0.01144	0.01102
cg2521727	GNG4	p53 [T006	173	179	0.211706	GGGCAA	0.36621	0.40082
cg2521727	GNG4	GR-alpha [	120	124	0.207689	AGAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	759	763	0.207689	CCTTT	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	883	887	0.207689	CCTTT	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1032	1036	0.207689	AGAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1101	1105	0.207689	AAAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1458	1462	0.207689	CCTCT	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1707	1711	0.207689	CCTCT	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1720	1724	0.207689	CCTCT	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1832	1836	0.207689	CCTCT	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1909	1913	0.207689	CCTCT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	51	55	0.207689	CCTCT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	108	112	0.207689	CCTCT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	142	146	0.207689	AAAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	150	154	0.207689	CCTTT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	266	270	0.207689	AAAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	284	288	0.207689	AAAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	301	305	0.207689	CCTTT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	314	318	0.207689	CCTCT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	433	437	0.207689	AAAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	621	625	0.207689	CCTCT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	641	645	0.207689	CCTTT	7.8125	7.79817

cg0457660	GNG4	GR-alpha [	724	728	0.207689	AGAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	749	753	0.207689	CCTTT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	845	849	0.207689	CCTCT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1022	1026	0.207689	CCTTT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1124	1128	0.207689	CCTTT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1205	1209	0.207689	CCTCT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1468	1472	0.207689	AAAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1502	1506	0.207689	AGAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1798	1802	0.207689	CCTTT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1819	1823	0.207689	CCTCT	7.8125	7.79817
cg2521727	GNG4	c-Ets-1 [T	1033	1039	0.128087	GAGGAA	0.24414	0.24982
cg2521727	GNG4	GR-beta [T	571	575	0	AAATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	706	710	0	AAATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	852	856	0	ACATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	870	874	0	ACATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1018	1022	0	AAATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1095	1099	0	ACATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1596	1600	0	AAATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1597	1601	0	AATTT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1605	1609	0	AAATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1606	1610	0	AATTT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1766	1770	0	AATTT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1774	1778	0	AAATT	3.90625	3.51525
cg2521727	GNG4	GR-beta [T	1775	1779	0	AATTT	3.90625	3.51525
cg2521727	GNG4	XBP-1 [T	164	169	0	CGTCAT	0.97656	0.94838
cg2521727	GNG4	XBP-1 [T	302	307	0	AGTCAT	0.97656	0.94838
cg2521727	GNG4	XBP-1 [T	717	722	0	ATGACT	0.97656	0.94838
cg2521727	GNG4	XBP-1 [T	839	844	0	ATGACG	0.97656	0.94838
cg2521727	GNG4	TFIID [T0	209	215	0	TTTTTTA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	210	216	0	TTTTTAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	567	573	0	TAGAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	699	705	0	TTTTTAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	701	707	0	TTTAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	702	708	0	TTAAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1026	1032	0	TTTAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1218	1224	0	TTTAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1219	1225	0	TTAAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1592	1598	0	TTTAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1599	1605	0	TTTAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1600	1606	0	TTAAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1601	1607	0	TAAAAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1614	1620	0	TTTTTGA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1768	1774	0	TTTTTAA	1.09863	0.95175
cg2521727	GNG4	TFIID [T0	1770	1776	0	TTTAAA	1.09863	0.95175
cg2521727	GNG4	GR-alpha [	220	224	0	ACAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	339	343	0	ACAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	387	391	0	ACAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	474	478	0	ACAGG	7.8125	7.79817

cg2521727	GNG4	GR-alpha [	648	652	0	ACAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	689	693	0	CCTAT	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1138	1142	0	ACAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1208	1212	0	ATAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1622	1626	0	ACAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1740	1744	0	ACAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1876	1880	0	ATAGG	7.8125	7.79817
cg2521727	GNG4	GR-alpha [	1900	1904	0	CCTAT	7.8125	7.79817
cg2521727	GNG4	FOXP3 [T	901	906	0	AACAAC	1.46484	1.44953
cg2521727	GNG4	FOXP3 [T	1279	1284	0	GTTGTT	1.46484	1.44953
cg2521727	GNG4	FOXP3 [T	1282	1287	0	GTTGTT	1.46484	1.44953
cg2521727	GNG4	FOXP3 [T	1285	1290	0	GTTGTT	1.46484	1.44953
cg2521727	GNG4	FOXP3 [T	1329	1334	0	GTTGTT	1.46484	1.44953
cg2521727	GNG4	HNF-3alpl	697	704	0	TATTTTT	0.09155	0.07727
cg2521727	GNG4	C/EBPbeta	5	8	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	42	45	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	140	143	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	175	178	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	228	231	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	379	382	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	403	406	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	520	523	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	542	545	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	583	586	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	589	592	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	678	681	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	713	716	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	727	730	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	743	746	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	763	766	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	828	831	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	873	876	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	886	889	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	902	905	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	929	932	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	935	938	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1021	1024	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1132	1135	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1153	1156	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1280	1283	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1283	1286	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1286	1289	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1330	1333	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1344	1347	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1395	1398	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1447	1450	0	ACAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1539	1542	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1638	1641	0	TTGC	15.625	15.26275

cg2521727	GNG4	C/EBPbeta	1662	1665	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1711	1714	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1781	1784	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1802	1805	0	TTGT	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1805	1808	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1836	1839	0	TTGC	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1838	1841	0	GCAA	15.625	15.26275
cg2521727	GNG4	C/EBPbeta	1989	1992	0	GCAA	15.625	15.26275
cg2521727	GNG4	YY1 [T00	261	264	0	CCAT	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	266	269	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	353	356	0	CCAT	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	910	913	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	989	992	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1091	1094	0	CCAT	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1166	1169	0	CCAT	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1172	1175	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1326	1329	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1336	1339	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1375	1378	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1389	1392	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1506	1509	0	CCAT	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1510	1513	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1954	1957	0	ATGG	7.8125	7.79459
cg2521727	GNG4	YY1 [T00	1980	1983	0	CCAT	7.8125	7.79459
cg2521727	GNG4	TFII-I [T0	1246	1251	0	CTTTCC	1.46484	1.48598
cg2521727	GNG4	TFII-I [T0	1516	1521	0	GGACAG	1.46484	1.48598
cg2521727	GNG4	TFII-I [T0	1579	1584	0	CTTTCC	1.46484	1.48598
cg2521727	GNG4	STAT4 [T	1230	1235	0	GGAAAT	0.48828	0.46235
cg2521727	GNG4	c-Ets-1 [T	319	325	0	CTTCCTC	0.24414	0.24982
cg2521727	GNG4	c-Ets-1 [T	780	786	0	CTTCCTC	0.24414	0.24982
cg2521727	GNG4	HOXD9 [	1606	1615	0	AATTTT	0.01144	0.00905
cg2521727	GNG4	HOXD10 [	1606	1615	0	AATTTT	0.01144	0.00905
cg2521727	GNG4	ER-alpha [	110	114	0	GGTCA	1.95312	1.99744
cg2521727	GNG4	GR [T050	375	381	0	TTTTTTG	0.36621	0.33174
cg2521727	GNG4	GR [T050	936	942	0	CAAAAA	0.36621	0.33174
cg2521727	GNG4	GR [T050	1430	1436	0	CAAAAA	0.36621	0.33174
cg2521727	GNG4	GR [T050	1613	1619	0	ATTTTT	0.36621	0.33174
cg2521727	GNG4	GR [T050	1777	1783	0	TTTTTTG	0.36621	0.33174
cg2521727	GNG4	AR [T000	1516	1524	0	GGACAG	0.00763	0.00819
cg2521727	GNG4	Pax-5 [T0	100	106	0	GGGCCT	1.09863	1.24633
cg2521727	GNG4	Pax-5 [T0	354	360	0	CATGCC	1.09863	1.24633
cg2521727	GNG4	Pax-5 [T0	783	789	0	CCTGCC	1.09863	1.24633
cg2521727	GNG4	p53 [T006	354	360	0	CATGCC	0.36621	0.40082
cg2521727	GNG4	p53 [T006	783	789	0	CCTGCC	0.36621	0.40082
cg2521727	GNG4	AP-2alpha	1304	1309	0	GCCTGC	0.97656	1.07867
cg2521727	GNG4	AP-2alpha	1378	1383	0	GCAGGC	0.97656	1.07867
cg2521727	GNG4	Elk-1 [T00	780	788	0	CTTCCTC	0.06104	0.06399
cg2521727	GNG4	IRF-2 [T0	85	90	0	AAGTGA	0.48828	0.46235

cg2521727	GNG4	IRF-2 [T01	1700	1705	0	AAGTGA	0.48828	0.46235
cg2521727	GNG4	IRF-2 [T01	1797	1802	0	TCACTT	0.48828	0.46235
cg0457660	GNG4	GR-beta [T	346	350	0	ACATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	428	432	0	AATGT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	755	759	0	AAATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	980	984	0	AATGT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1289	1293	0	AATTT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1515	1519	0	AATTT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1601	1605	0	AATTT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1641	1645	0	ACATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1710	1714	0	ACATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1721	1725	0	AATTT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1913	1917	0	AAATT	3.90625	3.51525
cg0457660	GNG4	GR-beta [T	1930	1934	0	AATGT	3.90625	3.51525
cg0457660	GNG4	TFIID [T0	71	77	0	TAAAAA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	531	537	0	TTTTATA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	949	955	0	TCTAAA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1137	1143	0	TTTTTGA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1306	1312	0	TTTTTTA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1536	1542	0	TTTTTTA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1537	1543	0	TTTTTAA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1603	1609	0	TTTTCTA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1664	1670	0	TTAAAA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1665	1671	0	TAAAAA	1.09863	0.95175
cg0457660	GNG4	TFIID [T0	1757	1763	0	TTTTTTA	1.09863	0.95175
cg0457660	GNG4	GR-alpha [	156	160	0	CCTGT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	177	181	0	ACAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	292	296	0	ACAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	452	456	0	ACAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	474	478	0	CCTGT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	661	665	0	CCTAT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1040	1044	0	ACAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1671	1675	0	ACAGG	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1747	1751	0	CCTAT	7.8125	7.79817
cg0457660	GNG4	GR-alpha [	1876	1880	0	ACAGG	7.8125	7.79817
cg0457660	GNG4	HNF-3alph	1474	1481	0	TATTTTT	0.09155	0.07727
cg0457660	GNG4	C/EBPbeta	38	41	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	222	225	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	251	254	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	408	411	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	425	428	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	526	529	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	552	555	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	589	592	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	647	650	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	680	683	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	814	817	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	876	879	0	TTGC	15.625	15.26275

cg0457660	GNG4	C/EBPbeta	878	881	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	937	940	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	959	962	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	967	970	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	978	981	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1025	1028	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1201	1204	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1221	1224	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1225	1228	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1294	1297	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1405	1408	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1407	1410	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1456	1459	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1481	1484	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1555	1558	0	ACAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1624	1627	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1661	1664	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1682	1685	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1703	1706	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1713	1716	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1719	1722	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1725	1728	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1741	1744	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1792	1795	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1795	1798	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1849	1852	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1870	1873	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1872	1875	0	GCAA	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1905	1908	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1916	1919	0	TTGC	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1923	1926	0	TTGT	15.625	15.26275
cg0457660	GNG4	C/EBPbeta	1937	1940	0	GCAA	15.625	15.26275
cg0457660	GNG4	YY1 [T00	325	328	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	338	341	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	444	447	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	594	597	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	608	611	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	673	676	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	942	945	0	ATGG	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1319	1322	0	ATGG	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1331	1334	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1333	1336	0	ATGG	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1440	1443	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1528	1531	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1613	1616	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1629	1632	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1813	1816	0	CCAT	7.8125	7.79459
cg0457660	GNG4	YY1 [T00	1901	1904	0	ATGG	7.8125	7.79459

cg0457660	GNG4	TFII-I [T0	302	307	0	CTTTCC	1.46484	1.48598
cg0457660	GNG4	TFII-I [T0	475	480	0	CTGTCC	1.46484	1.48598
cg0457660	GNG4	TFII-I [T0	689	694	0	CTGTCC	1.46484	1.48598
cg0457660	GNG4	TFII-I [T0	710	715	0	CTTTCC	1.46484	1.48598
cg0457660	GNG4	TFII-I [T0	731	736	0	CTTTCC	1.46484	1.48598
cg0457660	GNG4	STAT4 [T	1815	1820	0	ATTTCC	0.48828	0.46235
cg0457660	GNG4	ER-alpha [	166	170	0	TGACC	1.95312	1.99744
cg0457660	GNG4	ER-alpha [	398	402	0	GGTCA	1.95312	1.99744
cg0457660	GNG4	ER-alpha [	695	699	0	TGACC	1.95312	1.99744
cg0457660	GNG4	ER-alpha [	716	720	0	TGACC	1.95312	1.99744
cg0457660	GNG4	ER-alpha [	737	741	0	TGACC	1.95312	1.99744
cg0457660	GNG4	ER-alpha [	1360	1364	0	TGACC	1.95312	1.99744
cg0457660	GNG4	ER-alpha [	1370	1374	0	TGACC	1.95312	1.99744
cg0457660	GNG4	ER-alpha [	1975	1979	0	TGACC	1.95312	1.99744
cg0457660	GNG4	SRY [T00	1680	1688	0	CTTTGTT	0.03052	0.02847
cg0457660	GNG4	GR [T050	879	885	0	CAAAAA	0.36621	0.33174
cg0457660	GNG4	GR [T050	1136	1142	0	TTTTTTG	0.36621	0.33174
cg0457660	GNG4	GR [T050	1290	1296	0	ATTTTTG	0.36621	0.33174
cg0457660	GNG4	LEF-1 [T0	1775	1782	0	GATCAA	0.03052	0.02895
cg0457660	GNG4	GATA-1 [	915	920	0	TATCTG	0.97656	0.92541
cg0457660	GNG4	Pax-5 [T0	236	242	0	GGGCCC	1.09863	1.24633
cg0457660	GNG4	Pax-5 [T0	585	591	0	GGGCTT	1.09863	1.24633
cg0457660	GNG4	Pax-5 [T0	1422	1428	0	CGTGCC	1.09863	1.24633
cg0457660	GNG4	AP-2alpha	200	205	0	GCCTGC	0.97656	1.07867
cg0457660	GNG4	IRF-2 [T0	1367	1372	0	AAGTGA	0.48828	0.46235
cg0457660	GNG4	IRF-2 [T0	1491	1496	0	AAGTGA	0.48828	0.46235
cg0457660	GNG4	HNF-1A [	1537	1544	0	TTTTTAA	0.24414	0.20853
cg0457660	GNG4	HNF-1A [	1663	1670	0	GTTAAA	0.24414	0.20853
cg1103635	HCG4	c-Ets-1 [T	1398	1404	9.969337	ATTCCC	0.24414	0.23698
cg1103635	HCG4	STAT1bet	701	710	9.807397	AGAGGG	0.14877	0.14533
cg1103635	HCG4	XBP-1 [T	1941	1946	9.789909	ATGGCG	1.95312	1.94901
cg1103635	HCG4	PR B [T00	154	160	9.743489	AACACA	1.09863	1.0981
cg1103635	HCG4	PR B [T00	237	243	9.743489	GGGTGT	1.09863	1.0981
cg1103635	HCG4	PR B [T00	1029	1035	9.743489	AACACA	1.09863	1.0981
cg1103635	HCG4	PR A [T01	154	160	9.743489	AACACA	1.09863	1.0981
cg1103635	HCG4	PR A [T01	237	243	9.743489	GGGTGT	1.09863	1.0981
cg1103635	HCG4	PR A [T01	1029	1035	9.743489	AACACA	1.09863	1.0981
cg1103635	HCG4	c-Ets-1 [T	1734	1740	9.713162	ATTCCC	0.36621	0.37402
cg1103635	HCG4	Elk-1 [T00	660	668	9.62002	GGAGGG	0.07629	0.0786
cg1103635	HCG4	RAR-beta	34	43	9.567396	GCACAA	0.21362	0.22369
cg1103635	HCG4	TFIID [T0	163	169	9.552105	TTTGGA	1.46484	1.37777
cg1103635	HCG4	TFIID [T0	246	252	9.552105	TTTGCC	1.46484	1.37777
cg1103635	HCG4	TFIID [T0	713	719	9.552105	TTCGAA	1.46484	1.37777
cg1103635	HCG4	TFIID [T0	1141	1147	9.552105	TGGGAA	1.46484	1.37777
cg1103635	HCG4	TFIID [T0	1573	1579	9.552105	TTTCTCA	1.46484	1.37777
cg1103635	HCG4	Pax-5 [T0	1590	1596	9.552105	GGGCCA	1.46484	1.61918
cg1103635	HCG4	Pax-5 [T0	1943	1949	9.552105	GGCGCC	1.46484	1.61918
cg1103635	HCG4	NF-1 [T00	209	216	9.535536	CTGACC	0.73242	0.74634

cg1103635	HCG4	FOXP3 [T	6	11	9.512894	AAGAAC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	173	178	9.512894	CAGAAC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	554	559	9.512894	GAGAAC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	724	729	9.512894	CAGAAC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	801	806	9.512894	GTTGGC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	1286	1291	9.512894	ATAAAC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	1422	1427	9.512894	GGCAAC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	1500	1505	9.512894	GTTCTG	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	1769	1774	9.512894	CCCAAC	7.32422	7.22156
cg1103635	HCG4	FOXP3 [T	1818	1823	9.512894	GTTCTC	7.32422	7.22156
cg1103635	HCG4	TFII-I [T0	26	31	9.512894	GGAATT	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	664	669	9.512894	GGAAGG	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	910	915	9.512894	GGATAC	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	995	1000	9.512894	AAGTCC	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	1338	1343	9.512894	TTTTCC	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	1506	1511	9.512894	GGACGG	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	1541	1546	9.512894	GGACGG	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	1604	1609	9.512894	GGAAAC	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	1653	1658	9.512894	AAGTCC	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	1871	1876	9.512894	CGGTCC	7.32422	7.44385
cg1103635	HCG4	TFII-I [T0	1931	1936	9.512894	GGATGG	7.32422	7.44385
cg1103635	HCG4	c-Jun [T00	59	65	9.442241	TGACAG	0.73242	0.7366
cg1103635	HCG4	NFI/CTF [	1212	1219	9.352332	CCAAAG	0.54932	0.55369
cg1103635	HCG4	LEF-1 [T0	1692	1699	9.313676	CCCCAA	0.21362	0.21229
cg1103635	HCG4	c-Ets-1 [T	1887	1893	9.276861	GTTCCC	0.36621	0.37402
cg1103635	HCG4	AP-1 [T00	388	396	9.256161	ATTCAG	0.09155	0.08441
cg1103635	HCG4	VDR [T00	878	886	9.234242	GTTCAT	0.12207	0.11552
cg1103635	HCG4	NF-AT1 [	1143	1151	9.18189	GGAAAG	0.22888	0.22581
cg1103635	HCG4	LEF-1 [T0	794	801	9.099721	CTTTGC	0.54932	0.53171
cg1103635	HCG4	LEF-1 [T0	1743	1750	9.099721	CTTTGC	0.54932	0.53171
cg1103635	HCG4	STAT5A [	96	108	9.080962	CTGCCA	0.02816	0.02551
cg1103635	HCG4	c-Ets-1 [T	1087	1093	9.065503	ATGGAA	0.85449	0.84987
cg1103635	HCG4	NFI/CTF [	798	805	9.042931	GCAGTT	0.48828	0.48845
cg1103635	HCG4	GR [T050	160	166	8.971049	GCTTTC	0.61035	0.5928
cg1103635	HCG4	c-Ets-1 [T	493	499	8.937416	GTGGAA	0.85449	0.84987
cg1103635	HCG4	c-Ets-2 [T	1791	1799	8.912323	TTCCTG	0.27466	0.27171
cg1103635	HCG4	p53 [T006	1975	1981	8.912104	GGGCCC	0.12207	0.13824
cg1103635	HCG4	ETF [T002	631	641	8.876947	GAGAGG	0.02384	0.02809
cg1103635	HCG4	c-Ets-1 [T	459	465	8.809329	ATTCCA	0.85449	0.84987
cg1103635	HCG4	NF-1 [T00	1766	1773	8.790071	TCTCCC	0.24414	0.24339
cg1103635	HCG4	LEF-1 [T0	1162	1169	8.759086	CTTTGT	0.54932	0.53171
cg1103635	HCG4	LEF-1 [T0	1522	1529	8.759086	ATGCAA	0.54932	0.53171
cg1103635	HCG4	XBP-1 [T	149	154	8.75604	ATGAAA	2.92969	2.75329
cg1103635	HCG4	XBP-1 [T	380	385	8.75604	TTTCAT	2.92969	2.75329
cg1103635	HCG4	XBP-1 [T	421	426	8.75604	ATGAAC	2.92969	2.75329
cg1103635	HCG4	XBP-1 [T	649	654	8.75604	ATGAGA	2.92969	2.75329
cg1103635	HCG4	XBP-1 [T	878	883	8.75604	GTTCAT	2.92969	2.75329
cg1103635	HCG4	XBP-1 [T	936	941	8.75604	ATGAGC	2.92969	2.75329

cg1103635	HCG4	XBP-1 [T	1244	1249	8.75604	GATCAT	2.92969	2.75329
cg1103635	HCG4	XBP-1 [T	1317	1322	8.75604	TCTCAT	2.92969	2.75329
cg1103635	HCG4	RXR-alpha	1269	1275	8.664139	GCTACC	0.12207	0.13135
cg1103635	HCG4	IRF-1 [T0	686	694	8.661524	GTGAGG	0.20599	0.20245
cg1103635	HCG4	USF2 [T0	427	436	8.532138	CAGGTG	0.103	0.10815
cg1103635	HCG4	RelA [T00	1731	1741	8.46023	GGCATT	0.0248	0.02561
cg1103635	HCG4	RBP-Jkap	1886	1897	8.425028	AGTTCC	0.02074	0.02067
cg1103635	HCG4	c-Myb [T0	1299	1306	8.412632	AAACTG	0.30518	0.28602
cg1103635	HCG4	HNF-3alp	333	340	8.343064	TATTTA	0.27466	0.23078
cg1103635	HCG4	HNF-3alp	1101	1108	8.343064	AATTTA	0.27466	0.23078
cg1103635	HCG4	PR B [T00	74	80	8.338824	AACAGA	1.09863	1.09384
cg1103635	HCG4	PR B [T00	176	182	8.338824	AACAGG	1.09863	1.09384
cg1103635	HCG4	PR B [T00	924	930	8.338824	AACAGG	1.09863	1.09384
cg1103635	HCG4	PR B [T00	1171	1177	8.338824	TCCTGT	1.09863	1.09384
cg1103635	HCG4	PR A [T01	74	80	8.338824	AACAGA	1.09863	1.09384
cg1103635	HCG4	PR A [T01	176	182	8.338824	AACAGG	1.09863	1.09384
cg1103635	HCG4	PR A [T01	924	930	8.338824	AACAGG	1.09863	1.09384
cg1103635	HCG4	PR A [T01	1171	1177	8.338824	TCCTGT	1.09863	1.09384
cg1103635	HCG4	ATF3 [T0	1199	1206	8.313799	ATATGT	0.27466	0.27379
cg1103635	HCG4	PXR-1:RX	875	882	8.304332	AGTGTT	0.12207	0.11843
cg1103635	HCG4	GR-alpha [	69	73	8.281568	CAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	134	138	8.281568	GAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	137	141	8.281568	GGAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	214	218	8.281568	CAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	480	484	8.281568	CAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	610	614	8.281568	CAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	635	639	8.281568	GGAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	660	664	8.281568	GGAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	665	669	8.281568	GAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	682	686	8.281568	GGAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	780	784	8.281568	CCTTG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1042	1046	8.281568	CCTTG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1094	1098	8.281568	GAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1205	1209	8.281568	CAAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1393	1397	8.281568	CCTCC	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1484	1488	8.281568	GGAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1556	1560	8.281568	CGAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1716	1720	8.281568	GGAGG	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1786	1790	8.281568	CCTTC	7.8125	8.20394
cg1103635	HCG4	GR-alpha [	1928	1932	8.281568	CGAGG	7.8125	8.20394
cg1103635	HCG4	HNF-1B [	317	325	8.255112	TTCTTAA	0.11444	0.10456
cg1103635	HCG4	NFI/CTF [	1770	1777	8.241664	CCAACC	0.18311	0.1922
cg1103635	HCG4	p53 [T006	1545	1551	8.208781	GGGGCC	0.48828	0.55336
cg1103635	HCG4	p53 [T006	1974	1980	8.208781	GGGGCC	0.48828	0.55336
cg1103635	HCG4	NF-1 [T00	802	809	8.191058	TTGGCC	0.24414	0.24485
cg1103635	HCG4	c-Jun [T00	455	461	8.128539	TGACAT	0.48828	0.47447
cg1103635	HCG4	GR-alpha [	0	4	8.073878	GTAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	23	27	8.073878	CCAGG	7.8125	8.20289

cg1103635	HCG4	GR-alpha [	41	45	8.073878	CCTGC	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	415	419	8.073878	CCTAC	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	426	430	8.073878	CCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	538	542	8.073878	GCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	569	573	8.073878	GCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	679	683	8.073878	GCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	784	788	8.073878	GCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1010	1014	8.073878	CCTGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1060	1064	8.073878	CCTGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1402	1406	8.073878	CCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1434	1438	8.073878	CCTGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1481	1485	8.073878	GTAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1488	1492	8.073878	GCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1568	1572	8.073878	CCTGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1587	1591	8.073878	CCTGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1658	1662	8.073878	CCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1747	1751	8.073878	GCAGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1793	1797	8.073878	CCTGG	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1955	1959	8.073878	CCTGC	7.8125	8.20289
cg1103635	HCG4	GR-alpha [	1979	1983	8.073878	CCTGG	7.8125	8.20289
cg1103635	HCG4	TFIID [T0	1	7	8.014558	TAGGAA	2.19727	1.99811
cg1103635	HCG4	TFIID [T0	206	212	8.014558	TTTCTGA	2.19727	1.99811
cg1103635	HCG4	TFIID [T0	316	322	8.014558	TTTCTTA	2.19727	1.99811
cg1103635	HCG4	TFIID [T0	593	599	8.014558	TCACAA	2.19727	1.99811
cg1103635	HCG4	TFIID [T0	1163	1169	8.014558	TTTGTGA	2.19727	1.99811
cg1103635	HCG4	Pax-5 [T0	167	173	8.014558	GAAGCC	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	431	437	8.014558	TGTGCC	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	1545	1551	8.014558	GGGGCC	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	1546	1552	8.014558	GGGCCC	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	1661	1667	8.014558	GGGCCT	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	1717	1723	8.014558	GAGGCC	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	1807	1813	8.014558	GGGCTG	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	1809	1815	8.014558	GCTGCC	2.19727	2.42766
cg1103635	HCG4	Pax-5 [T0	1974	1980	8.014558	GGGGCC	2.19727	2.42766
cg1103635	HCG4	C/EBPalph	417	423	8.006685	TACAAT	0.24414	0.23098
cg1103635	HCG4	AhR:Arnt	1666	1675	8.006459	TCAGGC	0.01717	0.01925
cg1103635	HCG4	c-Ets-2 [T	21	29	7.84116	CACCAG	0.32043	0.30792
cg1103635	HCG4	c-Ets-2 [T	916	924	7.84116	TTCCTAA	0.32043	0.30792
cg1103635	HCG4	c-Ets-2 [T	1239	1247	7.84116	TTCCTGA	0.32043	0.30792
cg1103635	HCG4	EBF [T05	1076	1086	7.780217	AACTCA	0.04196	0.04563
cg1103635	HCG4	c-Jun [T00	558	564	7.686747	ACAGTC	0.48828	0.48672
cg1103635	HCG4	c-Ets-1 [T	1552	1558	7.642098	ATTCCG	0.48828	0.48642
cg1103635	HCG4	NFI/CTF [	160	167	7.587343	GCTTTTC	0.36621	0.36269
cg1103635	HCG4	c-Myb [T0	103	110	7.545286	AAACTG	0.42725	0.40917
cg1103635	HCG4	PPAR-alph	1653	1663	7.529496	AAGTCC	0.04482	0.04884
cg1103635	HCG4	PPAR-alph	1717	1727	7.529496	GAGGCC	0.04482	0.04884
cg1103635	HCG4	GR [T050	145	151	7.527031	CAAAAT	1.83105	1.71535
cg1103635	HCG4	GR [T050	596	602	7.527031	CAAATA	1.83105	1.71535

cg1103635	HCG4	GR [T050	1160	1166	7.527031	AGCTTT	1.83105	1.71535
cg1103635	HCG4	GR [T050	1356	1362	7.527031	CAAACA	1.83105	1.71535
cg1103635	HCG4	GR [T050	1360	1366	7.527031	CAAACA	1.83105	1.71535
cg1103635	HCG4	c-Ets-1 [T	1514	1520	7.514011	ATTCCG	0.48828	0.48642
cg1103635	HCG4	p53 [T006	1082	1088	7.47855	GGGCTA	0.73242	0.79826
cg1103635	HCG4	RAR-beta	1374	1383	7.459774	AAAAAA	0.24414	0.25121
cg1103635	HCG4	p53 [T006	1943	1949	7.458735	GGCGCC	0.73242	0.79826
cg1103635	HCG4	PEA3 [T0	1930	1938	7.421728	AGGATG	0.34332	0.35389
cg1103635	HCG4	POU2F2 (	756	766	7.236857	ATTTTA	0.00238	0.00196
cg1103635	HCG4	c-Ets-1 [T	1141	1147	7.199436	TGGGAA	0.73242	0.73732
cg1103635	HCG4	XBP-1 [T	270	275	7.172312	ATGAAT	2.92969	2.7512
cg1103635	HCG4	XBP-1 [T	278	283	7.172312	ATGAAT	2.92969	2.7512
cg1103635	HCG4	XBP-1 [T	373	378	7.172312	ACTCAT	2.92969	2.7512
cg1103635	HCG4	XBP-1 [T	384	389	7.172312	ATTCAT	2.92969	2.7512
cg1103635	HCG4	XBP-1 [T	436	441	7.172312	CCTCAT	2.92969	2.7512
cg1103635	HCG4	XBP-1 [T	988	993	7.172312	ATGAAT	2.92969	2.7512
cg1103635	HCG4	XBP-1 [T	1092	1097	7.172312	ATGAAG	2.92969	2.7512
cg1103635	HCG4	p53 [T006	1546	1552	7.153797	GGGCCC	1.09863	1.22478
cg1103635	HCG4	c-Myb [T0	1496	1503	7.127234	TCCAGT	0.18311	0.17765
cg1103635	HCG4	c-Jun [T00	959	965	7.096776	TGACTG	0.73242	0.73062
cg1103635	HCG4	c-Ets-1 [T	703	709	7.071349	AGGGAA	0.73242	0.73732
cg1103635	HCG4	c-Ets-1 [T	1602	1608	7.071349	AGGGAA	0.73242	0.73732
cg1103635	HCG4	C/EBPalp	1134	1140	7.00174	CATTGT	0.73242	0.68282
cg1103635	HCG4	HNF-3alp	144	151	7.000129	TCAAAA	0.82397	0.71909
cg1103635	HCG4	HNF-3alp	348	355	7.000129	AATTTC	0.82397	0.71909
cg1103635	HCG4	HNF-3alp	840	847	7.000129	AATTTT	0.82397	0.71909
cg1103635	HCG4	IRF-1 [T0	1139	1147	6.968314	TCTGGG	0.1297	0.12685
cg1103635	HCG4	NF-1 [T00	1690	1697	6.948522	GGCCCC	0.48828	0.50205
cg1103635	HCG4	ENKTF-1	1942	1949	6.942764	TGGCGC	1.46484	1.56616
cg1103635	HCG4	p53 [T006	1661	1667	6.938545	GGGCCT	1.09863	1.22478
cg1103635	HCG4	p53 [T006	1717	1723	6.938545	GAGGCC	1.09863	1.22478
cg1103635	HCG4	STAT1bet	1600	1609	6.908963	TCAGGG	0.103	0.09938
cg1103635	HCG4	ELF-1 [T0	912	924	6.870844	ATACTT	0.0056	0.00552
cg1103635	HCG4	c-Jun [T00	210	216	6.856451	TGACCA	0.73242	0.73062
cg1103635	HCG4	C/EBPalp	360	366	6.85549	TGCAAT	0.73242	0.68282
cg1103635	HCG4	AR [T000	1468	1476	6.817719	GGACAG	0.23651	0.23986
cg1103635	HCG4	NF-kappa	1729	1740	6.804252	TGGGCA	0.00608	0.00661
cg1103635	HCG4	NF-AT1 [	3	11	6.799037	GGAAAG	0.15259	0.14325
cg1103635	HCG4	NFI/CTF [	1708	1715	6.786076	TGGATT	0.73242	0.74795
cg1103635	HCG4	NFI/CTF [	1855	1862	6.786076	CCAATC	0.73242	0.74795
cg1103635	HCG4	NF-1 [T00	1226	1233	6.722386	TTGGCC	0.24414	0.2565
cg1103635	HCG4	c-Ets-2 [T	1170	1178	6.695187	TTCCTG	0.09155	0.08559
cg1103635	HCG4	FOXP3 [T	500	505	6.581441	GTTTTA	0.97656	0.904
cg1103635	HCG4	FOXP3 [T	747	752	6.581441	GTTTTA	0.97656	0.904
cg1103635	HCG4	TFII-I [T0	603	608	6.581441	GGAGTG	0.97656	0.9991
cg1103635	HCG4	TFII-I [T0	673	678	6.581441	GGAGAT	0.97656	0.9991
cg1103635	HCG4	TFII-I [T0	1052	1057	6.581441	GGAGAT	0.97656	0.9991
cg1103635	HCG4	TFII-I [T0	1823	1828	6.581441	CACTCC	0.97656	0.9991

cg1103635	HCG4	p53 [T006	167	173	6.563521	GAAGCC	0.48828	0.54643
cg1103635	HCG4	p53 [T006	1807	1813	6.563521	GGGCTG	0.48828	0.54643
cg1103635	HCG4	XBP-1 [T	951	956	6.478682	GGGCAT	0.97656	0.99906
cg1103635	HCG4	XBP-1 [T	1730	1735	6.478682	GGGCAT	0.97656	0.99906
cg1103635	HCG4	c-Fos [T00	1122	1131	6.448203	GAGTCA	0.04578	0.04485
cg1103635	HCG4	RAR-beta	1558	1567	6.378264	AGGGTT	0.18311	0.1857
cg1103635	HCG4	RAR-beta	1749	1758	6.378264	AGGGTT	0.18311	0.1857
cg1103635	HCG4	TCF-4E [T	1211	1217	6.302385	ACCAAA	0.61035	0.59686
cg1103635	HCG4	GR-alpha [	82	86	6.263098	CCTCA	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	436	440	6.263098	CCTCA	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	600	604	6.263098	TAAGG	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	625	629	6.263098	TAAGG	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	643	647	6.263098	TGAGG	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	687	691	6.263098	TGAGG	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	815	819	6.263098	CCTTA	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	947	951	6.263098	TGAGG	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	1475	1479	6.263098	TAAGG	3.90625	3.89624
cg1103635	HCG4	GR-alpha [	1664	1668	6.263098	CCTCA	3.90625	3.89624
cg1103635	HCG4	SRY [T00	1162	1170	6.176442	CTTTGTC	0.15259	0.14742
cg1103635	HCG4	SRY [T00	1209	1217	6.176442	GGACCA	0.15259	0.14742
cg1103635	HCG4	AR [T000	1053	1061	6.112954	GAGATG	0.24414	0.25115
cg1103635	HCG4	p53 [T006	1590	1596	6.095267	GGGCCA	0.61035	0.68483
cg1103635	HCG4	GR-alpha [	16	20	6.055408	TTAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	131	135	6.055408	CCTGA	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	453	457	6.055408	CCTGA	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	503	507	6.055408	TTAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	641	645	6.055408	CCTGA	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	730	734	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	830	834	6.055408	CCTAA	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	856	860	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	918	922	6.055408	CCTAA	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1049	1053	6.055408	TTAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1079	1083	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1155	1159	6.055408	TTAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1241	1245	6.055408	CCTGA	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1249	1253	6.055408	TTAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1327	1331	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1600	1604	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1645	1649	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1666	1670	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1679	1683	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1687	1691	6.055408	TCAGG	3.90625	3.89835
cg1103635	HCG4	GR-alpha [	1985	1989	6.055408	CCTGA	3.90625	3.89835
cg1103635	HCG4	c-Ets-1 [T	1339	1345	6.039428	TTTCCAC	0.36621	0.36174
cg1103635	HCG4	C/EBPalph	743	749	5.996794	CATTGTT	0.97656	0.91422
cg1103635	HCG4	RXR-alph	1796	1802	5.937582	GGGTAC	0.73242	0.78318
cg1103635	HCG4	STAT4 [T	664	669	5.882353	GGAAGG	0.48828	0.51201
cg1103635	HCG4	c-Ets-1 [T	1916	1922	5.814485	CTTCCC	0.36621	0.36174

cg1103635	HCG4	c-Jun [T00	1214	1220	5.783074	AAAGTC	0.36621	0.34478
cg1103635	HCG4	VDR [T00	418	426	5.771401	ACAATG	0.42725	0.41266
cg1103635	HCG4	NF-AT2 [	1334	1343	5.75046	CAACTT	0.04196	0.03934
cg1103635	HCG4	PPAR-alp	1586	1596	5.741676	TCCTGG	0.03529	0.03856
cg1103635	HCG4	RXR-alph	237	243	5.715466	GGGTGT	0.61035	0.65415
cg1103635	HCG4	c-Jun [T00	1641	1647	5.703976	GGGGTC	0.48828	0.49294
cg1103635	HCG4	ENKTF-1	1588	1595	5.687009	CTGGGC	0.73242	0.76357
cg1103635	HCG4	ENKTF-1	1626	1633	5.687009	TGGCAC	0.73242	0.76357
cg1103635	HCG4	c-Ets-1 [T	662	668	5.686398	AGGGAA	0.36621	0.38732
cg1103635	HCG4	IRF-1 [T0	1339	1347	5.65977	TTTCCA	0.22888	0.21959
cg1103635	HCG4	NF-1 [T00	1208	1215	5.626299	GGGACC	0.24414	0.25051
cg1103635	HCG4	c-Jun [T00	589	595	5.590308	AGTGTC	0.48828	0.49294
cg1103635	HCG4	AP-2alpha	44	49	5.568965	GCCTAT	0.48828	0.48642
cg1103635	HCG4	T3R-beta1	1435	1443	5.553412	CTGGGG	0.21362	0.21789
cg1103635	HCG4	TFIID [T0	917	923	5.544826	TCCTAA	0.73242	0.65314
cg1103635	HCG4	TFIID [T0	1880	1886	5.544826	TTCTAA	0.73242	0.65314
cg1103635	HCG4	Pax-5 [T0	1082	1088	5.544826	GGGCTA	0.73242	0.79
cg1103635	HCG4	C/EBPalp	1858	1864	5.455853	ATCAAT	0.73242	0.68229
cg1103635	HCG4	p53 [T006	1648	1654	5.345221	GGGCGA	0.61035	0.65765
cg1103635	HCG4	ELF-1 [T0	212	224	5.269599	ACCAAG	0.00453	0.00447
cg1103635	HCG4	HNF-1B [	850	858	5.261286	TGTTAA	0.03052	0.02776
cg1103635	HCG4	C/EBPalp	56	62	5.240291	TATTGA	0.97656	0.90302
cg1103635	HCG4	c-Ets-2 [T	67	75	5.162974	AGCAAG	0.13733	0.13279
cg1103635	HCG4	c-Ets-2 [T	212	220	5.162974	ACCAAG	0.13733	0.13279
cg1103635	HCG4	c-Myb [T0	1814	1821	5.137438	CCCAGT	0.30518	0.30087
cg1103635	HCG4	AP-2alpha	805	810	5.100982	GCCTTT	0.97656	0.97517
cg1103635	HCG4	AP-2alpha	1696	1701	5.100982	AAAGGC	0.97656	0.97517
cg1103635	HCG4	RXR-alph	787	793	5.089356	GGGTGA	0.48828	0.51407
cg1103635	HCG4	RXR-alph	1438	1444	5.089356	GGGTGA	0.48828	0.51407
cg1103635	HCG4	GR-beta [	55	59	5.042296	GTATT	3.90625	3.7093
cg1103635	HCG4	GR-beta [	140	144	5.042296	GGATT	3.90625	3.7093
cg1103635	HCG4	GR-beta [	181	185	5.042296	GGATT	3.90625	3.7093
cg1103635	HCG4	GR-beta [	332	336	5.042296	GTATT	3.90625	3.7093
cg1103635	HCG4	GR-beta [	411	415	5.042296	AATCC	3.90625	3.7093
cg1103635	HCG4	GR-beta [	761	765	5.042296	AATAC	3.90625	3.7093
cg1103635	HCG4	GR-beta [	811	815	5.042296	AATAC	3.90625	3.7093
cg1103635	HCG4	GR-beta [	868	872	5.042296	AATAC	3.90625	3.7093
cg1103635	HCG4	GR-beta [	1046	1050	5.042296	GTATT	3.90625	3.7093
cg1103635	HCG4	GR-beta [	1108	1112	5.042296	AATAC	3.90625	3.7093
cg1103635	HCG4	GR-beta [	1512	1516	5.042296	GGATT	3.90625	3.7093
cg1103635	HCG4	GR-beta [	1709	1713	5.042296	GGATT	3.90625	3.7093
cg1103635	HCG4	E2F-1 [T0	1118	1125	5.042045	GCGGGA	0.18311	0.20394
cg1103635	HCG4	c-Ets-1 [T	164	170	5.038739	TTGGAA	0.48828	0.48026
cg1103635	HCG4	Elk-1 [T00	915	923	5.027151	CTTCCTA	0.03052	0.02883
cg1103635	HCG4	c-Jun [T00	1935	1941	5.000337	GGTGTC	0.61035	0.60573
cg1103635	HCG4	c-Myb [T0	797	804	4.974489	TGCAGT	0.30518	0.30087
cg1103635	HCG4	EBF [T05	1431	1441	4.906683	CTCCCT	0.02289	0.02569
cg1103635	HCG4	XBP-1 [T	645	650	4.894955	AGGCAT	0.97656	0.99839

cg1103635	HCG4	AP-2alpha	16	21	4.890408	TTAGGC	0.97656	0.97517
cg1103635	HCG4	AP-2alpha	829	834	4.890408	GCCTAA	0.97656	0.97517
cg1103635	HCG4	c-Jun [T00	1200	1206	4.883696	TATGTC	0.61035	0.60573
cg1103635	HCG4	AP-1 [T00	1119	1127	4.868583	CGGGAG	0.12207	0.12309
cg1103635	HCG4	C/EBPalph	273	279	4.845599	AATTGA	0.97656	0.90302
cg1103635	HCG4	C/EBPalph	281	287	4.845599	AATTGA	0.97656	0.90302
cg1103635	HCG4	HNF-3alph	303	310	4.842999	ATAAAA	0.09155	0.07438
cg1103635	HCG4	HNF-3alph	308	315	4.842999	ATAAAA	0.09155	0.07438
cg1103635	HCG4	HNF-3alph	884	891	4.842999	ATAAAA	0.09155	0.07438
cg1103635	HCG4	FOXP3 [T	151	156	4.756447	GAAAAC	2.92969	2.82
cg1103635	HCG4	FOXP3 [T	244	249	4.756447	GTTTTG	2.92969	2.82
cg1103635	HCG4	FOXP3 [T	833	838	4.756447	AAAAAC	2.92969	2.82
cg1103635	HCG4	FOXP3 [T	921	926	4.756447	AAAAAC	2.92969	2.82
cg1103635	HCG4	FOXP3 [T	1351	1356	4.756447	AAAAAC	2.92969	2.82
cg1103635	HCG4	FOXP3 [T	1375	1380	4.756447	AAAAAC	2.92969	2.82
cg1103635	HCG4	TFII-I [T0	458	463	4.756447	CATTCC	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	495	500	4.756447	GGAATG	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	655	660	4.756447	GGAATG	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	690	695	4.756447	GGAAAT	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	1056	1061	4.756447	ATGTCC	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	1089	1094	4.756447	GGAATG	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	1397	1402	4.756447	CATTCC	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	1551	1556	4.756447	CATTCC	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	1709	1714	4.756447	GGATTG	2.92969	2.89715
cg1103635	HCG4	TFII-I [T0	1733	1738	4.756447	CATTCC	2.92969	2.89715
cg1103635	HCG4	PPAR-alph	1986	1996	4.727619	CTGACC	0.03242	0.03494
cg1103635	HCG4	HNF-1A [	317	324	4.684871	TTCTTA	0.12207	0.10966
cg1103635	HCG4	HNF-1C [	1282	1290	4.656597	GTTAAT	0.07629	0.06715
cg1103635	HCG4	EBF [T05	1655	1665	4.612817	GTCCCA	0.00572	0.00669
cg1103635	HCG4	RAR-alpha	1641	1653	4.596281	GGGGTC	0.00376	0.0041
cg1103635	HCG4	C/EBPalph	1854	1860	4.560723	GCCAAT	0.24414	0.24373
cg1103635	HCG4	c-Jun [T00	390	396	4.441904	TCAGTC	0.12207	0.11843
cg1103635	HCG4	RXR-alpha	36	42	4.423008	ACAACC	0.24414	0.25781
cg1103635	HCG4	STAT4 [T	166	171	4.411765	GGAAGC	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	458	463	4.411765	CATTCC	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	495	500	4.411765	GGAATG	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	655	660	4.411765	GGAATG	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	1089	1094	4.411765	GGAATG	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	1397	1402	4.411765	CATTCC	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	1551	1556	4.411765	CATTCC	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	1733	1738	4.411765	CATTCC	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	1789	1794	4.411765	TCTTCC	1.95312	1.99838
cg1103635	HCG4	STAT4 [T	1915	1920	4.411765	TCTTCC	1.95312	1.99838
cg1103635	HCG4	HOXD9 [	307	316	4.321431	AATAAA	0.03433	0.02831
cg1103635	HCG4	HOXD10 [	307	316	4.321431	AATAAA	0.03433	0.02831
cg1103635	HCG4	HNF-1C [	851	859	4.306318	GTTAAT	0.07629	0.06715
cg1103635	HCG4	c-Ets-1 [T	653	659	4.282938	GAGGAA	0.85449	0.8381
cg1103635	HCG4	GR-beta [	46	50	4.201913	CTATT	7.8125	7.23274

cg1103635	HCG4	GR-beta [T	307	311	4.201913	AATAA	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	368	372	4.201913	AATAG	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	598	602	4.201913	AATAA	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	854	858	4.201913	AATCA	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	991	995	4.201913	AATAA	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	1167	1171	4.201913	TGATT	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	1231	1235	4.201913	CGATT	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	1285	1289	4.201913	AATAA	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	1309	1313	4.201913	CTATT	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	1441	1445	4.201913	TGATT	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	1857	1861	4.201913	AATCA	7.8125	7.23274
cg1103635	HCG4	GR-beta [T	1911	1915	4.201913	CGATT	7.8125	7.23274
cg1103635	HCG4	NF-Y [T0	1711	1718	4.186615	ATTGGG	0.18311	0.17499
cg1103635	HCG4	c-Ets-1 [T	24	30	4.154851	CAGGAA	0.24414	0.23719
cg1103635	HCG4	c-Ets-1 [T	1169	1175	4.154851	ATTCCT	0.24414	0.23719
cg1103635	HCG4	c-Ets-1 [T	1238	1244	4.154851	ATTCCT	0.24414	0.23719
cg1103635	HCG4	p53 [T006	638	644	4.125254	GGGCCT	0.73242	0.82434
cg1103635	HCG4	p53 [T006	1688	1694	4.125254	CAGGCC	0.73242	0.82434
cg1103635	HCG4	PXR-1:RX	422	429	4.090374	TGAACC	0.12207	0.12474
cg1103635	HCG4	IRF-1 [T0	1600	1608	4.035054	TCAGGG	0.1297	0.12468
cg1103635	HCG4	RXR-alph	1559	1565	4.019014	GGGTTT	0.97656	1.02803
cg1103635	HCG4	RXR-alph	1750	1756	4.019014	GGGTTT	0.97656	1.02803
cg1103635	HCG4	RXR-alph	1840	1846	4.019014	GGGTTT	0.97656	1.02803
cg1103635	HCG4	EBF [T05	1399	1409	4.016439	TTCCCA	0.0248	0.02839
cg1103635	HCG4	TFIID [T0	343	349	4.007279	TTTATA	1.09863	0.94722
cg1103635	HCG4	TFIID [T0	365	371	4.007279	TTTAAT	1.09863	0.94722
cg1103635	HCG4	TFIID [T0	758	764	4.007279	TTTAAT	1.09863	0.94722
cg1103635	HCG4	TFIID [T0	808	814	4.007279	TTTAAT	1.09863	0.94722
cg1103635	HCG4	TFIID [T0	1284	1290	4.007279	TAATAA	1.09863	0.94722
cg1103635	HCG4	Pax-5 [T0	951	957	4.007279	GGGCAT	1.09863	1.18533
cg1103635	HCG4	Pax-5 [T0	1730	1736	4.007279	GGGCAT	1.09863	1.18533
cg1103635	HCG4	Pax-5 [T0	1975	1981	4.007279	GGGCCC	1.09863	1.18533
cg1103635	HCG4	AP-2alpha	779	784	3.970052	GCCTTG	0.97656	1.02535
cg1103635	HCG4	NFI/CTF [	1694	1701	3.793671	CCAAAG	0.18311	0.19063
cg1103635	HCG4	GR [T050	243	249	3.763516	TGTTTC	0.73242	0.6946
cg1103635	HCG4	GR [T050	792	798	3.763516	ATCTTT	0.73242	0.6946
cg1103635	HCG4	GR [T050	1741	1747	3.763516	ATCTTT	0.73242	0.6946
cg1103635	HCG4	p53 [T006	668	674	3.750231	GGGCTG	0.73242	0.82434
cg1103635	HCG4	c-Ets-1 [T	70	76	3.71855	AAGGAA	0.61035	0.61936
cg1103635	HCG4	CTF [T001	1852	1863	3.641537	AAGCCA	0.01001	0.00987
cg1103635	HCG4	p53 [T006	951	957	3.516613	GGGCAT	0.73242	0.80362
cg1103635	HCG4	p53 [T006	1730	1736	3.516613	GGGCAT	0.73242	0.80362
cg1103635	HCG4	HNF-3alph	864	871	3.500065	AAAAAA	0.27466	0.23175
cg1103635	HCG4	NF-AT1 [T	1335	1344	3.445347	AACTTT	0.07629	0.07204
cg1103635	HCG4	RXR-alph	1782	1788	3.392904	GGGTCC	1.09863	1.1653
cg1103635	HCG4	RXR-alph	1894	1900	3.392904	CGCACC	1.09863	1.1653
cg1103635	HCG4	GR-beta [T	203	207	3.361531	AGATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	312	316	3.361531	AATAT	3.90625	3.51525

cg1103635	HCG4	GR-beta [	313	317	3.361531	ATATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [	377	381	3.361531	ATATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [	754	758	3.361531	ATATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [	769	773	3.361531	AATCT	3.90625	3.51525
cg1103635	HCG4	GR-beta [	888	892	3.361531	AATAT	3.90625	3.51525
cg1103635	HCG4	GR-beta [	1236	1240	3.361531	AGATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [	1262	1266	3.361531	AGATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [	1344	1348	3.361531	AGATT	3.90625	3.51525
cg1103635	HCG4	c-Ets-2 [T	685	693	3.2883	GGTGAG	0.18311	0.18314
cg1103635	HCG4	RAR-beta	1948	1957	3.226064	CCCGAA	0.12207	0.12558
cg1103635	HCG4	RXR-alph	1376	1382	3.170788	AAAACC	0.24414	0.24551
cg1103635	HCG4	TCF-4E [T	794	800	3.151193	CTTTGC	0.24414	0.23169
cg1103635	HCG4	TCF-4E [T	1523	1529	3.151193	TGCAAA	0.24414	0.23169
cg1103635	HCG4	TCF-4E [T	1743	1749	3.151193	CTTTGC	0.24414	0.23169
cg1103635	HCG4	Elk-1 [T00	213	221	3.121991	CCAAGG	0.07629	0.07518
cg1103635	HCG4	POU2F2 (	746	756	3.116744	TGTTTTA	0.02575	0.02261
cg1103635	HCG4	c-Jun [T00	1987	1993	3.049104	TGACCC	0.24414	0.2435
cg1103635	HCG4	p53 [T006	431	437	3.028543	TGTGCC	0.48828	0.53227
cg1103635	HCG4	C/EBPalph	766	772	3.014837	ATCAAT	0.48828	0.47526
cg1103635	HCG4	C/EBPalph	954	960	2.981957	CATTGT	0.48828	0.47526
cg1103635	HCG4	STAT4 [T	3	8	2.941176	GGAAAG	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	72	77	2.941176	GGAACA	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	217	222	2.941176	GGAAGT	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	705	710	2.941176	GGAAAG	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	914	919	2.941176	ACTTCC	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	1143	1148	2.941176	GGAAAG	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	1168	1173	2.941176	GATTCC	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	1237	1242	2.941176	GATTCC	2.92969	2.92382
cg1103635	HCG4	STAT4 [T	1513	1518	2.941176	GATTCC	2.92969	2.92382
cg1103635	HCG4	NF-kappa	1714	1724	2.939121	GGGGAG	0.01669	0.01859
cg1103635	HCG4	STAT1bet	1139	1148	2.898434	TCTGGG	0.0515	0.04956
cg1103635	HCG4	p53 [T006	1809	1815	2.813291	GCTGCC	0.48828	0.53227
cg1103635	HCG4	c-Fos [T00	522	531	2.810503	ACTCTG	0.06104	0.06233
cg1103635	HCG4	PR B [T00	496	502	2.80933	GAATGT	0.73242	0.66711
cg1103635	HCG4	PR B [T00	743	749	2.80933	CATTGT	0.73242	0.66711
cg1103635	HCG4	PR B [T00	1607	1613	2.80933	AACATT	0.73242	0.66711
cg1103635	HCG4	PR A [T01	496	502	2.80933	GAATGT	0.73242	0.66711
cg1103635	HCG4	PR A [T01	743	749	2.80933	CATTGT	0.73242	0.66711
cg1103635	HCG4	PR A [T01	1607	1613	2.80933	AACATT	0.73242	0.66711
cg1103635	HCG4	TBP [T00	879	888	2.807313	TTCATA	0.12207	0.10444
cg1103635	HCG4	NF-AT2 [	705	714	2.800326	GGAAAG	0.03433	0.03159
cg1103635	HCG4	c-Jun [T00	1121	1127	2.654872	GGAGTC	0.48828	0.48077
cg1103635	HCG4	NF-AT1 [	1604	1612	2.595974	GGAAAC	0.09155	0.08666
cg1103635	HCG4	NF-kappa	1730	1740	2.575349	GGGCAT	0.0062	0.00658
cg1103635	HCG4	AP-2alpha	643	648	2.550491	TGAGGC	0.48828	0.51216
cg1103635	HCG4	AP-2alpha	1663	1668	2.550491	GCCTCA	0.48828	0.51216
cg1103635	HCG4	C/EBPalph	965	971	2.441016	CATTGA	0.48828	0.47439
cg1103635	HCG4	C/EBPalph	1609	1615	2.441016	CATTGA	0.48828	0.47439

cg1103635	HCG4	C/EBPalph	1829	1835	2.441016	CATTGA	0.48828	0.47439
cg1103635	HCG4	c-Jun [T00	516	522	2.345465	TGACAC	0.48828	0.48077
cg1103635	HCG4	RXR-alpha	823	829	2.322562	GGGTCT	0.85449	0.89683
cg1103635	HCG4	NF-AT2 [T	1604	1613	2.313293	GGAAAC	0.01144	0.01045
cg1103635	HCG4	Elk-1 [T00	1790	1798	2.299314	CTTCCTC	0.09155	0.09306
cg1103635	HCG4	T3R-beta1	681	689	2.259951	AGGAGG	0.03052	0.03203
cg1103635	HCG4	T3R-beta1	941	949	2.221365	CACTGG	0.15259	0.15303
cg1103635	HCG4	GATA-1 [	187	192	2.176375	TATCCA	3.90625	3.79558
cg1103635	HCG4	GATA-1 [	909	914	2.176375	TGGATA	3.90625	3.79558
cg1103635	HCG4	NF-Y [T0	1852	1859	2.12821	AAGCCA	0.21362	0.20748
cg1103635	HCG4	NF-1 [T00	1625	1632	2.067686	TTGGCA	0.12207	0.12476
cg1103635	HCG4	NF-AT1 [	1335	1343	1.970716	AACTTT	0.06866	0.0623
cg1103635	HCG4	PR B [T00	874	880	1.892895	AAGTGT	0.12207	0.1127
cg1103635	HCG4	PR B [T00	897	903	1.892895	AACACT	0.12207	0.1127
cg1103635	HCG4	PR A [T01	874	880	1.892895	AAGTGT	0.12207	0.1127
cg1103635	HCG4	PR A [T01	897	903	1.892895	AACACT	0.12207	0.1127
cg1103635	HCG4	AP-2alpha	1484	1489	1.871933	GGAGGC	0.97656	1.07805
cg1103635	HCG4	AP-2alpha	1716	1721	1.871933	GGAGGC	0.97656	1.07805
cg1103635	HCG4	TBP [T007	343	352	1.871542	TTTATAA	0.18311	0.15671
cg1103635	HCG4	C/EBPalph	28	34	1.830762	AATTGA	0.48828	0.46352
cg1103635	HCG4	FOXP3 [T	91	96	1.824994	TACAAC	0.48828	0.46414
cg1103635	HCG4	FOXP3 [T	1016	1021	1.824994	TACAAC	0.48828	0.46414
cg1103635	HCG4	FOXP3 [T	1175	1180	1.824994	GTTGTA	0.48828	0.46414
cg1103635	HCG4	TFII-I [T0	630	635	1.824994	GGAGAG	0.48828	0.51201
cg1103635	HCG4	TFII-I [T0	1765	1770	1.824994	CTCTCC	0.48828	0.51201
cg1103635	HCG4	c-Ets-1 [T	1	7	1.769212	TAGGAA	0.12207	0.11281
cg1103635	HCG4	HIF-1 [T0	448	456	1.730353	ACGTGC	0.09155	0.09676
cg1103635	HCG4	RXR-alpha	1642	1648	1.696452	GGGTCA	0.48828	0.52093
cg1103635	HCG4	RXR-alpha	1986	1992	1.696452	CTGACC	0.48828	0.52093
cg1103635	HCG4	GR-beta [T	27	31	1.680765	GAATT	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	108	112	1.680765	GCATT	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	272	276	1.680765	GAATT	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	280	284	1.680765	GAATT	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	710	714	1.680765	GAATT	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	711	715	1.680765	AATTC	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	953	957	1.680765	GCATT	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	964	968	1.680765	GCATT	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	1180	1184	1.680765	AATGC	3.90625	3.70067
cg1103635	HCG4	GR-beta [T	1732	1736	1.680765	GCATT	3.90625	3.70067
cg1103635	HCG4	HNF-1B [	1281	1289	1.651022	AGTTAA	0.00763	0.00634
cg1103635	HCG4	C/EBPbeta	164	167	1.639871	TTGG	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	213	216	1.639871	CCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	479	482	1.639871	CCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	802	805	1.639871	TTGG	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1212	1215	1.639871	CCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1226	1229	1.639871	TTGG	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1259	1262	1.639871	CCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1593	1596	1.639871	CCAA	15.625	15.23827

cg1103635	HCG4	C/EBPbeta	1625	1628	1.639871	TTGG	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1694	1697	1.639871	CCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1712	1715	1.639871	TTGG	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1770	1773	1.639871	CCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1855	1858	1.639871	CCAA	15.625	15.23827
cg1103635	HCG4	IRF-1 [T0	701	709	1.616539	AGAGGG	0.04578	0.04268
cg1103635	HCG4	XBP-1 [T	515	520	1.583727	ATGACA	0.97656	0.94995
cg1103635	HCG4	XBP-1 [T	1937	1942	1.583727	TGTCAT	0.97656	0.94995
cg1103635	HCG4	TFIID [T0	143	149	1.537547	TTCAAA	0.73242	0.65627
cg1103635	HCG4	TFIID [T0	162	168	1.537547	TTTTGG	0.73242	0.65627
cg1103635	HCG4	TFIID [T0	325	331	1.537547	TTTTTCA	0.73242	0.65627
cg1103635	HCG4	TFIID [T0	335	341	1.537547	TTTTACA	0.73242	0.65627
cg1103635	HCG4	TFIID [T0	1338	1344	1.537547	TTTTCCA	0.73242	0.65627
cg1103635	HCG4	Pax-5 [T0	196	202	1.537547	CTTGCC	0.73242	0.83087
cg1103635	HCG4	Pax-5 [T0	1405	1411	1.537547	GGGCAA	0.73242	0.83087
cg1103635	HCG4	c-Ets-1 [T	688	694	1.513038	GAGGAA	0.36621	0.35197
cg1103635	HCG4	STAT4 [T	26	31	1.470588	GGAATT	1.95312	1.90161
cg1103635	HCG4	STAT4 [T	1338	1343	1.470588	TTTTCC	1.95312	1.90161
cg1103635	HCG4	STAT4 [T	1604	1609	1.470588	GGAAAC	1.95312	1.90161
cg1103635	HCG4	STAT4 [T	1886	1891	1.470588	AGTTCC	1.95312	1.90161
cg1103635	HCG4	PR B [T00	9	15	1.404665	AACACT	0.36621	0.35143
cg1103635	HCG4	PR A [T01	9	15	1.404665	AACACT	0.36621	0.35143
cg1103635	HCG4	C/EBPbeta	30	33	1.366559	TTGA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	58	61	1.366559	TTGA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	144	147	1.366559	TCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	275	278	1.366559	TTGA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	283	286	1.366559	TTGA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	394	397	1.366559	TCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	767	770	1.366559	TCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	967	970	1.366559	TTGA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1204	1207	1.366559	TCAA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1611	1614	1.366559	TTGA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1831	1834	1.366559	TTGA	15.625	15.23827
cg1103635	HCG4	C/EBPbeta	1859	1862	1.366559	TCAA	15.625	15.23827
cg1103635	HCG4	AP-2alpha	925	930	1.357116	ACAGGC	0.48828	0.51319
cg1103635	HCG4	HNF-3alph	755	762	1.342935	TATTTTA	0.03052	0.02477
cg1103635	HCG4	HNF-3alph	1104	1111	1.342935	TTAAAA	0.03052	0.02477
cg1103635	HCG4	c-Ets-2 [T	650	658	1.071163	TGAGAG	0.06104	0.0583
cg1103635	HCG4	GATA-1 [	283	288	1.038567	TTGATA	1.95312	1.80234
cg1103635	HCG4	TBP [T00	1196	1205	0.935771	TTTATAT	0.12207	0.10448
cg1103635	HCG4	LEF-1 [T0	1210	1217	0.85582	GACCAA	0.03052	0.03064
cg1103635	HCG4	RXR-alpha	1950	1956	0.848226	CGAACC	0.48828	0.51313
cg1103635	HCG4	GR-beta [	28	32	0.840383	AATTG	7.8125	7.2174
cg1103635	HCG4	GR-beta [	148	152	0.840383	AATGA	7.8125	7.2174
cg1103635	HCG4	GR-beta [	234	238	0.840383	AATGG	7.8125	7.2174
cg1103635	HCG4	GR-beta [	269	273	0.840383	AATGA	7.8125	7.2174
cg1103635	HCG4	GR-beta [	273	277	0.840383	AATTG	7.8125	7.2174
cg1103635	HCG4	GR-beta [	281	285	0.840383	AATTG	7.8125	7.2174

cg1103635	HCG4	GR-beta [T	296	300	0.840383	TAATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	297	301	0.840383	AATTA	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	347	351	0.840383	TAATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	362	366	0.840383	CAATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	382	386	0.840383	TCATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	386	390	0.840383	TCATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	402	406	0.840383	AATTA	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	405	409	0.840383	TAATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	420	424	0.840383	AATGA	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	514	518	0.840383	AATGA	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	575	579	0.840383	AATGG	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	657	661	0.840383	AATGG	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	693	697	0.840383	AATGG	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	839	843	0.840383	TAATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	1091	1095	0.840383	AATGA	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	1246	1250	0.840383	TCATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	1396	1400	0.840383	CCATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	1550	1554	0.840383	CCATT	7.8125	7.2174
cg1103635	HCG4	GR-beta [T	1828	1832	0.840383	CCATT	7.8125	7.2174
cg1103635	HCG4	AP-2alpha	130	135	0.678558	GCCTGA	0.48828	0.51196
cg1103635	HCG4	AP-2alpha	452	457	0.678558	GCCTGA	0.48828	0.51196
cg1103635	HCG4	AP-2alpha	640	645	0.678558	GCCTGA	0.48828	0.51196
cg1103635	HCG4	AP-2alpha	1327	1332	0.678558	TCAGGC	0.48828	0.51196
cg1103635	HCG4	AP-2alpha	1666	1671	0.678558	TCAGGC	0.48828	0.51196
cg1103635	HCG4	AP-2alpha	1687	1692	0.678558	TCAGGC	0.48828	0.51196
cg1103635	HCG4	NF-AT1 [T	705	713	0.648993	GGAAAG	0.02289	0.02115
cg1103635	HCG4	C/EBPalph	1710	1716	0.540941	GATTGG	0.24414	0.24432
cg1103635	HCG4	AP-1 [T00	526	534	0.489074	TGACTC	0.09155	0.08806
cg1103635	HCG4	HNF-1A [	851	858	0.431647	GTTAAT	0.24414	0.21942
cg1103635	HCG4	c-Ets-1 [T	915	921	0.384261	CTTCCT	0.24414	0.23743
cg1103635	HCG4	c-Ets-1 [T	215	221	0.256174	AAGGAA	0.24414	0.23743
cg1103635	HCG4	p53 [T006	196	202	0.211706	CTTGCC	0.36621	0.40082
cg1103635	HCG4	p53 [T006	1405	1411	0.211706	GGGCAA	0.36621	0.40082
cg1103635	HCG4	GR-alpha [	119	123	0.207689	CCTCT	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	632	636	0.207689	AGAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	652	656	0.207689	AGAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	701	705	0.207689	AGAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	806	810	0.207689	CCTTT	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	1537	1541	0.207689	AGAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	1696	1700	0.207689	AAAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	1764	1768	0.207689	CCTCT	7.8125	7.79817
cg1103635	HCG4	GATA-1 [	1315	1320	0.105011	TATCTC	0.97656	0.92541
cg1103635	HCG4	GR-beta [T	339	343	0	ACATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	348	352	0	AATTT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	363	367	0	AATTT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	401	405	0	AAATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	406	410	0	AATTT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	457	461	0	ACATT	3.90625	3.51525

cg1103635	HCG4	GR-beta [T	497	501	0	AATGT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	742	746	0	ACATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	840	844	0	AATTT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	1100	1104	0	AAATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	1101	1105	0	AATTT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	1133	1137	0	ACATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	1193	1197	0	ACATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	1220	1224	0	ACATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	1608	1612	0	ACATT	3.90625	3.51525
cg1103635	HCG4	GR-beta [T	1861	1865	0	AATGT	3.90625	3.51525
cg1103635	HCG4	TFIID [T0	342	348	0	TTTTATA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	748	754	0	TTTTATA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	843	849	0	TTTTTTA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	861	867	0	TTTAAA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	862	868	0	TTAAAA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	863	869	0	TAAAAA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	883	889	0	TATAAA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	1103	1109	0	TTTAAA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	1185	1191	0	TTTTAG	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	1347	1353	0	TTTAAA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	1348	1354	0	TTAAAA	1.09863	0.95175
cg1103635	HCG4	TFIID [T0	1349	1355	0	TAAAAA	1.09863	0.95175
cg1103635	HCG4	c-Jun [T00	526	532	0	TGACTC	0.12207	0.11843
cg1103635	HCG4	GR-alpha [	45	49	0	CCTAT	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	177	181	0	ACAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	532	536	0	ACAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	925	929	0	ACAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	1172	1176	0	CCTGT	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	1381	1385	0	CCTGT	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	1470	1474	0	ACAGG	7.8125	7.79817
cg1103635	HCG4	GR-alpha [	1774	1778	0	CCTGT	7.8125	7.79817
cg1103635	HCG4	FOXP3 [T	35	40	0	CACAAC	1.46484	1.44953
cg1103635	HCG4	FOXP3 [T	241	246	0	GTTGTT	1.46484	1.44953
cg1103635	HCG4	FOXP3 [T	894	899	0	CACAAC	1.46484	1.44953
cg1103635	HCG4	FOXP3 [T	1332	1337	0	CACAAC	1.46484	1.44953
cg1103635	HCG4	FOXP3 [T	1362	1367	0	AACAAC	1.46484	1.44953
cg1103635	HCG4	FOXP3 [T	1365	1370	0	AACAAC	1.46484	1.44953
cg1103635	HCG4	FOXP3 [T	1368	1373	0	AACAAC	1.46484	1.44953
cg1103635	HCG4	PR B [T00	11	17	0	CACTGT	0.36621	0.35051
cg1103635	HCG4	PR B [T00	557	563	0	AACAGT	0.36621	0.35051
cg1103635	HCG4	PR A [T01	11	17	0	CACTGT	0.36621	0.35051
cg1103635	HCG4	PR A [T01	557	563	0	AACAGT	0.36621	0.35051
cg1103635	HCG4	C/EBPbeta	36	39	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	68	71	0	GCAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	92	95	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	197	200	0	TTGC	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	242	245	0	TTGT	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	247	250	0	TTGC	15.625	15.26275

cg1103635	HCG4	C/EBPbeta	361	364	0	GCAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	418	421	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	473	476	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	595	598	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	609	612	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	745	748	0	TTGT	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	782	785	0	TTGC	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	796	799	0	TTGC	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	895	898	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	956	959	0	TTGT	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	975	978	0	TTGC	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1017	1020	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1044	1047	0	TTGT	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1114	1117	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1136	1139	0	TTGT	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1164	1167	0	TTGT	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1176	1179	0	TTGT	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1290	1293	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1297	1300	0	GCAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1333	1336	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1355	1358	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1359	1362	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1363	1366	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1366	1369	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1369	1372	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1372	1375	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1407	1410	0	GCAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1423	1426	0	GCAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1426	1429	0	ACAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1524	1527	0	GCAA	15.625	15.26275
cg1103635	HCG4	C/EBPbeta	1745	1748	0	TTGC	15.625	15.26275
cg1103635	HCG4	NF-1 [T00	1589	1596	0	TGGGCC	0.12207	0.13147
cg1103635	HCG4	YY1 [T00	235	238	0	ATGG	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	576	579	0	ATGG	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	658	661	0	ATGG	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	694	697	0	ATGG	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1087	1090	0	ATGG	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1396	1399	0	CCAT	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1550	1553	0	CCAT	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1707	1710	0	ATGG	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1739	1742	0	CCAT	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1828	1831	0	CCAT	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1933	1936	0	ATGG	7.8125	7.79459
cg1103635	HCG4	YY1 [T00	1941	1944	0	ATGG	7.8125	7.79459
cg1103635	HCG4	TFII-I [T0	3	8	0	GGAAAG	1.46484	1.48598
cg1103635	HCG4	TFII-I [T0	186	191	0	CTATCC	1.46484	1.48598
cg1103635	HCG4	TFII-I [T0	579	584	0	GGACAG	1.46484	1.48598
cg1103635	HCG4	TFII-I [T0	705	710	0	GGAAAG	1.46484	1.48598

cg1103635	HCG4	TFII-I [T0	1143	1148	0	GGAAAG	1.46484	1.48598
cg1103635	HCG4	TFII-I [T0	1468	1473	0	GGACAG	1.46484	1.48598
cg1103635	HCG4	STAT4 [T	690	695	0	GGAAAT	0.48828	0.46235
cg1103635	HCG4	c-Ets-1 [T	1790	1796	0	CTTCCTC	0.24414	0.24982
cg1103635	HCG4	c-Myb [T0	93	100	0	CAACTG	0.03052	0.03205
cg1103635	HCG4	ER-alpha [	210	214	0	TGACC	1.95312	1.99744
cg1103635	HCG4	ER-alpha [	1643	1647	0	GGTCA	1.95312	1.99744
cg1103635	HCG4	ER-alpha [	1987	1991	0	TGACC	1.95312	1.99744
cg1103635	HCG4	PPAR-alpl	1810	1820	0	CTGCCC	0.00858	0.009
cg1103635	HCG4	NFI/CTF [	1621	1628	0	GCGCTT	0.18311	0.191
cg1103635	HCG4	GR [T050	1222	1228	0	ATTTTTC	0.36621	0.33174
cg1103635	HCG4	GR [T050	1291	1297	0	CAAAAA	0.36621	0.33174
cg1103635	HCG4	GR [T050	1373	1379	0	CAAAAA	0.36621	0.33174
cg1103635	HCG4	TBP [T007	749	758	0	TTTATAT	0.03052	0.02611
cg1103635	HCG4	AR [T000	579	587	0	GGACAG	0.00763	0.00819
cg1103635	HCG4	GATA-1 [	228	233	0	CAGATA	0.97656	0.92541
cg1103635	HCG4	GATA-1 [	1128	1133	0	CAGATA	0.97656	0.92541
cg1103635	HCG4	Pax-5 [T0	638	644	0	GGGCCT	1.09863	1.24633
cg1103635	HCG4	Pax-5 [T0	668	674	0	GGGCTG	1.09863	1.24633
cg1103635	HCG4	Pax-5 [T0	1688	1694	0	CAGGCC	1.09863	1.24633
cg1103635	HCG4	GCF [T00	1720	1728	0	GCCCAG	0.09155	0.10999
cg1103635	HCG4	GCF [T00	1725	1733	0	GCGCTG	0.09155	0.10999
cg1103635	HCG4	IRF-2 [T0	1146	1151	0	AAGTGA	0.48828	0.46235
cg1103635	HCG4	IRF-2 [T0	1527	1532	0	AAGTGA	0.48828	0.46235
cg1103635	HCG4	HNF-1A [	1282	1289	0	GTTAAT	0.24414	0.20853
cg1301955	HLA-B	c-Ets-1 [T	1544	1550	9.969337	TGGGAA	0.24414	0.23698
cg1301955	HLA-B	c-Myb [T0	1515	1522	9.815171	GAACTT	0.36621	0.34605
cg1301955	HLA-B	STAT1bet	923	932	9.807397	ATTTCCC	0.14877	0.14533
cg1301955	HLA-B	STAT1bet	1832	1841	9.807397	GTTTCCC	0.14877	0.14533
cg1301955	HLA-B	XBP-1 [T	1005	1010	9.789909	CGCCAT	1.95312	1.94901
cg2595453	HLA-B	XBP-1 [T	576	581	9.789909	CGCCAT	1.95312	1.94901
cg2595453	HLA-B	XBP-1 [T	1168	1173	9.789909	CGACAT	1.95312	1.94901
cg2595453	HLA-B	RBP-Jkapp	111	122	9.774182	GCTTCCC	0.02193	0.02186
cg1301955	HLA-B	PR B [T00	627	633	9.743489	GTGTGT	1.09863	1.0981
cg1301955	HLA-B	PR A [T01	627	633	9.743489	GTGTGT	1.09863	1.0981
cg2595453	HLA-B	PR B [T00	953	959	9.743489	AACACA	1.09863	1.0981
cg2595453	HLA-B	PR B [T00	1866	1872	9.743489	GTGTGT	1.09863	1.0981
cg2595453	HLA-B	PR A [T01	953	959	9.743489	AACACA	1.09863	1.0981
cg2595453	HLA-B	PR A [T01	1866	1872	9.743489	GTGTGT	1.09863	1.0981
cg1301955	HLA-B	LEF-1 [T0	1326	1333	9.72404	CTTTGTC	0.21362	0.21229
cg1301955	HLA-B	c-Jun [T00	519	525	9.717135	TGACCT	0.73242	0.7366
cg2595453	HLA-B	c-Jun [T00	590	596	9.717135	CAGGTC	0.73242	0.7366
cg2595453	HLA-B	c-Jun [T00	1758	1764	9.717135	TGACCT	0.73242	0.7366
cg1301955	HLA-B	c-Ets-1 [T	1207	1213	9.713162	GGGGAA	0.36621	0.37402
cg1301955	HLA-B	c-Ets-1 [T	1818	1824	9.713162	ATTCCCC	0.36621	0.37402
cg1301955	HLA-B	EBF [T054	1261	1271	9.706759	GACCCT	0.06866	0.07687
cg1301955	HLA-B	NF-AT1 [	1371	1379	9.691726	GGAAAC	0.16785	0.16528
cg2595453	HLA-B	EBF [T054	94	104	9.652631	GCCCCT	0.06866	0.07687

cg2595453	HLA-B	RAR-beta	614	623	9.622793	TAGAAA	0.21362	0.22369
cg1301955	HLA-B	TFIID [T0	1327	1333	9.552105	TTTGTCA	1.46484	1.37777
cg1301955	HLA-B	TFIID [T0	1718	1724	9.552105	TGTCAA	1.46484	1.37777
cg1301955	HLA-B	TFIID [T0	1765	1771	9.552105	TTTCCCA	1.46484	1.37777
cg1301955	HLA-B	Pax-5 [T0	250	256	9.552105	GGCGCC	1.46484	1.61918
cg1301955	HLA-B	Pax-5 [T0	524	530	9.552105	TGCGCC	1.46484	1.61918
cg1301955	HLA-B	Pax-5 [T0	671	677	9.552105	GGCGCC	1.46484	1.61918
cg1301955	HLA-B	Pax-5 [T0	739	745	9.552105	GTAGCC	1.46484	1.61918
cg1301955	HLA-B	Pax-5 [T0	880	886	9.552105	TGCGCC	1.46484	1.61918
cg1301955	HLA-B	Pax-5 [T0	1002	1008	9.552105	GGGCGC	1.46484	1.61918
cg1301955	HLA-B	Pax-5 [T0	1396	1402	9.552105	TGCGCC	1.46484	1.61918
cg2595453	HLA-B	TFIID [T0	325	331	9.552105	TGGGAA	1.46484	1.37777
cg2595453	HLA-B	Pax-5 [T0	91	97	9.552105	TTAGCC	1.46484	1.61918
cg2595453	HLA-B	Pax-5 [T0	1489	1495	9.552105	GGCGCC	1.46484	1.61918
cg2595453	HLA-B	Pax-5 [T0	1763	1769	9.552105	TGCGCC	1.46484	1.61918
cg2595453	HLA-B	Pax-5 [T0	1910	1916	9.552105	GGCGCC	1.46484	1.61918
cg2595453	HLA-B	Pax-5 [T0	1978	1984	9.552105	GTAGCC	1.46484	1.61918
cg1301955	HLA-B	NF-1 [T00	352	359	9.535536	CCGACC	0.73242	0.74634
cg2595453	HLA-B	NF-1 [T00	1591	1598	9.535536	CCGACC	0.73242	0.74634
cg1301955	HLA-B	FOXP3 [T	53	58	9.512894	GTTCTC	7.32422	7.22156
cg1301955	HLA-B	FOXP3 [T	355	360	9.512894	ACCAAC	7.32422	7.22156
cg1301955	HLA-B	FOXP3 [T	398	403	9.512894	GTAAAC	7.32422	7.22156
cg1301955	HLA-B	FOXP3 [T	1177	1182	9.512894	GTTGGG	7.32422	7.22156
cg1301955	HLA-B	FOXP3 [T	1215	1220	9.512894	CCCAAC	7.32422	7.22156
cg1301955	HLA-B	FOXP3 [T	1849	1854	9.512894	CAGAAC	7.32422	7.22156
cg1301955	HLA-B	FOXP3 [T	1927	1932	9.512894	GTTGCG	7.32422	7.22156
cg1301955	HLA-B	TFII-I [T0	2	7	9.512894	GGAAGG	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	42	47	9.512894	TTGTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	46	51	9.512894	CCTTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	162	167	9.512894	GTGTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	172	177	9.512894	CGGTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	255	260	9.512894	CCGTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	367	372	9.512894	GGATTT	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	506	511	9.512894	GGATGG	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	635	640	9.512894	CGGTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	781	786	9.512894	GGACAC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	894	899	9.512894	CGGTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	992	997	9.512894	GGACGG	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1061	1066	9.512894	GGACTT	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1075	1080	9.512894	GGACCG	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1150	1155	9.512894	GTATCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1274	1279	9.512894	CCGTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1288	1293	9.512894	GGACTT	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1353	1358	9.512894	GGACAA	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1371	1376	9.512894	GGAAAC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1407	1412	9.512894	CCTTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1499	1504	9.512894	GGAAAC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1634	1639	9.512894	GTTTCC	7.32422	7.44385

cg1301955	HLA-B	TFII-I [T0	1695	1700	9.512894	AATTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1832	1837	9.512894	GTTTCC	7.32422	7.44385
cg1301955	HLA-B	TFII-I [T0	1983	1988	9.512894	TTTTCC	7.32422	7.44385
cg2595453	HLA-B	FOXP3 [T	280	285	9.512894	AGCAAC	7.32422	7.22156
cg2595453	HLA-B	FOXP3 [T	806	811	9.512894	CAGAAC	7.32422	7.22156
cg2595453	HLA-B	FOXP3 [T	973	978	9.512894	GAGAAC	7.32422	7.22156
cg2595453	HLA-B	FOXP3 [T	1292	1297	9.512894	GTTCTC	7.32422	7.22156
cg2595453	HLA-B	FOXP3 [T	1594	1599	9.512894	ACCAAC	7.32422	7.22156
cg2595453	HLA-B	FOXP3 [T	1637	1642	9.512894	GTAAAC	7.32422	7.22156
cg2595453	HLA-B	TFII-I [T0	25	30	9.512894	CCATCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	166	171	9.512894	GGACAA	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	197	202	9.512894	CCTTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	300	305	9.512894	GGACGG	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	516	521	9.512894	GGAAGG	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	557	562	9.512894	GTGTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	578	583	9.512894	CCATCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	738	743	9.512894	GGACAC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	781	786	9.512894	GGACAC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	796	801	9.512894	GGAAGG	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	841	846	9.512894	GGATAA	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	890	895	9.512894	GGACTT	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	990	995	9.512894	GGAAAA	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1125	1130	9.512894	GGAAAC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1134	1139	9.512894	GGAAAA	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1190	1195	9.512894	TTTTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1214	1219	9.512894	CCATCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1241	1246	9.512894	GGAAGG	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1281	1286	9.512894	TTGTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1285	1290	9.512894	CCTTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1401	1406	9.512894	GTGTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1411	1416	9.512894	CGGTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1494	1499	9.512894	CCGTCC	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1606	1611	9.512894	GGATTT	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1745	1750	9.512894	GGATGG	7.32422	7.44385
cg2595453	HLA-B	TFII-I [T0	1874	1879	9.512894	CGGTCC	7.32422	7.44385
cg2595453	HLA-B	c-Jun [T00	252	258	9.511322	TGACCA	0.73242	0.7366
cg1301955	HLA-B	TCF-4E [T	1744	1750	9.453578	CTCAAA	0.48828	0.46934
cg1301955	HLA-B	TCF-4E [T	1921	1927	9.453578	CTCAAA	0.48828	0.46934
cg2595453	HLA-B	TCF-4E [T	1023	1029	9.453578	GTCAAA	0.48828	0.46934
cg1301955	HLA-B	PPAR-alph	608	618	9.39865	GCCTGG	0.00286	0.00313
cg2595453	HLA-B	PPAR-alph	1847	1857	9.39865	GCCTGG	0.00286	0.00313
cg2595453	HLA-B	c-Jun [T00	34	40	9.397655	ATTGTC	0.73242	0.7366
cg1301955	HLA-B	NFI/CTF [	1949	1956	9.352332	CCAATG	0.54932	0.55369
cg2595453	HLA-B	NFI/CTF [	680	687	9.352332	GTCTTT	0.54932	0.55369
cg2595453	HLA-B	NFI/CTF [	1006	1013	9.352332	CCAAGG	0.54932	0.55369
cg2595453	HLA-B	LEF-1 [T0	682	689	9.313676	CTTTGG	0.21362	0.21229
cg2595453	HLA-B	c-Ets-1 [T	1002	1008	9.276861	GTTCCC	0.36621	0.37402
cg2595453	HLA-B	SRY [T00	1021	1029	9.264664	GGGTCA	0.12207	0.11857

cg1301955	HLA-B	E2F-1 [T0	242	249	9.261732	GCGGAG	0.15259	0.16832
cg2595453	HLA-B	E2F-1 [T0	1481	1488	9.261732	GCGGAG	0.15259	0.16832
cg1301955	HLA-B	VDR [T00	1985	1993	9.234242	TTCCTG	0.12207	0.11552
cg2595453	HLA-B	VDR [T00	204	212	9.234242	TACCTG	0.12207	0.11552
cg1301955	HLA-B	c-Ets-1 [T	1696	1702	9.19359	ATTCCA	0.85449	0.84987
cg2595453	HLA-B	RAR-alph	1020	1032	9.192562	GGGGTC	0.02065	0.02209
cg2595453	HLA-B	c-Ets-1 [T	129	135	9.148774	AGGGAA	0.85449	0.84987
cg1301955	HLA-B	c-Myb [T0	1923	1930	9.142015	CAAAGT	0.39673	0.37851
cg1301955	HLA-B	E2F-1 [T0	363	370	9.028527	GCGGGG	0.27466	0.30178
cg1301955	HLA-B	E2F-1 [T0	763	770	9.028527	CTCCCC	0.27466	0.30178
cg2595453	HLA-B	E2F-1 [T0	1602	1609	9.028527	GCGGGG	0.27466	0.30178
cg1301955	HLA-B	c-Myb [T0	1501	1508	9.024874	AAACTG	0.39673	0.37851
cg1301955	HLA-B	c-Ets-1 [T	1512	1518	9.020687	GGGGAA	0.85449	0.84987
cg2595453	HLA-B	c-Ets-1 [T	881	887	9.020687	GGGGAA	0.85449	0.84987
cg1301955	HLA-B	GR [T050	368	374	8.971049	GATTTC	0.61035	0.5928
cg2595453	HLA-B	GR [T050	951	957	8.971049	CAAACA	0.61035	0.5928
cg2595453	HLA-B	GR [T050	1607	1613	8.971049	GATTTC	0.61035	0.5928
cg1301955	HLA-B	c-Ets-2 [T	1985	1993	8.912323	TTCCTG	0.27466	0.27171
cg2595453	HLA-B	c-Ets-2 [T	1129	1137	8.912323	ACTCAG	0.27466	0.27171
cg2595453	HLA-B	p53 [T006	347	353	8.912104	GGGCCC	0.12207	0.13824
cg2595453	HLA-B	p53 [T006	623	629	8.912104	AGGGCC	0.12207	0.13824
cg2595453	HLA-B	p53 [T006	1114	1120	8.912104	GGGCCC	0.12207	0.13824
cg1301955	HLA-B	ETF [T002	313	323	8.876947	GCCCCG	0.02384	0.02809
cg1301955	HLA-B	ETF [T002	674	684	8.876947	GCCCGC	0.02384	0.02809
cg2595453	HLA-B	ETF [T002	1552	1562	8.876947	GCCCCG	0.02384	0.02809
cg2595453	HLA-B	ETF [T002	1913	1923	8.876947	GCCCGC	0.02384	0.02809
cg1301955	HLA-B	NFI/CTF [	1479	1486	8.814757	CCTCTTC	0.48828	0.48845
cg1301955	HLA-B	c-Ets-1 [T	1428	1434	8.809329	CTGGAA	0.85449	0.84987
cg2595453	HLA-B	c-Ets-1 [T	936	942	8.809329	CTGGAA	0.85449	0.84987
cg1301955	HLA-B	NF-1 [T00	1178	1185	8.790071	TTGGGA	0.24414	0.24339
cg2595453	HLA-B	NF-AT1 [	860	868	8.769753	GGAAAG	0.22888	0.22581
cg1301955	HLA-B	E2F-1 [T0	111	118	8.76494	TGCTCC	0.27466	0.30178
cg2595453	HLA-B	E2F-1 [T0	1350	1357	8.76494	TGCTCC	0.27466	0.30178
cg2595453	HLA-B	LEF-1 [T0	722	729	8.759086	CTTTGC	0.54932	0.53171
cg1301955	HLA-B	XBP-1 [T	388	393	8.75604	ATGAAA	2.92969	2.75329
cg1301955	HLA-B	XBP-1 [T	1620	1625	8.75604	TCTCAT	2.92969	2.75329
cg2595453	HLA-B	XBP-1 [T	731	736	8.75604	TTTCAT	2.92969	2.75329
cg2595453	HLA-B	XBP-1 [T	1627	1632	8.75604	ATGAAA	2.92969	2.75329
cg1301955	HLA-B	HNF-1B [	1781	1789	8.696557	TCTGTA	0.11444	0.10456
cg2595453	HLA-B	RAR-beta	151	160	8.578216	TTGAAA	0.26703	0.27434
cg1301955	HLA-B	IRF-1 [T0	1367	1375	8.570857	CTGTGG	0.20599	0.20245
cg1301955	HLA-B	RAR-beta	1566	1575	8.55975	GGGGTT	0.26703	0.27434
cg1301955	HLA-B	RAR-beta	354	363	8.541284	GACCAA	0.26703	0.27434
cg2595453	HLA-B	RAR-beta	1593	1602	8.541284	GACCAA	0.26703	0.27434
cg1301955	HLA-B	p53 [T006	411	417	8.537081	GGGCTC	0.12207	0.13169
cg1301955	HLA-B	p53 [T006	1268	1274	8.537081	AGAGCC	0.12207	0.13169
cg2595453	HLA-B	p53 [T006	944	950	8.537081	AGAGCC	0.12207	0.13169
cg2595453	HLA-B	p53 [T006	1650	1656	8.537081	GGGCTC	0.12207	0.13169

cg2595453	HLA-B	NF-AT1 [	1187	1195	8.532897	CCATTT	0.10681	0.10494
cg1301955	HLA-B	c-Myb [T0	1173	1180	8.529773	ACAAGT	0.30518	0.28602
cg1301955	HLA-B	LEF-1 [T0	1920	1927	8.457856	CCTCAA	0.15259	0.154
cg1301955	HLA-B	c-Myb [T0	379	386	8.443873	CAACTG	0.30518	0.28602
cg2595453	HLA-B	c-Myb [T0	1618	1625	8.443873	CAACTG	0.30518	0.28602
cg2595453	HLA-B	ATF [T00	1080	1091	8.419848	AGACGT	0.07725	0.07664
cg1301955	HLA-B	c-Myb [T0	1630	1637	8.412632	ACCAGT	0.30518	0.28602
cg1301955	HLA-B	PR B [T00	1724	1730	8.338824	AACAGC	1.09863	1.09384
cg1301955	HLA-B	PR B [T00	1978	1984	8.338824	GCCTGT	1.09863	1.09384
cg1301955	HLA-B	PR A [T01	1724	1730	8.338824	AACAGC	1.09863	1.09384
cg1301955	HLA-B	PR A [T01	1978	1984	8.338824	GCCTGT	1.09863	1.09384
cg2595453	HLA-B	PR B [T00	885	891	8.338824	AACAGG	1.09863	1.09384
cg2595453	HLA-B	PR A [T01	885	891	8.338824	AACAGG	1.09863	1.09384
cg2595453	HLA-B	IRF-1 [T0	1071	1079	8.316022	TTTCCTC	0.20599	0.20245
cg2595453	HLA-B	ATF3 [T0	1080	1087	8.313799	AGACGT	0.27466	0.27379
cg1301955	HLA-B	GR-alpha [	3	7	8.281568	GAAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	46	50	8.281568	CCTTC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	91	95	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	130	134	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	190	194	8.281568	CCTCG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	211	215	8.281568	CCTTG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	244	248	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	247	251	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	289	293	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	425	429	8.281568	CGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	455	459	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	552	556	8.281568	CCTCG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	615	619	8.281568	CCTTG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	654	658	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	787	791	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	829	833	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	852	856	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	855	859	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	900	904	8.281568	CCTCG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	907	911	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	928	932	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	989	993	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1161	1165	8.281568	GAAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1227	1231	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1248	1252	8.281568	CCTCG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1356	1360	8.281568	CAAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1407	1411	8.281568	CCTTC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1413	1417	8.281568	CCTTC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1460	1464	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1551	1555	8.281568	GGAGG	7.8125	8.20394
cg1301955	HLA-B	GR-alpha [	1601	1605	8.281568	GAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	12	16	8.281568	CAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	29	33	8.281568	CCTTC	7.8125	8.20394

cg2595453	HLA-B	GR-alpha [	197	201	8.281568	CCTTC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	217	221	8.281568	CCTCC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	332	336	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	363	367	8.281568	GAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	408	412	8.281568	CCTCC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	488	492	8.281568	GAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	517	521	8.281568	GAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	573	577	8.281568	CCTCG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	797	801	8.281568	GAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	913	917	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	978	982	8.281568	CAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1007	1011	8.281568	CAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1065	1069	8.281568	CCTCC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1162	1166	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1194	1198	8.281568	CCTCC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1209	1213	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1242	1246	8.281568	GAAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1285	1289	8.281568	CCTTC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1330	1334	8.281568	CCTCC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1369	1373	8.281568	CCTCC	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1429	1433	8.281568	CCTCG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1450	1454	8.281568	CCTTG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1483	1487	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1486	1490	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1528	1532	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1664	1668	8.281568	CGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1694	1698	8.281568	GGAGG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1791	1795	8.281568	CCTCG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1854	1858	8.281568	CCTTG	7.8125	8.20394
cg2595453	HLA-B	GR-alpha [	1893	1897	8.281568	CCTCC	7.8125	8.20394
cg1301955	HLA-B	NFI/CTF [	356	363	8.241664	CCAACC	0.18311	0.1922
cg2595453	HLA-B	NFI/CTF [	1595	1602	8.241664	CCAACC	0.18311	0.1922
cg2595453	HLA-B	p53 [T006	346	352	8.208781	GGGGCC	0.48828	0.55336
cg2595453	HLA-B	p53 [T006	1113	1119	8.208781	GGGGCC	0.48828	0.55336
cg2595453	HLA-B	ENKTF-1	584	591	8.19852	CGCTGC	0.73242	0.80254
cg1301955	HLA-B	NF-1 [T00	372	379	8.191058	TTGGCC	0.24414	0.24485
cg2595453	HLA-B	NF-1 [T00	1611	1618	8.191058	TTGGCC	0.24414	0.24485
cg1301955	HLA-B	EBF [T05	448	458	8.152312	GCCTCA	0.04196	0.04563
cg2595453	HLA-B	EBF [T05	1687	1697	8.152312	GCCTCA	0.04196	0.04563
cg2595453	HLA-B	NF-AT1 [	990	998	8.12076	GGAAAA	0.1297	0.12846
cg2595453	HLA-B	NF-AT1 [	1134	1142	8.12076	GGAAAA	0.1297	0.12846
cg1301955	HLA-B	LEF-1 [T0	1743	1750	8.117221	TCTCAA	0.12207	0.11275
cg1301955	HLA-B	VDR [T00	194	202	8.079962	GTTCAG	0.24414	0.22992
cg1301955	HLA-B	VDR [T00	1440	1448	8.079962	TCCCTG	0.24414	0.22992
cg2595453	HLA-B	VDR [T00	1433	1441	8.079962	GTTCAG	0.24414	0.22992
cg1301955	HLA-B	AR [T000	39	47	8.079301	AGCTTG	0.19836	0.20641
cg2595453	HLA-B	AR [T000	1278	1286	8.079301	AGCTTG	0.19836	0.20641
cg1301955	HLA-B	GR-alpha [	20	24	8.073878	CCTGG	7.8125	8.20289

cg1301955	HLA-B	GR-alpha |	58	62	8.073878	CCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	94	98	8.073878	CCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	98	102	8.073878	GTAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	176	180	8.073878	CCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	184	188	8.073878	GCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	221	225	8.073878	GTAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	303	307	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	407	411	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	522	526	8.073878	CCTGC	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	576	580	8.073878	GCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	585	589	8.073878	GCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	609	613	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	657	661	8.073878	CCTGC	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	818	822	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	878	882	8.073878	CCTGC	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	890	894	8.073878	CCTGC	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	951	955	8.073878	CCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	968	972	8.073878	CCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	986	990	8.073878	GCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1154	1158	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1284	1288	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1312	1316	8.073878	CCTAC	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1350	1354	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1376	1380	8.073878	CCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1390	1394	8.073878	CCAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1427	1431	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1456	1460	8.073878	CCTGC	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1495	1499	8.073878	GTAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1542	1546	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1583	1587	8.073878	CCTGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1658	1662	8.073878	GTAGG	7.8125	8.20289
cg1301955	HLA-B	GR-alpha |	1874	1878	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	81	85	8.073878	CCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	127	131	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	143	147	8.073878	CCTGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	202	206	8.073878	CCTAC	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	220	224	8.073878	CCTAC	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	264	268	8.073878	CTAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	273	277	8.073878	CCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	357	361	8.073878	CCTGC	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	371	375	8.073878	CCTGC	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	530	534	8.073878	CCTGC	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	589	593	8.073878	CCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	608	612	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	621	625	8.073878	CCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	744	748	8.073878	CCTAG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	745	749	8.073878	CTAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha |	786	790	8.073878	CCTGG	7.8125	8.20289

cg2595453	HLA-B	GR-alpha [	823	827	8.073878	CCTGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	830	834	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	837	841	8.073878	CCTGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1017	1021	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1049	1053	8.073878	CTAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1259	1263	8.073878	CCTGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1297	1301	8.073878	CCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1333	1337	8.073878	CCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1337	1341	8.073878	GTAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1415	1419	8.073878	CCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1423	1427	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1460	1464	8.073878	GTAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1542	1546	8.073878	CCTGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1646	1650	8.073878	CCTGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1761	1765	8.073878	CCTGC	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1815	1819	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1824	1828	8.073878	GCAGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1848	1852	8.073878	CCTGG	7.8125	8.20289
cg2595453	HLA-B	GR-alpha [	1896	1900	8.073878	CCTGC	7.8125	8.20289
cg2595453	HLA-B	AR [T000	781	789	8.055836	GGACAC	0.19836	0.20641
cg1301955	HLA-B	TFIID [T0	1646	1652	8.014558	TTTGTTA	2.19727	1.99811
cg1301955	HLA-B	TFIID [T0	1703	1709	8.014558	TTTGTA	2.19727	1.99811
cg1301955	HLA-B	TFIID [T0	1743	1749	8.014558	TCTCAA	2.19727	1.99811
cg1301955	HLA-B	TFIID [T0	1880	1886	8.014558	TTTGTTA	2.19727	1.99811
cg1301955	HLA-B	Pax-5 [T0	124	130	8.014558	GGGCCG	2.19727	2.42766
cg1301955	HLA-B	Pax-5 [T0	322	328	8.014558	TCAGCC	2.19727	2.42766
cg1301955	HLA-B	Pax-5 [T0	760	766	8.014558	GGGCTC	2.19727	2.42766
cg1301955	HLA-B	Pax-5 [T0	833	839	8.014558	GGGCTG	2.19727	2.42766
cg1301955	HLA-B	Pax-5 [T0	971	977	8.014558	GGGCCG	2.19727	2.42766
cg1301955	HLA-B	Pax-5 [T0	1243	1249	8.014558	GCGGCC	2.19727	2.42766
cg2595453	HLA-B	TFIID [T0	706	712	8.014558	TCAGAA	2.19727	1.99811
cg2595453	HLA-B	TFIID [T0	858	864	8.014558	TTGGAA	2.19727	1.99811
cg2595453	HLA-B	Pax-5 [T0	346	352	8.014558	GGGGCC	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	366	372	8.014558	GGGCTC	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	433	439	8.014558	GGGCTT	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	441	447	8.014558	GCAGCC	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	503	509	8.014558	GCTGCC	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	624	630	8.014558	GGGCCC	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	801	807	8.014558	GGGCAC	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	1113	1119	8.014558	GGGGCC	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	1363	1369	8.014558	GGGCCG	2.19727	2.42766
cg2595453	HLA-B	Pax-5 [T0	1561	1567	8.014558	TCAGCC	2.19727	2.42766
cg2595453	HLA-B	C/EBPalp	856	862	8.006685	CATTGG	0.24414	0.23098
cg1301955	HLA-B	ETF [T002	307	317	7.870358	GCCCCG	0.07153	0.08737
cg1301955	HLA-B	ETF [T002	404	414	7.870358	GCGCCT	0.07153	0.08737
cg2595453	HLA-B	ATF-1 [T0	1080	1090	7.870358	AGACGT	0.07153	0.07126
cg2595453	HLA-B	ETF [T002	1546	1556	7.870358	GCCCCG	0.07153	0.08737
cg2595453	HLA-B	ETF [T002	1643	1653	7.870358	GCGCCT	0.07153	0.08737

cg1301955	HLA-B	p53 [T006	760	766	7.833758	GGGCTC	0.48828	0.55336
cg2595453	HLA-B	p53 [T006	366	372	7.833758	GGGCTC	0.48828	0.55336
cg1301955	HLA-B	IRF-1 [T0	1984	1992	7.82345	TTTCCTC	0.25177	0.2462
cg2595453	HLA-B	RXR-alpha	639	645	7.815913	GGGTGG	0.24414	0.26389
cg1301955	HLA-B	T3R-beta1	545	553	7.813363	TCACCG	0.27466	0.28753
cg1301955	HLA-B	T3R-beta1	943	951	7.813363	TCACCG	0.27466	0.28753
cg2595453	HLA-B	T3R-beta1	192	200	7.813363	TCACCC	0.27466	0.28753
cg2595453	HLA-B	T3R-beta1	1784	1792	7.813363	TCACCG	0.27466	0.28753
cg1301955	HLA-B	EBF [T05	1194	1204	7.780217	AACTCA	0.04196	0.04563
cg1301955	HLA-B	NF-AT1 [	1761	1769	7.744746	TTACTT	0.19836	0.19379
cg2595453	HLA-B	NF-AT1 [	327	335	7.744746	GGAAAG	0.19836	0.19379
cg2595453	HLA-B	NF-AT1 [	372	380	7.744746	CTGCTT	0.19836	0.19379
cg2595453	HLA-B	LEF-1 [T0	1022	1029	7.719635	GGTCAA	0.21362	0.21504
cg2595453	HLA-B	EBF [T05	633	643	7.659914	ACCTCA	0.01144	0.0122
cg1301955	HLA-B	p53 [T006	492	498	7.641867	GGGCCG	0.73242	0.79826
cg1301955	HLA-B	p53 [T006	612	618	7.641867	GGGCCT	0.73242	0.79826
cg2595453	HLA-B	p53 [T006	1731	1737	7.641867	GGGCCG	0.73242	0.79826
cg2595453	HLA-B	p53 [T006	1851	1857	7.641867	GGGCCT	0.73242	0.79826
cg2595453	HLA-B	c-Jun [T00	1081	1087	7.538568	GACGTC	0.48828	0.48672
cg1301955	HLA-B	PPAR-alp	1283	1293	7.529496	ACCTGG	0.04482	0.04884
cg2595453	HLA-B	PPAR-alp	142	152	7.529496	ACCTGG	0.04482	0.04884
cg1301955	HLA-B	GR [T050	1643	1649	7.527031	TTGTTTC	1.83105	1.71535
cg1301955	HLA-B	GR [T050	1746	1752	7.527031	CAAAGC	1.83105	1.71535
cg2595453	HLA-B	GR [T050	52	58	7.527031	CAAAAG	1.83105	1.71535
cg2595453	HLA-B	GR [T050	720	726	7.527031	CGCTTTC	1.83105	1.71535
cg1301955	HLA-B	c-Jun [T00	595	601	7.491008	TCGGTC	0.48828	0.48672
cg1301955	HLA-B	c-Jun [T00	958	964	7.491008	TCGGTC	0.48828	0.48672
cg2595453	HLA-B	c-Jun [T00	1834	1840	7.491008	TCGGTC	0.48828	0.48672
cg2595453	HLA-B	RAR-beta	171	180	7.47824	AGAAAA	0.24414	0.25121
cg2595453	HLA-B	RAR-beta	805	814	7.47824	ACAGAA	0.24414	0.25121
cg1301955	HLA-B	RAR-beta:	666	677	7.477995	TCCACG	0.02861	0.03163
cg2595453	HLA-B	RAR-beta:	1905	1916	7.477995	TCCACG	0.02861	0.03163
cg2595453	HLA-B	IRF-1 [T0	1130	1138	7.477948	CTCAGG	0.14496	0.14723
cg2595453	HLA-B	AR [T000	166	174	7.467081	GGACAA	0.25177	0.2544
cg1301955	HLA-B	C/EBPalp	1233	1239	7.465744	CATTGC	0.48828	0.45033
cg1301955	HLA-B	p53 [T006	250	256	7.458735	GGCGCC	0.73242	0.79826
cg1301955	HLA-B	p53 [T006	671	677	7.458735	GGCGCC	0.73242	0.79826
cg1301955	HLA-B	p53 [T006	1002	1008	7.458735	GGGCGC	0.73242	0.79826
cg2595453	HLA-B	p53 [T006	1489	1495	7.458735	GGCGCC	0.73242	0.79826
cg2595453	HLA-B	p53 [T006	1910	1916	7.458735	GGCGCC	0.73242	0.79826
cg1301955	HLA-B	NF-kappa	1223	1233	7.452991	TGCGCC	0.04435	0.04858
cg2595453	HLA-B	c-Myb [T0	861	868	7.442719	GAAAGT	0.42725	0.40917
cg1301955	HLA-B	C/EBPalp	1698	1704	7.396431	TCCAAT	0.48828	0.45033
cg1301955	HLA-B	C/EBPalp	1732	1738	7.396431	TACAAT	0.48828	0.45033
cg2595453	HLA-B	AR [T000	738	746	7.372454	GGACAC	0.25177	0.2544
cg1301955	HLA-B	PPAR-alp	406	416	7.370536	GCCTGG	0.04482	0.04884
cg2595453	HLA-B	PPAR-alp	1645	1655	7.370536	GCCTGG	0.04482	0.04884
cg1301955	HLA-B	PXR-1:RX	191	198	7.362674	CTCGTTC	0.24414	0.24326

cg2595453	HLA-B	PXR-1:RX	1430	1437	7.362674	CTCGTT	0.24414	0.24326
cg1301955	HLA-B	HOXD9 [T	1863	1872	7.270719	AATATA	0.06866	0.05771
cg1301955	HLA-B	HOXD10 [	1863	1872	7.270719	AATATA	0.06866	0.05771
cg1301955	HLA-B	c-Ets-1 [T	1765	1771	7.199436	TTTCCC	0.73242	0.73732
cg2595453	HLA-B	c-Ets-1 [T	325	331	7.199436	TGGGAA	0.73242	0.73732
cg1301955	HLA-B	GCF [T00	1219	1227	7.186486	ACGCTG	0.45776	0.50397
cg1301955	HLA-B	GCF [T00	1392	1400	7.186486	AGGCTG	0.45776	0.50397
cg1301955	HLA-B	XBP-1 [T	752	757	7.172312	ATGAAG	2.92969	2.7512
cg1301955	HLA-B	XBP-1 [T	802	807	7.172312	CCTCAT	2.92969	2.7512
cg1301955	HLA-B	XBP-1 [T	1687	1692	7.172312	ATGATT	2.92969	2.7512
cg1301955	HLA-B	XBP-1 [T	1814	1819	7.172312	CTTCAT	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	30	35	7.172312	CTTCAT	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	122	127	7.172312	ATGAGG	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	342	347	7.172312	ATGAGG	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	399	404	7.172312	CCTCAT	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	447	452	7.172312	CCTCAT	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	645	650	7.172312	CCTCAT	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	853	858	7.172312	ATTCAT	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	1139	1144	7.172312	ACTCAT	2.92969	2.7512
cg2595453	HLA-B	XBP-1 [T	1991	1996	7.172312	ATGAAG	2.92969	2.7512
cg1301955	HLA-B	MAZ [T00	925	937	7.171165	TTCCCT	0.00918	0.01018
cg2595453	HLA-B	p53 [T006	624	630	7.153797	GGGCCC	1.09863	1.22478
cg1301955	HLA-B	c-Myb [T0	1445	1452	7.127234	GAACTG	0.18311	0.17765
cg1301955	HLA-B	p53 [T006	199	205	7.103527	GGGCGA	1.09863	1.22478
cg2595453	HLA-B	p53 [T006	1438	1444	7.103527	GGGCGA	1.09863	1.22478
cg1301955	HLA-B	NF-AT1 [	1980	1988	7.095752	CTGTTT	0.15259	0.14325
cg1301955	HLA-B	Pax-5 [T0	199	205	7.082373	GGGCGA	0.12207	0.13135
cg2595453	HLA-B	Pax-5 [T0	1438	1444	7.082373	GGGCGA	0.12207	0.13135
cg1301955	HLA-B	c-Ets-1 [T	924	930	7.071349	TTTCCC	0.73242	0.73732
cg1301955	HLA-B	c-Ets-1 [T	1497	1503	7.071349	AGGGAA	0.73242	0.73732
cg1301955	HLA-B	c-Ets-1 [T	1833	1839	7.071349	TTTCCC	0.73242	0.73732
cg2595453	HLA-B	c-Ets-1 [T	376	382	7.071349	TTTCCC	0.73242	0.73732
cg2595453	HLA-B	IRF-1 [T0	986	994	7.044985	GAGAGG	0.1297	0.12685
cg2595453	HLA-B	C/EBPalp	33	39	7.00174	CATTGT	0.73242	0.68282
cg1301955	HLA-B	HNF-3alp	383	390	7.000129	TGAAAA	0.82397	0.71909
cg1301955	HLA-B	HNF-3alp	794	801	7.000129	TAGAAA	0.82397	0.71909
cg2595453	HLA-B	HNF-3alp	708	715	7.000129	AGAAAA	0.82397	0.71909
cg2595453	HLA-B	HNF-3alp	1622	1629	7.000129	TGAAAA	0.82397	0.71909
cg1301955	HLA-B	IRF-1 [T0	1765	1773	6.968314	TTTCCC	0.1297	0.12685
cg2595453	HLA-B	IRF-1 [T0	323	331	6.968314	TCTGGG	0.1297	0.12685
cg2595453	HLA-B	RXR-alph	662	668	6.967687	GGGTGG	0.36621	0.38841
cg2595453	HLA-B	RXR-alph	750	756	6.967687	ACCACC	0.36621	0.38841
cg2595453	HLA-B	NF-1 [T00	946	953	6.948522	AGCCCC	0.48828	0.50205
cg1301955	HLA-B	ENKTF-1	69	76	6.942764	CGGAGC	1.46484	1.56616
cg1301955	HLA-B	ENKTF-1	305	312	6.942764	TGGCCC	1.46484	1.56616
cg1301955	HLA-B	ENKTF-1	1002	1009	6.942764	GGGCGC	1.46484	1.56616
cg2595453	HLA-B	ENKTF-1	273	280	6.942764	CCAGGC	1.46484	1.56616
cg2595453	HLA-B	ENKTF-1	1308	1315	6.942764	CGGAGC	1.46484	1.56616

cg2595453	HLA-B	ENKTF-1	1544	1551	6.942764	TGGCCC	1.46484	1.56616
cg1301955	HLA-B	p53 [T006	124	130	6.938545	GGGCCG	1.09863	1.22478
cg1301955	HLA-B	p53 [T006	971	977	6.938545	GGGCCG	1.09863	1.22478
cg1301955	HLA-B	p53 [T006	1243	1249	6.938545	GCGGCC	1.09863	1.22478
cg2595453	HLA-B	p53 [T006	1363	1369	6.938545	GGGCCG	1.09863	1.22478
cg1301955	HLA-B	RelA [T00	1206	1216	6.926978	TGGGGA	0.01192	0.01233
cg1301955	HLA-B	E2F-1 [T0	579	586	6.839754	GGTTCC	0.30518	0.33862
cg2595453	HLA-B	E2F-1 [T0	1818	1825	6.839754	GGTTCC	0.30518	0.33862
cg2595453	HLA-B	PEA3 [T0	23	31	6.824411	ATCCAT	0.22888	0.22744
cg1301955	HLA-B	C/EBPalp	1109	1115	6.786177	TCCAAT	0.73242	0.68282
cg1301955	HLA-B	NFI/CTF [	1089	1096	6.786076	CTGATT	0.73242	0.74795
cg1301955	HLA-B	p53 [T006	739	745	6.775228	GTAGCC	1.09863	1.22478
cg2595453	HLA-B	p53 [T006	1978	1984	6.775228	GTAGCC	1.09863	1.22478
cg2595453	HLA-B	IRF-1 [T0	1121	1129	6.699483	CAGAGG	0.19073	0.1875
cg1301955	HLA-B	c-Ets-1 [T	580	586	6.693449	GTTCCG	0.48828	0.48842
cg2595453	HLA-B	c-Ets-1 [T	1819	1825	6.693449	GTTCCG	0.48828	0.48842
cg1301955	HLA-B	FOXP3 [T	1758	1763	6.581441	GTTTTA	0.97656	0.904
cg1301955	HLA-B	TFII-I [T0	75	80	6.581441	CACTCC	0.97656	0.9991
cg1301955	HLA-B	TFII-I [T0	808	813	6.581441	GGAGTG	0.97656	0.9991
cg1301955	HLA-B	TFII-I [T0	1123	1128	6.581441	GGAGTG	0.97656	0.9991
cg1301955	HLA-B	TFII-I [T0	1202	1207	6.581441	GGAGTG	0.97656	0.9991
cg1301955	HLA-B	TFII-I [T0	1465	1470	6.581441	CACTCC	0.97656	0.9991
cg1301955	HLA-B	TFII-I [T0	1855	1860	6.581441	ATCTCC	0.97656	0.9991
cg2595453	HLA-B	FOXP3 [T	1156	1161	6.581441	TTCAAC	0.97656	0.904
cg2595453	HLA-B	TFII-I [T0	526	531	6.581441	ATCTCC	0.97656	0.9991
cg2595453	HLA-B	TFII-I [T0	602	607	6.581441	ATCTCC	0.97656	0.9991
cg2595453	HLA-B	TFII-I [T0	846	851	6.581441	ATCTCC	0.97656	0.9991
cg2595453	HLA-B	TFII-I [T0	1233	1238	6.581441	GGAGAT	0.97656	0.9991
cg2595453	HLA-B	TFII-I [T0	1314	1319	6.581441	CACTCC	0.97656	0.9991
cg1301955	HLA-B	c-Ets-1 [T	631	637	6.565361	GTTCCG	0.48828	0.48842
cg2595453	HLA-B	c-Ets-1 [T	1870	1876	6.565361	GTTCCG	0.48828	0.48842
cg1301955	HLA-B	RXR-alph	726	732	6.563693	GGGTGT	0.24414	0.25119
cg1301955	HLA-B	RXR-alph	1112	1118	6.563693	AATACC	0.24414	0.25119
cg2595453	HLA-B	RXR-alph	739	745	6.563693	GACACC	0.24414	0.25119
cg2595453	HLA-B	RXR-alph	1965	1971	6.563693	GGGTGT	0.24414	0.25119
cg2595453	HLA-B	p53 [T006	433	439	6.563521	GGGCTT	0.48828	0.54643
cg2595453	HLA-B	p53 [T006	441	447	6.563521	GCAGCC	0.48828	0.54643
cg2595453	HLA-B	IRF-1 [T0	856	864	6.535281	CATTGG	0.19073	0.1875
cg1301955	HLA-B	NF-kappa	1207	1218	6.525226	GGGGAA	0.00405	0.00452
cg1301955	HLA-B	XBP-1 [T	236	241	6.478682	ATGCCC	0.97656	0.99906
cg1301955	HLA-B	XBP-1 [T	1522	1527	6.478682	ATGCCA	0.97656	0.99906
cg2595453	HLA-B	XBP-1 [T	287	292	6.478682	ATGCCC	0.97656	0.99906
cg2595453	HLA-B	XBP-1 [T	461	466	6.478682	TGGCAT	0.97656	0.99906
cg2595453	HLA-B	XBP-1 [T	1143	1148	6.478682	ATGCCA	0.97656	0.99906
cg2595453	HLA-B	XBP-1 [T	1475	1480	6.478682	ATGCCC	0.97656	0.99906
cg1301955	HLA-B	c-Jun [T00	1140	1146	6.475265	CGCGTC	0.61035	0.6179
cg1301955	HLA-B	c-Jun [T00	1910	1916	6.462218	GTAGTC	0.61035	0.6179
cg1301955	HLA-B	AR [T000	781	789	6.461025	GGACAC	0.19836	0.20813

cg1301955	HLA-B	AR [T0004	1353	1361	6.461025	GGACAA	0.19836	0.20813
cg2595453	HLA-B	c-Ets-1 [T(	858	864	6.423689	TTGGAA/	0.48828	0.48842
cg1301955	HLA-B	p53 [T006'	524	530	6.403751	TGCGCC(	0.48828	0.54643
cg1301955	HLA-B	p53 [T006'	880	886	6.403751	TGCGCC(	0.48828	0.54643
cg1301955	HLA-B	p53 [T006'	1396	1402	6.403751	TGCGCC(	0.48828	0.54643
cg2595453	HLA-B	p53 [T006'	1763	1769	6.403751	TGCGCC(	0.48828	0.54643
cg1301955	HLA-B	p53 [T006'	483	489	6.400205	GGGCGA	0.48828	0.54643
cg2595453	HLA-B	p53 [T006'	1165	1171	6.400205	GGGCGA	0.48828	0.54643
cg2595453	HLA-B	p53 [T006'	1722	1728	6.400205	GGGCGA	0.48828	0.54643
cg2595453	HLA-B	C/EBPalph	1094	1100	6.391486	AATTGT(	0.48828	0.47407
cg2595453	HLA-B	c-Jun [T00	353	359	6.293948	TGACCC7	0.61035	0.6179
cg1301955	HLA-B	GR-alpha [	118	122	6.263098	CCTCA	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	376	380	6.263098	CCTCA	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	449	453	6.263098	CCTCA	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	715	719	6.263098	CCTCA	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	802	806	6.263098	CCTCA	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	826	830	6.263098	TGAGG	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	870	874	6.263098	CCTCA	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	1029	1033	6.263098	TGAGG	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	1469	1473	6.263098	CCTTA	3.90625	3.89624
cg1301955	HLA-B	GR-alpha [	1920	1924	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	123	127	6.263098	TGAGG	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	190	194	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	343	347	6.263098	TGAGG	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	399	403	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	411	415	6.263098	CCTTA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	429	433	6.263098	TGAGG	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	447	451	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	634	638	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	645	649	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	966	970	6.263098	TGAGG	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	1074	1078	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	1090	1094	6.263098	CCTTA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	1118	1122	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	1357	1361	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	1615	1619	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	1688	1692	6.263098	CCTCA	3.90625	3.89624
cg2595453	HLA-B	GR-alpha [	1954	1958	6.263098	CCTCA	3.90625	3.89624
cg1301955	HLA-B	TCF-4 [T0	1919	1928	6.262917	ACCTCA/	0.04959	0.04686
cg1301955	HLA-B	C/EBPalph	1892	1898	6.245236	TATTGC/	0.97656	0.91422
cg2595453	HLA-B	IRF-1 [T0(	1191	1199	6.24301	TTTCCTC	0.16785	0.16217
cg1301955	HLA-B	NF-AT1 [T	1370	1379	6.201624	TGGAAA(	0.03815	0.03661
cg1301955	HLA-B	SRY [T009	1326	1334	6.176442	CTTTGTC	0.15259	0.14742
cg1301955	HLA-B	c-Ets-1 [T(	1369	1375	6.167515	GTGGAA.	0.36621	0.36174
cg1301955	HLA-B	c-Jun [T00	1327	1333	6.152811	TTTGTCA	0.36621	0.34478
cg1301955	HLA-B	RXR-alpha	485	491	6.119461	GCGACC(	0.73242	0.78318
cg2595453	HLA-B	RXR-alpha	1724	1730	6.119461	GCGACC(	0.73242	0.78318
cg2595453	HLA-B	c-Fos [T00	919	928	6.103724	AAAGTG.	0.09155	0.09198

cg1301955	HLA-B	GR-alpha [	196	200	6.055408	TCAGG	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	451	455	6.055408	TCAGG	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	872	876	6.055408	TCAGG	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	962	966	6.055408	TCAGG	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1197	1201	6.055408	TCAGG	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1256	1260	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1264	1268	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1297	1301	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1343	1347	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1442	1446	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1682	1686	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1753	1757	6.055408	CCTAA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1827	1831	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1859	1863	6.055408	CCTGA	3.90625	3.89835
cg1301955	HLA-B	GR-alpha [	1987	1991	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	206	210	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	351	355	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	380	384	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	423	427	6.055408	TCAGG	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	561	565	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	636	640	6.055408	TCAGG	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	715	719	6.055408	TCAGG	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	767	771	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	901	905	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	983	987	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	1036	1040	6.055408	CCTGA	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	1131	1135	6.055408	TCAGG	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	1435	1439	6.055408	TCAGG	3.90625	3.89835
cg2595453	HLA-B	GR-alpha [	1690	1694	6.055408	TCAGG	3.90625	3.89835
cg2595453	HLA-B	C/EBPalp	283	289	5.996794	AACAAT	0.97656	0.91422
cg2595453	HLA-B	AR [T000	776	784	5.953985	GGACAG	0.24414	0.25115
cg1301955	HLA-B	GCF [T00	569	577	5.917256	TAGCCG	0.64087	0.72542
cg1301955	HLA-B	GCF [T00	667	675	5.917256	CCACGG	0.64087	0.72542
cg1301955	HLA-B	GCF [T00	862	870	5.917256	GCGCGG	0.64087	0.72542
cg2595453	HLA-B	GCF [T00	1178	1186	5.917256	GCGCTG	0.64087	0.72542
cg2595453	HLA-B	GCF [T00	1808	1816	5.917256	TAGCCG	0.64087	0.72542
cg2595453	HLA-B	GCF [T00	1906	1914	5.917256	CCACGG	0.64087	0.72542
cg1301955	HLA-B	STAT4 [T	2	7	5.882353	GGAAGG	0.48828	0.51201
cg1301955	HLA-B	STAT4 [T	46	51	5.882353	CCTTCC	0.48828	0.51201
cg1301955	HLA-B	STAT4 [T	1407	1412	5.882353	CCTTCC	0.48828	0.51201
cg2595453	HLA-B	STAT4 [T	197	202	5.882353	CCTTCC	0.48828	0.51201
cg2595453	HLA-B	STAT4 [T	516	521	5.882353	GGAAGG	0.48828	0.51201
cg2595453	HLA-B	STAT4 [T	796	801	5.882353	GGAAGG	0.48828	0.51201
cg2595453	HLA-B	STAT4 [T	1241	1246	5.882353	GGAAGG	0.48828	0.51201
cg2595453	HLA-B	STAT4 [T	1285	1290	5.882353	CCTTCC	0.48828	0.51201
cg2595453	HLA-B	AR [T000	267	275	5.859358	GGACAG	0.24414	0.25115
cg1301955	HLA-B	c-Ets-1 [T	1127	1133	5.814485	TGGGAA	0.36621	0.36174
cg2595453	HLA-B	c-Ets-1 [T	112	118	5.814485	CTTCCC	0.36621	0.36174

cg2595453	HLA-B	c-Ets-1 [T	311	317	5.814485	TGGGAA	0.36621	0.36174
cg2595453	HLA-B	c-Ets-1 [T	697	703	5.814485	TGGGAA	0.36621	0.36174
cg1301955	HLA-B	AR [T000	1434	1442	5.811663	TCCCTGT	0.24414	0.25115
cg2595453	HLA-B	NF-kappa	1211	1221	5.806158	AGGCCA	0.04053	0.04443
cg2595453	HLA-B	c-Jun [T00	993	999	5.783074	AAAGTC	0.36621	0.34478
cg2595453	HLA-B	p53 [T006	91	97	5.720243	TTAGCC	0.61035	0.65765
cg1301955	HLA-B	c-Jun [T00	537	543	5.703976	GGGGTC	0.48828	0.49294
cg2595453	HLA-B	c-Jun [T00	394	400	5.703976	TGACCC	0.48828	0.49294
cg2595453	HLA-B	c-Jun [T00	1020	1026	5.703976	GGGGTC	0.48828	0.49294
cg2595453	HLA-B	c-Jun [T00	1776	1782	5.703976	GGGGTC	0.48828	0.49294
cg1301955	HLA-B	ENKTF-1	963	970	5.687009	CAGGGC	0.73242	0.76357
cg2595453	HLA-B	c-Ets-1 [T	198	204	5.686398	CTTCCCT	0.36621	0.38732
cg2595453	HLA-B	NF-1 [T00	568	575	5.626299	TTGGTC	0.24414	0.25051
cg1301955	HLA-B	AR [T000	159	167	5.597291	GCCGTG	0.05341	0.05856
cg2595453	HLA-B	AR [T000	1398	1406	5.597291	GCCGTG	0.05341	0.05856
cg1301955	HLA-B	T3R-beta1	1582	1590	5.591999	ACCTGG	0.21362	0.21789
cg1301955	HLA-B	T3R-beta1	820	828	5.572705	TGGGGG	0.21362	0.21789
cg2595453	HLA-B	T3R-beta1	11	19	5.572705	TCAAGG	0.21362	0.21789
cg1301955	HLA-B	NFI/CTF [	1318	1325	5.558661	CCAAGC	0.54932	0.55504
cg2595453	HLA-B	NFI/CTF [	564	571	5.558661	GAGTTT	0.54932	0.55504
cg2595453	HLA-B	NFI/CTF [	950	957	5.558661	CCAAAC	0.54932	0.55504
cg1301955	HLA-B	c-Ets-1 [T	0	6	5.558311	GGGGAA	0.36621	0.38732
cg1301955	HLA-B	c-Ets-1 [T	1408	1414	5.558311	CTTCCC	0.36621	0.38732
cg2595453	HLA-B	c-Ets-1 [T	335	341	5.558311	GGGGAA	0.36621	0.38732
cg2595453	HLA-B	c-Ets-1 [T	794	800	5.558311	GGGGAA	0.36621	0.38732
cg2595453	HLA-B	c-Ets-1 [T	1060	1066	5.558311	CTTCCC	0.36621	0.38732
cg2595453	HLA-B	c-Ets-1 [T	1239	1245	5.558311	GGGGAA	0.36621	0.38732
cg1301955	HLA-B	T3R-beta1	1959	1967	5.553412	TCACCG	0.21362	0.21789
cg1301955	HLA-B	TFIID [T0	1065	1071	5.544826	TTTAGA	0.73242	0.65314
cg1301955	HLA-B	p53 [T006	322	328	5.508538	TCAGCC	0.61035	0.65765
cg1301955	HLA-B	p53 [T006	833	839	5.508538	GGGCTG	0.61035	0.65765
cg2595453	HLA-B	p53 [T006	1561	1567	5.508538	TCAGCC	0.61035	0.65765
cg1301955	HLA-B	HNF-1C [	1780	1788	5.498706	ATCTGT	0.07629	0.06785
cg2595453	HLA-B	E2F-1 [T0	879	886	5.476857	GCGGGG	0.03052	0.03364
cg1301955	HLA-B	c-Ets-1 [T	47	53	5.430224	CTTCCC	0.36621	0.38732
cg2595453	HLA-B	c-Ets-1 [T	1286	1292	5.430224	CTTCCC	0.36621	0.38732
cg1301955	HLA-B	PPAR-alph	1070	1080	5.285833	AACTGG	0.03529	0.03856
cg1301955	HLA-B	RXR-alph	1047	1053	5.271235	GGGTGG	0.61035	0.65415
cg1301955	HLA-B	RXR-alph	1822	1828	5.271235	CCCACC	0.61035	0.65415
cg2595453	HLA-B	RXR-alph	184	190	5.271235	CCCACC	0.61035	0.65415
cg2595453	HLA-B	RXR-alph	611	617	5.271235	GGGTAG	0.61035	0.65415
cg2595453	HLA-B	RXR-alph	790	796	5.271235	GGGTGG	0.61035	0.65415
cg2595453	HLA-B	GR [T050	680	686	5.207533	GTCTTT	0.24414	0.24013
cg2595453	HLA-B	c-Ets-2 [T	1088	1096	5.162974	TTCCTTA	0.13733	0.13279
cg1301955	HLA-B	c-Myb [T0	721	728	5.137438	GAACTG	0.30518	0.30087
cg1301955	HLA-B	c-Myb [T0	1069	1076	5.137438	GAACTG	0.30518	0.30087
cg2595453	HLA-B	c-Myb [T0	1960	1967	5.137438	GAACTG	0.30518	0.30087
cg2595453	HLA-B	EBF [T05	618	628	5.130966	AACCCA	0.02289	0.02569

cg1301955	HLA-B	RXR-alph	145	151	5.089356	GGGTGA	0.48828	0.51407
cg2595453	HLA-B	RXR-alph	1384	1390	5.089356	GGGTGA	0.48828	0.51407
cg2595453	HLA-B	AP-1 [T00	700	708	5.059986	GAAGAG	0.12207	0.12309
cg2595453	HLA-B	USF2 [T0	831	840	5.052423	CAGGCA	0.103	0.10797
cg1301955	HLA-B	GR-beta [T	208	212	5.042296	AATCC	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	367	371	5.042296	GGATT	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	642	646	5.042296	AATAC	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	798	802	5.042296	AATAC	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	1112	1116	5.042296	AATAC	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	1211	1215	5.042296	AATCC	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	1432	1436	5.042296	AATCC	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	1616	1620	5.042296	GGATT	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	1652	1656	5.042296	AATAC	3.90625	3.7093
cg1301955	HLA-B	GR-beta [T	1678	1682	5.042296	AATCC	3.90625	3.7093
cg2595453	HLA-B	GR-beta [T	1044	1048	5.042296	GTATT	3.90625	3.7093
cg2595453	HLA-B	GR-beta [T	1447	1451	5.042296	AATCC	3.90625	3.7093
cg2595453	HLA-B	GR-beta [T	1606	1610	5.042296	GGATT	3.90625	3.7093
cg2595453	HLA-B	GR-beta [T	1881	1885	5.042296	AATAC	3.90625	3.7093
cg2595453	HLA-B	E2F-1 [T0	579	586	5.042045	CATCCC	0.18311	0.20394
cg1301955	HLA-B	NFI/CTF [	1117	1124	5.021086	CCAATG	0.24414	0.25666
cg1301955	HLA-B	p53 [T006	336	342	5.020467	CGAGCC	0.48828	0.53921
cg2595453	HLA-B	p53 [T006	1575	1581	5.020467	CGAGCC	0.48828	0.53921
cg1301955	HLA-B	RAR-beta:	331	342	4.98533	TCCCCC	0.00966	0.01077
cg2595453	HLA-B	RAR-beta:	1570	1581	4.98533	TCCCCC	0.00966	0.01077
cg2595453	HLA-B	c-Myb [T0	258	265	4.974489	CAACTG	0.30518	0.30087
cg1301955	HLA-B	NF-1 [T00	636	643	4.880836	GGTCCC	0.24414	0.24345
cg1301955	HLA-B	NF-1 [T00	1945	1952	4.880836	AGTCCC	0.24414	0.24345
cg2595453	HLA-B	NF-1 [T00	1875	1882	4.880836	GGTCCC	0.24414	0.24345
cg1301955	HLA-B	RXR-alph	298	304	4.86724	GAGACC	0.48828	0.51407
cg1301955	HLA-B	RXR-alph	838	844	4.86724	GAGACC	0.48828	0.51407
cg1301955	HLA-B	RXR-alph	1259	1265	4.86724	GAGACC	0.48828	0.51407
cg1301955	HLA-B	RXR-alph	1383	1389	4.86724	GAGACC	0.48828	0.51407
cg2595453	HLA-B	RXR-alph	1537	1543	4.86724	GAGACC	0.48828	0.51407
cg1301955	HLA-B	NF-Y [T0	637	644	4.867193	GTCCCA	0.36621	0.35921
cg1301955	HLA-B	NF-Y [T0	1696	1703	4.867193	ATTCCA	0.36621	0.35921
cg1301955	HLA-B	NF-Y [T0	1946	1953	4.867193	GTCCCA	0.36621	0.35921
cg2595453	HLA-B	NF-Y [T0	1876	1883	4.867193	GTCCCA	0.36621	0.35921
cg1301955	HLA-B	HNF-3alph	1804	1811	4.842999	TTAAAA	0.09155	0.07438
cg1301955	HLA-B	C/EBPalph	1671	1677	4.776286	TATTGG	0.97656	0.90302
cg1301955	HLA-B	FOXP3 [T	377	382	4.756447	CTCAAC	2.92969	2.82
cg1301955	HLA-B	FOXP3 [T	1569	1574	4.756447	GTTTTC	2.92969	2.82
cg1301955	HLA-B	FOXP3 [T	1592	1597	4.756447	GTTTTC	2.92969	2.82
cg1301955	HLA-B	FOXP3 [T	1721	1726	4.756447	CAAAAC	2.92969	2.82
cg1301955	HLA-B	FOXP3 [T	1982	1987	4.756447	GTTTTC	2.92969	2.82
cg1301955	HLA-B	TFII-I [T0	328	333	4.756447	CAGTCC	2.92969	2.89715
cg1301955	HLA-B	TFII-I [T0	923	928	4.756447	ATTTCC	2.92969	2.89715
cg1301955	HLA-B	TFII-I [T0	1106	1111	4.756447	ATATCC	2.92969	2.89715
cg1301955	HLA-B	TFII-I [T0	1546	1551	4.756447	GGAATG	2.92969	2.89715

cg1301955	HLA-B	TFII-I [T0	1817	1822	4.756447	CATTCC	2.92969	2.89715
cg1301955	HLA-B	TFII-I [T0	1944	1949	4.756447	CAGTCC	2.92969	2.89715
cg2595453	HLA-B	FOXP3 [T	172	177	4.756447	GAAAAC	2.92969	2.82
cg2595453	HLA-B	FOXP3 [T	1135	1140	4.756447	GAAAAC	2.92969	2.82
cg2595453	HLA-B	FOXP3 [T	1616	1621	4.756447	CTCAAC	2.92969	2.82
cg2595453	HLA-B	TFII-I [T0	307	312	4.756447	GGACTG	2.92969	2.89715
cg2595453	HLA-B	TFII-I [T0	1053	1058	4.756447	GGACTG	2.92969	2.89715
cg2595453	HLA-B	TFII-I [T0	1070	1075	4.756447	ATTTCC	2.92969	2.89715
cg2595453	HLA-B	TFII-I [T0	1086	1091	4.756447	CATTCC	2.92969	2.89715
cg2595453	HLA-B	TFII-I [T0	1567	1572	4.756447	CAGTCC	2.92969	2.89715
cg1301955	HLA-B	c-Ets-1 [T	1155	1161	4.654478	CTGGAA	0.85449	0.8381
cg2595453	HLA-B	c-Ets-1 [T	514	520	4.654478	CTGGAA	0.85449	0.8381
cg2595453	HLA-B	TCF-4 [T0	1021	1030	4.639022	GGGTCA	0.04196	0.04141
cg2595453	HLA-B	ATF-2 [T0	1079	1088	4.623667	GAGACG	0.03815	0.03703
cg1301955	HLA-B	TCF-4 [T0	1742	1751	4.575479	CTCTCA	0.04196	0.04141
cg1301955	HLA-B	C/EBPalph	1091	1097	4.560723	GATTGG	0.24414	0.24373
cg1301955	HLA-B	E2F-1 [T0	439	446	4.545253	GGTCCC	0.15259	0.16681
cg2595453	HLA-B	E2F-1 [T0	1678	1685	4.545253	GGTCCC	0.15259	0.16681
cg1301955	HLA-B	RXR-alpha	1792	1798	4.423008	GGGTTG	0.24414	0.25781
cg1301955	HLA-B	STAT4 [T	1157	1162	4.411765	GGAAGA	1.95312	1.99838
cg1301955	HLA-B	STAT4 [T	1546	1551	4.411765	GGAATG	1.95312	1.99838
cg1301955	HLA-B	STAT4 [T	1817	1822	4.411765	CATTCC	1.95312	1.99838
cg2595453	HLA-B	STAT4 [T	111	116	4.411765	GCTTCC	1.95312	1.99838
cg2595453	HLA-B	STAT4 [T	213	218	4.411765	TCTTCC	1.95312	1.99838
cg2595453	HLA-B	STAT4 [T	313	318	4.411765	GGAAGA	1.95312	1.99838
cg2595453	HLA-B	STAT4 [T	337	342	4.411765	GGAAGA	1.95312	1.99838
cg2595453	HLA-B	STAT4 [T	699	704	4.411765	GGAAGA	1.95312	1.99838
cg2595453	HLA-B	STAT4 [T	1059	1064	4.411765	TCTTCC	1.95312	1.99838
cg2595453	HLA-B	STAT4 [T	1086	1091	4.411765	CATTCC	1.95312	1.99838
cg2595453	HLA-B	c-Ets-1 [T	1087	1093	4.411026	ATTCCTT	0.85449	0.8381
cg1301955	HLA-B	p53 [T006	304	310	4.33696	CTGGCC	0.24414	0.28373
cg1301955	HLA-B	p53 [T006	965	971	4.33696	GGGCCA	0.24414	0.28373
cg2595453	HLA-B	p53 [T006	1543	1549	4.33696	CTGGCC	0.24414	0.28373
cg1301955	HLA-B	RXR-alpha	438	444	4.24113	GGGTCC	0.97656	1.02803
cg1301955	HLA-B	RXR-alpha	538	544	4.24113	GGGTCA	0.97656	1.02803
cg2595453	HLA-B	RXR-alpha	76	82	4.24113	GGGTCC	0.97656	1.02803
cg2595453	HLA-B	RXR-alpha	412	418	4.24113	CTTACC	0.97656	1.02803
cg2595453	HLA-B	RXR-alpha	669	675	4.24113	GGGTCA	0.97656	1.02803
cg2595453	HLA-B	RXR-alpha	1030	1036	4.24113	GGGACC	0.97656	1.02803
cg2595453	HLA-B	RXR-alpha	1677	1683	4.24113	GGGTCC	0.97656	1.02803
cg2595453	HLA-B	RXR-alpha	1777	1783	4.24113	GGGTCA	0.97656	1.02803
cg1301955	HLA-B	AP-2alpha	98	103	4.211849	GTAGGC	0.97656	1.02535
cg1301955	HLA-B	AP-2alpha	221	226	4.211849	GTAGGC	0.97656	1.02535
cg2595453	HLA-B	AP-2alpha	1337	1342	4.211849	GTAGGC	0.97656	1.02535
cg2595453	HLA-B	AP-2alpha	1460	1465	4.211849	GTAGGC	0.97656	1.02535
cg1301955	HLA-B	GR-beta [T	1090	1094	4.201913	TGATT	7.8125	7.23274
cg1301955	HLA-B	GR-beta [T	1688	1692	4.201913	TGATT	7.8125	7.23274
cg1301955	HLA-B	GR-beta [T	1891	1895	4.201913	CTATT	7.8125	7.23274

cg2595453	HLA-B	GR-beta [T	851	855	4.201913	CTATT	7.8125	7.23274
cg2595453	HLA-B	GR-beta [T	940	944	4.201913	AATCA	7.8125	7.23274
cg2595453	HLA-B	NF-Y [T0	857	864	4.186615	ATTGGA	0.18311	0.17499
cg1301955	HLA-B	p53 [T006	259	265	4.125254	CCGGCC	0.73242	0.82434
cg1301955	HLA-B	p53 [T006	310	316	4.125254	CCGGCC	0.73242	0.82434
cg1301955	HLA-B	p53 [T006	532	538	4.125254	GGGCCG	0.73242	0.82434
cg1301955	HLA-B	p53 [T006	648	654	4.125254	CCGGCC	0.73242	0.82434
cg1301955	HLA-B	p53 [T006	775	781	4.125254	GGGCCG	0.73242	0.82434
cg1301955	HLA-B	p53 [T006	946	952	4.125254	CCGGCC	0.73242	0.82434
cg2595453	HLA-B	p53 [T006	1498	1504	4.125254	CCGGCC	0.73242	0.82434
cg2595453	HLA-B	p53 [T006	1549	1555	4.125254	CCGGCC	0.73242	0.82434
cg2595453	HLA-B	p53 [T006	1771	1777	4.125254	GGGCCG	0.73242	0.82434
cg2595453	HLA-B	p53 [T006	1887	1893	4.125254	CCGGCC	0.73242	0.82434
cg1301955	HLA-B	EBF [T05	1539	1549	4.120419	CGCCCT	0.0248	0.02839
cg1301955	HLA-B	IRF-1 [T0	924	932	4.035054	TTTCCCT	0.1297	0.12468
cg1301955	HLA-B	IRF-1 [T0	1495	1503	4.035054	GTAGGG	0.1297	0.12468
cg2595453	HLA-B	IRF-1 [T0	376	384	4.035054	TTTCCCT	0.1297	0.12468
cg1301955	HLA-B	RXR-alph	292	298	4.019014	GGGTGT	0.97656	1.02803
cg2595453	HLA-B	RXR-alph	153	159	4.019014	GAAACC	0.97656	1.02803
cg2595453	HLA-B	RXR-alph	616	622	4.019014	GAAACC	0.97656	1.02803
cg2595453	HLA-B	RXR-alph	1531	1537	4.019014	GGGTGT	0.97656	1.02803
cg2595453	HLA-B	STAT1bet	375	384	4.01053	CTTTCCC	0.03433	0.03308
cg1301955	HLA-B	TFIID [T0	1704	1710	4.007279	TTGTAA	1.09863	0.94722
cg1301955	HLA-B	Pax-5 [T0	14	20	4.007279	ACTGCC	1.09863	1.18533
cg1301955	HLA-B	Pax-5 [T0	411	417	4.007279	GGGCTC	1.09863	1.18533
cg1301955	HLA-B	Pax-5 [T0	492	498	4.007279	GGGCCG	1.09863	1.18533
cg1301955	HLA-B	Pax-5 [T0	612	618	4.007279	GGGCCT	1.09863	1.18533
cg1301955	HLA-B	Pax-5 [T0	1268	1274	4.007279	AGAGCC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	286	292	4.007279	AATGCC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	347	353	4.007279	GGGCCC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	623	629	4.007279	AGGGCC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	944	950	4.007279	AGAGCC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	1114	1120	4.007279	GGGCCC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	1253	1259	4.007279	ACTGCC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	1650	1656	4.007279	GGGCTC	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	1731	1737	4.007279	GGGCCG	1.09863	1.18533
cg2595453	HLA-B	Pax-5 [T0	1851	1857	4.007279	GGGCCT	1.09863	1.18533
cg2595453	HLA-B	USF2 [T0	780	789	4.003951	AGGACA	0.01144	0.01199
cg2595453	HLA-B	USF1 [T0	669	678	3.987093	GGGTCA	0.08011	0.08435
cg1301955	HLA-B	AP-2alpha	614	619	3.970052	GCCTTG	0.97656	1.02535
cg2595453	HLA-B	AP-2alpha	978	983	3.970052	CAAGGC	0.97656	1.02535
cg2595453	HLA-B	AP-2alpha	1007	1012	3.970052	CAAGGC	0.97656	1.02535
cg2595453	HLA-B	AP-2alpha	1853	1858	3.970052	GCCTTG	0.97656	1.02535
cg1301955	HLA-B	RelA [T00	1830	1840	3.767912	GAGTTT	0.00811	0.0081
cg1301955	HLA-B	GR [T050	1324	1330	3.763516	CTCTTTC	0.73242	0.6946
cg1301955	HLA-B	GR [T050	1721	1727	3.763516	CAAAAC	0.73242	0.6946
cg1301955	HLA-B	p53 [T006	1401	1407	3.750231	CCAGCC	0.73242	0.82434
cg2595453	HLA-B	p53 [T006	147	153	3.750231	GGGCTT	0.73242	0.82434

cg1301955	HLA-B	AP-2alpha	3	8	3.743866	GAAGGC	0.48828	0.5124
cg1301955	HLA-B	AP-2alpha	1601	1606	3.743866	GAAGGC	0.48828	0.5124
cg2595453	HLA-B	AP-2alpha	488	493	3.743866	GAAGGC	0.48828	0.5124
cg2595453	HLA-B	AP-2alpha	1242	1247	3.743866	GAAGGC	0.48828	0.5124
cg2595453	HLA-B	PEA3 [T0(	19	27	3.710864	ATACAT(	0.09155	0.08745
cg1301955	HLA-B	NF-kappaI	758	768	3.634761	CGGGGC'	0.01812	0.02061
cg1301955	HLA-B	p53 [T006'	86	92	3.586914	CTCGCC(	0.73242	0.80362
cg1301955	HLA-B	p53 [T006'	1537	1543	3.586914	CTCGCC(	0.73242	0.80362
cg2595453	HLA-B	p53 [T006'	1325	1331	3.586914	CTCGCC(	0.73242	0.80362
cg1301955	HLA-B	RXR-alpha	847	853	3.574782	CCGACC(	1.09863	1.1653
cg1301955	HLA-B	RXR-alpha	932	938	3.574782	CCGACC(	1.09863	1.1653
cg1301955	HLA-B	p53 [T006'	14	20	3.516613	ACTGCC(	0.73242	0.80362
cg2595453	HLA-B	p53 [T006'	286	292	3.516613	AATGCC(	0.73242	0.80362
cg2595453	HLA-B	p53 [T006'	1253	1259	3.516613	ACTGCC(	0.73242	0.80362
cg1301955	HLA-B	GCF [T00:	574	582	3.409768	GCGCAG'	0.03052	0.03366
cg2595453	HLA-B	GCF [T00:	1813	1821	3.409768	GCGCAG'	0.03052	0.03366
cg1301955	HLA-B	RXR-alpha	396	402	3.392904	GGGTAA.	1.09863	1.1653
cg1301955	HLA-B	RXR-alpha	823	829	3.392904	GGGTGA'	1.09863	1.1653
cg1301955	HLA-B	RXR-alpha	1051	1057	3.392904	GGGTGC'	1.09863	1.1653
cg1301955	HLA-B	RXR-alpha	1163	1169	3.392904	AGGACC'	1.09863	1.1653
cg2595453	HLA-B	RXR-alpha	191	197	3.392904	CTCACC(	1.09863	1.1653
cg2595453	HLA-B	RXR-alpha	393	399	3.392904	ATGACC(	1.09863	1.1653
cg2595453	HLA-B	RXR-alpha	426	432	3.392904	GGGTGA'	1.09863	1.1653
cg2595453	HLA-B	RXR-alpha	1635	1641	3.392904	GGGTAA.	1.09863	1.1653
cg1301955	HLA-B	p53 [T006'	341	347	3.375208	CCCGCC(	0.73242	0.80362
cg1301955	HLA-B	p53 [T006'	346	352	3.375208	CCCGCC(	0.73242	0.80362
cg1301955	HLA-B	p53 [T006'	434	440	3.375208	GGGCGG	0.73242	0.80362
cg1301955	HLA-B	p53 [T006'	842	848	3.375208	CCCGCC(	0.73242	0.80362
cg2595453	HLA-B	p53 [T006'	1580	1586	3.375208	CCCGCC(	0.73242	0.80362
cg2595453	HLA-B	p53 [T006'	1585	1591	3.375208	CCCGCC(	0.73242	0.80362
cg2595453	HLA-B	p53 [T006'	1673	1679	3.375208	GGGCGG	0.73242	0.80362
cg1301955	HLA-B	GR-beta [T	1669	1673	3.361531	AATAT	3.90625	3.51525
cg1301955	HLA-B	GR-beta [T	1670	1674	3.361531	ATATT	3.90625	3.51525
cg1301955	HLA-B	GR-beta [T	1863	1867	3.361531	AATAT	3.90625	3.51525
cg2595453	HLA-B	GR-beta [T	845	849	3.361531	AATCT	3.90625	3.51525
cg1301955	HLA-B	GATA-2 ['	660	668	3.333333	GCTCTAT	0.30518	0.29349
cg2595453	HLA-B	GATA-2 ['	1899	1907	3.333333	GCTCTAT	0.30518	0.29349
cg2595453	HLA-B	c-Jun [T00	702	708	3.244843	AGAGTC.	0.24414	0.2435
cg1301955	HLA-B	AP-2alpha	916	921	3.229049	AGAGGC	0.48828	0.5124
cg1301955	HLA-B	AP-2alpha	1322	1327	3.229049	GCCTCT	0.48828	0.5124
cg1301955	HLA-B	RAR-beta	1876	1885	3.207598	AGGGTT'	0.12207	0.12558
cg1301955	HLA-B	RXR-alpha	1567	1573	3.170788	GGGTTT]	0.24414	0.24551
cg2595453	HLA-B	RXR-alpha	173	179	3.170788	AAAACC'	0.24414	0.24551
cg2595453	HLA-B	TCF-4E [T	722	728	3.151193	CTTTGCA	0.24414	0.23169
cg1301955	HLA-B	Pax-5 [T0(	86	92	3.075094	CTCGCC(	0.12207	0.13819
cg1301955	HLA-B	Pax-5 [T0(	1537	1543	3.075094	CTCGCC(	0.12207	0.13819
cg2595453	HLA-B	Pax-5 [T0(	1325	1331	3.075094	CTCGCC(	0.12207	0.13819
cg1301955	HLA-B	NF-Y [T0(	1107	1114	3.051543	TATCCA/	0.06104	0.05632

cg1301955	HLA-B	NF-Y [T0	1114	1121	3.051543	TACCCA	0.06104	0.05632
cg2595453	HLA-B	c-Jun [T00	668	674	3.049104	TGGGTC	0.24414	0.2435
cg2595453	HLA-B	USF1 [T0	673	682	3.033037	CACGTG	0.06294	0.06647
cg2595453	HLA-B	p53 [T006	801	807	3.028543	GGGCAC	0.48828	0.53227
cg1301955	HLA-B	C/EBPalp	1116	1122	2.981957	CCCAAT	0.48828	0.47526
cg1301955	HLA-B	C/EBPalp	1948	1954	2.981957	CCCAAT	0.48828	0.47526
cg1301955	HLA-B	c-Ets-2 [T	1636	1644	2.945838	TTCCTTT	0.06104	0.05567
cg1301955	HLA-B	STAT4 [T	579	584	2.941176	GGTTCC	2.92969	2.92382
cg1301955	HLA-B	STAT4 [T	630	635	2.941176	TGTTCC	2.92969	2.92382
cg1301955	HLA-B	STAT4 [T	1129	1134	2.941176	GGAAGT	2.92969	2.92382
cg1301955	HLA-B	STAT4 [T	1209	1214	2.941176	GGAATC	2.92969	2.92382
cg1301955	HLA-B	STAT4 [T	1430	1435	2.941176	GGAATC	2.92969	2.92382
cg1301955	HLA-B	STAT4 [T	1764	1769	2.941176	CTTTCC	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	131	136	2.941176	GGAACA	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	327	332	2.941176	GGAAAG	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	375	380	2.941176	CTTTCC	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	860	865	2.941176	GGAAAG	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	883	888	2.941176	GGAACA	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	938	943	2.941176	GGAATC	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	1001	1006	2.941176	GGTTCC	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	1818	1823	2.941176	GGTTCC	2.92969	2.92382
cg2595453	HLA-B	STAT4 [T	1869	1874	2.941176	TGTTCC	2.92969	2.92382
cg1301955	HLA-B	STAT1bet	1764	1773	2.898434	CTTTCCC	0.0515	0.04956
cg2595453	HLA-B	STAT1bet	323	332	2.898434	TCTGGG	0.0515	0.04956
cg2595453	HLA-B	p53 [T006	503	509	2.813291	GCTGCC	0.48828	0.53227
cg2595453	HLA-B	PR B [T00	283	289	2.80933	AACAAT	0.73242	0.66711
cg2595453	HLA-B	PR A [T01	283	289	2.80933	AACAAT	0.73242	0.66711
cg1301955	HLA-B	RXR-alph	356	362	2.726556	CCAACC	0.85449	0.89683
cg2595453	HLA-B	RXR-alph	1595	1601	2.726556	CCAACC	0.85449	0.89683
cg1301955	HLA-B	AP-2alpha	117	122	2.550491	GCCTCA	0.48828	0.51216
cg1301955	HLA-B	AP-2alpha	375	380	2.550491	GCCTCA	0.48828	0.51216
cg1301955	HLA-B	AP-2alpha	448	453	2.550491	GCCTCA	0.48828	0.51216
cg2595453	HLA-B	AP-2alpha	123	128	2.550491	TGAGGC	0.48828	0.51216
cg2595453	HLA-B	AP-2alpha	644	649	2.550491	GCCTCA	0.48828	0.51216
cg2595453	HLA-B	AP-2alpha	966	971	2.550491	TGAGGC	0.48828	0.51216
cg2595453	HLA-B	AP-2alpha	1356	1361	2.550491	GCCTCA	0.48828	0.51216
cg2595453	HLA-B	AP-2alpha	1614	1619	2.550491	GCCTCA	0.48828	0.51216
cg2595453	HLA-B	AP-2alpha	1687	1692	2.550491	GCCTCA	0.48828	0.51216
cg2595453	HLA-B	RXR-alph	807	813	2.544678	AGAACC	0.85449	0.89683
cg2595453	HLA-B	ENKTF-1	573	580	2.511511	CCTCGC	0.12207	0.13847
cg1301955	HLA-B	c-Jun [T00	1716	1722	2.345465	TGTGTC	0.48828	0.48077
cg1301955	HLA-B	GCF [T00	182	190	2.339499	GCGCAG	0.06104	0.06908
cg1301955	HLA-B	GCF [T00	520	528	2.339499	GACCTG	0.06104	0.06908
cg1301955	HLA-B	GCF [T00	876	884	2.339499	GTCCTG	0.06104	0.06908
cg2595453	HLA-B	GCF [T00	1421	1429	2.339499	GCGCAG	0.06104	0.06908
cg2595453	HLA-B	GCF [T00	1759	1767	2.339499	GACCTG	0.06104	0.06908
cg1301955	HLA-B	RXR-alph	428	434	2.322562	GGGTCT	0.85449	0.89683
cg2595453	HLA-B	RXR-alph	179	185	2.322562	CAGACC	0.85449	0.89683

cg2595453	HLA-B	RXR-alph	689	695	2.322562	GGGTCT	0.85449	0.89683
cg2595453	HLA-B	RXR-alph	1667	1673	2.322562	GGGTCT	0.85449	0.89683
cg1301955	HLA-B	T3R-beta1	1917	1925	2.240658	TCACCT	0.15259	0.15303
cg2595453	HLA-B	c-Ets-2 [T	1072	1080	2.217136	TTCCTC	0.16785	0.16456
cg1301955	HLA-B	Sp1 [T007	433	442	2.178662	TGGGCG	0.03624	0.04341
cg1301955	HLA-B	Sp1 [T007	840	849	2.178662	GACCCG	0.03624	0.04341
cg2595453	HLA-B	Sp1 [T007	1672	1681	2.178662	TGGGCG	0.03624	0.04341
cg1301955	HLA-B	GATA-1 [	664	669	2.176375	TATCCA	3.90625	3.79558
cg1301955	HLA-B	GATA-1 [	1107	1112	2.176375	TATCCA	3.90625	3.79558
cg1301955	HLA-B	GATA-1 [	1151	1156	2.176375	TATCCT	3.90625	3.79558
cg2595453	HLA-B	GATA-1 [	1903	1908	2.176375	TATCCA	3.90625	3.79558
cg1301955	HLA-B	NF-Y [T0	1092	1099	2.12821	ATTGGC	0.21362	0.20748
cg1301955	HLA-B	AP-2alpha	551	556	2.098119	GCCTCG	0.97656	1.07805
cg2595453	HLA-B	AP-2alpha	1790	1795	2.098119	GCCTCG	0.97656	1.07805
cg2595453	HLA-B	GATA-1 [	840	845	2.001358	GGGATA	3.90625	3.79558
cg2595453	HLA-B	PR B [T00	133	139	1.892895	AACACT	0.12207	0.1127
cg2595453	HLA-B	PR A [T01	133	139	1.892895	AACACT	0.12207	0.1127
cg1301955	HLA-B	AP-2alpha	129	134	1.871933	GCCTCC	0.97656	1.07805
cg1301955	HLA-B	AP-2alpha	247	252	1.871933	GGAGGC	0.97656	1.07805
cg1301955	HLA-B	AP-2alpha	455	460	1.871933	GGAGGC	0.97656	1.07805
cg1301955	HLA-B	AP-2alpha	1226	1231	1.871933	GCCTCC	0.97656	1.07805
cg1301955	HLA-B	AP-2alpha	1459	1464	1.871933	GCCTCC	0.97656	1.07805
cg2595453	HLA-B	AP-2alpha	1209	1214	1.871933	GGAGGC	0.97656	1.07805
cg2595453	HLA-B	AP-2alpha	1368	1373	1.871933	GCCTCC	0.97656	1.07805
cg2595453	HLA-B	AP-2alpha	1486	1491	1.871933	GGAGGC	0.97656	1.07805
cg2595453	HLA-B	AP-2alpha	1694	1699	1.871933	GGAGGC	0.97656	1.07805
cg1301955	HLA-B	TBP [T00	1861	1870	1.871542	TGAATA	0.18311	0.15671
cg1301955	HLA-B	NF-kappa	1207	1217	1.839527	GGGGAA	0.00572	0.00672
cg1301955	HLA-B	FOXP3 [T	562	567	1.824994	GTTGTA	0.48828	0.46414
cg1301955	HLA-B	TFII-I [T0	103	108	1.824994	CTCTCC	0.48828	0.51201
cg1301955	HLA-B	TFII-I [T0	1380	1385	1.824994	GGAGAG	0.48828	0.51201
cg1301955	HLA-B	TFII-I [T0	1475	1480	1.824994	CTCTCC	0.48828	0.51201
cg2595453	HLA-B	FOXP3 [T	1801	1806	1.824994	GTTGTA	0.48828	0.46414
cg2595453	HLA-B	TFII-I [T0	1342	1347	1.824994	CTCTCC	0.48828	0.51201
cg1301955	HLA-B	C/EBPalph	639	645	1.761449	CCCAAT	0.48828	0.46352
cg1301955	HLA-B	C/EBPalph	1666	1672	1.761449	CACAAT	0.48828	0.46352
cg2595453	HLA-B	C/EBPalph	1878	1884	1.761449	CCCAAT	0.48828	0.46352
cg1301955	HLA-B	PXR-1:RX	1989	1996	1.759733	TGAACT	0.06104	0.05771
cg2595453	HLA-B	PXR-1:RX	208	215	1.759733	TGAACT	0.06104	0.05771
cg1301955	HLA-B	RXR-alph	467	473	1.696452	CGGACC	0.48828	0.52093
cg2595453	HLA-B	RXR-alph	352	358	1.696452	CTGACC	0.48828	0.52093
cg2595453	HLA-B	RXR-alph	1706	1712	1.696452	CGGACC	0.48828	0.52093
cg1301955	HLA-B	GR-beta [	1694	1698	1.680765	GAATT	3.90625	3.70067
cg1301955	HLA-B	GR-beta [	1695	1699	1.680765	AATTC	3.90625	3.70067
cg1301955	HLA-B	GR-beta [	1728	1732	1.680765	GCATT	3.90625	3.70067
cg1301955	HLA-B	GR-beta [	1800	1804	1.680765	GCATT	3.90625	3.70067
cg1301955	HLA-B	GR-beta [	1951	1955	1.680765	AATGC	3.90625	3.70067
cg2595453	HLA-B	GR-beta [	286	290	1.680765	AATGC	3.90625	3.70067

cg2595453	HLA-B	GR-beta [T	712	716	1.680765	AATTC	3.90625	3.70067
cg2595453	HLA-B	c-Ets-2 [T	1192	1200	1.64415	TTCCTC	0.04578	0.04602
cg1301955	HLA-B	c-Ets-1 [T	1635	1641	1.641124	TTTCCT	0.36621	0.35197
cg1301955	HLA-B	C/EBPbeta	356	359	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	372	375	1.639871	TTGG	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	640	643	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1093	1096	1.639871	TTGG	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1110	1113	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1117	1120	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1178	1181	1.639871	TTGG	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1216	1219	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1318	1321	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1483	1486	1.639871	TTGG	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1673	1676	1.639871	TTGG	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1699	1702	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1949	1952	1.639871	CCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	568	571	1.639871	TTGG	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	684	687	1.639871	TTGG	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	858	861	1.639871	TTGG	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	950	953	1.639871	CCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	1006	1009	1.639871	CCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	1595	1598	1.639871	CCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	1611	1614	1.639871	TTGG	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	1879	1882	1.639871	CCAA	15.625	15.23827
cg1301955	HLA-B	IRF-1 [T0	1833	1841	1.616539	TTTCCC	0.04578	0.04268
cg1301955	HLA-B	XBP-1 [T	232	237	1.583727	GGTCAT	0.97656	0.94995
cg1301955	HLA-B	XBP-1 [T	1009	1014	1.583727	ATGACC	0.97656	0.94995
cg2595453	HLA-B	XBP-1 [T	251	256	1.583727	ATGACC	0.97656	0.94995
cg2595453	HLA-B	XBP-1 [T	393	398	1.583727	ATGACC	0.97656	0.94995
cg2595453	HLA-B	XBP-1 [T	1471	1476	1.583727	GGTCAT	0.97656	0.94995
cg1301955	HLA-B	TFIID [T0	1705	1711	1.537547	TGTAAA	0.73242	0.65627
cg1301955	HLA-B	Pax-5 [T0	304	310	1.537547	CTGGCC	0.73242	0.83087
cg1301955	HLA-B	Pax-5 [T0	341	347	1.537547	CCCGCC	0.73242	0.83087
cg1301955	HLA-B	Pax-5 [T0	346	352	1.537547	CCCGCC	0.73242	0.83087
cg1301955	HLA-B	Pax-5 [T0	434	440	1.537547	GGGCGG	0.73242	0.83087
cg1301955	HLA-B	Pax-5 [T0	842	848	1.537547	CCCGCC	0.73242	0.83087
cg1301955	HLA-B	Pax-5 [T0	965	971	1.537547	GGGCCA	0.73242	0.83087
cg2595453	HLA-B	Pax-5 [T0	1543	1549	1.537547	CTGGCC	0.73242	0.83087
cg2595453	HLA-B	Pax-5 [T0	1580	1586	1.537547	CCCGCC	0.73242	0.83087
cg2595453	HLA-B	Pax-5 [T0	1585	1591	1.537547	CCCGCC	0.73242	0.83087
cg2595453	HLA-B	Pax-5 [T0	1673	1679	1.537547	GGGCGG	0.73242	0.83087
cg1301955	HLA-B	NF-Y [T0	1672	1679	1.51343	ATTGGT	0.18311	0.17671
cg2595453	HLA-B	AR [T000	554	562	1.513096	TCAGTG	0.09155	0.09239
cg2595453	HLA-B	c-Ets-1 [T	988	994	1.513038	GAGGAA	0.36621	0.35197
cg2595453	HLA-B	c-Ets-1 [T	1071	1077	1.513038	TTTCCTC	0.36621	0.35197
cg2595453	HLA-B	c-Ets-1 [T	1123	1129	1.513038	GAGGAA	0.36621	0.35197
cg2595453	HLA-B	c-Ets-1 [T	1191	1197	1.513038	TTTCCTC	0.36621	0.35197
cg1301955	HLA-B	RXR-alph	1877	1883	1.474336	GGGTTT	0.48828	0.52093

cg1301955	HLA-B	STAT4 [T	1371	1376	1.470588	GGAAAC	1.95312	1.90161
cg1301955	HLA-B	STAT4 [T	1499	1504	1.470588	GGAAAC	1.95312	1.90161
cg1301955	HLA-B	STAT4 [T	1514	1519	1.470588	GGAACT	1.95312	1.90161
cg1301955	HLA-B	STAT4 [T	1634	1639	1.470588	GTTTCC	1.95312	1.90161
cg1301955	HLA-B	STAT4 [T	1695	1700	1.470588	AATTCC	1.95312	1.90161
cg1301955	HLA-B	STAT4 [T	1832	1837	1.470588	GTTTCC	1.95312	1.90161
cg1301955	HLA-B	STAT4 [T	1983	1988	1.470588	TTTTCC	1.95312	1.90161
cg2595453	HLA-B	STAT4 [T	990	995	1.470588	GGAAAA	1.95312	1.90161
cg2595453	HLA-B	STAT4 [T	1125	1130	1.470588	GGAAAC	1.95312	1.90161
cg2595453	HLA-B	STAT4 [T	1134	1139	1.470588	GGAAAA	1.95312	1.90161
cg2595453	HLA-B	STAT4 [T	1190	1195	1.470588	TTTTCC	1.95312	1.90161
cg1301955	HLA-B	c-Ets-1 [T	1984	1990	1.384951	TTTCCTC	0.36621	0.35197
cg2595453	HLA-B	c-Ets-1 [T	1132	1138	1.384951	CAGGAA	0.36621	0.35197
cg2595453	HLA-B	NF-AT1 [	859	868	1.378139	TGGAAA	0.01907	0.01758
cg1301955	HLA-B	C/EBPbeta	378	381	1.366559	TCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1519	1522	1.366559	TTGA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1720	1723	1.366559	TCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1745	1748	1.366559	TCAA	15.625	15.23827
cg1301955	HLA-B	C/EBPbeta	1922	1925	1.366559	TCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	11	14	1.366559	TCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	151	154	1.366559	TTGA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	1024	1027	1.366559	TCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	1157	1160	1.366559	TCAA	15.625	15.23827
cg2595453	HLA-B	C/EBPbeta	1617	1620	1.366559	TCAA	15.625	15.23827
cg1301955	HLA-B	AP-2alpha	1906	1911	1.357116	GCCTGT	0.48828	0.51319
cg1301955	HLA-B	AP-2alpha	1978	1983	1.357116	GCCTGT	0.48828	0.51319
cg1301955	HLA-B	IRF-1 [T0	1635	1643	1.274173	TTTCCTT	0.04578	0.04268
cg2595453	HLA-B	CREB [T0	1079	1087	1.217272	GAGACG	0.05341	0.05499
cg2595453	HLA-B	c-Ets-2 [T	985	993	1.071163	TGAGAG	0.06104	0.0583
cg2595453	HLA-B	c-Ets-2 [T	1120	1128	1.071163	TCAGAG	0.06104	0.0583
cg1301955	HLA-B	GCF [T00	25	33	1.070269	TACCAG	0.18311	0.21473
cg1301955	HLA-B	GCF [T00	140	148	1.070269	GCGCTG	0.18311	0.21473
cg2595453	HLA-B	GCF [T00	1264	1272	1.070269	TACCAG	0.18311	0.21473
cg2595453	HLA-B	GCF [T00	1379	1387	1.070269	GCGCTG	0.18311	0.21473
cg1301955	HLA-B	PXR-1:RX	1444	1451	0.941658	TGAACT	0.12207	0.11843
cg2595453	HLA-B	GATA-1 [	16	21	0.863549	GTGATA	1.95312	1.80234
cg2595453	HLA-B	RXR-alpha	1021	1027	0.848226	GGGTCA	0.48828	0.51313
cg1301955	HLA-B	GR-beta [	387	391	0.840383	AATGA	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	921	925	0.840383	CCATT	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1119	1123	0.840383	AATGG	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1232	1236	0.840383	CCATT	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1548	1552	0.840383	AATGG	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1686	1690	0.840383	AATGA	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1700	1704	0.840383	CAATT	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1734	1738	0.840383	CAATT	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1735	1739	0.840383	AATTA	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1808	1812	0.840383	AATTA	7.8125	7.2174
cg1301955	HLA-B	GR-beta [	1816	1820	0.840383	TCATT	7.8125	7.2174

cg2595453	HLA-B	GR-beta [T	32	36	0.840383	TCATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	121	125	0.840383	AATGA	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	773	777	0.840383	AATGG	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	855	859	0.840383	TCATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1068	1072	0.840383	CCATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1085	1089	0.840383	TCATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1093	1097	0.840383	TAATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1094	1098	0.840383	AATTG	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1146	1150	0.840383	CCATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1153	1157	0.840383	CCATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1187	1191	0.840383	CCATT	7.8125	7.2174
cg2595453	HLA-B	GR-beta [T	1626	1630	0.840383	AATGA	7.8125	7.2174
cg1301955	HLA-B	HNF-1A [	1649	1656	0.781639	GTTAAT	0.48828	0.45029
cg2595453	HLA-B	c-Fos [T00	703	712	0.768508	GAGTCA	0.00763	0.00741
cg1301955	HLA-B	AP-2alpha	1255	1260	0.678558	GCCTGA	0.48828	0.51196
cg1301955	HLA-B	AP-2alpha	1342	1347	0.678558	GCCTGA	0.48828	0.51196
cg2595453	HLA-B	AP-2alpha	715	720	0.678558	TCAGGC	0.48828	0.51196
cg2595453	HLA-B	AP-2alpha	766	771	0.678558	GCCTGA	0.48828	0.51196
cg2595453	HLA-B	AP-2alpha	982	987	0.678558	GCCTGA	0.48828	0.51196
cg2595453	HLA-B	c-Ets-2 [T	215	223	0.572986	TTCCTCC	0.00763	0.0074
cg2595453	HLA-B	AP-1 [T00	923	931	0.436196	TGACTC	0.09155	0.08806
cg1301955	HLA-B	GATA-1 [	1103	1108	0.280028	TAGATA	0.97656	0.8795
cg1301955	HLA-B	GATA-1 [	1811	1816	0.280028	TATCTT	0.97656	0.8795
cg1301955	HLA-B	AP-2alpha	406	411	0.226186	GCCTGG	0.97656	1.07867
cg1301955	HLA-B	AP-2alpha	608	613	0.226186	GCCTGG	0.97656	1.07867
cg1301955	HLA-B	AP-2alpha	817	822	0.226186	GCCTGG	0.97656	1.07867
cg1301955	HLA-B	AP-2alpha	1390	1395	0.226186	CCAGGC	0.97656	1.07867
cg2595453	HLA-B	AP-2alpha	81	86	0.226186	CCAGGC	0.97656	1.07867
cg2595453	HLA-B	AP-2alpha	273	278	0.226186	CCAGGC	0.97656	1.07867
cg2595453	HLA-B	AP-2alpha	822	827	0.226186	GCCTGG	0.97656	1.07867
cg2595453	HLA-B	AP-2alpha	1645	1650	0.226186	GCCTGG	0.97656	1.07867
cg2595453	HLA-B	AP-2alpha	1847	1852	0.226186	GCCTGG	0.97656	1.07867
cg1301955	HLA-B	GR-alpha [	684	688	0.207689	CCTCT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	916	920	0.207689	AGAGG	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1304	1308	0.207689	CCTCT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1323	1327	0.207689	CCTCT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1474	1478	0.207689	CCTCT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1479	1483	0.207689	CCTCT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1638	1642	0.207689	CCTTT	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	329	333	0.207689	AAAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	987	991	0.207689	AGAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	1026	1030	0.207689	AAAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	1109	1113	0.207689	AGAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	1122	1126	0.207689	AGAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	1197	1201	0.207689	CCTCT	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	1923	1927	0.207689	CCTCT	7.8125	7.79817
cg2595453	HLA-B	Elk-1 [T00	214	222	0.134348	CTTCCTC	0.06104	0.06399
cg2595453	HLA-B	c-Ets-1 [T	214	220	0.128087	CTTCCTC	0.24414	0.24982

cg2595453	HLA-B	GATA-1 [	388	393	0.105011	GAGATA	0.97656	0.92541
cg2595453	HLA-B	GATA-1 [	470	475	0.105011	TATCTC	0.97656	0.92541
cg2595453	HLA-B	GATA-1 [	525	530	0.105011	TATCTC	0.97656	0.92541
cg1301955	HLA-B	GR-beta [	1701	1705	0	AATTT	3.90625	3.51525
cg1301955	HLA-B	GR-beta [	1807	1811	0	AAATT	3.90625	3.51525
cg1301955	HLA-B	XBP-1 [T	1912	1917	0	AGTCAT	0.97656	0.94838
cg1301955	HLA-B	TFIID [T	1803	1809	0	TTTAAA	1.09863	0.95175
cg1301955	HLA-B	GR-alpha [	1436	1440	0	CCTGT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1563	1567	0	ACAGG	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1612	1616	0	ATAGG	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1714	1718	0	CCTGT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1837	1841	0	CCTGT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1907	1911	0	CCTGT	7.8125	7.79817
cg1301955	HLA-B	GR-alpha [	1979	1983	0	CCTGT	7.8125	7.79817
cg1301955	HLA-B	FOXP3 [T	1794	1799	0	GTTGTT	1.46484	1.44953
cg1301955	HLA-B	C/EBPbeta	42	45	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	138	141	0	TTGC	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	213	216	0	TTGC	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	563	566	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	617	620	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1173	1176	0	ACAA	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1235	1238	0	TTGC	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1328	1331	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1355	1358	0	ACAA	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1491	1494	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1643	1646	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1647	1650	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1667	1670	0	ACAA	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1704	1707	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1733	1736	0	ACAA	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1795	1798	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1798	1801	0	TTGC	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1881	1884	0	TTGT	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1894	1897	0	TTGC	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1896	1899	0	GCAA	15.625	15.26275
cg1301955	HLA-B	C/EBPbeta	1928	1931	0	TTGC	15.625	15.26275
cg1301955	HLA-B	YY1 [T00	508	511	0	ATGG	7.8125	7.79459
cg1301955	HLA-B	YY1 [T00	806	809	0	ATGG	7.8125	7.79459
cg1301955	HLA-B	YY1 [T00	921	924	0	CCAT	7.8125	7.79459
cg1301955	HLA-B	YY1 [T00	1007	1010	0	CCAT	7.8125	7.79459
cg1301955	HLA-B	YY1 [T00	1120	1123	0	ATGG	7.8125	7.79459
cg1301955	HLA-B	YY1 [T00	1232	1235	0	CCAT	7.8125	7.79459
cg1301955	HLA-B	YY1 [T00	1549	1552	0	ATGG	7.8125	7.79459
cg1301955	HLA-B	YY1 [T00	1939	1942	0	CCAT	7.8125	7.79459
cg1301955	HLA-B	TFII-I [T0	663	668	0	CTATCC	1.46484	1.48598
cg1301955	HLA-B	TFII-I [T0	1437	1442	0	CTGTCC	1.46484	1.48598
cg1301955	HLA-B	TFII-I [T0	1764	1769	0	CTTTCC	1.46484	1.48598
cg1301955	HLA-B	STAT4 [T	923	928	0	ATTTCC	0.48828	0.46235

cg1301955	HLA-B	ER-alpha [	232	236	0	GGTCA	1.95312	1.99744
cg1301955	HLA-B	ER-alpha [	320	324	0	GGTCA	1.95312	1.99744
cg1301955	HLA-B	ER-alpha [	519	523	0	TGACC	1.95312	1.99744
cg1301955	HLA-B	ER-alpha [	539	543	0	GGTCA	1.95312	1.99744
cg1301955	HLA-B	ER-alpha [	597	601	0	GGTCA	1.95312	1.99744
cg1301955	HLA-B	ER-alpha [	960	964	0	GGTCA	1.95312	1.99744
cg1301955	HLA-B	ER-alpha [	1010	1014	0	TGACC	1.95312	1.99744
cg1301955	HLA-B	GR [T050	1639	1645	0	CTTTTTG	0.36621	0.33174
cg1301955	HLA-B	GATA-1 [	63	68	0	TATCTG	0.97656	0.92541
cg1301955	HLA-B	CTF [T001	1088	1099	0	GCTGAT	0.00095	0.00098
cg1301955	HLA-B	Pax-5 [T0	235	241	0	CATGCC	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	259	265	0	CCGGCC	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	310	316	0	CCGGCC	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	336	342	0	CGAGCC	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	532	538	0	GGGCCG	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	648	654	0	CCGGCC	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	775	781	0	GGGCCG	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	946	952	0	CCGGCC	1.09863	1.24633
cg1301955	HLA-B	Pax-5 [T0	1401	1407	0	CCAGCC	1.09863	1.24633
cg1301955	HLA-B	p53 [T006	235	241	0	CATGCC	0.36621	0.40082
cg1301955	HLA-B	AP-2alpha	585	590	0	GCAGGC	0.97656	1.07867
cg1301955	HLA-B	AP-2alpha	889	894	0	GCCTGC	0.97656	1.07867
cg1301955	HLA-B	WT1 [T00	882	890	0	CGCCCC	0.00763	0.00958
cg1301955	HLA-B	GCF [T00	857	865	0	TCCCGG	0.09155	0.10999
cg1301955	HLA-B	Sp1 [T007	339	348	0	GCCCCG	0.00191	0.00246
cg1301955	HLA-B	Sp1 [T007	344	353	0	GCCCCG	0.00191	0.00246
cg1301955	HLA-B	IRF-2 [T0	1188	1193	0	AAGTGA	0.48828	0.46235
cg1301955	HLA-B	IRF-2 [T0	1416	1421	0	TCACTT	0.48828	0.46235
cg2595453	HLA-B	GR-beta [	711	715	0	AAATT	3.90625	3.51525
cg2595453	HLA-B	GR-beta [	1170	1174	0	ACATT	3.90625	3.51525
cg2595453	HLA-B	XBP-1 [T0	1083	1088	0	CGTCAT	0.97656	0.94838
cg2595453	HLA-B	c-Jun [T00	923	929	0	TGACTC	0.12207	0.11843
cg2595453	HLA-B	GR-alpha [	73	77	0	ACAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	97	101	0	CCTGT	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	778	782	0	ACAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	850	854	0	CCTAT	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	886	890	0	ACAGG	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	1227	1231	0	CCTAT	7.8125	7.79817
cg2595453	HLA-B	GR-alpha [	1230	1234	0	ATAGG	7.8125	7.79817
cg2595453	HLA-B	FOXP3 [T	3	8	0	CACAAC	1.46484	1.44953
cg2595453	HLA-B	FOXP3 [T	256	261	0	CACAAC	1.46484	1.44953
cg2595453	HLA-B	C/EBPbeta	4	7	0	ACAA	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	35	38	0	TTGT	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	51	54	0	ACAA	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	168	171	0	ACAA	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	257	260	0	ACAA	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	281	284	0	GCAA	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	284	287	0	ACAA	15.625	15.26275

cg2595453	HLA-B	C/EBPbeta	548	551	0	ACAA	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	724	727	0	TTGC	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	977	980	0	ACAA	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	1096	1099	0	TTGT	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	1281	1284	0	TTGT	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	1377	1380	0	TTGC	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	1452	1455	0	TTGC	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	1802	1805	0	TTGT	15.625	15.26275
cg2595453	HLA-B	C/EBPbeta	1856	1859	0	TTGT	15.625	15.26275
cg2595453	HLA-B	YY1 [T00	8	11	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	25	28	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	296	299	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	418	421	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	460	463	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	578	581	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	649	652	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	659	662	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	696	699	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	735	738	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	755	758	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	774	777	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	1068	1071	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	1146	1149	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	1153	1156	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	1187	1190	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	1214	1217	0	CCAT	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	1237	1240	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	YY1 [T00	1747	1750	0	ATGG	7.8125	7.79459
cg2595453	HLA-B	TFII-I [T0	267	272	0	GGACAG	1.46484	1.48598
cg2595453	HLA-B	TFII-I [T0	327	332	0	GGAAAG	1.46484	1.48598
cg2595453	HLA-B	TFII-I [T0	375	380	0	CTTTCC	1.46484	1.48598
cg2595453	HLA-B	TFII-I [T0	776	781	0	GGACAG	1.46484	1.48598
cg2595453	HLA-B	TFII-I [T0	860	865	0	GGAAAG	1.46484	1.48598
cg2595453	HLA-B	TFII-I [T0	1902	1907	0	CTATCC	1.46484	1.48598
cg2595453	HLA-B	STAT4 [T	1070	1075	0	ATTTCC	0.48828	0.46235
cg2595453	HLA-B	ER-alpha [	252	256	0	TGACC	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	353	357	0	TGACC	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	394	398	0	TGACC	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	592	596	0	GGTCA	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	651	655	0	GGTCA	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	670	674	0	GGTCA	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	760	764	0	TGACC	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	1022	1026	0	GGTCA	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	1471	1475	0	GGTCA	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	1559	1563	0	GGTCA	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	1758	1762	0	TGACC	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	1778	1782	0	GGTCA	1.95312	1.99744
cg2595453	HLA-B	ER-alpha [	1836	1840	0	GGTCA	1.95312	1.99744

cg2595453	HLA-B	c-Myc [T0	673	678	0	CACGTG	0.48828	0.51196
cg2595453	HLA-B	GATA-1 [	1302	1307	0	TATCTG	0.97656	0.92541
cg2595453	HLA-B	Pax-5 [T0	147	153	0	GGGCTT	1.09863	1.24633
cg2595453	HLA-B	Pax-5 [T0	1474	1480	0	CATGCC	1.09863	1.24633
cg2595453	HLA-B	Pax-5 [T0	1498	1504	0	CCGGCC	1.09863	1.24633
cg2595453	HLA-B	Pax-5 [T0	1549	1555	0	CCGGCC	1.09863	1.24633
cg2595453	HLA-B	Pax-5 [T0	1575	1581	0	CGAGCC	1.09863	1.24633
cg2595453	HLA-B	Pax-5 [T0	1771	1777	0	GGGCCG	1.09863	1.24633
cg2595453	HLA-B	Pax-5 [T0	1887	1893	0	CCGGCC	1.09863	1.24633
cg2595453	HLA-B	p53 [T006	1474	1480	0	CATGCC	0.36621	0.40082
cg2595453	HLA-B	AP-2alpha	830	835	0	GCAGGC	0.97656	1.07867
cg2595453	HLA-B	AP-2alpha	1824	1829	0	GCAGGC	0.97656	1.07867
cg2595453	HLA-B	Sp1 [T007	1578	1587	0	GCCCCG	0.00191	0.00246
cg2595453	HLA-B	Sp1 [T007	1583	1592	0	GCCCCG	0.00191	0.00246
cg2595453	HLA-B	IRF-2 [T01	920	925	0	AAGTGA	0.48828	0.46235
cg1120165	HLA-F	c-Myb [T0	944	951	9.815171	ACAAGT	0.36621	0.3712
cg1120165	HLA-F	XBP-1 [T	445	450	9.789909	ATGGCG	1.95312	1.95208
cg1120165	HLA-F	XBP-1 [T	1140	1145	9.789909	AGACAT	1.95312	1.95208
cg1120165	HLA-F	XBP-1 [T	1475	1480	9.789909	ATGGCG	1.95312	1.95208
cg1120165	HLA-F	RBP-Jkap	1405	1416	9.774182	AGTTCC	0.02193	0.02195
cg1120165	HLA-F	NF-1 [T00	959	966	9.761671	GGCACC	0.24414	0.24405
cg1120165	HLA-F	PR B [T00	354	360	9.743489	AACACG	1.09863	1.10292
cg1120165	HLA-F	PR A [T01	354	360	9.743489	AACACG	1.09863	1.10292
cg1120165	HLA-F	c-Jun [T00	1962	1968	9.717135	CAGGTC	0.73242	0.73031
cg1120165	HLA-F	c-Ets-1 [T	1270	1276	9.713162	ATTCCC	0.36621	0.36441
cg1120165	HLA-F	RAR-beta	1245	1254	9.641259	GGGGTT	0.21362	0.21243
cg1120165	HLA-F	RAR-beta	1301	1310	9.641259	TCCCAA	0.21362	0.21243
cg1120165	HLA-F	Pax-5 [T0	222	228	9.552105	GGGCCA	1.46484	1.43083
cg1120165	HLA-F	Pax-5 [T0	508	514	9.552105	GGGCGG	1.46484	1.43083
cg1120165	HLA-F	Pax-5 [T0	1185	1191	9.552105	GGGCAA	1.46484	1.43083
cg1120165	HLA-F	Pax-5 [T0	1366	1372	9.552105	GGGCGT	1.46484	1.43083
cg1120165	HLA-F	Pax-5 [T0	1477	1483	9.552105	GGCGCC	1.46484	1.43083
cg1120165	HLA-F	Pax-5 [T0	1601	1607	9.552105	GGGCGC	1.46484	1.43083
cg1120165	HLA-F	Pax-5 [T0	1893	1899	9.552105	GTGGCC	1.46484	1.43083
cg1120165	HLA-F	Pax-5 [T0	1957	1963	9.552105	GGGCGC	1.46484	1.43083
cg1120165	HLA-F	TFIID [T0	151	157	9.552105	TGGGAA	1.46484	1.48472
cg1120165	HLA-F	TFIID [T0	298	304	9.552105	TTTGGG	1.46484	1.48472
cg1120165	HLA-F	TFIID [T0	987	993	9.552105	TTCCAA	1.46484	1.48472
cg1120165	HLA-F	TFIID [T0	1053	1059	9.552105	TTTCGG	1.46484	1.48472
cg1120165	HLA-F	TFIID [T0	1111	1117	9.552105	TTTCTCA	1.46484	1.48472
cg1120165	HLA-F	TFIID [T0	1351	1357	9.552105	TTTCTCA	1.46484	1.48472
cg1120165	HLA-F	TFIID [T0	1450	1456	9.552105	TTTCCCA	1.46484	1.48472
cg1120165	HLA-F	NF-1 [T00	259	266	9.535536	TTGGTC	0.73242	0.73053
cg1120165	HLA-F	NF-1 [T00	1364	1371	9.535536	TTGGGC	0.73242	0.73053
cg1120165	HLA-F	NF-1 [T00	972	979	9.513281	TTGGGG	0.73242	0.73053
cg1120165	HLA-F	NF-1 [T00	1863	1870	9.513281	TACGCC	0.73242	0.73053
cg1120165	HLA-F	TFII-I [T0	343	348	9.512894	CCATCC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	686	691	9.512894	TTTTCC	7.32422	7.29728

cg1120165	HLA-F	TFII-I [T0	942	947	9.512894	GGACAA	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1050	1055	9.512894	GGATTT	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1190	1195	9.512894	AAGTCC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1269	1274	9.512894	AATTCC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1329	1334	9.512894	GGATAC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1420	1425	9.512894	AAGTCC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1449	1454	9.512894	TTTTCC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1762	1767	9.512894	AATTCC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1798	1803	9.512894	GGATGG	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1979	1984	9.512894	CCATCC	7.32422	7.29728
cg1120165	HLA-F	TFII-I [T0	1990	1995	9.512894	GGACCG	7.32422	7.29728
cg1120165	HLA-F	FOXP3 [T	1248	1253	9.512894	GTTGGG	7.32422	7.35678
cg1120165	HLA-F	FOXP3 [T	1302	1307	9.512894	CCCAAC	7.32422	7.35678
cg1120165	HLA-F	FOXP3 [T	1336	1341	9.512894	CATAAC	7.32422	7.35678
cg1120165	HLA-F	FOXP3 [T	1466	1471	9.512894	GTTGGG	7.32422	7.35678
cg1120165	HLA-F	FOXP3 [T	1872	1877	9.512894	GCCAAC	7.32422	7.35678
cg1120165	HLA-F	TCF-4E [T	53	59	9.453578	CTTTGT	0.48828	0.49215
cg1120165	HLA-F	c-Jun [T00	59	65	9.397655	ATTGTC	0.73242	0.73031
cg1120165	HLA-F	NFI/CTF [	1867	1874	9.352332	CCAAGG	0.54932	0.54821
cg1120165	HLA-F	c-Ets-1 [T	1406	1412	9.276861	GTTCCC	0.36621	0.36441
cg1120165	HLA-F	E2F-1 [T0	1912	1919	9.261732	TCCGCC	0.15259	0.14917
cg1120165	HLA-F	MEF-2A [	1446	1456	9.220261	TATTTTT	0.07343	0.07563
cg1120165	HLA-F	RAR-alpha	1469	1481	9.192562	GGGGTC	0.02065	0.02038
cg1120165	HLA-F	E2F [T002	1862	1871	9.126435	GTACGC	0.09537	0.09482
cg1120165	HLA-F	c-Ets-1 [T	101	107	9.065503	ATGGAA	0.85449	0.85523
cg1120165	HLA-F	c-Ets-1 [T	1014	1020	9.065503	ATGGAA	0.85449	0.85523
cg1120165	HLA-F	AhR [T01	444	454	9.058053	AATGGC	0.03242	0.03229
cg1120165	HLA-F	E2F-1 [T0	711	718	9.028527	GCGGGG	0.27466	0.26875
cg1120165	HLA-F	E2F-1 [T0	1717	1724	9.028527	GCGGGG	0.27466	0.26875
cg1120165	HLA-F	LEF-1 [T0	297	304	8.973041	CTTTGG	0.54932	0.55326
cg1120165	HLA-F	c-Ets-2 [T	1324	1332	8.912323	TTCCTG	0.27466	0.27495
cg1120165	HLA-F	p53 [T006	1197	1203	8.912104	AGGGCC	0.12207	0.11837
cg1120165	HLA-F	p53 [T006	1509	1515	8.912104	GGGCCC	0.12207	0.11837
cg1120165	HLA-F	HNF-4alph	1188	1200	8.87767	CAAAGT	0.01502	0.01524
cg1120165	HLA-F	NFI/CTF [	989	996	8.814757	CCAAAA	0.48828	0.48804
cg1120165	HLA-F	NF-1 [T00	299	306	8.790071	TTGGGA	0.24414	0.24467
cg1120165	HLA-F	NF-1 [T00	1249	1256	8.790071	TTGGGA	0.24414	0.24467
cg1120165	HLA-F	NF-1 [T00	1299	1306	8.790071	TCTCCC	0.24414	0.24467
cg1120165	HLA-F	E2F-1 [T0	1909	1916	8.76494	TGCTCC	0.27466	0.26875
cg1120165	HLA-F	LEF-1 [T0	53	60	8.759086	CTTTGT	0.54932	0.55326
cg1120165	HLA-F	XBP-1 [T	275	280	8.75604	GCTCAT	2.92969	2.9674
cg1120165	HLA-F	XBP-1 [T	665	670	8.75604	TTTCAT	2.92969	2.9674
cg1120165	HLA-F	XBP-1 [T	948	953	8.75604	GTTCAT	2.92969	2.9674
cg1120165	HLA-F	STAT1bet	729	738	8.695301	AGGAGG	0.22316	0.22446
cg1120165	HLA-F	LEF-1 [T0	223	230	8.575454	GGCCAA	0.15259	0.15214
cg1120165	HLA-F	c-Myb [T0	186	193	8.443873	CAACTG	0.30518	0.30924
cg1120165	HLA-F	c-Myb [T0	647	654	8.412632	AAACTG	0.30518	0.30924
cg1120165	HLA-F	LEF-1 [T0	1185	1192	8.361499	GGGCAA	0.15259	0.15214

cg1120165	HLA-F	c-Ets-2 [T	1764	1772	8.339336	TTCCTG	0.13733	0.13681
cg1120165	HLA-F	E2F-1 [T0	1535	1542	8.336446	GCGGGT	0.15259	0.14963
cg1120165	HLA-F	AR [T000	942	950	8.330815	GGACAA	0.10681	0.10625
cg1120165	HLA-F	GR-alpha [	108	112	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	218	222	8.281568	CAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	302	306	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	308	312	8.281568	CGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	315	319	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	324	328	8.281568	CGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	427	431	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	703	707	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	715	719	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	724	728	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	727	731	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	730	734	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	738	742	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	741	745	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	747	751	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	753	757	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	759	763	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	765	769	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	930	934	8.281568	CCTTC	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	970	974	8.281568	CCTTG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1022	1026	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1040	1044	8.281568	CAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1069	1073	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1095	1099	8.281568	GAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1164	1168	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1170	1174	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1176	1180	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1182	1186	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1217	1221	8.281568	CAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1232	1236	8.281568	CGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1252	1256	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1319	1323	8.281568	CCTTC	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1462	1466	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1489	1493	8.281568	CCTCC	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1492	1496	8.281568	CCTCC	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1575	1579	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1623	1627	8.281568	CCTCC	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1628	1632	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1631	1635	8.281568	GGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1654	1658	8.281568	CCTCC	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1657	1661	8.281568	CCTCG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1678	1682	8.281568	CCTTG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1795	1799	8.281568	CGAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1868	1872	8.281568	CAAGG	7.8125	7.72956
cg1120165	HLA-F	GR-alpha [	1931	1935	8.281568	CGAGG	7.8125	7.72956

cg1120165	HLA-F	c-Jun [T00	325	331	8.242207	GAGGTC	0.48828	0.49076
cg1120165	HLA-F	NFI/CTF [	1303	1310	8.241664	CCAACC	0.18311	0.1823
cg1120165	HLA-F	p53 [T006	1198	1204	8.208781	GGGCCC	0.48828	0.47377
cg1120165	HLA-F	p53 [T006	1508	1514	8.208781	GGGGCC	0.48828	0.47377
cg1120165	HLA-F	p53 [T006	1585	1591	8.208781	GGGGCC	0.48828	0.47377
cg1120165	HLA-F	ENKTF-1	398	405	8.19852	TGGCGG	0.73242	0.71737
cg1120165	HLA-F	ENKTF-1	1639	1646	8.19852	TGGCGG	0.73242	0.71737
cg1120165	HLA-F	NF-1 [T00	1869	1876	8.191058	AAGGCC	0.24414	0.24409
cg1120165	HLA-F	GR-alpha [	20	24	8.073878	CCTGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	74	78	8.073878	CCTGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	347	351	8.073878	CCTGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	505	509	8.073878	CCTGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	721	725	8.073878	GCAGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1008	1012	8.073878	CCAGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1106	1110	8.073878	CCTGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1156	1160	8.073878	CCTGC	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1195	1199	8.073878	CCAGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1203	1207	8.073878	CCAGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1326	1330	8.073878	CCTGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1410	1414	8.073878	CCAGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1495	1499	8.073878	CCTGC	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1513	1517	8.073878	CCTGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1605	1609	8.073878	GCAGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1665	1669	8.073878	CCAGG	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1766	1770	8.073878	CCTGC	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1907	1911	8.073878	CCTGC	7.8125	7.72238
cg1120165	HLA-F	GR-alpha [	1961	1965	8.073878	GCAGG	7.8125	7.72238
cg1120165	HLA-F	Pax-5 [T0	402	408	8.014558	GGGCAT	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1115	1121	8.014558	TCAGCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1198	1204	8.014558	GGGCCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1220	1226	8.014558	GGGCTC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1342	1348	8.014558	GCGGCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1508	1514	8.014558	GGGGCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1585	1591	8.014558	GGGGCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1648	1654	8.014558	TCAGCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1706	1712	8.014558	GCGGCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1721	1727	8.014558	GGAGCC	2.19727	2.14502
cg1120165	HLA-F	Pax-5 [T0	1833	1839	8.014558	GGGCCG	2.19727	2.14502
cg1120165	HLA-F	TFIID [T0	529	535	8.014558	TCTCAA	2.19727	2.24348
cg1120165	HLA-F	TFIID [T0	665	671	8.014558	TTTCAT	2.19727	2.24348
cg1120165	HLA-F	CTF [T001	9	20	7.899258	ATGTAT	0.02003	0.0203
cg1120165	HLA-F	POU2F2 (	188	198	7.84518	ACTGTA	0.01717	0.0176
cg1120165	HLA-F	c-Ets-2 [T	252	260	7.84116	TTCCTG	0.32043	0.32298
cg1120165	HLA-F	p53 [T006	1721	1727	7.833758	GGAGCC	0.48828	0.47377
cg1120165	HLA-F	T3R-beta1	1534	1542	7.813363	GGCGGG	0.27466	0.27236
cg1120165	HLA-F	EBF [T05	90	100	7.780217	AACTCA	0.04196	0.04106
cg1120165	HLA-F	NF-AT1 [	153	161	7.744746	GGAAAG	0.19836	0.19941
cg1120165	HLA-F	IRF-1 [T0	687	695	7.732782	TTTCCA	0.14496	0.14449

cg1120165	HLA-F	c-Ets-1 [T	1055	1061	7.642098	TCGGAA	0.48828	0.4878
cg1120165	HLA-F	c-Ets-1 [T	1791	1797	7.642098	ATTCCG	0.48828	0.4878
cg1120165	HLA-F	PPAR-alp	1190	1200	7.529496	AAGTCC	0.04482	0.04393
cg1120165	HLA-F	GR [T050	990	996	7.527031	CAAAAG	1.83105	1.86007
cg1120165	HLA-F	c-Jun [T00	1521	1527	7.491008	TGACCG	0.48828	0.48775
cg1120165	HLA-F	c-Jun [T00	1886	1892	7.491008	TGACCG	0.48828	0.48775
cg1120165	HLA-F	p53 [T006	96	102	7.47855	GGGCTA	0.73242	0.7186
cg1120165	HLA-F	p53 [T006	1477	1483	7.458735	GGCGCC	0.73242	0.7186
cg1120165	HLA-F	c-Myb [T0	1029	1036	7.442719	GAAAGT	0.42725	0.43114
cg1120165	HLA-F	PEA3 [T0	341	349	7.421728	GACCAT	0.34332	0.34161
cg1120165	HLA-F	c-Ets-1 [T	151	157	7.199436	TGGGAA	0.73242	0.73099
cg1120165	HLA-F	c-Ets-1 [T	1450	1456	7.199436	TTTCCC	0.73242	0.73099
cg1120165	HLA-F	XBP-1 [T	5	10	7.172312	ATGAAT	2.92969	2.97018
cg1120165	HLA-F	XBP-1 [T	106	111	7.172312	ATGAAG	2.92969	2.97018
cg1120165	HLA-F	XBP-1 [T	931	936	7.172312	CTTCAT	2.92969	2.97018
cg1120165	HLA-F	XBP-1 [T	1060	1065	7.172312	ATGAAT	2.92969	2.97018
cg1120165	HLA-F	XBP-1 [T	1067	1072	7.172312	ATGAAG	2.92969	2.97018
cg1120165	HLA-F	XBP-1 [T	1333	1338	7.172312	ACTCAT	2.92969	2.97018
cg1120165	HLA-F	XBP-1 [T	1441	1446	7.172312	ACTCAT	2.92969	2.97018
cg1120165	HLA-F	p53 [T006	1893	1899	7.150251	GTGGCC	1.09863	1.07125
cg1120165	HLA-F	NFI/CTF [	1245	1252	7.014249	GGGGTT	0.73242	0.73214
cg1120165	HLA-F	NFI/CTF [	1463	1470	7.014249	GAGGTT	0.73242	0.73214
cg1120165	HLA-F	C/EBPalp	951	957	7.00174	CATTGT	0.73242	0.74337
cg1120165	HLA-F	HNF-3alp	378	385	7.000129	AAAAAA	0.82397	0.84946
cg1120165	HLA-F	HNF-3alp	980	987	7.000129	AATTTC	0.82397	0.84946
cg1120165	HLA-F	HNF-3alp	1446	1453	7.000129	TATTTTT	0.82397	0.84946
cg1120165	HLA-F	IRF-1 [T0	149	157	6.968314	TCTGGG	0.1297	0.13036
cg1120165	HLA-F	IRF-1 [T0	1450	1458	6.968314	TTTCCC	0.1297	0.13036
cg1120165	HLA-F	RXR-alph	1971	1977	6.967687	ACCACC	0.36621	0.36214
cg1120165	HLA-F	NF-1 [T00	14	21	6.948522	TTGGCT	0.48828	0.4856
cg1120165	HLA-F	ENKTF-1	446	453	6.942764	TGGCGT	1.46484	1.44228
cg1120165	HLA-F	ENKTF-1	486	493	6.942764	TCGCGC	1.46484	1.44228
cg1120165	HLA-F	ENKTF-1	1476	1483	6.942764	TGGCGC	1.46484	1.44228
cg1120165	HLA-F	ENKTF-1	1981	1988	6.942764	ATCCGC	1.46484	1.44228
cg1120165	HLA-F	p53 [T006	1342	1348	6.938545	GCGGCC	1.09863	1.07125
cg1120165	HLA-F	p53 [T006	1706	1712	6.938545	GCGGCC	1.09863	1.07125
cg1120165	HLA-F	p53 [T006	1833	1839	6.938545	GGGCCG	1.09863	1.07125
cg1120165	HLA-F	AhR:Arnt	388	397	6.928166	CCGGGC	0.0515	0.04974
cg1120165	HLA-F	p53 [T006	1992	1998	6.891821	ACCGCC	1.09863	1.07125
cg1120165	HLA-F	PEA3 [T0	1797	1805	6.824411	AGGATG	0.22888	0.22933
cg1120165	HLA-F	NFI/CTF [	255	262	6.786076	CTGATT	0.73242	0.73214
cg1120165	HLA-F	NFI/CTF [	1388	1395	6.786076	CCAATC	0.73242	0.73214
cg1120165	HLA-F	p53 [T006	1220	1226	6.778774	GGGCTC	1.09863	1.07125
cg1120165	HLA-F	c-Ets-2 [T	576	584	6.769996	TTCCTG	0.03052	0.03102
cg1120165	HLA-F	NF-1 [T00	1531	1538	6.722386	TTGGGC	0.24414	0.24147
cg1120165	HLA-F	T3R-beta1	972	980	6.683388	TTGGGG	0.21362	0.21147
cg1120165	HLA-F	TFII-I [T0	66	71	6.581441	GGAGAT	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	332	337	6.581441	GGAGAT	0.97656	0.97366

cg1120165	HLA-F	TFII-I [T0	497	502	6.581441	CACTCC	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	1073	1078	6.581441	GGAGAT	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	1206	1211	6.581441	GGAGTG	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	1277	1282	6.581441	ATCTCC	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	1356	1361	6.581441	CACTCC	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	1578	1583	6.581441	GGAGTG	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	1674	1679	6.581441	CACTCC	0.97656	0.97366
cg1120165	HLA-F	TFII-I [T0	1847	1852	6.581441	GGAGTG	0.97656	0.97366
cg1120165	HLA-F	XBP-1 [T	402	407	6.478682	GGGCAT	0.97656	0.97062
cg1120165	HLA-F	c-Jun [T00	1309	1315	6.475265	CGTGTC	0.61035	0.60769
cg1120165	HLA-F	c-Fos [T00	132	141	6.448203	GAGTCA	0.04578	0.04589
cg1120165	HLA-F	RAR-beta	360	369	6.415195	GTGAAA	0.18311	0.183
cg1120165	HLA-F	p53 [T006	1601	1607	6.403751	GGGCGC	0.48828	0.47541
cg1120165	HLA-F	p53 [T006	1957	1963	6.403751	GGGCGC	0.48828	0.47541
cg1120165	HLA-F	TCF-4E [T	1186	1192	6.302385	GGCAAA	0.61035	0.61344
cg1120165	HLA-F	GR-alpha [	1582	1586	6.263098	TGAGG	3.90625	3.91061
cg1120165	HLA-F	GR-alpha [	1681	1685	6.263098	TGAGG	3.90625	3.91061
cg1120165	HLA-F	GR-alpha [	1900	1904	6.263098	TGAGG	3.90625	3.91061
cg1120165	HLA-F	C/EBPalph	26	32	6.245236	TGCAAT	0.97656	0.99
cg1120165	HLA-F	IRF-1 [T0	729	737	6.24301	AGGAGG	0.16785	0.16909
cg1120165	HLA-F	p53 [T006	508	514	6.188498	GGGCGG	0.61035	0.594
cg1120165	HLA-F	p53 [T006	1366	1372	6.188498	GGGCGT	0.61035	0.594
cg1120165	HLA-F	NF-AT2 [T	1445	1454	6.184331	ATATTT	0.04196	0.04255
cg1120165	HLA-F	PPAR-alph	1080	1090	6.14093	GACTGG	0.02003	0.01956
cg1120165	HLA-F	AR [T000	67	75	6.112954	GAGATG	0.24414	0.24229
cg1120165	HLA-F	p53 [T006	222	228	6.095267	GGGCCA	0.61035	0.594
cg1120165	HLA-F	GR-alpha [	63	67	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	93	97	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	165	169	6.055408	TTAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	254	258	6.055408	CCTGA	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	329	333	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	578	582	6.055408	CCTGA	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	587	591	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	675	679	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	939	943	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	1134	1138	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	1224	1228	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	1313	1317	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	1505	1509	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	1519	1523	6.055408	CCTGA	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	1612	1616	6.055408	TCAGG	3.90625	3.9065
cg1120165	HLA-F	GR-alpha [	1898	1902	6.055408	CCTGA	3.90625	3.9065
cg1120165	HLA-F	c-Myb [T0	916	923	6.04018	AAACTG	0.21362	0.21535
cg1120165	HLA-F	c-Ets-1 [T	687	693	6.039428	TTTCCAC	0.36621	0.36731
cg1120165	HLA-F	GCF [T00	267	275	5.917256	GCGCGG	0.64087	0.6219
cg1120165	HLA-F	EBF [T05	1502	1512	5.888853	CTCTCAC	0.00381	0.00372
cg1120165	HLA-F	STAT1bet	1449	1458	5.796867	TTTTCCC	0.1545	0.1557
cg1120165	HLA-F	C/EBPalph	12	18	5.781231	TATTGG	0.97656	0.99

cg1120165	HLA-F	C/EBPalpł	58	64	5.781231	TATTGTC	0.97656	0.99
cg1120165	HLA-F	NF-AT1 [T	733	741	5.77403	GGAAAG	0.06866	0.06922
cg1120165	HLA-F	VDR [T00	948	956	5.771401	GTTCATT	0.42725	0.42999
cg1120165	HLA-F	NF-AT2 [T	682	691	5.75046	CAACTTT	0.04196	0.04255
cg1120165	HLA-F	c-Jun [T00	1469	1475	5.703976	GGGGTC.	0.48828	0.48665
cg1120165	HLA-F	ENKTF-1	1515	1522	5.687009	TGGCCC'	0.73242	0.7249
cg1120165	HLA-F	ENKTF-1	1862	1869	5.687009	GTACGC(	0.73242	0.7249
cg1120165	HLA-F	ENKTF-1	1868	1875	5.687009	CAAGGC	0.73242	0.7249
cg1120165	HLA-F	ENKTF-1	1894	1901	5.687009	TGGCCC'	0.73242	0.7249
cg1120165	HLA-F	C/EBPalpł	33	39	5.565669	TACAAT(	0.73242	0.74391
cg1120165	HLA-F	NFI/CTF [	963	970	5.558661	CCAAGC'	0.54932	0.55038
cg1120165	HLA-F	Pax-5 [T0(	96	102	5.544826	GGGCTA'	0.73242	0.72046
cg1120165	HLA-F	Pax-5 [T0(	1992	1998	5.544826	ACCGCC(	0.73242	0.72046
cg1120165	HLA-F	TFIID [T0	117	123	5.544826	TTTAGA	0.73242	0.75085
cg1120165	HLA-F	TFIID [T0	1415	1421	5.544826	TTCTAA	0.73242	0.75085
cg1120165	HLA-F	p53 [T006	1115	1121	5.508538	TCAGCC(	0.61035	0.59991
cg1120165	HLA-F	p53 [T006	1648	1654	5.508538	TCAGCC(	0.61035	0.59991
cg1120165	HLA-F	p53 [T006	1586	1592	5.39549	GGGCCC	0.61035	0.59991
cg1120165	HLA-F	RAR-beta	449	458	5.389083	CGTGAA	0.15259	0.15189
cg1120165	HLA-F	p53 [T006	1124	1130	5.345221	GGGCGA	0.61035	0.59991
cg1120165	HLA-F	AP-1 [T00	129	137	5.321703	CAAGAG	0.09155	0.09214
cg1120165	HLA-F	NF-AT1 [T	1446	1454	5.125037	TATTTTT	0.05341	0.05402
cg1120165	HLA-F	AR [T000	654	662	5.104816	TCTCTGT	0.11444	0.11247
cg1120165	HLA-F	NF-Y [T0(	1843	1850	5.094053	ATTGGG.	0.36621	0.36847
cg1120165	HLA-F	GR-beta [T	11	15	5.042296	GTATT	3.90625	3.95351
cg1120165	HLA-F	GR-beta [T	57	61	5.042296	GTATT	3.90625	3.95351
cg1120165	HLA-F	GR-beta [T	122	126	5.042296	AATAC	3.90625	3.95351
cg1120165	HLA-F	GR-beta [T	1050	1054	5.042296	GGATT	3.90625	3.95351
cg1120165	HLA-F	GR-beta [T	1261	1265	5.042296	GTATT	3.90625	3.95351
cg1120165	HLA-F	GR-beta [T	1685	1689	5.042296	GTATT	3.90625	3.95351
cg1120165	HLA-F	GR-beta [T	1841	1845	5.042296	GTATT	3.90625	3.95351
cg1120165	HLA-F	E2F-1 [T0	312	319	5.042045	GCGGGA	0.18311	0.17901
cg1120165	HLA-F	E2F-1 [T0	1808	1815	5.042045	GCGGGA	0.18311	0.17901
cg1120165	HLA-F	c-Ets-1 [T(	986	992	5.038739	CTTCCA	0.48828	0.49031
cg1120165	HLA-F	C/EBPalpł	1034	1040	5.024728	TTCAATC	0.97656	0.99332
cg1120165	HLA-F	NFI/CTF [	1360	1367	5.021086	CCCATT(	0.24414	0.24103
cg1120165	HLA-F	XBP-1 [T(	279	284	4.894955	ATGCCT	0.97656	0.96979
cg1120165	HLA-F	XBP-1 [T(	1090	1095	4.894955	ATGCCG	0.97656	0.96979
cg1120165	HLA-F	RXR-alpha	1643	1649	4.86724	GGGTCT(	0.48828	0.484
cg1120165	HLA-F	TFII-I [T0	70	75	4.756447	ATGTCC	2.92969	2.93695
cg1120165	HLA-F	TFII-I [T0	103	108	4.756447	GGAATG	2.92969	2.93695
cg1120165	HLA-F	TFII-I [T0	1016	1021	4.756447	GGAATG	2.92969	2.93695
cg1120165	HLA-F	TFII-I [T0	1044	1049	4.756447	GGACTG	2.92969	2.93695
cg1120165	HLA-F	TFII-I [T0	1057	1062	4.756447	GGAATG	2.92969	2.93695
cg1120165	HLA-F	TFII-I [T0	1079	1084	4.756447	GGACTG	2.92969	2.93695
cg1120165	HLA-F	FOXP3 [T	159	164	4.756447	CAAAAC	2.92969	2.96063
cg1120165	HLA-F	FOXP3 [T	236	241	4.756447	GTTTTT	2.92969	2.96063
cg1120165	HLA-F	Ik-1 [T027	1040	1052	4.748597	CAAGGG	0.00313	0.00308

cg1120165	HLA-F	p53 [T006	265	271	4.645444	GGGCGC	0.24414	0.23584
cg1120165	HLA-F	VDR [T00	447	455	4.617121	GGCGTG	0.37384	0.37445
cg1120165	HLA-F	VDR [T00	1033	1041	4.617121	GTTCAA	0.37384	0.37445
cg1120165	HLA-F	EBF [T05	1192	1202	4.612817	GTCCCA	0.00572	0.00551
cg1120165	HLA-F	Sp1 [T007	507	516	4.572987	TGGGCG	0.08583	0.08339
cg1120165	HLA-F	C/EBPalph	1387	1393	4.560723	GCCAAT	0.24414	0.24411
cg1120165	HLA-F	E2F-1 [T0	1436	1443	4.545253	GCGGGA	0.15259	0.14941
cg1120165	HLA-F	RXR-alpha	1819	1825	4.423008	GGGTGG	0.24414	0.24292
cg1120165	HLA-F	STAT4 [T	103	108	4.411765	GGAATG	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	773	778	4.411765	GGAAGA	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	779	784	4.411765	GGAAGA	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	785	790	4.411765	GGAAGA	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	791	796	4.411765	GGAAGA	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	797	802	4.411765	GGAAGA	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	905	910	4.411765	GGAAGA	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	985	990	4.411765	TCTTCC	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	1016	1021	4.411765	GGAATG	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	1057	1062	4.411765	GGAATG	1.95312	1.94235
cg1120165	HLA-F	STAT4 [T	1322	1327	4.411765	TCTTCC	1.95312	1.94235
cg1120165	HLA-F	p53 [T006	1514	1520	4.33696	CTGGCC	0.24414	0.23584
cg1120165	HLA-F	HOXD9 [T	623	632	4.321431	AATAAA	0.03433	0.03596
cg1120165	HLA-F	HOXD10 [	623	632	4.321431	AATAAA	0.03433	0.03596
cg1120165	HLA-F	RAR-beta	1942	1951	4.307573	AGTGAA	0.14496	0.1447
cg1120165	HLA-F	c-Myb [T0	1402	1409	4.270092	CGCAGT	0.06104	0.06059
cg1120165	HLA-F	RXR-alpha	1860	1866	4.24113	GGGTAC	0.97656	0.9671
cg1120165	HLA-F	PXR-1:RX	451	458	4.213958	TGAACC	0.12207	0.12119
cg1120165	HLA-F	PXR-1:RX	1944	1951	4.213958	TGAACC	0.12207	0.12119
cg1120165	HLA-F	GR-beta [T	36	40	4.201913	AATCA	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	256	260	4.201913	TGATT	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	287	291	4.201913	AATCG	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	623	627	4.201913	AATAA	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	662	666	4.201913	CTATT	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	1037	1041	4.201913	AATCA	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	1063	1067	4.201913	AATAA	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	1390	1394	4.201913	AATCA	7.8125	7.94607
cg1120165	HLA-F	GR-beta [T	1789	1793	4.201913	CGATT	7.8125	7.94607
cg1120165	HLA-F	c-Ets-1 [T	251	257	4.154851	ATTCCT	0.24414	0.24526
cg1120165	HLA-F	c-Ets-1 [T	1763	1769	4.154851	ATTCCT	0.24414	0.24526
cg1120165	HLA-F	Sp1 [T007	1990	1999	4.134056	GGACCG	0.08965	0.08686
cg1120165	HLA-F	p53 [T006	1225	1231	4.125254	CAGGCC	0.73242	0.71379
cg1120165	HLA-F	SRY [T00	53	61	4.087393	CTTTGT	0.12207	0.12407
cg1120165	HLA-F	RXR-alpha	362	368	4.019014	GAAACC	0.97656	0.9671
cg1120165	HLA-F	RXR-alpha	1151	1157	4.019014	CACACC	0.97656	0.9671
cg1120165	HLA-F	Pax-5 [T0	1197	1203	4.007279	AGGGCC	1.09863	1.07975
cg1120165	HLA-F	Pax-5 [T0	1509	1515	4.007279	GGGCCC	1.09863	1.07975
cg1120165	HLA-F	TFIID [T0	622	628	4.007279	TAATAA	1.09863	1.13456
cg1120165	HLA-F	AP-2alpha	1868	1873	3.970052	CAAGGC	0.97656	0.96469
cg1120165	HLA-F	EBF [T05	1895	1905	3.842007	GGCCCT	0.0248	0.02398

cg1120165	HLA-F	E2F-1 [T0	510	517	3.784875	GCGGCA	0.15259	0.15068
cg1120165	HLA-F	GR [T050	159	165	3.763516	CAAAAC	0.73242	0.74251
cg1120165	HLA-F	NF-kappa	1719	1729	3.634761	GGGGAG	0.01812	0.01756
cg1120165	HLA-F	c-Ets-1 [T	1901	1907	3.590463	GAGGAA	0.61035	0.60765
cg1120165	HLA-F	p53 [T006	1658	1664	3.586914	CTCGCC	0.73242	0.7189
cg1120165	HLA-F	NF-Y [T0	1363	1370	3.580622	ATTGGG	0.48828	0.48904
cg1120165	HLA-F	C/EBPalph	257	263	3.555778	GATTGG	0.24414	0.24752
cg1120165	HLA-F	VDR [T00	1940	1948	3.462841	TGAGTG	0.21362	0.21341
cg1120165	HLA-F	c-Ets-1 [T	575	581	3.462376	GTTCCT	0.61035	0.60765
cg1120165	HLA-F	NF-AT1 [	683	692	3.445347	AACTTT	0.07629	0.07722
cg1120165	HLA-F	RXR-alph	591	597	3.392904	GGGTTA	1.09863	1.08572
cg1120165	HLA-F	RXR-alph	1428	1434	3.392904	CGCACC	1.09863	1.08572
cg1120165	HLA-F	RXR-alph	1470	1476	3.392904	GGGTCA	1.09863	1.08572
cg1120165	HLA-F	RXR-alph	1537	1543	3.392904	GGGTGA	1.09863	1.08572
cg1120165	HLA-F	p53 [T006	390	396	3.375208	GGGCGT	0.73242	0.7189
cg1120165	HLA-F	p53 [T006	709	715	3.375208	GGGCGG	0.73242	0.7189
cg1120165	HLA-F	p53 [T006	1533	1539	3.375208	GGGCGG	0.73242	0.7189
cg1120165	HLA-F	p53 [T006	1589	1595	3.375208	CCCGCC	0.73242	0.7189
cg1120165	HLA-F	T3R-beta1	1934	1942	3.370634	GGCTGG	0.27466	0.2755
cg1120165	HLA-F	GR-beta [	29	33	3.361531	AATAT	3.90625	3.99611
cg1120165	HLA-F	GR-beta [	249	253	3.361531	AGATT	3.90625	3.99611
cg1120165	HLA-F	GR-beta [	600	604	3.361531	AGATT	3.90625	3.99611
cg1120165	HLA-F	GR-beta [	1445	1449	3.361531	ATATT	3.90625	3.99611
cg1120165	HLA-F	c-Ets-2 [T	1898	1906	3.2883	CCTGAG	0.18311	0.18304
cg1120165	HLA-F	c-Jun [T00	131	137	3.244843	AGAGTC	0.24414	0.24403
cg1120165	HLA-F	AP-2alpha	1565	1570	3.229049	GCCTCT	0.48828	0.48238
cg1120165	HLA-F	Elk-1 [T00	901	909	3.121991	AAAAGG	0.07629	0.07656
cg1120165	HLA-F	Pax-5 [T0	1658	1664	3.075094	CTCGCC	0.12207	0.11895
cg1120165	HLA-F	C/EBPalph	1362	1368	2.981957	CATTGG	0.48828	0.4911
cg1120165	HLA-F	c-Ets-2 [T	900	908	2.945838	GAAAAG	0.06104	0.06231
cg1120165	HLA-F	STAT4 [T	153	158	2.941176	GGAAAG	2.92969	2.929
cg1120165	HLA-F	STAT4 [T	250	255	2.941176	GATTCC	2.92969	2.929
cg1120165	HLA-F	STAT4 [T	574	579	2.941176	GGTTCC	2.92969	2.929
cg1120165	HLA-F	STAT4 [T	733	738	2.941176	GGAAAG	2.92969	2.929
cg1120165	HLA-F	STAT4 [T	1790	1795	2.941176	GATTCC	2.92969	2.929
cg1120165	HLA-F	STAT4 [T	1903	1908	2.941176	GGAACC	2.92969	2.929
cg1120165	HLA-F	STAT1bet	149	158	2.898434	TCTGGG	0.0515	0.05191
cg1120165	HLA-F	p53 [T006	402	408	2.813291	GGGCAT	0.48828	0.47786
cg1120165	HLA-F	NF-1 [T00	221	228	2.813149	GGGGCC	0.24414	0.24101
cg1120165	HLA-F	CTF [T001	1385	1396	2.746279	AAGCCA	0.0062	0.0062
cg1120165	HLA-F	RXR-alph	1246	1252	2.726556	GGGTTG	0.85449	0.84796
cg1120165	HLA-F	RXR-alph	1303	1309	2.726556	CCAACC	0.85449	0.84796
cg1120165	HLA-F	RXR-alph	975	981	2.544678	GGGTGA	0.85449	0.84796
cg1120165	HLA-F	Sp1 [T007	1532	1541	2.515451	TGGGCG	0.04005	0.03892
cg1120165	HLA-F	C/EBPalph	1143	1149	2.441016	CATTGA	0.48828	0.49114
cg1120165	HLA-F	MAZ [T00	1165	1177	2.392122	GAGGGG	0.00405	0.00399
cg1120165	HLA-F	MAZ [T00	1171	1183	2.392122	GAGGGG	0.00405	0.00399
cg1120165	HLA-F	MAZ [T00	1177	1189	2.392122	GAGGGG	0.00405	0.00399

cg1120165	HLA-F	GCF [T00	1603	1611	2.339499	GCGCAG	0.06104	0.05925
cg1120165	HLA-F	GCF [T00	1959	1967	2.339499	GCGCAG	0.06104	0.05925
cg1120165	HLA-F	RXR-alpha	1634	1640	2.322562	GGGTCT	0.85449	0.84796
cg1120165	HLA-F	Elk-1 [T00	775	783	2.299314	AAGAGG	0.09155	0.09114
cg1120165	HLA-F	Elk-1 [T00	781	789	2.299314	AAGAGG	0.09155	0.09114
cg1120165	HLA-F	Elk-1 [T00	787	795	2.299314	AAGAGG	0.09155	0.09114
cg1120165	HLA-F	Elk-1 [T00	793	801	2.299314	AAGAGG	0.09155	0.09114
cg1120165	HLA-F	Elk-1 [T00	1323	1331	2.299314	CTTCCTC	0.09155	0.09114
cg1120165	HLA-F	GATA-1 [	1328	1333	2.176375	TGGATA	3.90625	3.92756
cg1120165	HLA-F	Elk-1 [T00	769	777	2.164966	GAGAGG	0.05341	0.05317
cg1120165	HLA-F	c-Ets-2 [T	768	776	2.142327	GGAGAG	0.16785	0.16856
cg1120165	HLA-F	NF-Y [T0	13	20	2.12821	ATTGGC	0.21362	0.21508
cg1120165	HLA-F	NF-Y [T0	1385	1392	2.12821	AAGCCA	0.21362	0.21508
cg1120165	HLA-F	AP-2alpha	308	313	2.098119	CGAGGC	0.97656	0.95407
cg1120165	HLA-F	AP-2alpha	1232	1237	2.098119	CGAGGC	0.97656	0.95407
cg1120165	HLA-F	AP-2alpha	1931	1936	2.098119	CGAGGC	0.97656	0.95407
cg1120165	HLA-F	NF-AT1 [	683	691	1.970716	AACTTT	0.06866	0.07012
cg1120165	HLA-F	p53 [T006	1185	1191	1.970013	GGGCAA	0.36621	0.36261
cg1120165	HLA-F	GATA-1 [	1524	1529	1.896347	CCGATA	3.90625	3.92756
cg1120165	HLA-F	AP-2alpha	302	307	1.871933	GGAGGC	0.97656	0.95407
cg1120165	HLA-F	AP-2alpha	427	432	1.871933	GGAGGC	0.97656	0.95407
cg1120165	HLA-F	AP-2alpha	1022	1027	1.871933	GGAGGC	0.97656	0.95407
cg1120165	HLA-F	AP-2alpha	1252	1257	1.871933	GGAGGC	0.97656	0.95407
cg1120165	HLA-F	AP-2alpha	1488	1493	1.871933	GCCTCC	0.97656	0.95407
cg1120165	HLA-F	AP-2alpha	1622	1627	1.871933	GCCTCC	0.97656	0.95407
cg1120165	HLA-F	C/EBPalph	1759	1765	1.830762	CGCAAT	0.48828	0.49438
cg1120165	HLA-F	TFII-I [T0	768	773	1.824994	GGAGAG	0.48828	0.48408
cg1120165	HLA-F	TFII-I [T0	1298	1303	1.824994	CTCTCC	0.48828	0.48408
cg1120165	HLA-F	FOXP3 [T	124	129	1.824994	TACAAC	0.48828	0.49451
cg1120165	HLA-F	FOXP3 [T	180	185	1.824994	GTTGTA	0.48828	0.49451
cg1120165	HLA-F	FOXP3 [T	184	189	1.824994	TACAAC	0.48828	0.49451
cg1120165	HLA-F	FOXP3 [T	680	685	1.824994	TACAAC	0.48828	0.49451
cg1120165	HLA-F	FOXP3 [T	1920	1925	1.824994	TACAAC	0.48828	0.49451
cg1120165	HLA-F	C/EBPalph	1842	1848	1.761449	TATTGG	0.48828	0.49438
cg1120165	HLA-F	GR-beta [	193	197	1.680765	AATGC	3.90625	3.94936
cg1120165	HLA-F	GR-beta [	196	200	1.680765	GCATT	3.90625	3.94936
cg1120165	HLA-F	GR-beta [	584	588	1.680765	AATTC	3.90625	3.94936
cg1120165	HLA-F	GR-beta [	979	983	1.680765	GAATT	3.90625	3.94936
cg1120165	HLA-F	GR-beta [	1268	1272	1.680765	GAATT	3.90625	3.94936
cg1120165	HLA-F	GR-beta [	1269	1273	1.680765	AATTC	3.90625	3.94936
cg1120165	HLA-F	GR-beta [	1762	1766	1.680765	AATTC	3.90625	3.94936
cg1120165	HLA-F	c-Ets-2 [T	728	736	1.64415	GAGGAG	0.04578	0.04579
cg1120165	HLA-F	C/EBPbeta	14	17	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	225	228	1.639871	CCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	259	262	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	299	302	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	597	600	1.639871	CCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	963	966	1.639871	CCAA	15.625	15.72563

cg1120165	HLA-F	C/EBPbeta	972	975	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	989	992	1.639871	CCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1249	1252	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1303	1306	1.639871	CCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1364	1367	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1388	1391	1.639871	CCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1467	1470	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1531	1534	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1844	1847	1.639871	TTGG	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1867	1870	1.639871	CCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1873	1876	1.639871	CCAA	15.625	15.72563
cg1120165	HLA-F	PXR-1:RX	1030	1037	1.63615	AAAGTT	0.06104	0.06239
cg1120165	HLA-F	Sp1 [T007	1587	1596	1.628725	GGCCCG	0.03242	0.03129
cg1120165	HLA-F	XBP-1 [T	1471	1476	1.583727	GGTCAT	0.97656	0.98146
cg1120165	HLA-F	Pax-5 [T0	265	271	1.537547	GGGCGC	0.73242	0.71311
cg1120165	HLA-F	Pax-5 [T0	390	396	1.537547	GGGCGT	0.73242	0.71311
cg1120165	HLA-F	Pax-5 [T0	709	715	1.537547	GGGCGG	0.73242	0.71311
cg1120165	HLA-F	Pax-5 [T0	1514	1520	1.537547	CTGGCC	0.73242	0.71311
cg1120165	HLA-F	Pax-5 [T0	1533	1539	1.537547	GGGCGG	0.73242	0.71311
cg1120165	HLA-F	Pax-5 [T0	1589	1595	1.537547	CCCGCC	0.73242	0.71311
cg1120165	HLA-F	TFIID [T0	238	244	1.537547	TTTTACA	0.73242	0.75096
cg1120165	HLA-F	TFIID [T0	374	380	1.537547	TACAAA	0.73242	0.75096
cg1120165	HLA-F	TFIID [T0	686	692	1.537547	TTTTCCA	0.73242	0.75096
cg1120165	HLA-F	TFIID [T0	988	994	1.537547	TCCAAA	0.73242	0.75096
cg1120165	HLA-F	c-Ets-1 [T	731	737	1.513038	GAGGAA	0.36621	0.36952
cg1120165	HLA-F	STAT4 [T	686	691	1.470588	TTTTCC	1.95312	1.96333
cg1120165	HLA-F	STAT4 [T	1269	1274	1.470588	AATTCC	1.95312	1.96333
cg1120165	HLA-F	STAT4 [T	1405	1410	1.470588	AGTTCC	1.95312	1.96333
cg1120165	HLA-F	STAT4 [T	1449	1454	1.470588	TTTTCC	1.95312	1.96333
cg1120165	HLA-F	STAT4 [T	1762	1767	1.470588	AATTCC	1.95312	1.96333
cg1120165	HLA-F	C/EBPbeta	217	220	1.366559	TCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	531	534	1.366559	TCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1035	1038	1.366559	TCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1039	1042	1.366559	TCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1145	1148	1.366559	TTGA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1216	1219	1.366559	TCAA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1264	1267	1.366559	TTGA	15.625	15.72563
cg1120165	HLA-F	C/EBPbeta	1680	1683	1.366559	TTGA	15.625	15.72563
cg1120165	HLA-F	AP-2alpha	281	286	1.357116	GCCTGT	0.48828	0.48203
cg1120165	HLA-F	C/EBPalph	1262	1268	1.220508	TATTGA	0.24414	0.247
cg1120165	HLA-F	c-Ets-2 [T	774	782	1.071163	GAAGAG	0.06104	0.06166
cg1120165	HLA-F	c-Ets-2 [T	780	788	1.071163	GAAGAG	0.06104	0.06166
cg1120165	HLA-F	c-Ets-2 [T	786	794	1.071163	GAAGAG	0.06104	0.06166
cg1120165	HLA-F	c-Ets-2 [T	792	800	1.071163	GAAGAG	0.06104	0.06166
cg1120165	HLA-F	GATA-1 [	215	220	1.038567	TATCAA	1.95312	1.98662
cg1120165	HLA-F	NF-Y [T0	258	265	0.907437	ATTGGT	0.12207	0.12315
cg1120165	HLA-F	RXR-alpha	1084	1090	0.848226	GGGTCC	0.48828	0.48333
cg1120165	HLA-F	RXR-alpha	1548	1554	0.848226	GGGTCC	0.48828	0.48333

cg1120165	HLA-F	GR-beta [T	4	8	0.840383	AATGA	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	105	109	0.840383	AATGA	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	113	117	0.840383	TAATT	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	382	386	0.840383	AATTA	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	444	448	0.840383	AATGG	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	583	587	0.840383	TAATT	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	933	937	0.840383	TCATT	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	950	954	0.840383	TCATT	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	1018	1022	0.840383	AATGG	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	1059	1063	0.840383	AATGA	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	1066	1070	0.840383	AATGA	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	1348	1352	0.840383	CCATT	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	1361	1365	0.840383	CCATT	7.8125	7.94706
cg1120165	HLA-F	GR-beta [T	1761	1765	0.840383	CAATT	7.8125	7.94706
cg1120165	HLA-F	PXR-1:RX	945	952	0.818075	CAAGTT	0.12207	0.12266
cg1120165	HLA-F	GATA-1 [	579	584	0.758539	CTGATA	1.95312	1.98662
cg1120165	HLA-F	AP-2alpha	1224	1229	0.678558	TCAGGC	0.48828	0.48199
cg1120165	HLA-F	Sp1 [T007	708	717	0.574521	GGGGCG	0.00763	0.00733
cg1120165	HLA-F	PR B [T00	232	238	0.48823	AACAGT	0.12207	0.12407
cg1120165	HLA-F	PR A [T01	232	238	0.48823	AACAGT	0.12207	0.12407
cg1120165	HLA-F	c-Ets-1 [T	903	909	0.256174	AAGGAA	0.24414	0.24569
cg1120165	HLA-F	AP-2alpha	504	509	0.226186	GCCTGG	0.97656	0.95305
cg1120165	HLA-F	AP-2alpha	1665	1670	0.226186	CCAGGC	0.97656	0.95305
cg1120165	HLA-F	GR-alpha [	571	575	0.207689	AAAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	700	704	0.207689	AGAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	770	774	0.207689	AGAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	776	780	0.207689	AGAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	782	786	0.207689	AGAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	788	792	0.207689	AGAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	794	798	0.207689	AGAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	902	906	0.207689	AAAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	1566	1570	0.207689	CCTCT	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	1829	1833	0.207689	AGAGG	7.8125	7.81264
cg1120165	HLA-F	c-Ets-1 [T	771	777	0.128087	GAGGAA	0.24414	0.2429
cg1120165	HLA-F	c-Ets-1 [T	777	783	0.128087	GAGGAA	0.24414	0.2429
cg1120165	HLA-F	c-Ets-1 [T	783	789	0.128087	GAGGAA	0.24414	0.2429
cg1120165	HLA-F	c-Ets-1 [T	789	795	0.128087	GAGGAA	0.24414	0.2429
cg1120165	HLA-F	c-Ets-1 [T	795	801	0.128087	GAGGAA	0.24414	0.2429
cg1120165	HLA-F	GR-alpha [	282	286	0	CCTGT	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	661	665	0	CCTAT	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	1161	1165	0	ACAGG	7.8125	7.81264
cg1120165	HLA-F	GR-alpha [	1857	1861	0	ACAGG	7.8125	7.81264
cg1120165	HLA-F	RXR-alph	451	457	0	TGAACC	0.24414	0.2444
cg1120165	HLA-F	RXR-alph	1944	1950	0	TGAACC	0.24414	0.2444
cg1120165	HLA-F	Pax-5 [T0	1225	1231	0	CAGGCC	1.09863	1.06846
cg1120165	HLA-F	Pax-5 [T0	1586	1592	0	GGGCCC	1.09863	1.06846
cg1120165	HLA-F	TFII-I [T0	153	158	0	GGAAAG	1.46484	1.45997
cg1120165	HLA-F	TFII-I [T0	657	662	0	CTGTCC	1.46484	1.45997

cg1120165	HLA-F	TFII-I [T0	733	738	0	GGAAAG	1.46484	1.45997
cg1120165	HLA-F	c-Ets-1 [T	1323	1329	0	CTTCCTC	0.24414	0.2429
cg1120165	HLA-F	YY1 [T00	101	104	0	ATGG	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	343	346	0	CCAT	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	445	448	0	ATGG	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1014	1017	0	ATGG	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1019	1022	0	ATGG	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1077	1080	0	ATGG	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1088	1091	0	CCAT	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1275	1278	0	CCAT	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1348	1351	0	CCAT	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1361	1364	0	CCAT	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1475	1478	0	ATGG	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1800	1803	0	ATGG	7.8125	7.81711
cg1120165	HLA-F	YY1 [T00	1979	1982	0	CCAT	7.8125	7.81711
cg1120165	HLA-F	ER-alpha [	327	331	0	GGTCA	1.95312	1.9404
cg1120165	HLA-F	ER-alpha [	1471	1475	0	GGTCA	1.95312	1.9404
cg1120165	HLA-F	ER-alpha [	1521	1525	0	TGACC	1.95312	1.9404
cg1120165	HLA-F	ER-alpha [	1886	1890	0	TGACC	1.95312	1.9404
cg1120165	HLA-F	ER-alpha [	1964	1968	0	GGTCA	1.95312	1.9404
cg1120165	HLA-F	GATA-1 [	138	143	0	CAGATA	0.97656	0.98738
cg1120165	HLA-F	C/EBPbeta	25	28	0	TTGC	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	27	30	0	GCAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	34	37	0	ACAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	45	48	0	TTGT	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	55	58	0	TTGT	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	60	63	0	TTGT	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	125	128	0	ACAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	128	131	0	ACAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	158	161	0	GCAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	181	184	0	TTGT	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	185	188	0	ACAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	375	378	0	ACAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	470	473	0	TTGC	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	681	684	0	ACAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	944	947	0	ACAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	953	956	0	TTGT	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	1187	1190	0	GCAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	1760	1763	0	GCAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	1826	1829	0	GCAA	15.625	15.71349
cg1120165	HLA-F	C/EBPbeta	1921	1924	0	ACAA	15.625	15.71349
cg1120165	HLA-F	TFIID [T0	116	122	0	TTTTAG	1.09863	1.13474
cg1120165	HLA-F	TFIID [T0	531	537	0	TCAAAA	1.09863	1.13474
cg1120165	HLA-F	TFIID [T0	625	631	0	TAAAAA	1.09863	1.13474
cg1120165	HLA-F	FOXP3 [T	44	49	0	GTTGTG	1.46484	1.47315
cg1120165	HLA-F	GR-beta [	8	12	0	AATGT	3.90625	3.99611
cg1120165	HLA-F	GR-beta [	114	118	0	AATTT	3.90625	3.99611
cg1120165	HLA-F	GR-beta [	206	210	0	ACATT	3.90625	3.99611

cg1120165	HLA-F	GR-beta [T	381	385	0	AAATT	3.90625	3.99611
cg1120165	HLA-F	GR-beta [T	980	984	0	AATTT	3.90625	3.99611
cg1120165	HLA-F	GR-beta [T	1142	1146	0	ACATT	3.90625	3.99611
cg1120165	HLA-F	GR [T050	376	382	0	CAAAAA	0.36621	0.37562
cg1120165	HLA-F	GR [T050	532	538	0	CAAAAA	0.36621	0.37562
cg1120165	HLA-F	TBP [T007	209	218	0	TTTATAT	0.03052	0.03159
cg0645773	HRH1	PEA3 [T0	750	758	9.937959	GGGATG	0.18311	0.18382
cg0883107	HRH1	PEA3 [T0	688	696	9.937959	GGGATG	0.18311	0.18382
cg0645773	HRH1	RelA [T00	1061	1071	9.900897	TCGGGA	0.02623	0.02693
cg0883107	HRH1	RelA [T00	999	1009	9.900897	TCGGGA	0.02623	0.02693
cg0645773	HRH1	c-Myb [T0	1032	1039	9.815171	ACAAGT	0.36621	0.34605
cg0883107	HRH1	c-Myb [T0	970	977	9.815171	ACAAGT	0.36621	0.34605
cg0645773	HRH1	XBP-1 [T	1620	1625	9.789909	ATGGCT	1.95312	1.94901
cg0645773	HRH1	XBP-1 [T	1857	1862	9.789909	ATGGCG	1.95312	1.94901
cg0883107	HRH1	XBP-1 [T	1558	1563	9.789909	ATGGCT	1.95312	1.94901
cg0883107	HRH1	XBP-1 [T	1795	1800	9.789909	ATGGCG	1.95312	1.94901
cg0645773	HRH1	NF-1 [T00	923	930	9.761671	AGCACC	0.24414	0.24488
cg0883107	HRH1	NF-1 [T00	861	868	9.761671	AGCACC	0.24414	0.24488
cg0645773	HRH1	PR B [T00	577	583	9.743489	AACACA	1.09863	1.0981
cg0645773	HRH1	PR A [T01	577	583	9.743489	AACACA	1.09863	1.0981
cg0883107	HRH1	PR B [T00	515	521	9.743489	AACACA	1.09863	1.0981
cg0883107	HRH1	PR A [T01	515	521	9.743489	AACACA	1.09863	1.0981
cg0645773	HRH1	AhR:Arnt	1432	1441	9.738501	TGGGGC	0.17929	0.20119
cg0883107	HRH1	AhR:Arnt	1370	1379	9.738501	TGGGGC	0.17929	0.20119
cg0645773	HRH1	LEF-1 [T0	743	750	9.72404	AGGCAA	0.21362	0.21229
cg0883107	HRH1	LEF-1 [T0	681	688	9.72404	AGGCAA	0.21362	0.21229
cg0645773	HRH1	Elk-1 [T00	1232	1240	9.719998	CTTCCG	0.07629	0.0786
cg0883107	HRH1	Elk-1 [T00	1170	1178	9.719998	CTTCCG	0.07629	0.0786
cg0645773	HRH1	c-Ets-1 [T	1062	1068	9.585075	CGGGAA	0.36621	0.37402
cg0883107	HRH1	c-Ets-1 [T	1000	1006	9.585075	CGGGAA	0.36621	0.37402
cg0645773	HRH1	TFIID [T0	1	7	9.552105	TTTGCC	1.46484	1.37777
cg0645773	HRH1	TFIID [T0	63	69	9.552105	TCCCAA	1.46484	1.37777
cg0645773	HRH1	TFIID [T0	340	346	9.552105	TGGGAA	1.46484	1.37777
cg0645773	HRH1	TFIID [T0	843	849	9.552105	TTCCAA	1.46484	1.37777
cg0645773	HRH1	TFIID [T0	977	983	9.552105	TTTCCC	1.46484	1.37777
cg0645773	HRH1	TFIID [T0	1141	1147	9.552105	TGGGAA	1.46484	1.37777
cg0645773	HRH1	Pax-5 [T0	763	769	9.552105	GGGCCA	1.46484	1.61918
cg0883107	HRH1	TFIID [T0	1	7	9.552105	TCCCAA	1.46484	1.37777
cg0883107	HRH1	TFIID [T0	278	284	9.552105	TGGGAA	1.46484	1.37777
cg0883107	HRH1	TFIID [T0	781	787	9.552105	TTCCAA	1.46484	1.37777
cg0883107	HRH1	TFIID [T0	915	921	9.552105	TTTCCC	1.46484	1.37777
cg0883107	HRH1	TFIID [T0	1079	1085	9.552105	TGGGAA	1.46484	1.37777
cg0883107	HRH1	Pax-5 [T0	701	707	9.552105	GGGCCA	1.46484	1.61918
cg0645773	HRH1	NF-1 [T00	1148	1155	9.535536	CTGACC	0.73242	0.74634
cg0883107	HRH1	NF-1 [T00	1086	1093	9.535536	CTGACC	0.73242	0.74634
cg0645773	HRH1	NF-1 [T00	515	522	9.513281	TACCCC	0.73242	0.74634
cg0883107	HRH1	NF-1 [T00	453	460	9.513281	TACCCC	0.73242	0.74634
cg0645773	HRH1	FOXP3 [T	9	14	9.512894	GTTGGC	7.32422	7.22156

cg0645773	HRH1	FOXP3 [T	107	112	9.512894	CTAAAC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	268	273	9.512894	CAGAAC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	472	477	9.512894	AGCAAC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	518	523	9.512894	CCCAAC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	596	601	9.512894	AGCAAC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	735	740	9.512894	GTTTAT	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	982	987	9.512894	CATAAC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	1151	1156	9.512894	ACCAAC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	1158	1163	9.512894	GTTTAG	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	1672	1677	9.512894	GTTCTG	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	1692	1697	9.512894	GTTATT	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	1745	1750	9.512894	GTTATC	7.32422	7.22156
cg0645773	HRH1	FOXP3 [T	1854	1859	9.512894	GTTATG	7.32422	7.22156
cg0645773	HRH1	TFII-I [T0	138	143	9.512894	AATTCC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	369	374	9.512894	GGAAAA	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	624	629	9.512894	GTTTCC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	630	635	9.512894	CCATCC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	823	828	9.512894	GGAAGG	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	841	846	9.512894	CCTTCC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	942	947	9.512894	GTGTCC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1087	1092	9.512894	CCGTCC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1143	1148	9.512894	GGAAAC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1272	1277	9.512894	TTGTCC	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1296	1301	9.512894	GGATTT	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1580	1585	9.512894	GGATGG	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1630	1635	9.512894	GGATGG	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1715	1720	9.512894	GGATGG	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1733	1738	9.512894	GGAACG	7.32422	7.44385
cg0645773	HRH1	TFII-I [T0	1816	1821	9.512894	TTGTCC	7.32422	7.44385
cg0883107	HRH1	FOXP3 [T	45	50	9.512894	CTAAAC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	206	211	9.512894	CAGAAC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	410	415	9.512894	AGCAAC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	456	461	9.512894	CCCAAC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	534	539	9.512894	AGCAAC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	673	678	9.512894	GTTTAT	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	920	925	9.512894	CATAAC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	1089	1094	9.512894	ACCAAC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	1096	1101	9.512894	GTTTAG	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	1610	1615	9.512894	GTTCTG	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	1630	1635	9.512894	GTTATT	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	1683	1688	9.512894	GTTATC	7.32422	7.22156
cg0883107	HRH1	FOXP3 [T	1792	1797	9.512894	GTTATG	7.32422	7.22156
cg0883107	HRH1	TFII-I [T0	76	81	9.512894	AATTCC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	307	312	9.512894	GGAAAA	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	562	567	9.512894	GTTTCC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	568	573	9.512894	CCATCC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	761	766	9.512894	GGAAGG	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	779	784	9.512894	CCTTCC	7.32422	7.44385

cg0883107	HRH1	TFII-I [T0	880	885	9.512894	GTGTCC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1025	1030	9.512894	CCGTCC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1081	1086	9.512894	GGAAAC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1210	1215	9.512894	TTGTCC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1234	1239	9.512894	GGATTT	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1518	1523	9.512894	GGATGG	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1568	1573	9.512894	GGATGG	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1653	1658	9.512894	GGATGG	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1671	1676	9.512894	GGAACG	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1754	1759	9.512894	TTGTCC	7.32422	7.44385
cg0883107	HRH1	TFII-I [T0	1994	1999	9.512894	TTGTCC	7.32422	7.44385
cg0645773	HRH1	c-Jun [T00	386	392	9.511322	TGACCA	0.73242	0.7366
cg0883107	HRH1	c-Jun [T00	324	330	9.511322	TGACCA	0.73242	0.7366
cg0645773	HRH1	TCF-4E [T	670	676	9.453578	CTTTGA	0.48828	0.46934
cg0883107	HRH1	TCF-4E [T	608	614	9.453578	CTTTGA	0.48828	0.46934
cg0645773	HRH1	NF-kappa	1719	1729	9.399522	GGGGAA	0.02193	0.02416
cg0883107	HRH1	NF-kappa	1657	1667	9.399522	GGGGAA	0.02193	0.02416
cg0645773	HRH1	NFI/CTF [	126	133	9.352332	AACATT	0.54932	0.55369
cg0645773	HRH1	NFI/CTF [	238	245	9.352332	CCAAGG	0.54932	0.55369
cg0883107	HRH1	NFI/CTF [	64	71	9.352332	AACATT	0.54932	0.55369
cg0883107	HRH1	NFI/CTF [	176	183	9.352332	CCAAGG	0.54932	0.55369
cg0645773	HRH1	c-Myb [T0	558	565	9.29064	AAACTC	0.36621	0.34746
cg0645773	HRH1	c-Myb [T0	1012	1019	9.29064	AAACTC	0.36621	0.34746
cg0883107	HRH1	c-Myb [T0	496	503	9.29064	AAACTC	0.36621	0.34746
cg0883107	HRH1	c-Myb [T0	950	957	9.29064	AAACTC	0.36621	0.34746
cg0645773	HRH1	c-Ets-1 [T	705	711	9.276861	GTTCCC	0.36621	0.37402
cg0883107	HRH1	c-Ets-1 [T	643	649	9.276861	GTTCCC	0.36621	0.37402
cg0645773	HRH1	SRY [T00	670	678	9.264664	CTTTGA	0.12207	0.11857
cg0883107	HRH1	SRY [T00	608	616	9.264664	CTTTGA	0.12207	0.11857
cg0645773	HRH1	ATF [T00	580	591	9.257019	ACACGT	0.07725	0.07678
cg0883107	HRH1	ATF [T00	518	529	9.257019	ACACGT	0.07725	0.07678
cg0645773	HRH1	RBP-Jkap	1137	1148	9.256527	GTGCTG	0.01884	0.01884
cg0883107	HRH1	RBP-Jkap	1075	1086	9.256527	GTGCTG	0.01884	0.01884
cg0645773	HRH1	AP-1 [T00	1571	1579	9.203282	TGACTG	0.24414	0.23028
cg0883107	HRH1	AP-1 [T00	1509	1517	9.203282	TGACTG	0.24414	0.23028
cg0645773	HRH1	c-Ets-1 [T	572	578	9.19359	ATTCCA	0.85449	0.84987
cg0883107	HRH1	c-Ets-1 [T	510	516	9.19359	ATTCCA	0.85449	0.84987
cg0645773	HRH1	c-Ets-1 [T	463	469	9.148774	GTTCCC	0.85449	0.84987
cg0883107	HRH1	c-Ets-1 [T	401	407	9.148774	GTTCCC	0.85449	0.84987
cg0645773	HRH1	c-Myb [T0	1811	1818	9.142015	CTAAGT	0.39673	0.37851
cg0883107	HRH1	c-Myb [T0	1749	1756	9.142015	CTAAGT	0.39673	0.37851
cg0645773	HRH1	E2F-1 [T0	1272	1279	9.140572	TTGTCC	0.27466	0.30178
cg0883107	HRH1	E2F-1 [T0	1210	1217	9.140572	TTGTCC	0.27466	0.30178
cg0645773	HRH1	c-Ets-1 [T	139	145	9.065503	ATTCCA	0.85449	0.84987
cg0883107	HRH1	c-Ets-1 [T	77	83	9.065503	ATTCCA	0.85449	0.84987
cg0645773	HRH1	NFI/CTF [	1152	1159	9.042931	CCAACA	0.48828	0.48845
cg0883107	HRH1	NFI/CTF [	1090	1097	9.042931	CCAACA	0.48828	0.48845
cg0645773	HRH1	c-Myb [T0	620	627	9.024874	CTCAGT	0.39673	0.37851

cg0883107	HRH1	c-Myb [T0	558	565	9.024874	CTCAGT	0.39673	0.37851
cg0645773	HRH1	c-Ets-1 [T	1719	1725	9.020687	GGGGAA	0.85449	0.84987
cg0883107	HRH1	c-Ets-1 [T	1657	1663	9.020687	GGGGAA	0.85449	0.84987
cg0645773	HRH1	c-Jun [T00	581	587	9.013496	CACGTC	0.61035	0.60549
cg0883107	HRH1	c-Jun [T00	519	525	9.013496	CACGTC	0.61035	0.60549
cg0645773	HRH1	LEF-1 [T0	63	70	8.973041	TCCCAA	0.54932	0.53171
cg0883107	HRH1	LEF-1 [T0	1	8	8.973041	TCCCAA	0.54932	0.53171
cg0645773	HRH1	GR [T050	351	357	8.971049	GCTTTC	0.61035	0.5928
cg0883107	HRH1	GR [T050	289	295	8.971049	GCTTTC	0.61035	0.5928
cg0645773	HRH1	AP-1 [T00	1158	1166	8.907204	GTTTAG	0.24414	0.23028
cg0883107	HRH1	AP-1 [T00	1096	1104	8.907204	GTTTAG	0.24414	0.23028
cg0645773	HRH1	GATA-2 [	1990	1998	8.888889	TGATAC	0.22888	0.22339
cg0883107	HRH1	GATA-2 [	1928	1936	8.888889	TGATAC	0.22888	0.22339
cg0645773	HRH1	AP-1 [T00	1052	1060	8.862731	TGACTT	0.24414	0.23028
cg0883107	HRH1	AP-1 [T00	990	998	8.862731	TGACTT	0.24414	0.23028
cg0645773	HRH1	NFI/CTF [	1909	1916	8.814757	CCAAAA	0.48828	0.48845
cg0883107	HRH1	NFI/CTF [	1847	1854	8.814757	CCAAAA	0.48828	0.48845
cg0645773	HRH1	c-Ets-1 [T	1486	1492	8.809329	CTGGAA	0.85449	0.84987
cg0883107	HRH1	c-Ets-1 [T	1424	1430	8.809329	CTGGAA	0.85449	0.84987
cg0645773	HRH1	Elk-1 [T00	589	597	8.797343	GGCTGG	0.24414	0.26271
cg0883107	HRH1	Elk-1 [T00	527	535	8.797343	GGCTGG	0.24414	0.26271
cg0645773	HRH1	NF-1 [T00	61	68	8.790071	CCTCCC	0.24414	0.24339
cg0645773	HRH1	NF-1 [T00	481	488	8.790071	TTGGGA	0.24414	0.24339
cg0883107	HRH1	NF-1 [T00	419	426	8.790071	TTGGGA	0.24414	0.24339
cg0645773	HRH1	XBP-1 [T	116	121	8.75604	GCTCAT	2.92969	2.75329
cg0645773	HRH1	XBP-1 [T	920	925	8.75604	ATGAGC	2.92969	2.75329
cg0645773	HRH1	XBP-1 [T	1301	1306	8.75604	TTTCAT	2.92969	2.75329
cg0645773	HRH1	XBP-1 [T	1344	1349	8.75604	ATGAAC	2.92969	2.75329
cg0883107	HRH1	XBP-1 [T	54	59	8.75604	GCTCAT	2.92969	2.75329
cg0883107	HRH1	XBP-1 [T	858	863	8.75604	ATGAGC	2.92969	2.75329
cg0883107	HRH1	XBP-1 [T	1239	1244	8.75604	TTTCAT	2.92969	2.75329
cg0883107	HRH1	XBP-1 [T	1282	1287	8.75604	ATGAAC	2.92969	2.75329
cg0645773	HRH1	STAT1bet	338	347	8.695301	AGTGGG	0.22316	0.2175
cg0645773	HRH1	STAT1bet	976	985	8.695301	CTTTCC	0.22316	0.2175
cg0883107	HRH1	STAT1bet	276	285	8.695301	AGTGGG	0.22316	0.2175
cg0883107	HRH1	STAT1bet	914	923	8.695301	CTTTCC	0.22316	0.2175
cg0645773	HRH1	c-Jun [T00	503	509	8.571705	TGACTG	0.12207	0.1249
cg0645773	HRH1	c-Jun [T00	1656	1662	8.571705	CCAGTC	0.12207	0.1249
cg0883107	HRH1	c-Jun [T00	441	447	8.571705	TGACTG	0.12207	0.1249
cg0883107	HRH1	c-Jun [T00	1594	1600	8.571705	CCAGTC	0.12207	0.1249
cg0645773	HRH1	RAR-beta	517	526	8.55975	CCCCAA	0.26703	0.27434
cg0883107	HRH1	RAR-beta	455	464	8.55975	CCCCAA	0.26703	0.27434
cg0645773	HRH1	p53 [T006	1463	1469	8.537081	GGGCTC	0.12207	0.13169
cg0883107	HRH1	p53 [T006	1401	1407	8.537081	GGGCTC	0.12207	0.13169
cg0645773	HRH1	HNF-3alp	119	126	8.343064	CATTTA	0.27466	0.23078
cg0883107	HRH1	HNF-3alp	57	64	8.343064	CATTTA	0.27466	0.23078
cg0645773	HRH1	PR B [T00	1723	1729	8.338824	AACAGC	1.09863	1.09384
cg0645773	HRH1	PR B [T00	1741	1747	8.338824	CCCTGT	1.09863	1.09384

cg0645773	HRH1	PR A [T01	1723	1729	8.338824	AACAGC	1.09863	1.09384
cg0645773	HRH1	PR A [T01	1741	1747	8.338824	CCCTGTT	1.09863	1.09384
cg0883107	HRH1	PR B [T00	1661	1667	8.338824	AACAGC	1.09863	1.09384
cg0883107	HRH1	PR B [T00	1679	1685	8.338824	CCCTGTT	1.09863	1.09384
cg0883107	HRH1	PR B [T00	1989	1995	8.338824	CTCTGTT	1.09863	1.09384
cg0883107	HRH1	PR A [T01	1661	1667	8.338824	AACAGC	1.09863	1.09384
cg0883107	HRH1	PR A [T01	1679	1685	8.338824	CCCTGTT	1.09863	1.09384
cg0883107	HRH1	PR A [T01	1989	1995	8.338824	CTCTGTT	1.09863	1.09384
cg0645773	HRH1	ATF3 [T0	1072	1079	8.313799	TGACGC	0.27466	0.27379
cg0883107	HRH1	ATF3 [T0	1010	1017	8.313799	TGACGC	0.27466	0.27379
cg0645773	HRH1	RelA [T00	339	349	8.296767	GTGGGA	0.0248	0.02561
cg0883107	HRH1	RelA [T00	277	287	8.296767	GTGGGA	0.0248	0.02561
cg0645773	HRH1	GR-alpha [	55	59	8.281568	CCTTG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	61	65	8.281568	CCTCC	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	171	175	8.281568	CCTCC	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	201	205	8.281568	CCTCC	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	239	243	8.281568	CAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	276	280	8.281568	CCTTG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	376	380	8.281568	CAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	445	449	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	479	483	8.281568	CCTTG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	484	488	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	586	590	8.281568	CAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	731	735	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	755	759	8.281568	GAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	824	828	8.281568	GAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	841	845	8.281568	CCTTC	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	928	932	8.281568	CAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	969	973	8.281568	CGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1126	1130	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1180	1184	8.281568	CAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1183	1187	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1452	1456	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1548	1552	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1591	1595	8.281568	CAAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1598	1602	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1648	1652	8.281568	GGAGG	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1706	1710	8.281568	CCTTC	7.8125	8.20394
cg0645773	HRH1	GR-alpha [	1764	1768	8.281568	CCTCC	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	109	113	8.281568	CCTCC	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	139	143	8.281568	CCTCC	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	177	181	8.281568	CAAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	214	218	8.281568	CCTTG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	314	318	8.281568	CAAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	383	387	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	417	421	8.281568	CCTTG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	422	426	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	524	528	8.281568	CAAGG	7.8125	8.20394

cg0883107	HRH1	GR-alpha [	669	673	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	693	697	8.281568	GAAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	762	766	8.281568	GAAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	779	783	8.281568	CCTTC	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	866	870	8.281568	CAAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	907	911	8.281568	CGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1064	1068	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1118	1122	8.281568	CAAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1121	1125	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1390	1394	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1486	1490	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1529	1533	8.281568	CAAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1536	1540	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1586	1590	8.281568	GGAGG	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1644	1648	8.281568	CCTTC	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1702	1706	8.281568	CCTCC	7.8125	8.20394
cg0883107	HRH1	GR-alpha [	1955	1959	8.281568	CAAGG	7.8125	8.20394
cg0645773	HRH1	c-Jun [T00	34	40	8.242207	TGACCT	0.48828	0.47447
cg0645773	HRH1	NFI/CTF [	519	526	8.241664	CCAACC	0.18311	0.1922
cg0883107	HRH1	NFI/CTF [	457	464	8.241664	CCAACC	0.18311	0.1922
cg0645773	HRH1	NF-AT1 [	973	981	8.236182	GCTCTT	0.1297	0.12846
cg0883107	HRH1	NF-AT1 [	911	919	8.236182	GCTCTT	0.1297	0.12846
cg0645773	HRH1	NF-AT1 [	342	350	8.223794	GGAAAG	0.1297	0.12846
cg0883107	HRH1	NF-AT1 [	280	288	8.223794	GGAAAG	0.1297	0.12846
cg0645773	HRH1	ENKTF-1	11	18	8.19852	TGGCCA	0.73242	0.80254
cg0645773	HRH1	ENKTF-1	300	307	8.19852	AGTCGC	0.73242	0.80254
cg0645773	HRH1	ENKTF-1	1858	1865	8.19852	TGGCGG	0.73242	0.80254
cg0883107	HRH1	ENKTF-1	238	245	8.19852	AGTCGC	0.73242	0.80254
cg0883107	HRH1	ENKTF-1	1796	1803	8.19852	TGGCGG	0.73242	0.80254
cg0645773	HRH1	NF-1 [T00	57	64	8.191058	TTGGCC	0.24414	0.24485
cg0645773	HRH1	c-Jun [T00	696	702	8.128539	AATGTC	0.48828	0.47447
cg0883107	HRH1	c-Jun [T00	634	640	8.128539	AATGTC	0.48828	0.47447
cg0645773	HRH1	LEF-1 [T0	1097	1104	8.117221	TTTCAA	0.12207	0.11275
cg0883107	HRH1	LEF-1 [T0	1035	1042	8.117221	TTTCAA	0.12207	0.11275
cg0645773	HRH1	VDR [T00	1341	1349	8.079962	GAAATG	0.24414	0.22992
cg0883107	HRH1	VDR [T00	1279	1287	8.079962	GAAATG	0.24414	0.22992
cg0645773	HRH1	GR-alpha [	14	18	8.073878	CCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	51	55	8.073878	CCTGC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	165	169	8.073878	CCTGC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	206	210	8.073878	CCTAC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	212	216	8.073878	CCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	219	223	8.073878	CCTGC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	251	255	8.073878	CCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	399	403	8.073878	CCTGC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	459	463	8.073878	CCTGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	467	471	8.073878	CCTGC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	530	534	8.073878	GTAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	537	541	8.073878	CCAGG	7.8125	8.20289

cg0645773	HRH1	GR-alpha [	852	856	8.073878	CCTGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	880	884	8.073878	CCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	895	899	8.073878	CTAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	932	936	8.073878	GCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	953	957	8.073878	CCTGC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1006	1010	8.073878	CCTAG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1024	1028	8.073878	CCTGC	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1279	1283	8.073878	CCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1399	1403	8.073878	CCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1420	1424	8.073878	CCTAG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1509	1513	8.073878	CCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1772	1776	8.073878	CCTGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1783	1787	8.073878	GCAGG	7.8125	8.20289
cg0645773	HRH1	GR-alpha [	1900	1904	8.073878	CCTAC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	103	107	8.073878	CCTGC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	144	148	8.073878	CCTAC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	150	154	8.073878	CCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	157	161	8.073878	CCTGC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	189	193	8.073878	CCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	337	341	8.073878	CCTGC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	397	401	8.073878	CCTGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	405	409	8.073878	CCTGC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	468	472	8.073878	GTAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	475	479	8.073878	CCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	790	794	8.073878	CCTGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	818	822	8.073878	CCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	833	837	8.073878	CTAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	870	874	8.073878	GCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	891	895	8.073878	CCTGC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	944	948	8.073878	CCTAG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	962	966	8.073878	CCTGC	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	1217	1221	8.073878	CCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	1337	1341	8.073878	CCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	1358	1362	8.073878	CCTAG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	1447	1451	8.073878	CCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	1710	1714	8.073878	CCTGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	1721	1725	8.073878	GCAGG	7.8125	8.20289
cg0883107	HRH1	GR-alpha [	1838	1842	8.073878	CCTAC	7.8125	8.20289
cg0883107	HRH1	AR [T000	1991	1999	8.055836	CTGTTG	0.19836	0.20641
cg0645773	HRH1	TFIID [T0	23	29	8.014558	TTGCAA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	291	297	8.014558	TTAGAA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	550	556	8.014558	TTTCTA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	554	560	8.014558	TAACAA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	714	720	8.014558	TTTGAG	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	1008	1014	8.014558	TAGCAA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	1097	1103	8.014558	TTTCAA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	1250	1256	8.014558	TTTGAT	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	1308	1314	8.014558	TAAGAA	2.19727	1.99811

cg0645773	HRH1	TFIID [T0	1851	1857	8.014558	TTTGTTA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	1931	1937	8.014558	TTAGAA	2.19727	1.99811
cg0645773	HRH1	TFIID [T0	1968	1974	8.014558	TTTGCA	2.19727	1.99811
cg0645773	HRH1	Pax-5 [T0	96	102	8.014558	TGTGCC	2.19727	2.42766
cg0645773	HRH1	Pax-5 [T0	616	622	8.014558	GGGCCT	2.19727	2.42766
cg0645773	HRH1	Pax-5 [T0	1283	1289	8.014558	GCAGCC	2.19727	2.42766
cg0645773	HRH1	Pax-5 [T0	1472	1478	8.014558	GGGCTG	2.19727	2.42766
cg0645773	HRH1	Pax-5 [T0	1660	1666	8.014558	TCAGCC	2.19727	2.42766
cg0645773	HRH1	Pax-5 [T0	1915	1921	8.014558	GGAGCC	2.19727	2.42766
cg0883107	HRH1	TFIID [T0	229	235	8.014558	TTAGAA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	488	494	8.014558	TTTCTAA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	492	498	8.014558	TAACAA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	652	658	8.014558	TTTGAG	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	946	952	8.014558	TAGCAA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	1035	1041	8.014558	TTTCAA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	1188	1194	8.014558	TTTGAT	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	1246	1252	8.014558	TAAGAA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	1789	1795	8.014558	TTTGTTA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	1869	1875	8.014558	TTAGAA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	1906	1912	8.014558	TTTGCA	2.19727	1.99811
cg0883107	HRH1	TFIID [T0	1972	1978	8.014558	TTTGAG	2.19727	1.99811
cg0883107	HRH1	Pax-5 [T0	34	40	8.014558	TGTGCC	2.19727	2.42766
cg0883107	HRH1	Pax-5 [T0	554	560	8.014558	GGGCCT	2.19727	2.42766
cg0883107	HRH1	Pax-5 [T0	1221	1227	8.014558	GCAGCC	2.19727	2.42766
cg0883107	HRH1	Pax-5 [T0	1410	1416	8.014558	GGGCTG	2.19727	2.42766
cg0883107	HRH1	Pax-5 [T0	1598	1604	8.014558	TCAGCC	2.19727	2.42766
cg0883107	HRH1	Pax-5 [T0	1853	1859	8.014558	GGAGCC	2.19727	2.42766
cg0645773	HRH1	USF2 [T0	1982	1991	8.007902	AGTACA	0.01717	0.01801
cg0883107	HRH1	USF2 [T0	1920	1929	8.007902	AGTACA	0.01717	0.01801
cg0883107	HRH1	USF2 [T0	1933	1942	8.007902	CAGGTG	0.01717	0.01801
cg0645773	HRH1	AhR:Arnt	1767	1776	8.006459	CCACGC	0.01717	0.01925
cg0883107	HRH1	AhR:Arnt	1705	1714	8.006459	CCACGC	0.01717	0.01925
cg0645773	HRH1	p53 [T006	1915	1921	7.833758	GGAGCC	0.48828	0.55336
cg0883107	HRH1	p53 [T006	1853	1859	7.833758	GGAGCC	0.48828	0.55336
cg0645773	HRH1	T3R-beta1	1453	1461	7.813363	GAGGGG	0.27466	0.28753
cg0883107	HRH1	T3R-beta1	1391	1399	7.813363	GAGGGG	0.27466	0.28753
cg0645773	HRH1	c-Ets-2 [T	364	372	7.76635	AGACAG	0.32043	0.30792
cg0645773	HRH1	c-Ets-2 [T	1376	1384	7.76635	AGACAG	0.32043	0.30792
cg0883107	HRH1	c-Ets-2 [T	302	310	7.76635	AGACAG	0.32043	0.30792
cg0883107	HRH1	c-Ets-2 [T	1314	1322	7.76635	AGACAG	0.32043	0.30792
cg0645773	HRH1	c-Myb [T0	1267	1274	7.662426	AGAAGT	0.42725	0.40917
cg0883107	HRH1	c-Myb [T0	1205	1212	7.662426	AGAAGT	0.42725	0.40917
cg0645773	HRH1	AR [T000	1269	1277	7.623968	AAGTTG	0.25177	0.2544
cg0645773	HRH1	AR [T000	1813	1821	7.623968	AAGTTG	0.25177	0.2544
cg0883107	HRH1	AR [T000	1207	1215	7.623968	AAGTTG	0.25177	0.2544
cg0883107	HRH1	AR [T000	1751	1759	7.623968	AAGTTG	0.25177	0.2544
cg0645773	HRH1	LEF-1 [T0	612	619	7.6105	CTTTGG	0.21362	0.21504
cg0883107	HRH1	LEF-1 [T0	550	557	7.6105	CTTTGG	0.21362	0.21504

cg0645773	HRH1	RBP-Jkapp	976	987	7.593528	CTTTCCC	0.02337	0.02319
cg0883107	HRH1	RBP-Jkapp	914	925	7.593528	CTTTCCC	0.02337	0.02319
cg0645773	HRH1	NFI/CTF [	351	358	7.587343	GCTTTTC	0.36621	0.36269
cg0645773	HRH1	NFI/CTF [	1120	1127	7.587343	GCACTT	0.36621	0.36269
cg0883107	HRH1	NFI/CTF [	289	296	7.587343	GCTTTTC	0.36621	0.36269
cg0883107	HRH1	NFI/CTF [	1058	1065	7.587343	GCACTT	0.36621	0.36269
cg0645773	HRH1	NF-AT1 [	369	377	7.574801	GGAAAA	0.19836	0.19379
cg0883107	HRH1	NF-AT1 [	307	315	7.574801	GGAAAA	0.19836	0.19379
cg0645773	HRH1	c-Myb [T0	327	334	7.545286	AGCAGT	0.42725	0.40917
cg0883107	HRH1	c-Myb [T0	265	272	7.545286	AGCAGT	0.42725	0.40917
cg0645773	HRH1	GR [T050	1100	1106	7.527031	CAAAGC	1.83105	1.71535
cg0645773	HRH1	GR [T050	1247	1253	7.527031	TCTTTTG	1.83105	1.71535
cg0645773	HRH1	GR [T050	1848	1854	7.527031	TCTTTTG	1.83105	1.71535
cg0645773	HRH1	GR [T050	1910	1916	7.527031	CAAAAG	1.83105	1.71535
cg0645773	HRH1	GR [T050	1965	1971	7.527031	ATATTTC	1.83105	1.71535
cg0883107	HRH1	GR [T050	1038	1044	7.527031	CAAAGC	1.83105	1.71535
cg0883107	HRH1	GR [T050	1185	1191	7.527031	TCTTTTG	1.83105	1.71535
cg0883107	HRH1	GR [T050	1786	1792	7.527031	TCTTTTG	1.83105	1.71535
cg0883107	HRH1	GR [T050	1848	1854	7.527031	CAAAAG	1.83105	1.71535
cg0883107	HRH1	GR [T050	1903	1909	7.527031	ATATTTC	1.83105	1.71535
cg0645773	HRH1	RAR-beta	987	996	7.47824	CCGGAA	0.24414	0.25121
cg0645773	HRH1	RAR-beta	1042	1051	7.47824	GCCTAA	0.24414	0.25121
cg0883107	HRH1	RAR-beta	925	934	7.47824	CCGGAA	0.24414	0.25121
cg0883107	HRH1	RAR-beta	980	989	7.47824	GCCTAA	0.24414	0.25121
cg0645773	HRH1	PEA3 [T0	159	167	7.421728	GAGCAT	0.34332	0.35389
cg0645773	HRH1	PEA3 [T0	1714	1722	7.421728	AGGATG	0.34332	0.35389
cg0883107	HRH1	PEA3 [T0	97	105	7.421728	GAGCAT	0.34332	0.35389
cg0883107	HRH1	PEA3 [T0	1652	1660	7.421728	AGGATG	0.34332	0.35389
cg0645773	HRH1	p53 [T006	254	260	7.266844	GGGCTT	0.73242	0.79826
cg0645773	HRH1	p53 [T006	1562	1568	7.266844	GGGCTG	0.73242	0.79826
cg0645773	HRH1	p53 [T006	1612	1618	7.266844	GGGCTG	0.73242	0.79826
cg0883107	HRH1	p53 [T006	192	198	7.266844	GGGCTT	0.73242	0.79826
cg0883107	HRH1	p53 [T006	1500	1506	7.266844	GGGCTG	0.73242	0.79826
cg0883107	HRH1	p53 [T006	1550	1556	7.266844	GGGCTG	0.73242	0.79826
cg0645773	HRH1	c-Ets-1 [T	340	346	7.199436	TGGGAA	0.73242	0.73732
cg0645773	HRH1	c-Ets-1 [T	977	983	7.199436	TTTCCCA	0.73242	0.73732
cg0645773	HRH1	c-Ets-1 [T	1141	1147	7.199436	TGGGAA	0.73242	0.73732
cg0883107	HRH1	c-Ets-1 [T	278	284	7.199436	TGGGAA	0.73242	0.73732
cg0883107	HRH1	c-Ets-1 [T	915	921	7.199436	TTTCCCA	0.73242	0.73732
cg0883107	HRH1	c-Ets-1 [T	1079	1085	7.199436	TGGGAA	0.73242	0.73732
cg0645773	HRH1	XBP-1 [T	153	158	7.172312	ATGATG	2.92969	2.7512
cg0645773	HRH1	XBP-1 [T	569	574	7.172312	ATGATT	2.92969	2.7512
cg0645773	HRH1	XBP-1 [T	753	758	7.172312	ATGAAG	2.92969	2.7512
cg0645773	HRH1	XBP-1 [T	916	921	7.172312	ACTCAT	2.92969	2.7512
cg0645773	HRH1	XBP-1 [T	1092	1097	7.172312	CCTCAT	2.92969	2.7512
cg0645773	HRH1	XBP-1 [T	1491	1496	7.172312	ATGATG	2.92969	2.7512
cg0645773	HRH1	XBP-1 [T	1606	1611	7.172312	CATCAT	2.92969	2.7512
cg0645773	HRH1	XBP-1 [T	1974	1979	7.172312	ACTCAT	2.92969	2.7512

cg0883107	HRH1	XBP-1 [T	91	96	7.172312	ATGATG	2.92969	2.7512
cg0883107	HRH1	XBP-1 [T	507	512	7.172312	ATGATT	2.92969	2.7512
cg0883107	HRH1	XBP-1 [T	691	696	7.172312	ATGAAG	2.92969	2.7512
cg0883107	HRH1	XBP-1 [T	854	859	7.172312	ACTCAT	2.92969	2.7512
cg0883107	HRH1	XBP-1 [T	1030	1035	7.172312	CCTCAT	2.92969	2.7512
cg0883107	HRH1	XBP-1 [T	1429	1434	7.172312	ATGATG	2.92969	2.7512
cg0883107	HRH1	XBP-1 [T	1544	1549	7.172312	CATCAT	2.92969	2.7512
cg0883107	HRH1	XBP-1 [T	1912	1917	7.172312	ACTCAT	2.92969	2.7512
cg0645773	HRH1	p53 [T006	763	769	7.150251	GGGCCA	1.09863	1.22478
cg0883107	HRH1	p53 [T006	701	707	7.150251	GGGCCA	1.09863	1.22478
cg0645773	HRH1	Ik-1 [T027	1016	1028	7.122895	TCCCAG	0.01064	0.01145
cg0883107	HRH1	Ik-1 [T027	954	966	7.122895	TCCCAG	0.01064	0.01145
cg0645773	HRH1	HNF-3alp	548	555	7.000129	TATTTCT	0.82397	0.71909
cg0645773	HRH1	HNF-3alp	1925	1932	7.000129	TGTAAA	0.82397	0.71909
cg0645773	HRH1	HNF-3alp	1966	1973	7.000129	TATTTG	0.82397	0.71909
cg0883107	HRH1	HNF-3alp	486	493	7.000129	TATTTCT	0.82397	0.71909
cg0883107	HRH1	HNF-3alp	1863	1870	7.000129	TGTAAA	0.82397	0.71909
cg0883107	HRH1	HNF-3alp	1904	1911	7.000129	TATTTG	0.82397	0.71909
cg0645773	HRH1	IRF-1 [T0	1139	1147	6.968314	GCTGGG	0.1297	0.12685
cg0883107	HRH1	IRF-1 [T0	1077	1085	6.968314	GCTGGG	0.1297	0.12685
cg0645773	HRH1	c-Ets-1 [T	625	631	6.943262	TTTCCC	0.73242	0.73732
cg0883107	HRH1	c-Ets-1 [T	563	569	6.943262	TTTCCC	0.73242	0.73732
cg0645773	HRH1	ENKTF-1	334	341	6.942764	TGGCAG	1.46484	1.56616
cg0645773	HRH1	ENKTF-1	680	687	6.942764	CACGGC	1.46484	1.56616
cg0645773	HRH1	ENKTF-1	1274	1281	6.942764	GTCCGC	1.46484	1.56616
cg0645773	HRH1	ENKTF-1	1881	1888	6.942764	TGGCTG	1.46484	1.56616
cg0883107	HRH1	ENKTF-1	272	279	6.942764	TGGCAG	1.46484	1.56616
cg0883107	HRH1	ENKTF-1	618	625	6.942764	CACGGC	1.46484	1.56616
cg0883107	HRH1	ENKTF-1	1212	1219	6.942764	GTCCGC	1.46484	1.56616
cg0883107	HRH1	ENKTF-1	1819	1826	6.942764	TGGCTG	1.46484	1.56616
cg0645773	HRH1	p53 [T006	616	622	6.938545	GGGCCT	1.09863	1.22478
cg0883107	HRH1	p53 [T006	554	560	6.938545	GGGCCT	1.09863	1.22478
cg0645773	HRH1	c-Jun [T00	1149	1155	6.856451	TGACCA	0.73242	0.73062
cg0883107	HRH1	c-Jun [T00	1087	1093	6.856451	TGACCA	0.73242	0.73062
cg0645773	HRH1	C/EBPalp	135	141	6.85549	TTCAAT	0.73242	0.68282
cg0883107	HRH1	C/EBPalp	73	79	6.85549	TTCAAT	0.73242	0.68282
cg0645773	HRH1	NFI/CTF [	329	336	6.786076	CAGTTT	0.73242	0.74795
cg0645773	HRH1	NFI/CTF [	1525	1532	6.786076	CTGATT	0.73242	0.74795
cg0645773	HRH1	NFI/CTF [	1574	1581	6.786076	CTGATT	0.73242	0.74795
cg0645773	HRH1	NFI/CTF [	1624	1631	6.786076	CTGATT	0.73242	0.74795
cg0883107	HRH1	NFI/CTF [	267	274	6.786076	CAGTTT	0.73242	0.74795
cg0883107	HRH1	NFI/CTF [	1463	1470	6.786076	CTGATT	0.73242	0.74795
cg0883107	HRH1	NFI/CTF [	1512	1519	6.786076	CTGATT	0.73242	0.74795
cg0883107	HRH1	NFI/CTF [	1562	1569	6.786076	CTGATT	0.73242	0.74795
cg0645773	HRH1	LEF-1 [T0	670	677	6.75468	CTTTGA	0.06104	0.05927
cg0883107	HRH1	LEF-1 [T0	608	615	6.75468	CTTTGA	0.06104	0.05927
cg0645773	HRH1	TCF-4 [T0	669	678	6.735684	TCTTTG	0.04959	0.04686
cg0883107	HRH1	TCF-4 [T0	607	616	6.735684	TCTTTG	0.04959	0.04686

cg0645773	HRH1	NF-1 [T00	10	17	6.722386	TTGGCC	0.24414	0.2565
cg0645773	HRH1	c-Myb [T0	180	187	6.719843	CAACTC	0.30518	0.30272
cg0883107	HRH1	c-Myb [T0	118	125	6.719843	CAACTC	0.30518	0.30272
cg0645773	HRH1	T3R-beta1	908	916	6.664094	CTCGGG	0.21362	0.2251
cg0883107	HRH1	T3R-beta1	846	854	6.664094	CTCGGG	0.21362	0.2251
cg0645773	HRH1	c-Fos [T00	1171	1180	6.660217	GAGTCA	0.04578	0.04485
cg0883107	HRH1	c-Fos [T00	1109	1118	6.660217	GAGTCA	0.04578	0.04485
cg0645773	HRH1	E2F-1 [T0	1413	1420	6.611004	ATTACC	0.12207	0.1297
cg0883107	HRH1	E2F-1 [T0	1351	1358	6.611004	ATTACC	0.12207	0.1297
cg0645773	HRH1	HNF-1C [	488	496	6.596946	GTTAAA	0.05341	0.04756
cg0883107	HRH1	HNF-1C [	426	434	6.596946	GTTAAA	0.05341	0.04756
cg0645773	HRH1	FOXP3 [T	640	645	6.581441	TAAAAC	0.97656	0.904
cg0645773	HRH1	TFII-I [T0	1188	1193	6.581441	GGAGTG	0.97656	0.9991
cg0645773	HRH1	TFII-I [T0	1538	1543	6.581441	GGAGTG	0.97656	0.9991
cg0645773	HRH1	TFII-I [T0	1637	1642	6.581441	GGAGTG	0.97656	0.9991
cg0883107	HRH1	FOXP3 [T	578	583	6.581441	TAAAAC	0.97656	0.904
cg0883107	HRH1	TFII-I [T0	1126	1131	6.581441	GGAGTG	0.97656	0.9991
cg0883107	HRH1	TFII-I [T0	1476	1481	6.581441	GGAGTG	0.97656	0.9991
cg0883107	HRH1	TFII-I [T0	1575	1580	6.581441	GGAGTG	0.97656	0.9991
cg0645773	HRH1	c-Ets-1 [T	987	993	6.565361	CCGGAA	0.48828	0.48842
cg0645773	HRH1	c-Ets-1 [T	1731	1737	6.565361	CCGGAA	0.48828	0.48842
cg0883107	HRH1	c-Ets-1 [T	925	931	6.565361	CCGGAA	0.48828	0.48842
cg0883107	HRH1	c-Ets-1 [T	1669	1675	6.565361	CCGGAA	0.48828	0.48842
cg0645773	HRH1	p53 [T006	1283	1289	6.563521	GCAGCC	0.48828	0.54643
cg0883107	HRH1	p53 [T006	1221	1227	6.563521	GCAGCC	0.48828	0.54643
cg0645773	HRH1	AR [T000	939	947	6.50872	TGTGTG	0.19836	0.20813
cg0883107	HRH1	AR [T000	877	885	6.50872	TGTGTG	0.19836	0.20813
cg0645773	HRH1	c-Jun [T00	1215	1221	6.475265	TGACAC	0.61035	0.6179
cg0883107	HRH1	c-Jun [T00	1153	1159	6.475265	TGACAC	0.61035	0.6179
cg0645773	HRH1	TCF-4E [T	744	750	6.302385	GGCAAA	0.61035	0.59686
cg0645773	HRH1	TCF-4E [T	1098	1104	6.302385	TTCAAA	0.61035	0.59686
cg0883107	HRH1	TCF-4E [T	682	688	6.302385	GGCAAA	0.61035	0.59686
cg0883107	HRH1	TCF-4E [T	1036	1042	6.302385	TTCAAA	0.61035	0.59686
cg0645773	HRH1	c-Jun [T00	411	417	6.293948	TGACCC	0.61035	0.6179
cg0883107	HRH1	c-Jun [T00	349	355	6.293948	TGACCC	0.61035	0.6179
cg0645773	HRH1	GR-alpha [	37	41	6.263098	CCTCA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	229	233	6.263098	CCTCA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	405	409	6.263098	CCTCA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	432	436	6.263098	CCTTA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	545	549	6.263098	CCTTA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	619	623	6.263098	CCTCA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	677	681	6.263098	CCTCA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	820	824	6.263098	TAAGG	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	994	998	6.263098	CCTTA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1092	1096	6.263098	CCTCA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1288	1292	6.263098	CCTCA	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1366	1370	6.263098	TGAGG	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1517	1521	6.263098	TGAGG	3.90625	3.89624

cg0645773	HRH1	GR-alpha [	1712	1716	6.263098	TGAGG	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1804	1808	6.263098	TGAGG	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1829	1833	6.263098	TGAGG	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1885	1889	6.263098	TGAGG	3.90625	3.89624
cg0645773	HRH1	GR-alpha [	1893	1897	6.263098	TAAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	167	171	6.263098	CCTCA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	343	347	6.263098	CCTCA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	370	374	6.263098	CCTTA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	483	487	6.263098	CCTTA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	557	561	6.263098	CCTCA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	615	619	6.263098	CCTCA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	758	762	6.263098	TAAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	932	936	6.263098	CCTTA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1030	1034	6.263098	CCTCA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1226	1230	6.263098	CCTCA	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1304	1308	6.263098	TGAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1455	1459	6.263098	TGAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1650	1654	6.263098	TGAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1742	1746	6.263098	TGAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1767	1771	6.263098	TGAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1823	1827	6.263098	TGAGG	3.90625	3.89624
cg0883107	HRH1	GR-alpha [	1831	1835	6.263098	TAAGG	3.90625	3.89624
cg0645773	HRH1	IRF-1 [T0	365	373	6.206911	GACAGG	0.16785	0.16217
cg0883107	HRH1	IRF-1 [T0	303	311	6.206911	GACAGG	0.16785	0.16217
cg0645773	HRH1	SRY [T00	1096	1104	6.176442	ATTTCA	0.15259	0.14742
cg0883107	HRH1	SRY [T00	1034	1042	6.176442	ATTTCA	0.15259	0.14742
cg0645773	HRH1	RXR-alph	206	212	6.119461	CCTACC	0.73242	0.78318
cg0883107	HRH1	RXR-alph	144	150	6.119461	CCTACC	0.73242	0.78318
cg0645773	HRH1	GR-alpha [	32	36	6.055408	CCTGA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	106	110	6.055408	CCTAA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	434	438	6.055408	TTAGG	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	808	812	6.055408	CCTAA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	818	822	6.055408	CCTAA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	864	868	6.055408	TCAGG	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	1028	1032	6.055408	CCTGA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	1043	1047	6.055408	CCTAA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	1070	1074	6.055408	CCTGA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	1364	1368	6.055408	CCTGA	3.90625	3.89835
cg0645773	HRH1	GR-alpha [	1988	1992	6.055408	CCTGA	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	44	48	6.055408	CCTAA	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	372	376	6.055408	TTAGG	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	746	750	6.055408	CCTAA	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	756	760	6.055408	CCTAA	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	802	806	6.055408	TCAGG	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	966	970	6.055408	CCTGA	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	981	985	6.055408	CCTAA	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	1008	1012	6.055408	CCTGA	3.90625	3.89835
cg0883107	HRH1	GR-alpha [	1302	1306	6.055408	CCTGA	3.90625	3.89835

cg0883107	HRH1	GR-alpha [	1926	1930	6.055408	CCTGA	3.90625	3.89835
cg0645773	HRH1	ATF-2 [T0	579	588	6.05134	CACACG	0.11826	0.11557
cg0883107	HRH1	ATF-2 [T0	517	526	6.05134	CACACG	0.11826	0.11557
cg0645773	HRH1	c-Myb [T0	1145	1152	6.04018	AAACTG	0.21362	0.2053
cg0883107	HRH1	c-Myb [T0	1083	1090	6.04018	AAACTG	0.21362	0.2053
cg0645773	HRH1	C/EBPalph	128	134	5.996794	CATTGG	0.97656	0.91422
cg0645773	HRH1	C/EBPalph	701	707	5.996794	CATTGT	0.97656	0.91422
cg0883107	HRH1	C/EBPalph	66	72	5.996794	CATTGG	0.97656	0.91422
cg0883107	HRH1	C/EBPalph	639	645	5.996794	CATTGT	0.97656	0.91422
cg0645773	HRH1	RXR-alph	911	917	5.937582	GGGTGA	0.73242	0.78318
cg0645773	HRH1	RXR-alph	1205	1211	5.937582	GGGTGC	0.73242	0.78318
cg0645773	HRH1	RXR-alph	1456	1462	5.937582	GGGTGA	0.73242	0.78318
cg0645773	HRH1	RXR-alph	1943	1949	5.937582	AGTACC	0.73242	0.78318
cg0883107	HRH1	RXR-alph	849	855	5.937582	GGGTGA	0.73242	0.78318
cg0883107	HRH1	RXR-alph	1143	1149	5.937582	GGGTGC	0.73242	0.78318
cg0883107	HRH1	RXR-alph	1394	1400	5.937582	GGGTGA	0.73242	0.78318
cg0883107	HRH1	RXR-alph	1881	1887	5.937582	AGTACC	0.73242	0.78318
cg0645773	HRH1	GCF [T00	785	793	5.917256	TTTCGG	0.64087	0.72542
cg0883107	HRH1	GCF [T00	723	731	5.917256	TTTCGG	0.64087	0.72542
cg0645773	HRH1	STAT4 [T	823	828	5.882353	GGAAGG	0.48828	0.51201
cg0645773	HRH1	STAT4 [T	841	846	5.882353	CCTTCC	0.48828	0.51201
cg0883107	HRH1	STAT4 [T	761	766	5.882353	GGAAGG	0.48828	0.51201
cg0883107	HRH1	STAT4 [T	779	784	5.882353	CCTTCC	0.48828	0.51201
cg0645773	HRH1	HNF-1B [	487	495	5.881318	GGTTAA	0.09918	0.08736
cg0883107	HRH1	HNF-1B [	425	433	5.881318	GGTTAA	0.09918	0.08736
cg0645773	HRH1	C/EBPalph	1409	1415	5.850545	GGCAAT	0.97656	0.91422
cg0883107	HRH1	C/EBPalph	1347	1353	5.850545	GGCAAT	0.97656	0.91422
cg0645773	HRH1	AP-1 [T00	1500	1508	5.818984	GACGAG	0.09155	0.09438
cg0883107	HRH1	AP-1 [T00	1438	1446	5.818984	GACGAG	0.09155	0.09438
cg0645773	HRH1	c-Ets-1 [T	721	727	5.814485	TGGGAA	0.36621	0.36174
cg0883107	HRH1	c-Ets-1 [T	659	665	5.814485	TGGGAA	0.36621	0.36174
cg0645773	HRH1	c-Fos [T00	910	919	5.679695	CGGGTG	0.04578	0.04712
cg0883107	HRH1	c-Fos [T00	848	857	5.679695	CGGGTG	0.04578	0.04712
cg0645773	HRH1	T3R-beta1	1398	1406	5.591999	GCCAGG	0.21362	0.21789
cg0883107	HRH1	T3R-beta1	1336	1344	5.591999	GCCAGG	0.21362	0.21789
cg0645773	HRH1	C/EBPalph	1527	1533	5.565669	GATTGG	0.73242	0.68229
cg0645773	HRH1	C/EBPalph	1576	1582	5.565669	GATTGG	0.73242	0.68229
cg0645773	HRH1	C/EBPalph	1626	1632	5.565669	GATTGG	0.73242	0.68229
cg0883107	HRH1	C/EBPalph	1465	1471	5.565669	GATTGG	0.73242	0.68229
cg0883107	HRH1	C/EBPalph	1514	1520	5.565669	GATTGG	0.73242	0.68229
cg0883107	HRH1	C/EBPalph	1564	1570	5.565669	GATTGG	0.73242	0.68229
cg0645773	HRH1	NFI/CTF [	845	852	5.558661	CCAAAC	0.54932	0.55504
cg0883107	HRH1	NFI/CTF [	783	790	5.558661	CCAAAC	0.54932	0.55504
cg0645773	HRH1	c-Ets-1 [T	1440	1446	5.558311	GGGGAA	0.36621	0.38732
cg0883107	HRH1	c-Ets-1 [T	1378	1384	5.558311	GGGGAA	0.36621	0.38732
cg0645773	HRH1	TFIID [T0	290	296	5.544826	TTTAGA	0.73242	0.65314
cg0883107	HRH1	TFIID [T0	228	234	5.544826	TTTAGA	0.73242	0.65314
cg0645773	HRH1	p53 [T006	1472	1478	5.508538	GGGCTG	0.61035	0.65765

cg0645773	HRH1	p53 [T006	1660	1666	5.508538	TCAGCC	0.61035	0.65765
cg0883107	HRH1	p53 [T006	1410	1416	5.508538	GGGCTG	0.61035	0.65765
cg0883107	HRH1	p53 [T006	1598	1604	5.508538	TCAGCC	0.61035	0.65765
cg0645773	HRH1	RAR-beta	844	853	5.389083	TCCAAA	0.15259	0.15813
cg0883107	HRH1	RAR-beta	782	791	5.389083	TCCAAA	0.15259	0.15813
cg0645773	HRH1	NF-1 [T00	1905	1912	5.377909	CAGCCC	0.24414	0.25051
cg0883107	HRH1	NF-1 [T00	1843	1850	5.377909	CAGCCC	0.24414	0.25051
cg0645773	HRH1	IRF-1 [T0	977	985	5.351774	TTTCCC	0.22888	0.21959
cg0883107	HRH1	IRF-1 [T0	915	923	5.351774	TTTCCC	0.22888	0.21959
cg0645773	HRH1	RXR-alph	513	519	5.271235	TCTACC	0.61035	0.65415
cg0645773	HRH1	RXR-alph	759	765	5.271235	GGGTGG	0.61035	0.65415
cg0645773	HRH1	RXR-alph	856	862	5.271235	GGGTAG	0.61035	0.65415
cg0883107	HRH1	RXR-alph	451	457	5.271235	TCTACC	0.61035	0.65415
cg0883107	HRH1	RXR-alph	697	703	5.271235	GGGTGG	0.61035	0.65415
cg0883107	HRH1	RXR-alph	794	800	5.271235	GGGTAG	0.61035	0.65415
cg0645773	HRH1	C/EBPalp	320	326	5.240291	TATTGC	0.97656	0.90302
cg0883107	HRH1	C/EBPalp	258	264	5.240291	TATTGC	0.97656	0.90302
cg0645773	HRH1	HNF-1C [	549	557	5.214027	ATTTCT	0.04578	0.04128
cg0883107	HRH1	HNF-1C [	487	495	5.214027	ATTTCT	0.04578	0.04128
cg0645773	HRH1	c-Ets-2 [T	818	826	5.162974	CCTAAG	0.13733	0.13279
cg0883107	HRH1	c-Ets-2 [T	756	764	5.162974	CCTAAG	0.13733	0.13279
cg0645773	HRH1	c-Fos [T00	886	895	5.119614	GAGTCA	0.02289	0.02181
cg0883107	HRH1	c-Fos [T00	824	833	5.119614	GAGTCA	0.02289	0.02181
cg0645773	HRH1	AP-1 [T00	883	891	5.112864	GGAGAG	0.12207	0.12309
cg0883107	HRH1	AP-1 [T00	821	829	5.112864	GGAGAG	0.12207	0.12309
cg0645773	HRH1	AP-2alpha	1937	1942	5.100982	AAAGGC	0.97656	0.97517
cg0883107	HRH1	AP-2alpha	1875	1880	5.100982	AAAGGC	0.97656	0.97517
cg0645773	HRH1	USF2 [T0	213	222	5.052423	CAGGTG	0.103	0.10797
cg0645773	HRH1	USF2 [T0	1400	1409	5.052423	CAGGTG	0.103	0.10797
cg0883107	HRH1	USF2 [T0	151	160	5.052423	CAGGTG	0.103	0.10797
cg0883107	HRH1	USF2 [T0	1338	1347	5.052423	CAGGTG	0.103	0.10797
cg0645773	HRH1	GR-beta [	76	80	5.042296	GGATT	3.90625	3.7093
cg0645773	HRH1	GR-beta [	319	323	5.042296	GTATT	3.90625	3.7093
cg0645773	HRH1	GR-beta [	437	441	5.042296	GGATT	3.90625	3.7093
cg0645773	HRH1	GR-beta [	495	499	5.042296	AATAC	3.90625	3.7093
cg0645773	HRH1	GR-beta [	835	839	5.042296	AATCC	3.90625	3.7093
cg0645773	HRH1	GR-beta [	1066	1070	5.042296	AATCC	3.90625	3.7093
cg0645773	HRH1	GR-beta [	1296	1300	5.042296	GGATT	3.90625	3.7093
cg0883107	HRH1	GR-beta [	14	18	5.042296	GGATT	3.90625	3.7093
cg0883107	HRH1	GR-beta [	257	261	5.042296	GTATT	3.90625	3.7093
cg0883107	HRH1	GR-beta [	375	379	5.042296	GGATT	3.90625	3.7093
cg0883107	HRH1	GR-beta [	433	437	5.042296	AATAC	3.90625	3.7093
cg0883107	HRH1	GR-beta [	773	777	5.042296	AATCC	3.90625	3.7093
cg0883107	HRH1	GR-beta [	1004	1008	5.042296	AATCC	3.90625	3.7093
cg0883107	HRH1	GR-beta [	1234	1238	5.042296	GGATT	3.90625	3.7093
cg0883107	HRH1	GR-beta [	1949	1953	5.042296	AATAC	3.90625	3.7093
cg0645773	HRH1	c-Ets-1 [T	842	848	5.038739	CTTCCA	0.48828	0.48026
cg0883107	HRH1	c-Ets-1 [T	780	786	5.038739	CTTCCA	0.48828	0.48026

cg0645773	HRH1	MAZ [T00	168	180	5.034163	GCCCCT	0.00611	0.00711
cg0883107	HRH1	MAZ [T00	106	118	5.034163	GCCCCT	0.00611	0.00711
cg0645773	HRH1	IRF-1 [T0	625	633	4.968836	TTTCCCC	0.1297	0.12724
cg0883107	HRH1	IRF-1 [T0	563	571	4.968836	TTTCCCC	0.1297	0.12724
cg0645773	HRH1	XBP-1 [T	1111	1116	4.894955	ATGCCG	0.97656	0.99839
cg0883107	HRH1	XBP-1 [T	1049	1054	4.894955	ATGCCG	0.97656	0.99839
cg0645773	HRH1	AP-2alpha	1042	1047	4.890408	GCCTAA	0.97656	0.97517
cg0883107	HRH1	AP-2alpha	980	985	4.890408	GCCTAA	0.97656	0.97517
cg0645773	HRH1	RXR-alph	508	514	4.86724	GGGTCT	0.48828	0.51407
cg0883107	HRH1	RXR-alph	446	452	4.86724	GGGTCT	0.48828	0.51407
cg0645773	HRH1	FOXP3 [T	294	299	4.756447	GAAAAC	2.92969	2.82
cg0645773	HRH1	TFII-I [T0	1488	1493	4.756447	GGAATG	2.92969	2.89715
cg0645773	HRH1	TFII-I [T0	1513	1518	4.756447	GGACTG	2.92969	2.89715
cg0883107	HRH1	FOXP3 [T	232	237	4.756447	GAAAAC	2.92969	2.82
cg0883107	HRH1	TFII-I [T0	1426	1431	4.756447	GGAATG	2.92969	2.89715
cg0883107	HRH1	TFII-I [T0	1451	1456	4.756447	GGACTG	2.92969	2.89715
cg0645773	HRH1	c-Ets-1 [T	359	365	4.654478	CTTCCA	0.85449	0.8381
cg0645773	HRH1	c-Ets-1 [T	591	597	4.654478	CTGGAA	0.85449	0.8381
cg0883107	HRH1	c-Ets-1 [T	297	303	4.654478	CTTCCA	0.85449	0.8381
cg0883107	HRH1	c-Ets-1 [T	529	535	4.654478	CTGGAA	0.85449	0.8381
cg0645773	HRH1	AP-1 [T00	1599	1607	4.553988	GAGGAG	0.03052	0.03196
cg0883107	HRH1	AP-1 [T00	1537	1545	4.553988	GAGGAG	0.03052	0.03196
cg0645773	HRH1	IRF-1 [T0	338	346	4.549799	AGTGGG	0.05341	0.05056
cg0883107	HRH1	IRF-1 [T0	276	284	4.549799	AGTGGG	0.05341	0.05056
cg0645773	HRH1	NF-kappa	197	207	4.443744	TGAGCC	0.03242	0.03571
cg0883107	HRH1	NF-kappa	135	145	4.443744	TGAGCC	0.03242	0.03571
cg0645773	HRH1	c-Jun [T00	1571	1577	4.441904	TGACTG	0.12207	0.11843
cg0883107	HRH1	c-Jun [T00	1509	1515	4.441904	TGACTG	0.12207	0.11843
cg0645773	HRH1	AP-2alpha	895	900	4.438035	CTAGGC	0.97656	0.99839
cg0645773	HRH1	AP-2alpha	1419	1424	4.438035	GCCTAG	0.97656	0.99839
cg0883107	HRH1	AP-2alpha	833	838	4.438035	CTAGGC	0.97656	0.99839
cg0883107	HRH1	AP-2alpha	1357	1362	4.438035	GCCTAG	0.97656	0.99839
cg0645773	HRH1	AP-2alpha	431	436	4.422424	GCCTTA	0.97656	0.99839
cg0883107	HRH1	AP-2alpha	369	374	4.422424	GCCTTA	0.97656	0.99839
cg0645773	HRH1	STAT4 [T	358	363	4.411765	GCTTCC	1.95312	1.99838
cg0645773	HRH1	STAT4 [T	593	598	4.411765	GGAAGC	1.95312	1.99838
cg0645773	HRH1	STAT4 [T	723	728	4.411765	GGAAGA	1.95312	1.99838
cg0645773	HRH1	STAT4 [T	1231	1236	4.411765	GCTTCC	1.95312	1.99838
cg0645773	HRH1	STAT4 [T	1381	1386	4.411765	GGAAGC	1.95312	1.99838
cg0645773	HRH1	STAT4 [T	1442	1447	4.411765	GGAAGA	1.95312	1.99838
cg0645773	HRH1	STAT4 [T	1488	1493	4.411765	GGAATG	1.95312	1.99838
cg0645773	HRH1	STAT4 [T	1733	1738	4.411765	GGAACG	1.95312	1.99838
cg0883107	HRH1	STAT4 [T	296	301	4.411765	GCTTCC	1.95312	1.99838
cg0883107	HRH1	STAT4 [T	531	536	4.411765	GGAAGC	1.95312	1.99838
cg0883107	HRH1	STAT4 [T	661	666	4.411765	GGAAGA	1.95312	1.99838
cg0883107	HRH1	STAT4 [T	1169	1174	4.411765	GCTTCC	1.95312	1.99838
cg0883107	HRH1	STAT4 [T	1319	1324	4.411765	GGAAGC	1.95312	1.99838
cg0883107	HRH1	STAT4 [T	1380	1385	4.411765	GGAAGA	1.95312	1.99838

cg0883107	HRH1	STAT4 [T	1426	1431	4.411765	GGAATG	1.95312	1.99838
cg0883107	HRH1	STAT4 [T	1671	1676	4.411765	GGAACG	1.95312	1.99838
cg0645773	HRH1	RAR-beta	795	804	4.326039	GGGGTT	0.14496	0.14853
cg0883107	HRH1	RAR-beta	733	742	4.326039	GGGGTT	0.14496	0.14853
cg0645773	HRH1	RAR-beta	106	115	4.307573	CCTAAA	0.14496	0.14853
cg0883107	HRH1	RAR-beta	44	53	4.307573	CCTAAA	0.14496	0.14853
cg0645773	HRH1	HNF-1B [	1691	1699	4.252262	AGTTAT	0.05341	0.04718
cg0883107	HRH1	HNF-1B [	1629	1637	4.252262	AGTTAT	0.05341	0.04718
cg0645773	HRH1	RXR-alph	410	416	4.24113	GTGACC	0.97656	1.02803
cg0883107	HRH1	RXR-alph	348	354	4.24113	GTGACC	0.97656	1.02803
cg0645773	HRH1	C/EBPalp	1694	1700	4.235345	TATTGA	0.48828	0.46347
cg0883107	HRH1	C/EBPalp	1632	1638	4.235345	TATTGA	0.48828	0.46347
cg0645773	HRH1	Elk-1 [T00	819	827	4.204473	CTAAGG	0.09155	0.08816
cg0883107	HRH1	Elk-1 [T00	757	765	4.204473	CTAAGG	0.09155	0.08816
cg0645773	HRH1	GR-beta [	547	551	4.201913	TTATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	570	574	4.201913	TGATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	602	606	4.201913	CGATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1056	1060	4.201913	TTATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1315	1319	4.201913	AATCA	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1476	1480	4.201913	TGATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1526	1530	4.201913	TGATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1575	1579	4.201913	TGATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1625	1629	4.201913	TGATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1693	1697	4.201913	TTATT	7.8125	7.23274
cg0645773	HRH1	GR-beta [	1697	1701	4.201913	TGATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	485	489	4.201913	TTATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	508	512	4.201913	TGATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	540	544	4.201913	CGATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	994	998	4.201913	TTATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	1253	1257	4.201913	AATCA	7.8125	7.23274
cg0883107	HRH1	GR-beta [	1414	1418	4.201913	TGATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	1464	1468	4.201913	TGATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	1513	1517	4.201913	TGATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	1563	1567	4.201913	TGATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	1631	1635	4.201913	TTATT	7.8125	7.23274
cg0883107	HRH1	GR-beta [	1635	1639	4.201913	TGATT	7.8125	7.23274
cg0645773	HRH1	c-Jun [T00	1502	1508	4.1298	CGAGTC	0.24414	0.23729
cg0883107	HRH1	c-Jun [T00	1440	1446	4.1298	CGAGTC	0.24414	0.23729
cg0645773	HRH1	p53 [T006	101	107	4.125254	CCGGCC	0.73242	0.82434
cg0883107	HRH1	p53 [T006	39	45	4.125254	CCGGCC	0.73242	0.82434
cg0883107	HRH1	c-Ets-2 [T	1953	1961	4.091811	CACAAG	0.16022	0.15061
cg0645773	HRH1	RXR-alph	875	881	4.019014	CACACC	0.97656	1.02803
cg0883107	HRH1	RXR-alph	813	819	4.019014	CACACC	0.97656	1.02803
cg0645773	HRH1	TFIID [T0	121	127	4.007279	TTTTAA	1.09863	0.94722
cg0645773	HRH1	TFIID [T0	1306	1312	4.007279	TTTAAG	1.09863	0.94722
cg0645773	HRH1	Pax-5 [T0	254	260	4.007279	GGGCTT	1.09863	1.18533
cg0645773	HRH1	Pax-5 [T0	1463	1469	4.007279	GGGCTC	1.09863	1.18533
cg0645773	HRH1	Pax-5 [T0	1562	1568	4.007279	GGGCTG	1.09863	1.18533

cg0645773	HRH1	Pax-5 [T0	1612	1618	4.007279	GGGCTG	1.09863	1.18533
cg0883107	HRH1	TFIID [T0	59	65	4.007279	TTTTAA	1.09863	0.94722
cg0883107	HRH1	TFIID [T0	1244	1250	4.007279	TTTAAG	1.09863	0.94722
cg0883107	HRH1	Pax-5 [T0	192	198	4.007279	GGGCTT	1.09863	1.18533
cg0883107	HRH1	Pax-5 [T0	1401	1407	4.007279	GGGCTC	1.09863	1.18533
cg0883107	HRH1	Pax-5 [T0	1500	1506	4.007279	GGGCTG	1.09863	1.18533
cg0883107	HRH1	Pax-5 [T0	1550	1556	4.007279	GGGCTG	1.09863	1.18533
cg0645773	HRH1	AP-2alpha	54	59	3.970052	GCCTTG	0.97656	1.02535
cg0645773	HRH1	AP-2alpha	239	244	3.970052	CAAGGC	0.97656	1.02535
cg0645773	HRH1	AP-2alpha	376	381	3.970052	CAAGGC	0.97656	1.02535
cg0645773	HRH1	AP-2alpha	586	591	3.970052	CAAGGC	0.97656	1.02535
cg0645773	HRH1	AP-2alpha	928	933	3.970052	CAAGGC	0.97656	1.02535
cg0883107	HRH1	AP-2alpha	177	182	3.970052	CAAGGC	0.97656	1.02535
cg0883107	HRH1	AP-2alpha	314	319	3.970052	CAAGGC	0.97656	1.02535
cg0883107	HRH1	AP-2alpha	524	529	3.970052	CAAGGC	0.97656	1.02535
cg0883107	HRH1	AP-2alpha	866	871	3.970052	CAAGGC	0.97656	1.02535
cg0645773	HRH1	NF-Y [T0	1528	1535	3.95898	ATTGGA	0.18311	0.17499
cg0645773	HRH1	NF-Y [T0	1577	1584	3.95898	ATTGGA	0.18311	0.17499
cg0645773	HRH1	NF-Y [T0	1627	1634	3.95898	ATTGGA	0.18311	0.17499
cg0883107	HRH1	NF-Y [T0	1466	1473	3.95898	ATTGGA	0.18311	0.17499
cg0883107	HRH1	NF-Y [T0	1515	1522	3.95898	ATTGGA	0.18311	0.17499
cg0883107	HRH1	NF-Y [T0	1565	1572	3.95898	ATTGGA	0.18311	0.17499
cg0645773	HRH1	c-Jun [T00	1160	1166	3.807346	TTAGTC	0.24414	0.23729
cg0883107	HRH1	c-Jun [T00	1098	1104	3.807346	TTAGTC	0.24414	0.23729
cg0645773	HRH1	GR [T050	610	616	3.763516	TTCTTTG	0.73242	0.6946
cg0645773	HRH1	GR [T050	668	674	3.763516	TTCTTTG	0.73242	0.6946
cg0883107	HRH1	GR [T050	548	554	3.763516	TTCTTTG	0.73242	0.6946
cg0883107	HRH1	GR [T050	606	612	3.763516	TTCTTTG	0.73242	0.6946
cg0645773	HRH1	p53 [T006	223	229	3.750231	CAAGCC	0.73242	0.82434
cg0645773	HRH1	p53 [T006	1359	1365	3.750231	CAAGCC	0.73242	0.82434
cg0645773	HRH1	p53 [T006	1904	1910	3.750231	CCAGCC	0.73242	0.82434
cg0883107	HRH1	p53 [T006	161	167	3.750231	CAAGCC	0.73242	0.82434
cg0883107	HRH1	p53 [T006	1297	1303	3.750231	CAAGCC	0.73242	0.82434
cg0883107	HRH1	p53 [T006	1842	1848	3.750231	CCAGCC	0.73242	0.82434
cg0645773	HRH1	AP-2alpha	824	829	3.743866	GAAGGC	0.48828	0.5124
cg0645773	HRH1	AP-2alpha	840	845	3.743866	GCCTTC	0.48828	0.5124
cg0883107	HRH1	AP-2alpha	762	767	3.743866	GAAGGC	0.48828	0.5124
cg0883107	HRH1	AP-2alpha	778	783	3.743866	GCCTTC	0.48828	0.5124
cg0645773	HRH1	EBF [T05	1361	1371	3.738028	AGCCCT	0.00381	0.0041
cg0883107	HRH1	EBF [T05	1299	1309	3.738028	AGCCCT	0.00381	0.0041
cg0645773	HRH1	CREB [T0	579	587	3.729071	CACACG	0.10681	0.10808
cg0883107	HRH1	CREB [T0	517	525	3.729071	CACACG	0.10681	0.10808
cg0883107	HRH1	c-Ets-1 [T	1956	1962	3.71855	AAGGAA	0.61035	0.61936
cg0645773	HRH1	c-Ets-1 [T	1886	1892	3.590463	GAGGAA	0.61035	0.61936
cg0883107	HRH1	c-Ets-1 [T	1824	1830	3.590463	GAGGAA	0.61035	0.61936
cg0645773	HRH1	HNF-3alph	491	498	3.500065	AAAAAA	0.27466	0.23175
cg0645773	HRH1	HNF-3alph	1960	1967	3.500065	AGAAAA	0.27466	0.23175
cg0883107	HRH1	HNF-3alph	429	436	3.500065	AAAAAA	0.27466	0.23175

cg0883107	HRH1	HNF-3alp	1898	1905	3.500065	AGAAAA	0.27466	0.23175
cg0645773	HRH1	PPAR-alp	504	514	3.498013	GACTGG	0.01431	0.015
cg0883107	HRH1	PPAR-alp	442	452	3.498013	GACTGG	0.01431	0.015
cg0645773	HRH1	RXR-alph	989	995	3.392904	GGAACC	1.09863	1.1653
cg0883107	HRH1	RXR-alph	927	933	3.392904	GGAACC	1.09863	1.1653
cg0645773	HRH1	p53 [T006	1434	1440	3.375208	GGGCGT	0.73242	0.80362
cg0883107	HRH1	p53 [T006	1372	1378	3.375208	GGGCGT	0.73242	0.80362
cg0645773	HRH1	GR-beta [	664	668	3.361531	AATCT	3.90625	3.51525
cg0645773	HRH1	GR-beta [	1754	1758	3.361531	AGATT	3.90625	3.51525
cg0645773	HRH1	GR-beta [	1964	1968	3.361531	AATAT	3.90625	3.51525
cg0645773	HRH1	GR-beta [	1965	1969	3.361531	ATATT	3.90625	3.51525
cg0883107	HRH1	GR-beta [	602	606	3.361531	AATCT	3.90625	3.51525
cg0883107	HRH1	GR-beta [	1692	1696	3.361531	AGATT	3.90625	3.51525
cg0883107	HRH1	GR-beta [	1902	1906	3.361531	AATAT	3.90625	3.51525
cg0883107	HRH1	GR-beta [	1903	1907	3.361531	ATATT	3.90625	3.51525
cg0645773	HRH1	c-Ets-1 [T	1232	1238	3.359159	CTTCCG	0.61035	0.61936
cg0883107	HRH1	c-Ets-1 [T	1170	1176	3.359159	CTTCCG	0.61035	0.61936
cg0645773	HRH1	T3R-beta1	1506	1514	3.332047	TCACCA	0.27466	0.27326
cg0883107	HRH1	T3R-beta1	1444	1452	3.332047	TCACCA	0.27466	0.27326
cg0645773	HRH1	c-Ets-2 [T	1883	1891	3.2883	GCTGAG	0.18311	0.18314
cg0883107	HRH1	c-Ets-2 [T	1821	1829	3.2883	GCTGAG	0.18311	0.18314
cg0645773	HRH1	c-Jun [T00	885	891	3.244843	AGAGTC	0.24414	0.2435
cg0883107	HRH1	c-Jun [T00	823	829	3.244843	AGAGTC	0.24414	0.2435
cg0645773	HRH1	AP-2alpha	313	318	3.229049	GCCTCT	0.48828	0.5124
cg0645773	HRH1	AP-2alpha	424	429	3.229049	AGAGGC	0.48828	0.5124
cg0645773	HRH1	AP-2alpha	741	746	3.229049	AGAGGC	0.48828	0.5124
cg0645773	HRH1	AP-2alpha	1406	1411	3.229049	AGAGGC	0.48828	0.5124
cg0883107	HRH1	AP-2alpha	251	256	3.229049	GCCTCT	0.48828	0.5124
cg0883107	HRH1	AP-2alpha	362	367	3.229049	AGAGGC	0.48828	0.5124
cg0883107	HRH1	AP-2alpha	679	684	3.229049	AGAGGC	0.48828	0.5124
cg0883107	HRH1	AP-2alpha	1344	1349	3.229049	AGAGGC	0.48828	0.5124
cg0645773	HRH1	c-Fos [T00	1503	1512	3.081206	GAGTCA	0.06104	0.06233
cg0883107	HRH1	c-Fos [T00	1441	1450	3.081206	GAGTCA	0.06104	0.06233
cg0645773	HRH1	p53 [T006	96	102	3.028543	TGTGCC	0.48828	0.53227
cg0883107	HRH1	p53 [T006	34	40	3.028543	TGTGCC	0.48828	0.53227
cg0645773	HRH1	STAT4 [T	342	347	2.941176	GGAAAG	2.92969	2.92382
cg0645773	HRH1	STAT4 [T	462	467	2.941176	GGTTCC	2.92969	2.92382
cg0645773	HRH1	STAT4 [T	571	576	2.941176	GATTCC	2.92969	2.92382
cg0645773	HRH1	STAT4 [T	704	709	2.941176	TGTTCC	2.92969	2.92382
cg0645773	HRH1	STAT4 [T	976	981	2.941176	CTTTCC	2.92969	2.92382
cg0645773	HRH1	STAT4 [T	989	994	2.941176	GGAACC	2.92969	2.92382
cg0645773	HRH1	STAT4 [T	1064	1069	2.941176	GGAATC	2.92969	2.92382
cg0645773	HRH1	STAT4 [T	1721	1726	2.941176	GGAACA	2.92969	2.92382
cg0883107	HRH1	STAT4 [T	280	285	2.941176	GGAAAG	2.92969	2.92382
cg0883107	HRH1	STAT4 [T	400	405	2.941176	GGTTCC	2.92969	2.92382
cg0883107	HRH1	STAT4 [T	509	514	2.941176	GATTCC	2.92969	2.92382
cg0883107	HRH1	STAT4 [T	642	647	2.941176	TGTTCC	2.92969	2.92382
cg0883107	HRH1	STAT4 [T	914	919	2.941176	CTTTCC	2.92969	2.92382

cg0883107	HRH1	STAT4 [T	927	932	2.941176	GGAACC	2.92969	2.92382
cg0883107	HRH1	STAT4 [T	1002	1007	2.941176	GGAATC	2.92969	2.92382
cg0883107	HRH1	STAT4 [T	1659	1664	2.941176	GGAACA	2.92969	2.92382
cg0645773	HRH1	NF-1 [T00	614	621	2.813149	TTGGGC	0.24414	0.2566
cg0883107	HRH1	NF-1 [T00	552	559	2.813149	TTGGGC	0.24414	0.2566
cg0645773	HRH1	PR B [T00	126	132	2.80933	AACATT	0.73242	0.66711
cg0645773	HRH1	PR B [T00	701	707	2.80933	CATTGT	0.73242	0.66711
cg0645773	HRH1	PR A [T01	126	132	2.80933	AACATT	0.73242	0.66711
cg0645773	HRH1	PR A [T01	701	707	2.80933	CATTGT	0.73242	0.66711
cg0883107	HRH1	PR B [T00	64	70	2.80933	AACATT	0.73242	0.66711
cg0883107	HRH1	PR B [T00	639	645	2.80933	CATTGT	0.73242	0.66711
cg0883107	HRH1	PR A [T01	64	70	2.80933	AACATT	0.73242	0.66711
cg0883107	HRH1	PR A [T01	639	645	2.80933	CATTGT	0.73242	0.66711
cg0645773	HRH1	TBP [T007	736	745	2.807313	TTTATAC	0.12207	0.10444
cg0883107	HRH1	TBP [T007	674	683	2.807313	TTTATAC	0.12207	0.10444
cg0645773	HRH1	RXR-alph	519	525	2.726556	CCAACC	0.85449	0.89683
cg0883107	HRH1	RXR-alph	457	463	2.726556	CCAACC	0.85449	0.89683
cg0645773	HRH1	c-Jun [T00	1601	1607	2.654872	GGAGTC	0.48828	0.48077
cg0883107	HRH1	c-Jun [T00	1539	1545	2.654872	GGAGTC	0.48828	0.48077
cg0645773	HRH1	PPAR-alph	1916	1926	2.642917	GAGCCC	0.00858	0.00898
cg0883107	HRH1	PPAR-alph	1854	1864	2.642917	GAGCCC	0.00858	0.00898
cg0645773	HRH1	AP-2alpha	618	623	2.550491	GCCTCA	0.48828	0.51216
cg0645773	HRH1	AP-2alpha	676	681	2.550491	GCCTCA	0.48828	0.51216
cg0645773	HRH1	AP-2alpha	1829	1834	2.550491	TGAGGC	0.48828	0.51216
cg0883107	HRH1	AP-2alpha	556	561	2.550491	GCCTCA	0.48828	0.51216
cg0883107	HRH1	AP-2alpha	614	619	2.550491	GCCTCA	0.48828	0.51216
cg0883107	HRH1	AP-2alpha	1767	1772	2.550491	TGAGGC	0.48828	0.51216
cg0645773	HRH1	RXR-alph	145	151	2.544678	TTCACCC	0.85449	0.89683
cg0883107	HRH1	RXR-alph	83	89	2.544678	TTCACCC	0.85449	0.89683
cg0645773	HRH1	c-Jun [T00	1052	1058	2.538231	TGACTT	0.48828	0.48077
cg0883107	HRH1	c-Jun [T00	990	996	2.538231	TGACTT	0.48828	0.48077
cg0645773	HRH1	PXR-1:RX	1345	1352	2.454225	TGAACT	0.12207	0.11843
cg0883107	HRH1	PXR-1:RX	1283	1290	2.454225	TGAACT	0.12207	0.11843
cg0645773	HRH1	C/EBPalph	1289	1295	2.441016	CTCAATC	0.48828	0.47439
cg0883107	HRH1	C/EBPalph	1227	1233	2.441016	CTCAATC	0.48828	0.47439
cg0645773	HRH1	Ik-1 [T027	66	78	2.374299	CAAAGT	0.00063	0.00068
cg0883107	HRH1	Ik-1 [T027	4	16	2.374299	CAAAGT	0.00063	0.00068
cg0645773	HRH1	HNF-1C [	1692	1700	2.372238	GTTATTC	0.04578	0.04064
cg0883107	HRH1	HNF-1C [	1630	1638	2.372238	GTTATTC	0.04578	0.04064
cg0645773	HRH1	c-Jun [T00	1072	1078	2.345465	TGACGC	0.48828	0.48077
cg0883107	HRH1	c-Jun [T00	1010	1016	2.345465	TGACGC	0.48828	0.48077
cg0645773	HRH1	GATA-2 [	1542	1550	2.222222	TGATAG	0.22888	0.21978
cg0883107	HRH1	GATA-2 [	1480	1488	2.222222	TGATAG	0.22888	0.21978
cg0883107	HRH1	GATA-1 [	1942	1947	2.176375	TATCCA	3.90625	3.79558
cg0645773	HRH1	Elk-1 [T00	1377	1385	2.164966	GACAGG	0.05341	0.05461
cg0883107	HRH1	Elk-1 [T00	1315	1323	2.164966	GACAGG	0.05341	0.05461
cg0645773	HRH1	AP-2alpha	969	974	2.098119	CGAGGC	0.97656	1.07805
cg0883107	HRH1	AP-2alpha	907	912	2.098119	CGAGGC	0.97656	1.07805

cg0645773	HRH1	AP-2alpha	60	65	1.871933	GCCTCC	0.97656	1.07805
cg0645773	HRH1	AP-2alpha	200	205	1.871933	GCCTCC	0.97656	1.07805
cg0883107	HRH1	AP-2alpha	138	143	1.871933	GCCTCC	0.97656	1.07805
cg0645773	HRH1	TFII-I [T0	262	267	1.824994	CTCTCC	0.48828	0.51201
cg0645773	HRH1	TFII-I [T0	448	453	1.824994	GGAGAG	0.48828	0.51201
cg0645773	HRH1	TFII-I [T0	883	888	1.824994	GGAGAG	0.48828	0.51201
cg0645773	HRH1	TFII-I [T0	1863	1868	1.824994	GGAGAG	0.48828	0.51201
cg0883107	HRH1	TFII-I [T0	200	205	1.824994	CTCTCC	0.48828	0.51201
cg0883107	HRH1	TFII-I [T0	386	391	1.824994	GGAGAG	0.48828	0.51201
cg0883107	HRH1	TFII-I [T0	821	826	1.824994	GGAGAG	0.48828	0.51201
cg0883107	HRH1	TFII-I [T0	1801	1806	1.824994	GGAGAG	0.48828	0.51201
cg0645773	HRH1	RXR-alph	1737	1743	1.696452	CGGACC	0.48828	0.52093
cg0883107	HRH1	RXR-alph	1675	1681	1.696452	CGGACC	0.48828	0.52093
cg0645773	HRH1	GR-beta [	138	142	1.680765	AATTC	3.90625	3.70067
cg0645773	HRH1	GR-beta [	1076	1080	1.680765	GCATT	3.90625	3.70067
cg0645773	HRH1	GR-beta [	1241	1245	1.680765	GCATT	3.90625	3.70067
cg0883107	HRH1	GR-beta [	76	80	1.680765	AATTC	3.90625	3.70067
cg0883107	HRH1	GR-beta [	1014	1018	1.680765	GCATT	3.90625	3.70067
cg0883107	HRH1	GR-beta [	1179	1183	1.680765	GCATT	3.90625	3.70067
cg0645773	HRH1	C/EBPbeta	10	13	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	57	60	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	65	68	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	130	133	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	238	241	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	333	336	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	355	358	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	481	484	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	519	522	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	575	578	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	614	617	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	634	637	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	845	848	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	927	930	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	946	949	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1124	1127	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1152	1155	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1529	1532	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1578	1581	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1628	1631	1.639871	TTGG	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1909	1912	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	3	6	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	68	71	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	176	179	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	271	274	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	293	296	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	419	422	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	457	460	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	513	516	1.639871	CCAA	15.625	15.23827

cg0883107	HRH1	C/EBPbeta	552	555	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	572	575	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	783	786	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	865	868	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	884	887	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1062	1065	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1090	1093	1.639871	CCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1467	1470	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1516	1519	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1566	1569	1.639871	TTGG	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1847	1850	1.639871	CCAA	15.625	15.23827
cg0645773	HRH1	XBP-1 [T	698	703	1.583727	TGTCAT	0.97656	0.94995
cg0645773	HRH1	XBP-1 [T	772	777	1.583727	GGTCAT	0.97656	0.94995
cg0645773	HRH1	XBP-1 [T	1214	1219	1.583727	ATGACA	0.97656	0.94995
cg0883107	HRH1	XBP-1 [T	636	641	1.583727	TGTCAT	0.97656	0.94995
cg0883107	HRH1	XBP-1 [T	710	715	1.583727	GGTCAT	0.97656	0.94995
cg0883107	HRH1	XBP-1 [T	1152	1157	1.583727	ATGACA	0.97656	0.94995
cg0645773	HRH1	c-Fos [T00	1602	1611	1.540603	GAGTCA	0.00763	0.00739
cg0883107	HRH1	c-Fos [T00	1540	1549	1.540603	GAGTCA	0.00763	0.00739
cg0645773	HRH1	TFIID [T0	1299	1305	1.537547	TTTTTCA	0.73242	0.65627
cg0645773	HRH1	Pax-5 [T0	1434	1440	1.537547	GGGCGT	0.73242	0.83087
cg0883107	HRH1	TFIID [T0	1237	1243	1.537547	TTTTTCA	0.73242	0.65627
cg0883107	HRH1	Pax-5 [T0	1372	1378	1.537547	GGGCGT	0.73242	0.83087
cg0645773	HRH1	E2F-1 [T0	1860	1867	1.490375	GCGGGA	0.06104	0.0656
cg0883107	HRH1	E2F-1 [T0	1798	1805	1.490375	GCGGGA	0.06104	0.0656
cg0645773	HRH1	RXR-alph	796	802	1.474336	GGGTTT	0.48828	0.52093
cg0645773	HRH1	RXR-alph	846	852	1.474336	CAAACC	0.48828	0.52093
cg0883107	HRH1	RXR-alph	734	740	1.474336	GGGTTT	0.48828	0.52093
cg0883107	HRH1	RXR-alph	784	790	1.474336	CAAACC	0.48828	0.52093
cg0645773	HRH1	STAT4 [T	138	143	1.470588	AATTCC	1.95312	1.90161
cg0645773	HRH1	STAT4 [T	369	374	1.470588	GGAAAA	1.95312	1.90161
cg0645773	HRH1	STAT4 [T	624	629	1.470588	GTTTCC	1.95312	1.90161
cg0645773	HRH1	STAT4 [T	1143	1148	1.470588	GGAAAC	1.95312	1.90161
cg0645773	HRH1	STAT4 [T	1888	1893	1.470588	GGAACT	1.95312	1.90161
cg0883107	HRH1	STAT4 [T	76	81	1.470588	AATTCC	1.95312	1.90161
cg0883107	HRH1	STAT4 [T	307	312	1.470588	GGAAAA	1.95312	1.90161
cg0883107	HRH1	STAT4 [T	562	567	1.470588	GTTTCC	1.95312	1.90161
cg0883107	HRH1	STAT4 [T	1081	1086	1.470588	GGAAAC	1.95312	1.90161
cg0883107	HRH1	STAT4 [T	1826	1831	1.470588	GGAACT	1.95312	1.90161
cg0883107	HRH1	STAT4 [T	1958	1963	1.470588	GGAACT	1.95312	1.90161
cg0645773	HRH1	PR B [T00	1668	1674	1.404665	CAGTGT	0.36621	0.35143
cg0645773	HRH1	PR A [T01	1668	1674	1.404665	CAGTGT	0.36621	0.35143
cg0883107	HRH1	PR B [T00	1606	1612	1.404665	CAGTGT	0.36621	0.35143
cg0883107	HRH1	PR A [T01	1606	1612	1.404665	CAGTGT	0.36621	0.35143
cg0645773	HRH1	c-Ets-1 [T	367	373	1.384951	CAGGAA	0.36621	0.35197
cg0883107	HRH1	c-Ets-1 [T	305	311	1.384951	CAGGAA	0.36621	0.35197
cg0645773	HRH1	C/EBPbeta	39	42	1.366559	TCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	136	139	1.366559	TCAA	15.625	15.23827

cg0645773	HRH1	C/EBPbeta	278	281	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	585	588	1.366559	TCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	672	675	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	715	718	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	800	803	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1099	1102	1.366559	TCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1179	1182	1.366559	TCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1251	1254	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1290	1293	1.366559	TCAA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1680	1683	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1696	1699	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1700	1703	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1711	1714	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	C/EBPbeta	1824	1827	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	74	77	1.366559	TCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	216	219	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	523	526	1.366559	TCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	610	613	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	653	656	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	738	741	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1037	1040	1.366559	TCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1117	1120	1.366559	TCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1189	1192	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1228	1231	1.366559	TCAA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1618	1621	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1634	1637	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1638	1641	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1649	1652	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1762	1765	1.366559	TTGA	15.625	15.23827
cg0883107	HRH1	C/EBPbeta	1973	1976	1.366559	TTGA	15.625	15.23827
cg0645773	HRH1	AP-2alpha	936	941	1.357116	GCCTGT	0.48828	0.51319
cg0645773	HRH1	AP-2alpha	958	963	1.357116	ACAGGC	0.48828	0.51319
cg0883107	HRH1	AP-2alpha	874	879	1.357116	GCCTGT	0.48828	0.51319
cg0883107	HRH1	AP-2alpha	896	901	1.357116	ACAGGC	0.48828	0.51319
cg0645773	HRH1	p53 [T006	1000	1006	1.270236	CGTGCC	0.12207	0.13816
cg0883107	HRH1	p53 [T006	938	944	1.270236	CGTGCC	0.12207	0.13816
cg0645773	HRH1	TCF-4 [T0	1096	1105	1.235198	ATTTCA	0.05722	0.05422
cg0883107	HRH1	TCF-4 [T0	1034	1043	1.235198	ATTTCA	0.05722	0.05422
cg0645773	HRH1	PEA3 [T0	270	278	1.194633	GAACAT	0.06866	0.06787
cg0883107	HRH1	PEA3 [T0	208	216	1.194633	GAACAT	0.06866	0.06787
cg0645773	HRH1	T3R-beta1	1565	1573	1.110682	CTGTGG	0.07629	0.07886
cg0883107	HRH1	T3R-beta1	1503	1511	1.110682	CTGTGG	0.07629	0.07886
cg0645773	HRH1	GCF [T00	790	798	1.070269	GCGCTG	0.18311	0.21473
cg0883107	HRH1	GCF [T00	728	736	1.070269	GCGCTG	0.18311	0.21473
cg0645773	HRH1	NF-Y [T0	129	136	1.058936	ATTGGT	0.12207	0.11765
cg0883107	HRH1	NF-Y [T0	67	74	1.058936	ATTGGT	0.12207	0.11765
cg0645773	HRH1	GATA-1 [	278	283	1.038567	TTGATA	1.95312	1.80234
cg0645773	HRH1	GATA-1 [	1251	1256	1.038567	TTGATA	1.95312	1.80234

cg0883107	HRH1	GATA-1 [	216	221	1.038567	TTGATA	1.95312	1.80234
cg0883107	HRH1	GATA-1 [	1189	1194	1.038567	TTGATA	1.95312	1.80234
cg0645773	HRH1	EBF [T05	849	859	0.984797	ACCCCT	0.00763	0.00886
cg0883107	HRH1	EBF [T05	787	797	0.984797	ACCCCT	0.00763	0.00886
cg0645773	HRH1	GATA-1 [	1541	1546	0.863549	GTGATA	1.95312	1.80234
cg0883107	HRH1	GATA-1 [	1479	1484	0.863549	GTGATA	1.95312	1.80234
cg0645773	HRH1	RXR-alph	1044	1050	0.848226	CTAACC	0.48828	0.51313
cg0883107	HRH1	RXR-alph	982	988	0.848226	CTAACC	0.48828	0.51313
cg0645773	HRH1	GR-beta [	118	122	0.840383	TCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	137	141	0.840383	CAATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	142	146	0.840383	CCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	309	313	0.840383	AATGG	7.8125	7.2174
cg0645773	HRH1	GR-beta [	700	704	0.840383	TCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	709	713	0.840383	CCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	728	732	0.840383	AATGG	7.8125	7.2174
cg0645773	HRH1	GR-beta [	774	778	0.840383	TCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	889	893	0.840383	TCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1094	1098	0.840383	TCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1292	1296	0.840383	AATGG	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1303	1307	0.840383	TCATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1343	1347	0.840383	AATGA	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1411	1415	0.840383	CAATT	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1412	1416	0.840383	AATTA	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1449	1453	0.840383	AATGG	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1490	1494	0.840383	AATGA	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1929	1933	0.840383	AATTA	7.8125	7.2174
cg0645773	HRH1	GR-beta [	1954	1958	0.840383	AATGG	7.8125	7.2174
cg0883107	HRH1	GR-beta [	56	60	0.840383	TCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	75	79	0.840383	CAATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	80	84	0.840383	CCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	247	251	0.840383	AATGG	7.8125	7.2174
cg0883107	HRH1	GR-beta [	638	642	0.840383	TCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	647	651	0.840383	CCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	666	670	0.840383	AATGG	7.8125	7.2174
cg0883107	HRH1	GR-beta [	712	716	0.840383	TCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	827	831	0.840383	TCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1032	1036	0.840383	TCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1230	1234	0.840383	AATGG	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1241	1245	0.840383	TCATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1281	1285	0.840383	AATGA	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1349	1353	0.840383	CAATT	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1350	1354	0.840383	AATTA	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1387	1391	0.840383	AATGG	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1428	1432	0.840383	AATGA	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1867	1871	0.840383	AATTA	7.8125	7.2174
cg0883107	HRH1	GR-beta [	1892	1896	0.840383	AATGG	7.8125	7.2174
cg0645773	HRH1	GATA-1 [	1837	1842	0.758539	CTGATA	1.95312	1.80234
cg0645773	HRH1	GATA-1 [	1989	1994	0.758539	CTGATA	1.95312	1.80234

cg0883107	HRH1	GATA-1 [	1775	1780	0.758539	CTGATA	1.95312	1.80234
cg0883107	HRH1	GATA-1 [	1927	1932	0.758539	CTGATA	1.95312	1.80234
cg0645773	HRH1	AP-2alpha	864	869	0.678558	TCAGGC	0.48828	0.51196
cg0645773	HRH1	AP-2alpha	1027	1032	0.678558	GCCTGA	0.48828	0.51196
cg0883107	HRH1	AP-2alpha	802	807	0.678558	TCAGGC	0.48828	0.51196
cg0883107	HRH1	AP-2alpha	965	970	0.678558	GCCTGA	0.48828	0.51196
cg0645773	HRH1	RXR-alph	108	114	0.62611	TAAACC	0.12207	0.11915
cg0883107	HRH1	RXR-alph	46	52	0.62611	TAAACC	0.12207	0.11915
cg0645773	HRH1	PEA3 [T0	1758	1766	0.597316	TCACAT	0.04578	0.04362
cg0883107	HRH1	PEA3 [T0	1696	1704	0.597316	TCACAT	0.04578	0.04362
cg0645773	HRH1	PR B [T00	1154	1160	0.48823	AACAGT	0.12207	0.11255
cg0645773	HRH1	PR A [T01	1154	1160	0.48823	AACAGT	0.12207	0.11255
cg0883107	HRH1	PR B [T00	1092	1098	0.48823	AACAGT	0.12207	0.11255
cg0883107	HRH1	PR A [T01	1092	1098	0.48823	AACAGT	0.12207	0.11255
cg0645773	HRH1	AP-1 [T00	1168	1176	0.348957	ACTGAG	0.09155	0.08806
cg0883107	HRH1	AP-1 [T00	1106	1114	0.348957	ACTGAG	0.09155	0.08806
cg0645773	HRH1	GATA-1 [	659	664	0.280028	TAGATA	0.97656	0.8795
cg0645773	HRH1	GATA-1 [	1747	1752	0.280028	TATCTT	0.97656	0.8795
cg0883107	HRH1	GATA-1 [	597	602	0.280028	TAGATA	0.97656	0.8795
cg0883107	HRH1	GATA-1 [	1685	1690	0.280028	TATCTT	0.97656	0.8795
cg0645773	HRH1	AP-1 [T00	914	922	0.261718	TGACTC	0.09155	0.08806
cg0883107	HRH1	AP-1 [T00	852	860	0.261718	TGACTC	0.09155	0.08806
cg0645773	HRH1	c-Ets-1 [T	821	827	0.256174	AAGGAA	0.24414	0.23743
cg0883107	HRH1	c-Ets-1 [T	759	765	0.256174	AAGGAA	0.24414	0.23743
cg0645773	HRH1	AP-2alpha	14	19	0.226186	CCAGGC	0.97656	1.07867
cg0645773	HRH1	AP-2alpha	1279	1284	0.226186	CCAGGC	0.97656	1.07867
cg0645773	HRH1	AP-2alpha	1771	1776	0.226186	GCCTGG	0.97656	1.07867
cg0883107	HRH1	AP-2alpha	1217	1222	0.226186	CCAGGC	0.97656	1.07867
cg0883107	HRH1	AP-2alpha	1709	1714	0.226186	GCCTGG	0.97656	1.07867
cg0645773	HRH1	GR-alpha [	314	318	0.207689	CCTCT	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	415	419	0.207689	CCTCT	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	424	428	0.207689	AGAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	741	745	0.207689	AGAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	747	751	0.207689	AAAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1406	1410	0.207689	AGAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1796	1800	0.207689	AAAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1820	1824	0.207689	CCTCT	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1912	1916	0.207689	AAAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1937	1941	0.207689	AAAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	252	256	0.207689	CCTCT	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	353	357	0.207689	CCTCT	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	362	366	0.207689	AGAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	679	683	0.207689	AGAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	685	689	0.207689	AAAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1344	1348	0.207689	AGAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1734	1738	0.207689	AAAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1758	1762	0.207689	CCTCT	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1850	1854	0.207689	AAAGG	7.8125	7.79817

cg0883107	HRH1	GR-alpha [	1875	1879	0.207689	AAAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1988	1992	0.207689	CCTCT	7.8125	7.79817
cg0645773	HRH1	GR-beta [T	127	131	0	ACATT	3.90625	3.51525
cg0645773	HRH1	GR-beta [T	287	291	0	ACATT	3.90625	3.51525
cg0645773	HRH1	GR-beta [T	696	700	0	AATGT	3.90625	3.51525
cg0645773	HRH1	GR-beta [T	1928	1932	0	AAATT	3.90625	3.51525
cg0645773	HRH1	XBP-1 [T	502	507	0	ATGACT	0.97656	0.94838
cg0645773	HRH1	XBP-1 [T	887	892	0	AGTCAT	0.97656	0.94838
cg0645773	HRH1	XBP-1 [T	1603	1608	0	AGTCAT	0.97656	0.94838
cg0645773	HRH1	TFIID [T0	292	298	0	TAGAAA	1.09863	0.95175
cg0645773	HRH1	TFIID [T0	489	495	0	TTAAAA	1.09863	0.95175
cg0645773	HRH1	TFIID [T0	490	496	0	TAAAAA	1.09863	0.95175
cg0645773	HRH1	TFIID [T0	688	694	0	TCTAAA	1.09863	0.95175
cg0645773	HRH1	TFIID [T0	690	696	0	TAAAAA	1.09863	0.95175
cg0645773	HRH1	TFIID [T0	712	718	0	TTTTTGA	1.09863	0.95175
cg0645773	HRH1	TFIID [T0	1932	1938	0	TAGAAA	1.09863	0.95175
cg0645773	HRH1	c-Jun [T00	914	920	0	TGACTC	0.12207	0.11843
cg0645773	HRH1	c-Jun [T00	1170	1176	0	TGAGTC	0.12207	0.11843
cg0645773	HRH1	GR-alpha [	150	154	0	CCTAT	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	366	370	0	ACAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	650	654	0	ACAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	937	941	0	CCTGT	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	958	962	0	ACAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1378	1382	0	ACAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1544	1548	0	ATAGG	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1742	1746	0	CCTGT	7.8125	7.79817
cg0645773	HRH1	GR-alpha [	1994	1998	0	ACAGG	7.8125	7.79817
cg0645773	HRH1	FOXP3 [T	178	183	0	GACAAC	1.46484	1.44953
cg0645773	HRH1	FOXP3 [T	1271	1276	0	GTTGTC	1.46484	1.44953
cg0645773	HRH1	FOXP3 [T	1815	1820	0	GTTGTC	1.46484	1.44953
cg0645773	HRH1	PR B [T00	297	303	0	AACAGT	0.36621	0.35051
cg0645773	HRH1	PR A [T01	297	303	0	AACAGT	0.36621	0.35051
cg0645773	HRH1	C/EBPbeta	2	5	0	TTGC	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	23	26	0	TTGC	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	25	28	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	179	182	0	ACAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	222	225	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	322	325	0	TTGC	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	375	378	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	473	476	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	556	559	0	ACAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	597	600	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	703	706	0	TTGT	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	745	748	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1010	1013	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1032	1035	0	ACAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1272	1275	0	TTGT	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1351	1354	0	ACAA	15.625	15.26275

cg0645773	HRH1	C/EBPbeta	1358	1361	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1410	1413	0	GCAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1590	1593	0	ACAA	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1816	1819	0	TTGT	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1852	1855	0	TTGT	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1969	1972	0	TTGC	15.625	15.26275
cg0645773	HRH1	C/EBPbeta	1971	1974	0	GCAA	15.625	15.26275
cg0645773	HRH1	YY1 [T00	5	8	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	142	145	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	156	159	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	186	189	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	310	313	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	630	633	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	685	688	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	709	712	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	720	723	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	729	732	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	770	773	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	981	984	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1109	1112	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1293	1296	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1336	1339	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1450	1453	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1494	1497	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1582	1585	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1610	1613	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1620	1623	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1632	1635	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1643	1646	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1717	1720	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1788	1791	0	CCAT	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1857	1860	0	ATGG	7.8125	7.79459
cg0645773	HRH1	YY1 [T00	1955	1958	0	ATGG	7.8125	7.79459
cg0645773	HRH1	C/EBPalp	1698	1704	0	GATTGA	0.24414	0.24342
cg0645773	HRH1	TFII-I [T0	342	347	0	GGAAAG	1.46484	1.48598
cg0645773	HRH1	TFII-I [T0	976	981	0	CTTTCC	1.46484	1.48598
cg0645773	HRH1	c-Ets-1 [T	1379	1385	0	CAGGAA	0.24414	0.24982
cg0645773	HRH1	ER-alpha [	34	38	0	TGACC	1.95312	1.99744
cg0645773	HRH1	ER-alpha [	386	390	0	TGACC	1.95312	1.99744
cg0645773	HRH1	ER-alpha [	411	415	0	TGACC	1.95312	1.99744
cg0645773	HRH1	ER-alpha [	772	776	0	GGTCA	1.95312	1.99744
cg0645773	HRH1	ER-alpha [	1149	1153	0	TGACC	1.95312	1.99744
cg0645773	HRH1	NFI/CTF [	946	953	0	CCAAGC	0.18311	0.191
cg0645773	HRH1	GR [T050	711	717	0	ATTTTT	0.36621	0.33174
cg0645773	HRH1	GATA-1 [	1869	1874	0	TATCTG	0.97656	0.92541
cg0645773	HRH1	Pax-5 [T0	101	107	0	CCGGCC	1.09863	1.24633
cg0645773	HRH1	Pax-5 [T0	165	171	0	CCTGCC	1.09863	1.24633
cg0645773	HRH1	Pax-5 [T0	223	229	0	CAAGCC	1.09863	1.24633

cg0645773	HRH1	Pax-5 [T0	1000	1006	0	CGTGCC	1.09863	1.24633
cg0645773	HRH1	Pax-5 [T0	1359	1365	0	CAAGCC	1.09863	1.24633
cg0645773	HRH1	Pax-5 [T0	1904	1910	0	CCAGCC	1.09863	1.24633
cg0645773	HRH1	p53 [T006	165	171	0	CCTGCC	0.36621	0.40082
cg0645773	HRH1	AP-2alpha	50	55	0	GCCTGC	0.97656	1.07867
cg0645773	HRH1	AP-2alpha	218	223	0	GCCTGC	0.97656	1.07867
cg0645773	HRH1	AP-2alpha	398	403	0	GCCTGC	0.97656	1.07867
cg0645773	HRH1	AP-2alpha	932	937	0	GCAGGC	0.97656	1.07867
cg0645773	HRH1	AP-2alpha	952	957	0	GCCTGC	0.97656	1.07867
cg0645773	HRH1	AP-2alpha	1783	1788	0	GCAGGC	0.97656	1.07867
cg0645773	HRH1	IRF-2 [T01	41	46	0	AAGTGA	0.48828	0.46235
cg0645773	HRH1	IRF-2 [T01	1174	1179	0	TCACTT	0.48828	0.46235
cg0645773	HRH1	HNF-1A [	488	495	0	GTTAAA	0.24414	0.20853
cg0883107	HRH1	GR-beta [	65	69	0	ACATT	3.90625	3.51525
cg0883107	HRH1	GR-beta [	225	229	0	ACATT	3.90625	3.51525
cg0883107	HRH1	GR-beta [	634	638	0	AATGT	3.90625	3.51525
cg0883107	HRH1	GR-beta [	1866	1870	0	AAATT	3.90625	3.51525
cg0883107	HRH1	XBP-1 [T0	440	445	0	ATGACT	0.97656	0.94838
cg0883107	HRH1	XBP-1 [T0	825	830	0	AGTCAT	0.97656	0.94838
cg0883107	HRH1	XBP-1 [T0	1541	1546	0	AGTCAT	0.97656	0.94838
cg0883107	HRH1	TFIID [T0	230	236	0	TAGAAA	1.09863	0.95175
cg0883107	HRH1	TFIID [T0	427	433	0	TTAAAA	1.09863	0.95175
cg0883107	HRH1	TFIID [T0	428	434	0	TAAAAA	1.09863	0.95175
cg0883107	HRH1	TFIID [T0	626	632	0	TCTAAA	1.09863	0.95175
cg0883107	HRH1	TFIID [T0	628	634	0	TAAAAA	1.09863	0.95175
cg0883107	HRH1	TFIID [T0	650	656	0	TTTTTGA	1.09863	0.95175
cg0883107	HRH1	TFIID [T0	1870	1876	0	TAGAAA	1.09863	0.95175
cg0883107	HRH1	TFIID [T0	1970	1976	0	TTTTTGA	1.09863	0.95175
cg0883107	HRH1	c-Jun [T00	852	858	0	TGACTC	0.12207	0.11843
cg0883107	HRH1	c-Jun [T00	1108	1114	0	TGAGTC	0.12207	0.11843
cg0883107	HRH1	GR-alpha [	88	92	0	CCTAT	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	304	308	0	ACAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	588	592	0	ACAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	875	879	0	CCTGT	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	896	900	0	ACAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1316	1320	0	ACAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1482	1486	0	ATAGG	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1680	1684	0	CCTGT	7.8125	7.79817
cg0883107	HRH1	GR-alpha [	1932	1936	0	ACAGG	7.8125	7.79817
cg0883107	HRH1	FOXP3 [T	116	121	0	GACAAC	1.46484	1.44953
cg0883107	HRH1	FOXP3 [T	1209	1214	0	GTTGTC	1.46484	1.44953
cg0883107	HRH1	FOXP3 [T	1753	1758	0	GTTGTC	1.46484	1.44953
cg0883107	HRH1	FOXP3 [T	1993	1998	0	GTTGTC	1.46484	1.44953
cg0883107	HRH1	PR B [T00	235	241	0	AACAGT	0.36621	0.35051
cg0883107	HRH1	PR A [T01	235	241	0	AACAGT	0.36621	0.35051
cg0883107	HRH1	C/EBPbeta	117	120	0	ACAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	160	163	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	260	263	0	TTGC	15.625	15.26275

cg0883107	HRH1	C/EBPbeta	313	316	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	411	414	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	494	497	0	ACAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	535	538	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	641	644	0	TTGT	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	683	686	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	948	951	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	970	973	0	ACAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1210	1213	0	TTGT	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1289	1292	0	ACAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1296	1299	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1348	1351	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1528	1531	0	ACAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1754	1757	0	TTGT	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1790	1793	0	TTGT	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1907	1910	0	TTGC	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1909	1912	0	GCAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1954	1957	0	ACAA	15.625	15.26275
cg0883107	HRH1	C/EBPbeta	1994	1997	0	TTGT	15.625	15.26275
cg0883107	HRH1	YY1 [T00	80	83	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	94	97	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	124	127	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	248	251	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	568	571	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	623	626	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	647	650	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	658	661	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	667	670	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	708	711	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	919	922	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1047	1050	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1231	1234	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1274	1277	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1388	1391	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1432	1435	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1520	1523	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1548	1551	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1558	1561	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1570	1573	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1581	1584	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1655	1658	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1726	1729	0	CCAT	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1795	1798	0	ATGG	7.8125	7.79459
cg0883107	HRH1	YY1 [T00	1893	1896	0	ATGG	7.8125	7.79459
cg0883107	HRH1	C/EBPalph	1636	1642	0	GATTGA	0.24414	0.24342
cg0883107	HRH1	TFII-I [T0	280	285	0	GGAAAG	1.46484	1.48598
cg0883107	HRH1	TFII-I [T0	914	919	0	CTTTCC	1.46484	1.48598
cg0883107	HRH1	TFII-I [T0	1941	1946	0	CTATCC	1.46484	1.48598

cg0883107	HRH1	c-Ets-1 [T	1317	1323	0	CAGGAA	0.24414	0.24982
cg0883107	HRH1	ER-alpha [	324	328	0	TGACC	1.95312	1.99744
cg0883107	HRH1	ER-alpha [	349	353	0	TGACC	1.95312	1.99744
cg0883107	HRH1	ER-alpha [	710	714	0	GGTCA	1.95312	1.99744
cg0883107	HRH1	ER-alpha [	1087	1091	0	TGACC	1.95312	1.99744
cg0883107	HRH1	NFI/CTF [	884	891	0	CCAAGC	0.18311	0.191
cg0883107	HRH1	GR [T050	649	655	0	ATTTTT	0.36621	0.33174
cg0883107	HRH1	GR [T050	1969	1975	0	TTTTTTG	0.36621	0.33174
cg0883107	HRH1	GATA-1 [	1807	1812	0	TATCTG	0.97656	0.92541
cg0883107	HRH1	Pax-5 [T0	39	45	0	CCGGCC	1.09863	1.24633
cg0883107	HRH1	Pax-5 [T0	103	109	0	CCTGCC	1.09863	1.24633
cg0883107	HRH1	Pax-5 [T0	161	167	0	CAAGCC	1.09863	1.24633
cg0883107	HRH1	Pax-5 [T0	938	944	0	CGTGCC	1.09863	1.24633
cg0883107	HRH1	Pax-5 [T0	1297	1303	0	CAAGCC	1.09863	1.24633
cg0883107	HRH1	Pax-5 [T0	1842	1848	0	CCAGCC	1.09863	1.24633
cg0883107	HRH1	p53 [T006	103	109	0	CCTGCC	0.36621	0.40082
cg0883107	HRH1	AP-2alpha	156	161	0	GCCTGC	0.97656	1.07867
cg0883107	HRH1	AP-2alpha	336	341	0	GCCTGC	0.97656	1.07867
cg0883107	HRH1	AP-2alpha	870	875	0	GCAGGC	0.97656	1.07867
cg0883107	HRH1	AP-2alpha	890	895	0	GCCTGC	0.97656	1.07867
cg0883107	HRH1	AP-2alpha	1721	1726	0	GCAGGC	0.97656	1.07867
cg0883107	HRH1	IRF-2 [T0	1112	1117	0	TCACTT	0.48828	0.46235
cg0883107	HRH1	HNF-1A [	426	433	0	GTTAAA	0.24414	0.20853
cg2362236	HSD17B1	RAR-beta:	241	252	9.97066	TTCCCC	0.06974	0.06822
cg2362236	HSD17B1	RAR-beta:	589	600	9.97066	TCCCCA	0.06974	0.06822
cg2362236	HSD17B1	c-Ets-1 [T	1791	1797	9.969337	TGGGAA	0.24414	0.2459
cg2362236	HSD17B1	COUP-TF	463	475	9.828903	CCCAAG	0.02503	0.0249
cg2362236	HSD17B1	STAT1bet	600	609	9.807397	CTTTCC	0.14877	0.1495
cg2362236	HSD17B1	XBP-1 [T	1121	1126	9.789909	CGCCAT	1.95312	1.95208
cg2362236	HSD17B1	XBP-1 [T	1417	1422	9.789909	ATGGCT	1.95312	1.95208
cg2362236	HSD17B1	XBP-1 [T	1837	1842	9.789909	AGCCAT	1.95312	1.95208
cg2362236	HSD17B1	NF-1 [T00	1104	1111	9.761671	GGCTCC	0.24414	0.24405
cg2362236	HSD17B1	PR B [T00	231	237	9.743489	AACACC	1.09863	1.10292
cg2362236	HSD17B1	PR B [T00	1501	1507	9.743489	AACACA	1.09863	1.10292
cg2362236	HSD17B1	PR A [T01	231	237	9.743489	AACACC	1.09863	1.10292
cg2362236	HSD17B1	PR A [T01	1501	1507	9.743489	AACACA	1.09863	1.10292
cg2362236	HSD17B1	c-Myb [T0	1109	1116	9.704537	CAACTA	0.36621	0.37054
cg2362236	HSD17B1	c-Myb [T0	1478	1485	9.704537	CGGAGT	0.36621	0.37054
cg2362236	HSD17B1	RAR-beta	672	681	9.641259	GGGGTT	0.21362	0.21243
cg2362236	HSD17B1	EBF [T05	509	519	9.574945	ACACCA	0.06866	0.06676
cg2362236	HSD17B1	Pax-5 [T0	367	373	9.552105	GGGCGC	1.46484	1.43083
cg2362236	HSD17B1	Pax-5 [T0	705	711	9.552105	TCCGCC	1.46484	1.43083
cg2362236	HSD17B1	Pax-5 [T0	1260	1266	9.552105	GCCGCC	1.46484	1.43083
cg2362236	HSD17B1	Pax-5 [T0	1342	1348	9.552105	GGGCGG	1.46484	1.43083
cg2362236	HSD17B1	Pax-5 [T0	1606	1612	9.552105	GGGCCA	1.46484	1.43083
cg2362236	HSD17B1	TFIID [T0	540	546	9.552105	TTTGGG	1.46484	1.48472
cg2362236	HSD17B1	TFIID [T0	1443	1449	9.552105	TTTGGG	1.46484	1.48472
cg2362236	HSD17B1	NF-1 [T00	1797	1804	9.513281	TTGGCT	0.73242	0.73053

cg2362236	HSD17B1	NF-1 [T00	1802	1809	9.513281	TTGGGG	0.73242	0.73053
cg2362236	HSD17B1	TFII-I [T0	239	244	9.512894	CGTTCC	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	537	542	9.512894	GGATTT	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	586	591	9.512894	TTATCC	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	816	821	9.512894	GGACCG	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	836	841	9.512894	CCTTCC	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1148	1153	9.512894	CGTTCC	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1250	1255	9.512894	CGATCC	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1309	1314	9.512894	TTGTCC	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1337	1342	9.512894	GGATGG	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1463	1468	9.512894	GGATCG	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1726	1731	9.512894	AAGTCC	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1757	1762	9.512894	GGATAA	7.32422	7.29728
cg2362236	HSD17B1	TFII-I [T0	1793	1798	9.512894	GGAATT	7.32422	7.29728
cg2362236	HSD17B1	FOXP3 [T	147	152	9.512894	GTTTAT	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	198	203	9.512894	GTTCTG	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	414	419	9.512894	GTTGGT	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	423	428	9.512894	GTTATG	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	579	584	9.512894	GTTCTG	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	585	590	9.512894	GTTATC	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	657	662	9.512894	GTTGGG	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	675	680	9.512894	GTTGGG	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	722	727	9.512894	GTTGCT	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	792	797	9.512894	GTTGGG	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	895	900	9.512894	CAGAAC	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	1498	1503	9.512894	AGCAAC	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	1663	1668	9.512894	ACCAAC	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	1667	1672	9.512894	ACCAAC	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	1758	1763	9.512894	GATAAC	7.32422	7.35678
cg2362236	HSD17B1	FOXP3 [T	1935	1940	9.512894	GTTGCC	7.32422	7.35678
cg2362236	HSD17B1	c-Jun [T00	48	54	9.442241	GCCGTC	0.73242	0.73031
cg2362236	HSD17B1	NFI/CTF [	464	471	9.352332	CCAAGG	0.54932	0.54821
cg2362236	HSD17B1	NFI/CTF [	1688	1695	9.352332	CCAAGG	0.54932	0.54821
cg2362236	HSD17B1	LEF-1 [T0	212	219	9.313676	CTTTGG	0.21362	0.2139
cg2362236	HSD17B1	ATF [T00	1112	1123	9.257019	CTACGT	0.07725	0.07724
cg2362236	HSD17B1	PPAR-alpl	301	311	9.158357	CTCTGG	0.0515	0.04986
cg2362236	HSD17B1	c-Ets-1 [T	240	246	9.020687	GTTCCC	0.85449	0.85523
cg2362236	HSD17B1	LEF-1 [T0	1442	1449	8.973041	CTTTGG	0.54932	0.55326
cg2362236	HSD17B1	Elk-1 [T00	837	845	8.931691	CTTCCA	0.24414	0.24034
cg2362236	HSD17B1	c-Ets-2 [T	102	110	8.912323	CCTCAG	0.27466	0.27495
cg2362236	HSD17B1	ETF [T002	921	931	8.876947	GAGCGC	0.02384	0.02303
cg2362236	HSD17B1	c-Jun [T00	466	472	8.832178	AAGGTC	0.61035	0.61059
cg2362236	HSD17B1	NF-1 [T00	541	548	8.790071	TTGGGA	0.24414	0.24467
cg2362236	HSD17B1	NF-1 [T00	1444	1451	8.790071	TTGGGA	0.24414	0.24467
cg2362236	HSD17B1	E2F-1 [T0	889	896	8.76494	GCGGCG	0.27466	0.26875
cg2362236	HSD17B1	XBP-1 [T	1659	1664	8.75604	ATGAAC	2.92969	2.9674
cg2362236	HSD17B1	XBP-1 [T	1841	1846	8.75604	ATGAGA	2.92969	2.9674
cg2362236	HSD17B1	c-Jun [T00	456	462	8.571705	TGACTG	0.12207	0.12139

cg2362236	HSD17B1	LEF-1 [T0	1307	1314	8.361499	CTTTGTC	0.15259	0.15214
cg2362236	HSD17B1	HNF-3alpl	1538	1545	8.343064	AATTTA/	0.27466	0.28528
cg2362236	HSD17B1	c-Ets-2 [T(	556	564	8.339336	CGGCAG(	0.13733	0.13681
cg2362236	HSD17B1	c-Ets-2 [T(	1065	1073	8.339336	TTCCTGC	0.13733	0.13681
cg2362236	HSD17B1	GR-alpha [	10	14	8.281568	CCTTG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	14	18	8.281568	GAAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	59	63	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	111	115	8.281568	CCTCG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	174	178	8.281568	GAAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	465	469	8.281568	CAAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	521	525	8.281568	CCTTG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	544	548	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	712	716	8.281568	CCTCC	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	776	780	8.281568	CCTTC	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	786	790	8.281568	GAAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	807	811	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	836	840	8.281568	CCTTC	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	858	862	8.281568	CCTCG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	885	889	8.281568	CGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	906	910	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	915	919	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	959	963	8.281568	CCTCC	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	989	993	8.281568	CCTCC	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1163	1167	8.281568	CGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1175	1179	8.281568	CGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1211	1215	8.281568	CGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1254	1258	8.281568	CCTCC	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1303	1307	8.281568	CCTTC	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1447	1451	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1453	1457	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1460	1464	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1567	1571	8.281568	CCTTG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1584	1588	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1689	1693	8.281568	CAAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1764	1768	8.281568	CAAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1779	1783	8.281568	GGAGG	7.8125	7.72956
cg2362236	HSD17B1	GR-alpha [	1860	1864	8.281568	CCTTG	7.8125	7.72956
cg2362236	HSD17B1	NFI/CTF [	1664	1671	8.241664	CCAACC/	0.18311	0.1823
cg2362236	HSD17B1	p53 [T006'	594	600	8.162057	AGCGCC(	0.48828	0.47377
cg2362236	HSD17B1	c-Jun [T00	143	149	8.128539	TGACGT	0.48828	0.49076
cg2362236	HSD17B1	E2F-1 [T0	1347	1354	8.101379	GCGGTA(	0.30518	0.3
cg2362236	HSD17B1	GR-alpha [	18	22	8.073878	GCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	89	93	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	265	269	8.073878	CCTAG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	288	292	8.073878	CCTGC	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	316	320	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	352	356	8.073878	CCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	391	395	8.073878	CCTGC	7.8125	7.72238

cg2362236	HSD17B1	GR-alpha [	399	403	8.073878	CCTAG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	481	485	8.073878	CCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	512	516	8.073878	CCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	558	562	8.073878	GCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	694	698	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	938	942	8.073878	CCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1001	1005	8.073878	GCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1040	1044	8.073878	CCTGC	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1067	1071	8.073878	CCTGC	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1073	1077	8.073878	CCTGC	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1088	1092	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1197	1201	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1315	1319	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1332	1336	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1408	1412	8.073878	CTAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1457	1461	8.073878	GCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1575	1579	8.073878	CCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1623	1627	8.073878	CCTGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1711	1715	8.073878	CCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1776	1780	8.073878	GCAGG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1939	1943	8.073878	CCTAG	7.8125	7.72238
cg2362236	HSD17B1	GR-alpha [	1940	1944	8.073878	CTAGG	7.8125	7.72238
cg2362236	HSD17B1	Pax-5 [T0	63	69	8.014558	GGGCAC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	71	77	8.014558	TCTGCC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	129	135	8.014558	GGGCTG	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	206	212	8.014558	GCTGCC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	326	332	8.014558	TCTGCC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	515	521	8.014558	GGGCTC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	547	553	8.014558	GGGCTG	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	758	764	8.014558	GCGGCC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	795	801	8.014558	GGGCAG	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	797	803	8.014558	GCAGCC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	1171	1177	8.014558	GGGCCG	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	1201	1207	8.014558	GGGCAG	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	1570	1576	8.014558	TGAGCC	2.19727	2.14502
cg2362236	HSD17B1	Pax-5 [T0	1768	1774	8.014558	GGGCAT	2.19727	2.14502
cg2362236	HSD17B1	TFIID [T0	571	577	8.014558	TTTCAA	2.19727	2.24348
cg2362236	HSD17B1	TFIID [T0	1681	1687	8.014558	TCAGAA	2.19727	2.24348
cg2362236	HSD17B1	TFIID [T0	1911	1917	8.014558	TTTCTG	2.19727	2.24348
cg2362236	HSD17B1	MAZ [T00	709	721	7.982153	CCCCCT	0.00915	0.009
cg2362236	HSD17B1	ETF [T002	1194	1204	7.870358	GGGCCT	0.07153	0.06862
cg2362236	HSD17B1	p53 [T006	515	521	7.833758	GGGCTC	0.48828	0.47377
cg2362236	HSD17B1	RXR-alpha	1361	1367	7.815913	GGGTGG	0.24414	0.24104
cg2362236	HSD17B1	T3R-beta1	1012	1020	7.813363	TCACCG	0.27466	0.27236
cg2362236	HSD17B1	T3R-beta1	1623	1631	7.774776	CCTGGG	0.27466	0.27236
cg2362236	HSD17B1	NFI/CTF [	356	363	7.587343	GCACTT	0.36621	0.36674
cg2362236	HSD17B1	EBF [T05	898	908	7.555934	AACCCT	0.01144	0.01125
cg2362236	HSD17B1	GR [T050	1016	1022	7.527031	CGCTTT	1.83105	1.86007

cg2362236	HSD17B1	GR [T050	1440	1446	7.527031	CGCTTT	1.83105	1.86007
cg2362236	HSD17B1	RAR-beta:	1565	1576	7.477995	TTCCTT	0.02861	0.02796
cg2362236	HSD17B1	C/EBPalp	138	144	7.465744	TTCAAT	0.48828	0.49653
cg2362236	HSD17B1	C/EBPalp	1951	1957	7.465744	TGCAAT	0.48828	0.49653
cg2362236	HSD17B1	LEF-1 [T0	1018	1025	7.396545	CTTTGC	0.21362	0.21302
cg2362236	HSD17B1	PPAR-alp	662	672	7.370536	GGCTGG	0.04482	0.04393
cg2362236	HSD17B1	PPAR-alp	680	690	7.370536	GGCTGG	0.04482	0.04393
cg2362236	HSD17B1	GCF [T00	94	102	7.186486	CCGCTG	0.45776	0.44706
cg2362236	HSD17B1	GCF [T00	619	627	7.186486	GCGCAG	0.45776	0.44706
cg2362236	HSD17B1	GCF [T00	892	900	7.186486	GCGCAG	0.45776	0.44706
cg2362236	HSD17B1	GCF [T00	967	975	7.186486	GCGCAG	0.45776	0.44706
cg2362236	HSD17B1	GCF [T00	1402	1410	7.186486	GCGCAG	0.45776	0.44706
cg2362236	HSD17B1	XBP-1 [T	777	782	7.172312	CTTCAT	2.92969	2.97018
cg2362236	HSD17B1	XBP-1 [T	1600	1605	7.172312	ATGATG	2.92969	2.97018
cg2362236	HSD17B1	PPAR-alp	686	696	7.154987	GACTGG	0.01431	0.01397
cg2362236	HSD17B1	p53 [T006	1606	1612	7.150251	GGGCCA	1.09863	1.07125
cg2362236	HSD17B1	p53 [T006	306	312	7.103527	GGGCGA	1.09863	1.07125
cg2362236	HSD17B1	Pax-5 [T0	306	312	7.082373	GGGCGA	0.12207	0.12014
cg2362236	HSD17B1	NFI/CTF [	654	661	7.014249	GTGGTT	0.73242	0.73214
cg2362236	HSD17B1	NFI/CTF [	672	679	7.014249	GGGGTT	0.73242	0.73214
cg2362236	HSD17B1	HNF-3alp	1525	1532	7.000129	CAAAAA	0.82397	0.84946
cg2362236	HSD17B1	HNF-3alp	1534	1541	7.000129	AGAAAA	0.82397	0.84946
cg2362236	HSD17B1	HNF-3alp	1542	1549	7.000129	TAAAAA	0.82397	0.84946
cg2362236	HSD17B1	NF-1 [T00	658	665	6.948522	TTGGGG	0.48828	0.4856
cg2362236	HSD17B1	NF-1 [T00	676	683	6.948522	TTGGGG	0.48828	0.4856
cg2362236	HSD17B1	NF-1 [T00	1660	1667	6.948522	TGAACC	0.48828	0.4856
cg2362236	HSD17B1	ENKTF-1	193	200	6.942764	TGGCGG	1.46484	1.44228
cg2362236	HSD17B1	ENKTF-1	700	707	6.942764	TGGCGT	1.46484	1.44228
cg2362236	HSD17B1	ENKTF-1	1798	1805	6.942764	TGGCTT	1.46484	1.44228
cg2362236	HSD17B1	p53 [T006	758	764	6.938545	GCGGCC	1.09863	1.07125
cg2362236	HSD17B1	p53 [T006	948	954	6.891821	GGGCGG	1.09863	1.07125
cg2362236	HSD17B1	E2F-1 [T0	21	28	6.839754	GGTTCC	0.30518	0.29782
cg2362236	HSD17B1	c-Jun [T00	1629	1635	6.787369	TGACAG	0.73242	0.73173
cg2362236	HSD17B1	NFI/CTF [	53	60	6.786076	CAGCTT	0.73242	0.73214
cg2362236	HSD17B1	NFI/CTF [	1798	1805	6.786076	TGGCTT	0.73242	0.73214
cg2362236	HSD17B1	p53 [T006	1570	1576	6.778774	TGAGCC	1.09863	1.07125
cg2362236	HSD17B1	AR [T000	825	833	6.725174	GGACAT	0.19836	0.19597
cg2362236	HSD17B1	NF-1 [T00	793	800	6.722386	TTGGGC	0.24414	0.24147
cg2362236	HSD17B1	c-Ets-1 [T	22	28	6.693449	GTTCCG	0.48828	0.48798
cg2362236	HSD17B1	AR [T000	281	289	6.675397	ACCCTG	0.19836	0.19597
cg2362236	HSD17B1	c-Jun [T00	1821	1827	6.668031	TGACTT	0.61035	0.60769
cg2362236	HSD17B1	TFII-I [T0	38	43	6.581441	GGAGTG	0.97656	0.97366
cg2362236	HSD17B1	TFII-I [T0	311	316	6.581441	ATCTCC	0.97656	0.97366
cg2362236	HSD17B1	TFII-I [T0	941	946	6.581441	GGAGTG	0.97656	0.97366
cg2362236	HSD17B1	TFII-I [T0	1615	1620	6.581441	CACTCC	0.97656	0.97366
cg2362236	HSD17B1	TFII-I [T0	1947	1952	6.581441	GGAGTG	0.97656	0.97366
cg2362236	HSD17B1	TFII-I [T0	1979	1984	6.581441	ATCTCC	0.97656	0.97366
cg2362236	HSD17B1	FOXP3 [T	1393	1398	6.581441	GTTTTA	0.97656	0.99397

cg2362236	HSD17B1	c-Ets-1 [T	1149	1155	6.565361	GTTCCG	0.48828	0.48798
cg2362236	HSD17B1	p53 [T006	129	135	6.563521	GGGCTG	0.48828	0.47541
cg2362236	HSD17B1	p53 [T006	547	553	6.563521	GGGCTG	0.48828	0.47541
cg2362236	HSD17B1	p53 [T006	797	803	6.563521	GCAGCC	0.48828	0.47541
cg2362236	HSD17B1	PPAR-alp	1314	1324	6.51544	CCCTGG	0.03719	0.03639
cg2362236	HSD17B1	IRF-1 [T0	601	609	6.497844	TTTCCG	0.19073	0.19127
cg2362236	HSD17B1	XBP-1 [T	1433	1438	6.478682	ATGCCA	0.97656	0.97062
cg2362236	HSD17B1	XBP-1 [T	1768	1773	6.478682	GGGCAT	0.97656	0.97062
cg2362236	HSD17B1	p53 [T006	367	373	6.403751	GGGCGC	0.48828	0.47541
cg2362236	HSD17B1	C/EBPalp	1795	1801	6.391486	AATTGG	0.48828	0.49071
cg2362236	HSD17B1	TCF-4E [T	1018	1024	6.302385	CTTTGC	0.61035	0.61344
cg2362236	HSD17B1	TCF-4E [T	1154	1160	6.302385	GGCAAA	0.61035	0.61344
cg2362236	HSD17B1	PPAR-alp	758	768	6.299891	GCGGCC	0.03719	0.03639
cg2362236	HSD17B1	GR-alpha [	102	106	6.263098	CCTCA	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	126	130	6.263098	TAAGG	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	529	533	6.263098	CCTCA	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	607	611	6.263098	CCTCA	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	903	907	6.263098	TGAGG	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	1010	1014	6.263098	CCTCA	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	1281	1285	6.263098	CCTCA	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	1722	1726	6.263098	CCTCA	3.90625	3.91061
cg2362236	HSD17B1	GR-alpha [	1847	1851	6.263098	CCTCA	3.90625	3.91061
cg2362236	HSD17B1	p53 [T006	1260	1266	6.188498	GCCGCC	0.61035	0.594
cg2362236	HSD17B1	p53 [T006	1342	1348	6.188498	GGGCGG	0.61035	0.594
cg2362236	HSD17B1	SRY [T00	1307	1315	6.176442	CTTTGT	0.15259	0.15366
cg2362236	HSD17B1	GR-alpha [	104	108	6.055408	TCAGG	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	124	128	6.055408	CCTAA	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	451	455	6.055408	TTAGG	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	505	509	6.055408	CCTGA	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	747	751	6.055408	CCTGA	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	901	905	6.055408	CCTGA	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	1239	1243	6.055408	CCTGA	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	1786	1790	6.055408	TTAGG	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	1813	1817	6.055408	TCAGG	3.90625	3.9065
cg2362236	HSD17B1	GR-alpha [	1849	1853	6.055408	TCAGG	3.90625	3.9065
cg2362236	HSD17B1	RXR-alph	44	50	5.937582	GGGTGC	0.73242	0.72249
cg2362236	HSD17B1	RXR-alph	1626	1632	5.937582	GGGTGA	0.73242	0.72249
cg2362236	HSD17B1	NF-kappa	583	593	5.917275	TGGTTA	0.04053	0.03971
cg2362236	HSD17B1	GCF [T00	887	895	5.917256	AGGCGG	0.64087	0.6219
cg2362236	HSD17B1	p53 [T006	1171	1177	5.883561	GGGCCG	0.61035	0.594
cg2362236	HSD17B1	STAT4 [T	836	841	5.882353	CCTTCC	0.48828	0.48408
cg2362236	HSD17B1	C/EBPalp	1646	1652	5.850545	GTCAAT	0.97656	0.99
cg2362236	HSD17B1	E2F-1 [T0	600	607	5.846171	CTTTCC	0.18311	0.18044
cg2362236	HSD17B1	c-Ets-1 [T	612	618	5.814485	CTTCCC	0.36621	0.36731
cg2362236	HSD17B1	c-Ets-1 [T	1986	1992	5.814485	CTTCCC	0.36621	0.36731
cg2362236	HSD17B1	VDR [T00	1656	1664	5.771401	CAAATG	0.42725	0.42999
cg2362236	HSD17B1	ATF-2 [T0	142	151	5.75773	ATGACG	0.11826	0.11873
cg2362236	HSD17B1	AR [T000	1306	1314	5.754178	TCTTTGT	0.24414	0.24229

cg2362236	HSD17B1	RXR-alph	231	237	5.715466	AACACC	0.61035	0.6044
cg2362236	HSD17B1	c-Jun [T00	83	89	5.703976	TGACCC	0.48828	0.48665
cg2362236	HSD17B1	ENKTF-1	152	159	5.687009	TTGCGC	0.73242	0.7249
cg2362236	HSD17B1	NF-1 [T00	1825	1832	5.626299	TTGGAC	0.24414	0.24258
cg2362236	HSD17B1	c-Jun [T00	262	268	5.587335	TGACCT	0.48828	0.48665
cg2362236	HSD17B1	c-Jun [T00	396	402	5.587335	TGACCT	0.48828	0.48665
cg2362236	HSD17B1	T3R-beta1	1117	1125	5.572705	TCACCG	0.21362	0.21287
cg2362236	HSD17B1	c-Ets-1 [T	428	434	5.558311	GGGGAA	0.36621	0.3623
cg2362236	HSD17B1	Pax-5 [T0	594	600	5.544826	AGCGCC	0.73242	0.72046
cg2362236	HSD17B1	Pax-5 [T0	948	954	5.544826	GGGCGG	0.73242	0.72046
cg2362236	HSD17B1	Pax-5 [T0	1958	1964	5.544826	GGGCAA	0.73242	0.72046
cg2362236	HSD17B1	TFIID [T0	1395	1401	5.544826	TTTACC	0.73242	0.75085
cg2362236	HSD17B1	EBF [T05	1312	1322	5.519385	TCCCCT	0.01907	0.0183
cg2362236	HSD17B1	HNF-1A [	252	259	5.466509	CTCTTA	0.24414	0.2469
cg2362236	HSD17B1	ATF [T00	139	150	5.46568	TCAATG	0.02575	0.02579
cg2362236	HSD17B1	c-Ets-1 [T	1131	1137	5.430224	CGGGAA	0.36621	0.3623
cg2362236	HSD17B1	NF-1 [T00	360	367	5.377909	TTGGGC	0.24414	0.24258
cg2362236	HSD17B1	RAR-beta	894	903	5.31522	GCAGAA	0.15259	0.15189
cg2362236	HSD17B1	RXR-alph	1093	1099	5.271235	ACGACC	0.61035	0.6044
cg2362236	HSD17B1	RXR-alph	1805	1811	5.271235	GGGTAG	0.61035	0.6044
cg2362236	HSD17B1	ETF [T002	1182	1192	5.246906	GGGGGC	0.02861	0.02737
cg2362236	HSD17B1	RelA [T00	427	437	5.177167	TGGGGA	0.01001	0.00994
cg2362236	HSD17B1	c-Ets-2 [T	1565	1573	5.162974	TTCCTT	0.13733	0.13828
cg2362236	HSD17B1	c-Ets-2 [T	1858	1866	5.162974	TTCCTT	0.13733	0.13828
cg2362236	HSD17B1	NF-kappa	78	88	5.154475	GGGGAT	0.02432	0.02374
cg2362236	HSD17B1	p53 [T006	705	711	5.133514	TCCGCC	0.48828	0.47747
cg2362236	HSD17B1	AP-1 [T00	1807	1815	5.112864	GTAGAG	0.12207	0.12162
cg2362236	HSD17B1	AP-2alpha	134	139	5.100982	GCCTTT	0.97656	0.97567
cg2362236	HSD17B1	AP-2alpha	1157	1162	5.100982	AAAGGC	0.97656	0.97567
cg2362236	HSD17B1	AP-2alpha	1273	1278	5.100982	AAAGGC	0.97656	0.97567
cg2362236	HSD17B1	AP-2alpha	1737	1742	5.100982	AAAGGC	0.97656	0.97567
cg2362236	HSD17B1	RXR-alph	278	284	5.089356	AGCACC	0.48828	0.484
cg2362236	HSD17B1	USF2 [T0	385	394	5.052423	GTGCCA	0.103	0.10178
cg2362236	HSD17B1	GR-beta [	418	422	5.042296	GTATT	3.90625	3.95351
cg2362236	HSD17B1	GR-beta [	502	506	5.042296	AATCC	3.90625	3.95351
cg2362236	HSD17B1	GR-beta [	537	541	5.042296	GGATT	3.90625	3.95351
cg2362236	HSD17B1	GR-beta [	854	858	5.042296	AATAC	3.90625	3.95351
cg2362236	HSD17B1	E2F-1 [T0	291	298	5.042045	GCGGGA	0.18311	0.17901
cg2362236	HSD17B1	E2F-1 [T0	989	996	5.042045	CCTCCC	0.18311	0.17901
cg2362236	HSD17B1	NFI/CTF [	210	217	5.021086	CCCTTT	0.24414	0.24103
cg2362236	HSD17B1	NFI/CTF [	1763	1770	5.021086	CCAAGG	0.24414	0.24103
cg2362236	HSD17B1	c-Jun [T00	507	513	5.000337	TGACAC	0.61035	0.61057
cg2362236	HSD17B1	ATF3 [T0	1112	1119	4.941398	CTACGT	0.09155	0.09183
cg2362236	HSD17B1	EBF [T05	1329	1339	4.906683	GTCCCT	0.02289	0.02224
cg2362236	HSD17B1	c-Jun [T00	1113	1119	4.883696	TACGTC	0.61035	0.61057
cg2362236	HSD17B1	RXR-alph	1509	1515	4.86724	GAGACC	0.48828	0.484
cg2362236	HSD17B1	RXR-alph	1638	1644	4.86724	GAGACC	0.48828	0.484
cg2362236	HSD17B1	GCF [T00	1220	1228	4.846987	GCGCGG	0.27466	0.26486

cg2362236	HSD17B1	c-Myb [T0	160	167	4.840682	GCAAGT	0.30518	0.30568
cg2362236	HSD17B1	c-Myb [T0	1853	1860	4.840682	GCAAGT	0.30518	0.30568
cg2362236	HSD17B1	c-Ets-1 [T	837	843	4.782565	CTTCCAC	0.48828	0.49031
cg2362236	HSD17B1	C/EBPalph	419	425	4.776286	TATTGTT	0.97656	0.99332
cg2362236	HSD17B1	C/EBPalph	851	857	4.776286	ACCAAT	0.97656	0.99332
cg2362236	HSD17B1	TFII-I [T0	667	672	4.756447	GGACTG	2.92969	2.93695
cg2362236	HSD17B1	TFII-I [T0	685	690	4.756447	GGACTG	2.92969	2.93695
cg2362236	HSD17B1	TFII-I [T0	825	830	4.756447	GGACAT	2.92969	2.93695
cg2362236	HSD17B1	TFII-I [T0	1563	1568	4.756447	CATTCC	2.92969	2.93695
cg2362236	HSD17B1	FOXP3 [T	228	233	4.756447	GTCAAC	2.92969	2.96063
cg2362236	HSD17B1	FOXP3 [T	1675	1680	4.756447	AAAAAC	2.92969	2.96063
cg2362236	HSD17B1	PPAR-alph	1196	1206	4.727619	GCCTGG	0.03242	0.03183
cg2362236	HSD17B1	CTF [T001	1792	1803	4.70535	GGGAAT	0.01001	0.01006
cg2362236	HSD17B1	p53 [T006	1023	1029	4.645444	CGCGCC	0.24414	0.23584
cg2362236	HSD17B1	p53 [T006	1218	1224	4.645444	GGGCGC	0.24414	0.23584
cg2362236	HSD17B1	p53 [T006	1298	1304	4.645444	CGCGCC	0.24414	0.23584
cg2362236	HSD17B1	c-Ets-1 [T	601	607	4.616023	TTTCCGC	0.85449	0.85764
cg2362236	HSD17B1	T3R-beta1	450	458	4.481316	GTTAGG	0.27466	0.27551
cg2362236	HSD17B1	AP-2alpha	1408	1413	4.438035	CTAGGC	0.97656	0.96979
cg2362236	HSD17B1	AP-2alpha	1938	1943	4.438035	GCCTAG	0.97656	0.96979
cg2362236	HSD17B1	AP-2alpha	1940	1945	4.438035	CTAGGC	0.97656	0.96979
cg2362236	HSD17B1	RXR-alph	34	40	4.423008	GGGTGG	0.24414	0.24292
cg2362236	HSD17B1	STAT4 [T	239	244	4.411765	CGTTCC	1.95312	1.94235
cg2362236	HSD17B1	STAT4 [T	430	435	4.411765	GGAAGC	1.95312	1.94235
cg2362236	HSD17B1	STAT4 [T	1006	1011	4.411765	TCTTCC	1.95312	1.94235
cg2362236	HSD17B1	STAT4 [T	1063	1068	4.411765	GCTTCC	1.95312	1.94235
cg2362236	HSD17B1	STAT4 [T	1148	1153	4.411765	CGTTCC	1.95312	1.94235
cg2362236	HSD17B1	STAT4 [T	1277	1282	4.411765	GCTTCC	1.95312	1.94235
cg2362236	HSD17B1	STAT4 [T	1563	1568	4.411765	CATTCC	1.95312	1.94235
cg2362236	HSD17B1	STAT4 [T	1985	1990	4.411765	GCTTCC	1.95312	1.94235
cg2362236	HSD17B1	c-Ets-1 [T	1564	1570	4.411026	ATTCCTT	0.85449	0.85764
cg2362236	HSD17B1	p53 [T006	317	323	4.33696	CTGGCC	0.24414	0.23584
cg2362236	HSD17B1	p53 [T006	459	465	4.33696	CTGGCC	0.24414	0.23584
cg2362236	HSD17B1	HOXD9 [T	1902	1911	4.321431	TTTTTTT	0.03433	0.03596
cg2362236	HSD17B1	HOXD10 [	1902	1911	4.321431	TTTTTTT	0.03433	0.03596
cg2362236	HSD17B1	PEA3 [T0	825	833	4.30818	GGACAT	0.13733	0.13791
cg2362236	HSD17B1	CREB [T0	1111	1119	4.261795	ACTACG	0.04578	0.04561
cg2362236	HSD17B1	RXR-alph	484	490	4.24113	GGGACC	0.97656	0.9671
cg2362236	HSD17B1	RXR-alph	1234	1240	4.24113	GGGACC	0.97656	0.9671
cg2362236	HSD17B1	GR-beta [T	149	153	4.201913	TTATT	7.8125	7.94607
cg2362236	HSD17B1	GR-beta [T	1529	1533	4.201913	AATAA	7.8125	7.94607
cg2362236	HSD17B1	GR-beta [T	1546	1550	4.201913	AATCA	7.8125	7.94607
cg2362236	HSD17B1	GR-beta [T	1653	1657	4.201913	AATCA	7.8125	7.94607
cg2362236	HSD17B1	GR-beta [T	1907	1911	4.201913	TTATT	7.8125	7.94607
cg2362236	HSD17B1	p53 [T006	644	650	4.125254	GGGCCG	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	691	697	4.125254	GGGCCT	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	1189	1195	4.125254	GGGCCG	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	1194	1200	4.125254	GGGCCT	0.73242	0.71379

cg2362236	HSD17B1	p53 [T006	63	69	4.083527	GGGCAC	0.73242	0.71379
cg2362236	HSD17B1	C/EBPalph	1959	1965	4.019783	GGCAAT	0.48828	0.49358
cg2362236	HSD17B1	TFIID [T0	1733	1739	4.007279	TATTAA	1.09863	1.13456
cg2362236	HSD17B1	AP-2alpha	9	14	3.970052	GCCTTG	0.97656	0.96469
cg2362236	HSD17B1	GR [T050	1305	1311	3.763516	TTCTTTG	0.73242	0.74251
cg2362236	HSD17B1	p53 [T006	362	368	3.750231	GGGCTG	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	437	443	3.750231	CCAGCC	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	661	667	3.750231	GGGCTG	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	679	685	3.750231	GGGCTG	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	928	934	3.750231	GGGCTG	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	1471	1477	3.750231	CAAGCC	0.73242	0.71379
cg2362236	HSD17B1	p53 [T006	1706	1712	3.750231	CCAGCC	0.73242	0.71379
cg2362236	HSD17B1	AP-2alpha	14	19	3.743866	GAAGGC	0.48828	0.48238
cg2362236	HSD17B1	AP-2alpha	174	179	3.743866	GAAGGC	0.48828	0.48238
cg2362236	HSD17B1	AP-2alpha	775	780	3.743866	GCCTTC	0.48828	0.48238
cg2362236	HSD17B1	p53 [T006	1958	1964	3.728319	GGGCAA	0.73242	0.7189
cg2362236	HSD17B1	c-Ets-1 [T	1857	1863	3.71855	GTTCCT	0.61035	0.60765
cg2362236	HSD17B1	c-Fos [T00	226	235	3.637699	GAGTCA	0.05341	0.05347
cg2362236	HSD17B1	p53 [T006	859	865	3.586914	CTCGCC	0.73242	0.7189
cg2362236	HSD17B1	RXR-alph	1035	1041	3.574782	CCGACC	1.09863	1.08572
cg2362236	HSD17B1	HNF-3alph	1908	1915	3.500065	TATTTC	0.27466	0.28532
cg2362236	HSD17B1	c-Ets-1 [T	105	111	3.462376	CAGGAA	0.61035	0.60765
cg2362236	HSD17B1	c-Ets-1 [T	559	565	3.462376	CAGGAA	0.61035	0.60765
cg2362236	HSD17B1	c-Myb [T0	1389	1396	3.438142	GCCAGT	0.12207	0.12203
cg2362236	HSD17B1	RXR-alph	82	88	3.392904	ATGACC	1.09863	1.08572
cg2362236	HSD17B1	RXR-alph	561	567	3.392904	GGAACC	1.09863	1.08572
cg2362236	HSD17B1	Elk-1 [T00	1278	1286	3.381796	CTTCCT	0.04578	0.04588
cg2362236	HSD17B1	p53 [T006	1184	1190	3.375208	GGGCGG	0.73242	0.7189
cg2362236	HSD17B1	GR-beta [	495	499	3.361531	AGATT	3.90625	3.99611
cg2362236	HSD17B1	GR-beta [	1732	1736	3.361531	ATATT	3.90625	3.99611
cg2362236	HSD17B1	GR-beta [	1962	1966	3.361531	AATCT	3.90625	3.99611
cg2362236	HSD17B1	GR-beta [	1978	1982	3.361531	AATCT	3.90625	3.99611
cg2362236	HSD17B1	GR-beta [	1992	1996	3.361531	AGATT	3.90625	3.99611
cg2362236	HSD17B1	NF-kappa	428	439	3.321549	GGGGAA	0.00513	0.00506
cg2362236	HSD17B1	PR B [T00	575	581	3.29756	AAATGT	0.24414	0.25122
cg2362236	HSD17B1	PR A [T01	575	581	3.29756	AAATGT	0.24414	0.25122
cg2362236	HSD17B1	c-Ets-2 [T	1008	1016	3.2883	TTCCTC	0.18311	0.18304
cg2362236	HSD17B1	c-Ets-2 [T	1279	1287	3.2883	TTCCTC	0.18311	0.18304
cg2362236	HSD17B1	PXR-1:RX	1660	1667	3.2723	TGAACC	0.12207	0.12271
cg2362236	HSD17B1	Elk-1 [T00	1007	1015	3.247448	CTTCCT	0.07629	0.07656
cg2362236	HSD17B1	c-Jun [T00	1809	1815	3.244843	AGAGTC	0.24414	0.24403
cg2362236	HSD17B1	RAR-beta	244	253	3.226064	CCCGAA	0.12207	0.12169
cg2362236	HSD17B1	ATF-2 [T0	1111	1120	3.201112	ACTACG	0.06104	0.0608
cg2362236	HSD17B1	CREB [T0	143	151	3.196569	TGACGT	0.06104	0.06133
cg2362236	HSD17B1	Sp1 [T007	703	712	3.170707	CGTCCG	0.03433	0.03306
cg2362236	HSD17B1	Sp1 [T007	1258	1267	3.170707	CGGCCG	0.03433	0.03306
cg2362236	HSD17B1	Pax-5 [T0	859	865	3.075094	CTCGCC	0.12207	0.11895
cg2362236	HSD17B1	C/EBPalph	381	387	2.981957	CATTGT	0.48828	0.4911

cg2362236	HSD17B1	STAT4 [T	21	26	2.941176	GGTTCC	2.92969	2.929
cg2362236	HSD17B1	STAT4 [T	107	112	2.941176	GGAACC	2.92969	2.929
cg2362236	HSD17B1	STAT4 [T	561	566	2.941176	GGAACC	2.92969	2.929
cg2362236	HSD17B1	STAT4 [T	600	605	2.941176	CTTTCC	2.92969	2.929
cg2362236	HSD17B1	STAT4 [T	611	616	2.941176	ACTTCC	2.92969	2.929
cg2362236	HSD17B1	STAT4 [T	1133	1138	2.941176	GGAAGT	2.92969	2.929
cg2362236	HSD17B1	p53 [T006	206	212	2.813291	GCTGCC	0.48828	0.47786
cg2362236	HSD17B1	p53 [T006	795	801	2.813291	GGGCAG	0.48828	0.47786
cg2362236	HSD17B1	p53 [T006	1768	1774	2.813291	GGGCAT	0.48828	0.47786
cg2362236	HSD17B1	PR B [T00	419	425	2.80933	TATTGT	0.73242	0.74818
cg2362236	HSD17B1	PR A [T01	419	425	2.80933	TATTGT	0.73242	0.74818
cg2362236	HSD17B1	RXR-alph	673	679	2.726556	GGGTTG	0.85449	0.84796
cg2362236	HSD17B1	NFI/CTF [	1668	1675	2.683003	CCAACC	0.06104	0.06008
cg2362236	HSD17B1	c-Fos [T00	1810	1819	2.598489	GAGTCA	0.03052	0.03034
cg2362236	HSD17B1	AP-2alpha	101	106	2.550491	GCCTCA	0.48828	0.48266
cg2362236	HSD17B1	AP-2alpha	528	533	2.550491	GCCTCA	0.48828	0.48266
cg2362236	HSD17B1	AP-2alpha	606	611	2.550491	GCCTCA	0.48828	0.48266
cg2362236	HSD17B1	RXR-alph	896	902	2.544678	AGAACC	0.85449	0.84796
cg2362236	HSD17B1	RXR-alph	1587	1593	2.544678	GGGTGC	0.85449	0.84796
cg2362236	HSD17B1	Sp1 [T007	947	956	2.505331	GGGGCG	0.04005	0.03892
cg2362236	HSD17B1	Sp1 [T007	1341	1350	2.491373	GGGGCG	0.04005	0.03892
cg2362236	HSD17B1	NF-Y [T0	849	856	2.420868	CTACCA	0.21362	0.21485
cg2362236	HSD17B1	GCF [T00	1038	1046	2.339499	ACCCTG	0.06104	0.05925
cg2362236	HSD17B1	RXR-alph	1318	1324	2.322562	GGGTCT	0.85449	0.84796
cg2362236	HSD17B1	T3R-beta1	1971	1979	2.240658	TCACCA	0.15259	0.15262
cg2362236	HSD17B1	GATA-1 [	1756	1761	2.176375	TGGATA	3.90625	3.92756
cg2362236	HSD17B1	GCF [T00	960	968	2.140539	CTCCGG	0.09155	0.08882
cg2362236	HSD17B1	GCF [T00	1294	1302	2.140539	CTCCCG	0.09155	0.08882
cg2362236	HSD17B1	NF-Y [T0	1796	1803	2.12821	ATTGGC	0.21362	0.21508
cg2362236	HSD17B1	AP-2alpha	885	890	2.098119	CGAGGC	0.97656	0.95407
cg2362236	HSD17B1	AP-2alpha	1163	1168	2.098119	CGAGGC	0.97656	0.95407
cg2362236	HSD17B1	AP-2alpha	1175	1180	2.098119	CGAGGC	0.97656	0.95407
cg2362236	HSD17B1	AP-2alpha	1211	1216	2.098119	CGAGGC	0.97656	0.95407
cg2362236	HSD17B1	GATA-1 [	587	592	2.001358	TATCCC	3.90625	3.92756
cg2362236	HSD17B1	PR B [T00	410	416	1.892895	AAGTGT	0.12207	0.12429
cg2362236	HSD17B1	PR B [T00	1135	1141	1.892895	AAGTGT	0.12207	0.12429
cg2362236	HSD17B1	PR A [T01	410	416	1.892895	AAGTGT	0.12207	0.12429
cg2362236	HSD17B1	PR A [T01	1135	1141	1.892895	AAGTGT	0.12207	0.12429
cg2362236	HSD17B1	AP-2alpha	1447	1452	1.871933	GGAGGC	0.97656	0.95407
cg2362236	HSD17B1	AP-2alpha	1453	1458	1.871933	GGAGGC	0.97656	0.95407
cg2362236	HSD17B1	TFII-I [T0	726	731	1.824994	CTCTCC	0.48828	0.48408
cg2362236	HSD17B1	TFII-I [T0	985	990	1.824994	CTCTCC	0.48828	0.48408
cg2362236	HSD17B1	p53 [T006	71	77	1.758307	TCTGCC	0.36621	0.36261
cg2362236	HSD17B1	p53 [T006	326	332	1.758307	TCTGCC	0.36621	0.36261
cg2362236	HSD17B1	p53 [T006	1201	1207	1.758307	GGGCAG	0.36621	0.36261
cg2362236	HSD17B1	NF-kappa	428	438	1.729152	GGGGAA	0.00525	0.00511
cg2362236	HSD17B1	GR-beta [	380	384	1.680765	GCATT	3.90625	3.94936
cg2362236	HSD17B1	GR-beta [	1432	1436	1.680765	AATGC	3.90625	3.94936

cg2362236	HSD17B1	GR-beta [T	1794	1798	1.680765	GAATT	3.90625	3.94936
cg2362236	HSD17B1	C/EBPbeta	57	60	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	214	217	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	360	363	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	415	418	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	464	467	1.639871	CCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	541	544	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	658	661	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	676	679	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	793	796	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	852	855	1.639871	CCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1108	1111	1.639871	CCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1444	1447	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1483	1486	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1582	1585	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1664	1667	1.639871	CCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1668	1671	1.639871	CCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1688	1691	1.639871	CCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1763	1766	1.639871	CCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1797	1800	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1802	1805	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1825	1828	1.639871	TTGG	15.625	15.72563
cg2362236	HSD17B1	XBP-1 [T0	82	87	1.583727	ATGACC	0.97656	0.98146
cg2362236	HSD17B1	Pax-5 [T0	317	323	1.537547	CTGGCC	0.73242	0.71311
cg2362236	HSD17B1	Pax-5 [T0	459	465	1.537547	CTGGCC	0.73242	0.71311
cg2362236	HSD17B1	Pax-5 [T0	1023	1029	1.537547	CGCGCC	0.73242	0.71311
cg2362236	HSD17B1	Pax-5 [T0	1184	1190	1.537547	GGGCGG	0.73242	0.71311
cg2362236	HSD17B1	Pax-5 [T0	1218	1224	1.537547	GGGCGC	0.73242	0.71311
cg2362236	HSD17B1	Pax-5 [T0	1298	1304	1.537547	CGCGCC	0.73242	0.71311
cg2362236	HSD17B1	TFIID [T0	1523	1529	1.537547	TACAAA	0.73242	0.75096
cg2362236	HSD17B1	E2F-1 [T0	1293	1300	1.490375	TCTCCC	0.06104	0.06008
cg2362236	HSD17B1	STAT4 [T	1793	1798	1.470588	GGAATT	1.95312	1.96333
cg2362236	HSD17B1	STAT4 [T	1856	1861	1.470588	AGTTCC	1.95312	1.96333
cg2362236	HSD17B1	C/EBPbeta	12	15	1.366559	TTGA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	139	142	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	229	232	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	573	576	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	742	745	1.366559	TTGA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1470	1473	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1569	1572	1.366559	TTGA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1647	1650	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1655	1658	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1724	1727	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	C/EBPbeta	1996	1999	1.366559	TCAA	15.625	15.72563
cg2362236	HSD17B1	AP-2alpha	1426	1431	1.357116	GCCTGT	0.48828	0.48203
cg2362236	HSD17B1	ENKTF-1	911	918	1.255756	TGGCGG	0.24414	0.23904
cg2362236	HSD17B1	ENKTF-1	1118	1125	1.255756	CACCGC	0.24414	0.23904
cg2362236	HSD17B1	C/EBPalph	150	156	1.220508	TATTGC	0.24414	0.247

cg2362236	HSD17B1	GCF [T00	590	598	1.070269	CCCCAG	0.18311	0.17647
cg2362236	HSD17B1	GCF [T00	1397	1405	1.070269	TACCAG	0.18311	0.17647
cg2362236	HSD17B1	RXR-alpha	217	223	0.848226	GGGTCC	0.48828	0.48333
cg2362236	HSD17B1	RXR-alpha	246	252	0.848226	CGAACC	0.48828	0.48333
cg2362236	HSD17B1	RXR-alpha	1826	1832	0.848226	TGGACC	0.48828	0.48333
cg2362236	HSD17B1	GR-beta [T	141	145	0.840383	AATGA	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1368	1372	0.840383	TAATT	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1369	1373	0.840383	AATTA	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1562	1566	0.840383	CCATT	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1648	1652	0.840383	CAATT	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1649	1653	0.840383	AATTA	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1658	1662	0.840383	AATGA	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1795	1799	0.840383	AATTG	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1832	1836	0.840383	CCATT	7.8125	7.94706
cg2362236	HSD17B1	GR-beta [T	1954	1958	0.840383	AATGG	7.8125	7.94706
cg2362236	HSD17B1	AP-2alpha	746	751	0.678558	GCCTGA	0.48828	0.48199
cg2362236	HSD17B1	AP-2alpha	1849	1854	0.678558	TCAGGC	0.48828	0.48199
cg2362236	HSD17B1	C/EBPalph	1975	1981	0.540941	CACAAT	0.24414	0.24507
cg2362236	HSD17B1	AP-1 [T00	223	231	0.401835	AGTGAG	0.09155	0.09215
cg2362236	HSD17B1	GATA-1 [	1373	1378	0.280028	AAGATA	0.97656	0.99875
cg2362236	HSD17B1	AP-2alpha	352	357	0.226186	CCAGGC	0.97656	0.95305
cg2362236	HSD17B1	AP-2alpha	693	698	0.226186	GCCTGG	0.97656	0.95305
cg2362236	HSD17B1	AP-2alpha	1087	1092	0.226186	GCCTGG	0.97656	0.95305
cg2362236	HSD17B1	AP-2alpha	1196	1201	0.226186	GCCTGG	0.97656	0.95305
cg2362236	HSD17B1	AP-2alpha	1622	1627	0.226186	GCCTGG	0.97656	0.95305
cg2362236	HSD17B1	GR-alpha [	135	139	0.207689	CCTTT	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	211	215	0.207689	CCTTT	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	251	255	0.207689	CCTCT	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	322	326	0.207689	CCTCT	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	446	450	0.207689	AGAGG	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	599	603	0.207689	CCTTT	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	804	808	0.207689	AGAGG	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	1157	1161	0.207689	AAAGG	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	1205	1209	0.207689	AGAGG	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	1273	1277	0.207689	AAAGG	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	1737	1741	0.207689	AAAGG	7.8125	7.81264
cg2362236	HSD17B1	c-Ets-1 [T	1007	1013	0.128087	CTTCCTC	0.24414	0.2429
cg2362236	HSD17B1	c-Ets-1 [T	1278	1284	0.128087	CTTCCTC	0.24414	0.2429
cg2362236	HSD17B1	GR-alpha [	283	287	0	CCTGT	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	1427	1431	0	CCTGT	7.8125	7.81264
cg2362236	HSD17B1	GR-alpha [	1643	1647	0	CCTGT	7.8125	7.81264
cg2362236	HSD17B1	XBP-1 [T	142	147	0	ATGACG	0.97656	0.98127
cg2362236	HSD17B1	Pax-5 [T0	362	368	0	GGGCTG	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	437	443	0	CCAGCC	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	644	650	0	GGGCCG	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	661	667	0	GGGCTG	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	679	685	0	GGGCTG	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	691	697	0	GGGCCT	1.09863	1.06846

cg2362236	HSD17B1	Pax-5 [T0	928	934	0	GGGCTG	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	1067	1073	0	CCTGCC	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	1189	1195	0	GGGCCG	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	1194	1200	0	GGGCCT	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	1471	1477	0	CAAGCC	1.09863	1.06846
cg2362236	HSD17B1	Pax-5 [T0	1706	1712	0	CCAGCC	1.09863	1.06846
cg2362236	HSD17B1	p53 [T006	1067	1073	0	CCTGCC	0.36621	0.35912
cg2362236	HSD17B1	Sp1 [T007	1183	1192	0	GGGGCG	0.00191	0.00182
cg2362236	HSD17B1	TFII-I [T0	284	289	0	CTGTCC	1.46484	1.45997
cg2362236	HSD17B1	TFII-I [T0	600	605	0	CTTTCC	1.46484	1.45997
cg2362236	HSD17B1	c-Ets-1 [T	1064	1070	0	CTTCCT	0.24414	0.2429
cg2362236	HSD17B1	YY1 [T00	373	376	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	426	429	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	535	538	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	781	784	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1123	1126	0	CCAT	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1339	1342	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1417	1420	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1516	1519	0	CCAT	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1562	1565	0	CCAT	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1603	1606	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1730	1733	0	CCAT	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1832	1835	0	CCAT	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1839	1842	0	CCAT	7.8125	7.81711
cg2362236	HSD17B1	YY1 [T00	1955	1958	0	ATGG	7.8125	7.81711
cg2362236	HSD17B1	Elk-1 [T00	1064	1072	0	CTTCCT	0.06104	0.06047
cg2362236	HSD17B1	GCF [T00	614	622	0	TCCCAG	0.09155	0.08765
cg2362236	HSD17B1	GCF [T00	923	931	0	GCGCCG	0.09155	0.08765
cg2362236	HSD17B1	GCF [T00	1434	1442	0	TGCCAG	0.09155	0.08765
cg2362236	HSD17B1	ER-alpha [	83	87	0	TGACC	1.95312	1.9404
cg2362236	HSD17B1	ER-alpha [	262	266	0	TGACC	1.95312	1.9404
cg2362236	HSD17B1	ER-alpha [	396	400	0	TGACC	1.95312	1.9404
cg2362236	HSD17B1	ER-alpha [	468	472	0	GGTCA	1.95312	1.9404
cg2362236	HSD17B1	T3R-beta1	914	922	0	CGGAGG	0.01526	0.01505
cg2362236	HSD17B1	T3R-beta1	1051	1059	0	TCACCA	0.01526	0.01505
cg2362236	HSD17B1	C/EBPbeta	152	155	0	TTGC	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	160	163	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	383	386	0	TTGT	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	421	424	0	TTGT	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	523	526	0	TTGT	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	723	726	0	TTGC	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	869	872	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	873	876	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1020	1023	0	TTGC	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1155	1158	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1309	1312	0	TTGT	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1499	1502	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1524	1527	0	ACAA	15.625	15.71349

cg2362236	HSD17B1	C/EBPbeta	1818	1821	0	TTGT	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1853	1856	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1862	1865	0	TTGC	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1933	1936	0	TTGT	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1936	1939	0	TTGC	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1952	1955	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1960	1963	0	GCAA	15.625	15.71349
cg2362236	HSD17B1	C/EBPbeta	1976	1979	0	ACAA	15.625	15.71349
cg2362236	HSD17B1	NF-1 [T00	460	467	0	TGGCCC	0.12207	0.11983
cg2362236	HSD17B1	c-Jun [T00	225	231	0	TGAGTC	0.12207	0.12266
cg2362236	HSD17B1	TFIID [T0	1540	1546	0	TTTAAA	1.09863	1.13474
cg2362236	HSD17B1	TFIID [T0	1541	1547	0	TTAAAA	1.09863	1.13474
cg2362236	HSD17B1	TFIID [T0	1903	1909	0	TTTTTTA	1.09863	1.13474
cg2362236	HSD17B1	FOXP3 [T	1817	1822	0	GTTGTG	1.46484	1.47315
cg2362236	HSD17B1	GR-beta [	338	342	0	ACATT	3.90625	3.99611
cg2362236	HSD17B1	GR-beta [	576	580	0	AATGT	3.90625	3.99611
cg2362236	HSD17B1	GR-beta [	1537	1541	0	AAATT	3.90625	3.99611
cg2362236	HSD17B1	GR-beta [	1538	1542	0	AATTT	3.90625	3.99611
cg2362236	HSD17B1	GR [T050	1525	1531	0	CAAAAA	0.36621	0.37562
cg2362236	HSD17B1	IRF-2 [T01	609	614	0	TCACTT	0.48828	0.49387
cg1346255	INADL	NF-AT2 [	334	343	9.999272	GGAAAG	0.08774	0.08903
cg1346255	INADL	HNF-1C [	92	100	9.870625	TTGTCTA	0.10681	0.10839
cg1346255	INADL	c-Ets-1 [T	963	969	9.841249	AGGGAA	0.24414	0.2459
cg1346255	INADL	Egr-3 [T0	1438	1450	9.828903	CAGAGT	0.02503	0.02488
cg1346255	INADL	c-Myb [T0	101	108	9.815171	ACAAGT	0.36621	0.3712
cg1346255	INADL	STAT1bet	330	339	9.807397	TAAAGG	0.14877	0.1495
cg1346255	INADL	XBP-1 [T	1036	1041	9.789909	ATGTCT	1.95312	1.95208
cg1346255	INADL	XBP-1 [T	1148	1153	9.789909	AGACAT	1.95312	1.95208
cg1346255	INADL	XBP-1 [T	1350	1355	9.789909	AGACAT	1.95312	1.95208
cg1346255	INADL	XBP-1 [T	1704	1709	9.789909	ATGGCT	1.95312	1.95208
cg1346255	INADL	PR B [T00	98	104	9.743489	AACACA	1.09863	1.10292
cg1346255	INADL	PR B [T00	174	180	9.743489	GTGTGT	1.09863	1.10292
cg1346255	INADL	PR B [T00	1601	1607	9.743489	AACACC	1.09863	1.10292
cg1346255	INADL	PR B [T00	1629	1635	9.743489	CTGTGT	1.09863	1.10292
cg1346255	INADL	PR A [T01	98	104	9.743489	AACACA	1.09863	1.10292
cg1346255	INADL	PR A [T01	174	180	9.743489	GTGTGT	1.09863	1.10292
cg1346255	INADL	PR A [T01	1601	1607	9.743489	AACACC	1.09863	1.10292
cg1346255	INADL	PR A [T01	1629	1635	9.743489	CTGTGT	1.09863	1.10292
cg1346255	INADL	c-Myb [T0	544	551	9.729271	TTCAGT	0.36621	0.37054
cg1346255	INADL	c-Ets-1 [T	995	1001	9.585075	ATTCCC	0.36621	0.36441
cg1346255	INADL	Pax-5 [T0	1073	1079	9.552105	TTTGCC	1.46484	1.43083
cg1346255	INADL	Pax-5 [T0	1155	1161	9.552105	TTGGCC	1.46484	1.43083
cg1346255	INADL	TFIID [T0	71	77	9.552105	TTTGGG	1.46484	1.48472
cg1346255	INADL	TFIID [T0	570	576	9.552105	TTTGAC	1.46484	1.48472
cg1346255	INADL	TFIID [T0	1550	1556	9.552105	TGGGAA	1.46484	1.48472
cg1346255	INADL	TFIID [T0	1730	1736	9.552105	TTTGGG	1.46484	1.48472
cg1346255	INADL	TFIID [T0	1818	1824	9.552105	TACCAA	1.46484	1.48472
cg1346255	INADL	NF-1 [T00	1782	1789	9.535536	ATGGCC	0.73242	0.73053

cg1346255	INADL	NF-1 [T00	1191	1198	9.513281	CACCCC	0.73242	0.73053
cg1346255	INADL	TFII-I [T0	66	71	9.512894	GGAATT	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	179	184	9.512894	TTTTCC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	435	440	9.512894	GGAAGG	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	527	532	9.512894	GGAAAC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	622	627	9.512894	GGACAC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	729	734	9.512894	TTATCC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	965	970	9.512894	GGAATT	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	983	988	9.512894	TTATCC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1106	1111	9.512894	TTATCC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1160	1165	9.512894	CCATCC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1188	1193	9.512894	GGACAC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1269	1274	9.512894	GGAAAC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1295	1300	9.512894	GTTTCC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1498	1503	9.512894	GGACAC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1525	1530	9.512894	GGAAAA	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1552	1557	9.512894	GGAAAA	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1556	1561	9.512894	AAGTCC	7.32422	7.29728
cg1346255	INADL	TFII-I [T0	1620	1625	9.512894	AATTCC	7.32422	7.29728
cg1346255	INADL	FOXP3 [T	52	57	9.512894	GTAAAC	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	289	294	9.512894	GTTCTC	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	493	498	9.512894	GAGAAC	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	513	518	9.512894	AAGAAC	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	981	986	9.512894	GTTTAT	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	1001	1006	9.512894	GTTGGT	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	1562	1567	9.512894	GTTATC	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	1633	1638	9.512894	GTTCTC	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	1785	1790	9.512894	GCCAAC	7.32422	7.35678
cg1346255	INADL	FOXP3 [T	1838	1843	9.512894	GTTGGC	7.32422	7.35678
cg1346255	INADL	TCF-4E [T	569	575	9.453578	CTTTGA	0.48828	0.49215
cg1346255	INADL	TCF-4E [T	1638	1644	9.453578	CTTTGA	0.48828	0.49215
cg1346255	INADL	SRY [T00	569	577	9.264664	CTTTGA	0.12207	0.12265
cg1346255	INADL	MEF-2A [	1809	1819	9.220261	TACTAA	0.07343	0.07563
cg1346255	INADL	LEF-1 [T0	569	576	9.082175	CTTTGA	0.54932	0.55326
cg1346255	INADL	USF2 [T0	552	561	9.056375	CCTCCA	0.1545	0.15287
cg1346255	INADL	USF2 [T0	1708	1717	9.056375	CTCACA	0.1545	0.15287
cg1346255	INADL	PXR-1:RX	664	671	8.998824	GTTGTT	0.24414	0.2439
cg1346255	INADL	LEF-1 [T0	1729	1736	8.973041	CTTTGG	0.54932	0.55326
cg1346255	INADL	GR [T050	240	246	8.971049	GCTTTT	0.61035	0.61632
cg1346255	INADL	GR [T050	610	616	8.971049	GATTTT	0.61035	0.61632
cg1346255	INADL	HNF-1C [	136	144	8.969184	TTTTATA	0.12207	0.12495
cg1346255	INADL	IRF-1 [T0	180	188	8.916359	TTTCCA	0.09155	0.09147
cg1346255	INADL	c-Ets-2 [T	1622	1630	8.912323	TTCCTG	0.27466	0.27495
cg1346255	INADL	T3R-beta1	1537	1545	8.904753	TCACCC	0.2594	0.25766
cg1346255	INADL	ETF [T002	1121	1131	8.876947	GAGGGC	0.02384	0.02303
cg1346255	INADL	PR B [T00	1272	1278	8.827054	AACAGC	0.36621	0.36944
cg1346255	INADL	PR B [T00	1529	1535	8.827054	AACAGG	0.36621	0.36944
cg1346255	INADL	PR A [T01	1272	1278	8.827054	AACAGC	0.36621	0.36944

cg1346255	INADL	PR A [T01	1529	1535	8.827054	AACAGG	0.36621	0.36944
cg1346255	INADL	NF-1 [T00	72	79	8.790071	TTGGGA	0.24414	0.24467
cg1346255	INADL	NF-1 [T00	1731	1738	8.790071	TTGGGA	0.24414	0.24467
cg1346255	INADL	XBP-1 [T	16	21	8.75604	TATCAT	2.92969	2.9674
cg1346255	INADL	XBP-1 [T	130	135	8.75604	TTTCAT	2.92969	2.9674
cg1346255	INADL	XBP-1 [T	303	308	8.75604	ATGAAA	2.92969	2.9674
cg1346255	INADL	XBP-1 [T	606	611	8.75604	ATGAGA	2.92969	2.9674
cg1346255	INADL	XBP-1 [T	667	672	8.75604	GTTCAT	2.92969	2.9674
cg1346255	INADL	XBP-1 [T	704	709	8.75604	TATCAT	2.92969	2.9674
cg1346255	INADL	XBP-1 [T	1423	1428	8.75604	TCTCAT	2.92969	2.9674
cg1346255	INADL	c-Myb [T0	1685	1692	8.728118	GAAAGT	0.30518	0.30924
cg1346255	INADL	STAT1bet	523	532	8.695301	TGGGGG	0.22316	0.22446
cg1346255	INADL	STAT1bet	1548	1557	8.695301	TGTGGG	0.22316	0.22446
cg1346255	INADL	AP-1 [T00	11	19	8.513775	TGACTT	0.03052	0.03084
cg1346255	INADL	LEF-1 [T0	1638	1645	8.457856	CTTTGA	0.15259	0.15214
cg1346255	INADL	c-Ets-1 [T	929	935	8.373028	ATGGAA	0.24414	0.24529
cg1346255	INADL	POU2F2 (	93	103	8.346865	TGTCTA	0.0515	0.05239
cg1346255	INADL	c-Ets-2 [T	61	69	8.339336	GGGCAG	0.13733	0.13681
cg1346255	INADL	PR B [T00	285	291	8.338824	GTCTGT	1.09863	1.10009
cg1346255	INADL	PR B [T00	516	522	8.338824	AACAGC	1.09863	1.10009
cg1346255	INADL	PR B [T00	977	983	8.338824	CCCTGT	1.09863	1.10009
cg1346255	INADL	PR B [T00	1129	1135	8.338824	GGCTGT	1.09863	1.10009
cg1346255	INADL	PR B [T00	1347	1353	8.338824	AACAGA	1.09863	1.10009
cg1346255	INADL	PR B [T00	1471	1477	8.338824	AACAGA	1.09863	1.10009
cg1346255	INADL	PR A [T01	285	291	8.338824	GTCTGT	1.09863	1.10009
cg1346255	INADL	PR A [T01	516	522	8.338824	AACAGC	1.09863	1.10009
cg1346255	INADL	PR A [T01	977	983	8.338824	CCCTGT	1.09863	1.10009
cg1346255	INADL	PR A [T01	1129	1135	8.338824	GGCTGT	1.09863	1.10009
cg1346255	INADL	PR A [T01	1347	1353	8.338824	AACAGA	1.09863	1.10009
cg1346255	INADL	PR A [T01	1471	1477	8.338824	AACAGA	1.09863	1.10009
cg1346255	INADL	GR-alpha	268	272	8.281568	CCTTG	7.8125	7.72956
cg1346255	INADL	GR-alpha	399	403	8.281568	CAAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	416	420	8.281568	CCTTC	7.8125	7.72956
cg1346255	INADL	GR-alpha	425	429	8.281568	CAAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	436	440	8.281568	GAAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	552	556	8.281568	CCTCC	7.8125	7.72956
cg1346255	INADL	GR-alpha	961	965	8.281568	GAAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	987	991	8.281568	CCTTG	7.8125	7.72956
cg1346255	INADL	GR-alpha	1165	1169	8.281568	CGAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	1429	1433	8.281568	CCTTG	7.8125	7.72956
cg1346255	INADL	GR-alpha	1734	1738	8.281568	GGAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	1740	1744	8.281568	CAAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	1901	1905	8.281568	GGAGG	7.8125	7.72956
cg1346255	INADL	GR-alpha	1907	1911	8.281568	GGAGG	7.8125	7.72956
cg1346255	INADL	ENKTF-1	1377	1384	8.19852	CCCTGC	0.73242	0.71737
cg1346255	INADL	NF-1 [T00	1735	1742	8.191058	GAGGCC	0.24414	0.24409
cg1346255	INADL	NF-AT1 [	176	184	8.12076	GTGTTT	0.1297	0.12988
cg1346255	INADL	NF-AT1 [	1552	1560	8.12076	GGAAAA	0.1297	0.12988

cg1346255	INADL	VDR [T00	667	675	8.079962	GTTCAT	0.24414	0.24712
cg1346255	INADL	VDR [T00	968	976	8.079962	ATTCTG	0.24414	0.24712
cg1346255	INADL	GR-alpha [	63	67	8.073878	GCAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	432	436	8.073878	GCAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	558	562	8.073878	CCTGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	935	939	8.073878	CCAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1089	1093	8.073878	GCAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1125	1129	8.073878	GCAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1140	1144	8.073878	CCTAG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1182	1186	8.073878	CTAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1371	1375	8.073878	CCTAC	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1378	1382	8.073878	CCTGC	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1382	1386	8.073878	CCAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1763	1767	8.073878	CCAGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1897	1901	8.073878	CCTGG	7.8125	7.72238
cg1346255	INADL	GR-alpha [	1947	1951	8.073878	CCTGG	7.8125	7.72238
cg1346255	INADL	Pax-5 [T0	371	377	8.014558	GGGCCT	2.19727	2.14502
cg1346255	INADL	Pax-5 [T0	938	944	8.014558	GGGCAG	2.19727	2.14502
cg1346255	INADL	Pax-5 [T0	1096	1102	8.014558	TCTGCC	2.19727	2.14502
cg1346255	INADL	Pax-5 [T0	1651	1657	8.014558	GGGCCT	2.19727	2.14502
cg1346255	INADL	Pax-5 [T0	1746	1752	8.014558	GGGCAG	2.19727	2.14502
cg1346255	INADL	TFIID [T0	141	147	8.014558	TAACAA	2.19727	2.24348
cg1346255	INADL	TFIID [T0	302	308	8.014558	TATGAA	2.19727	2.24348
cg1346255	INADL	TFIID [T0	759	765	8.014558	TTTGTT	2.19727	2.24348
cg1346255	INADL	TFIID [T0	1278	1284	8.014558	TCAGAA	2.19727	2.24348
cg1346255	INADL	TFIID [T0	1656	1662	8.014558	TAAGAA	2.19727	2.24348
cg1346255	INADL	TFIID [T0	1971	1977	8.014558	TCTCAA	2.19727	2.24348
cg1346255	INADL	c-Myb [T0	457	464	8.005241	GAACTA	0.21362	0.21454
cg1346255	INADL	p53 [T006	1202	1208	7.853573	ATGGCC	0.48828	0.47377
cg1346255	INADL	T3R-beta1	613	621	7.79407	TTTGGG	0.27466	0.27236
cg1346255	INADL	NF-AT1 [	1679	1687	7.744746	GGAAAG	0.19836	0.19941
cg1346255	INADL	IRF-1 [T0	1521	1529	7.732782	CTCTGG	0.14496	0.14449
cg1346255	INADL	c-Jun [T00	0	6	7.686747	ACAGTC	0.48828	0.48775
cg1346255	INADL	c-Jun [T00	1626	1632	7.686747	TGACTG	0.48828	0.48775
cg1346255	INADL	NFI/CTF [	240	247	7.587343	GCTTTC	0.36621	0.36674
cg1346255	INADL	NF-AT1 [	1678	1687	7.579763	TGGAAA	0.00763	0.00769
cg1346255	INADL	c-Jun [T00	951	957	7.538568	GATGTC	0.48828	0.48775
cg1346255	INADL	GR [T050	68	74	7.527031	AATTTC	1.83105	1.86007
cg1346255	INADL	GR [T050	88	94	7.527031	CATTTC	1.83105	1.86007
cg1346255	INADL	GR [T050	144	150	7.527031	CAAAGC	1.83105	1.86007
cg1346255	INADL	GR [T050	186	192	7.527031	CAAACA	1.83105	1.86007
cg1346255	INADL	GR [T050	205	211	7.527031	CAAACA	1.83105	1.86007
cg1346255	INADL	GR [T050	409	415	7.527031	CAAAGC	1.83105	1.86007
cg1346255	INADL	GR [T050	756	762	7.527031	ATATTC	1.83105	1.86007
cg1346255	INADL	GR [T050	786	792	7.527031	CAAAAT	1.83105	1.86007
cg1346255	INADL	GR [T050	797	803	7.527031	CAAAGC	1.83105	1.86007
cg1346255	INADL	GR [T050	1151	1157	7.527031	CATTTC	1.83105	1.86007
cg1346255	INADL	GR [T050	1337	1343	7.527031	ACTTTC	1.83105	1.86007

cg1346255	INADL	GR [T050	1609	1615	7.527031	CAAACA	1.83105	1.86007
cg1346255	INADL	GR [T050	1821	1827	7.527031	CAAAAT	1.83105	1.86007
cg1346255	INADL	C/EBPalph	1015	1021	7.465744	CATTGC	0.48828	0.49653
cg1346255	INADL	C/EBPalph	657	663	7.396431	AATTGT	0.48828	0.49653
cg1346255	INADL	C/EBPalph	1617	1623	7.396431	TACAAT	0.48828	0.49653
cg1346255	INADL	IRF-1 [T0	523	531	7.387351	TGGGGG	0.14496	0.14449
cg1346255	INADL	c-Ets-2 [T	430	438	7.268173	CAGCAG	0.09155	0.09191
cg1346255	INADL	p53 [T006	1128	1134	7.266844	GGGCTG	0.73242	0.7186
cg1346255	INADL	NF-AT1 [	334	342	7.211175	GGAAAG	0.15259	0.1548
cg1346255	INADL	c-Ets-1 [T	1550	1556	7.199436	TGGGAA	0.73242	0.73099
cg1346255	INADL	SRY [T00	405	413	7.175614	GAAGCA	0.30518	0.30739
cg1346255	INADL	XBP-1 [T	110	115	7.172312	ATGATT	2.92969	2.97018
cg1346255	INADL	XBP-1 [T	444	449	7.172312	ATGAAT	2.92969	2.97018
cg1346255	INADL	XBP-1 [T	452	457	7.172312	ATGAGG	2.92969	2.97018
cg1346255	INADL	XBP-1 [T	540	545	7.172312	ATGATT	2.92969	2.97018
cg1346255	INADL	XBP-1 [T	884	889	7.172312	CCTCAT	2.92969	2.97018
cg1346255	INADL	XBP-1 [T	1213	1218	7.172312	ATGAGG	2.92969	2.97018
cg1346255	INADL	XBP-1 [T	1263	1268	7.172312	ACTCAT	2.92969	2.97018
cg1346255	INADL	XBP-1 [T	1494	1499	7.172312	ATGAGG	2.92969	2.97018
cg1346255	INADL	NF-AT1 [	1525	1533	7.095752	GGAAAA	0.15259	0.1548
cg1346255	INADL	HNF-3alph	112	119	7.000129	GATTTT	0.82397	0.84946
cg1346255	INADL	HNF-3alph	133	140	7.000129	CATTTT	0.82397	0.84946
cg1346255	INADL	HNF-3alph	324	331	7.000129	AATTTA	0.82397	0.84946
cg1346255	INADL	IRF-1 [T0	1548	1556	6.968314	TGTGGG	0.1297	0.13036
cg1346255	INADL	TCF-4 [T0	1637	1646	6.961804	TCTTTG	0.01144	0.01152
cg1346255	INADL	c-Ets-1 [T	525	531	6.943262	GGGGAA	0.73242	0.73099
cg1346255	INADL	ENKTF-1	625	632	6.942764	CACAGC	1.46484	1.44228
cg1346255	INADL	ENKTF-1	1781	1788	6.942764	CATGGC	1.46484	1.44228
cg1346255	INADL	ENKTF-1	1871	1878	6.942764	TGGCTG	1.46484	1.44228
cg1346255	INADL	ENKTF-1	1928	1935	6.942764	TCGCGC	1.46484	1.44228
cg1346255	INADL	p53 [T006	371	377	6.938545	GGGCCT	1.09863	1.07125
cg1346255	INADL	STAT1bet	1265	1274	6.908963	TCATGG	0.103	0.10372
cg1346255	INADL	p53 [T006	1290	1296	6.891821	GGGCGG	1.09863	1.07125
cg1346255	INADL	c-Ets-1 [T	1513	1519	6.821536	GTTCCG	0.73242	0.73099
cg1346255	INADL	Egr-3 [T0	1601	1613	6.820034	AACACC	0.00894	0.00899
cg1346255	INADL	C/EBPalph	865	871	6.786177	TATTGT	0.73242	0.74337
cg1346255	INADL	C/EBPalph	911	917	6.786177	TACAAT	0.73242	0.74337
cg1346255	INADL	NFI/CTF [	630	637	6.786076	CCAAAC	0.73242	0.73214
cg1346255	INADL	NFI/CTF [	821	828	6.786076	CCAATC	0.73242	0.73214
cg1346255	INADL	NFI/CTF [	1110	1117	6.786076	CCAATC	0.73242	0.73214
cg1346255	INADL	T3R-beta1	1789	1797	6.702681	ACATGG	0.21362	0.21147
cg1346255	INADL	GATA-2 [	634	642	6.666667	ACCATA	0.24414	0.24583
cg1346255	INADL	TFII-I [T0	1020	1025	6.581441	CACTCC	0.97656	0.97366
cg1346255	INADL	TFII-I [T0	1403	1408	6.581441	GGAGAT	0.97656	0.97366
cg1346255	INADL	TFII-I [T0	1939	1944	6.581441	CACTCC	0.97656	0.97366
cg1346255	INADL	FOXP3 [T	474	479	6.581441	TAAAAC	0.97656	0.99397
cg1346255	INADL	FOXP3 [T	816	821	6.581441	TTCAAC	0.97656	0.99397
cg1346255	INADL	FOXP3 [T	1344	1349	6.581441	TTCAAC	0.97656	0.99397

cg1346255	INADL	RXR-alph	1189	1195	6.563693	GACACC	0.24414	0.2434
cg1346255	INADL	PXR-1:RX	1340	1347	6.5446	TTTGTTC	0.24414	0.24672
cg1346255	INADL	PPAR-alp	1853	1863	6.51544	TAGTCC	0.03719	0.03639
cg1346255	INADL	AR [T000	1498	1506	6.50872	GGACAC	0.19836	0.19597
cg1346255	INADL	XBP-1 [T	650	655	6.478682	ATGCCA	0.97656	0.97062
cg1346255	INADL	NFI/CTF [	998	1005	6.476675	CCCGTT	0.06104	0.05991
cg1346255	INADL	c-Jun [T00	572	578	6.475265	TGACAC	0.61035	0.60769
cg1346255	INADL	c-Myb [T0	54	61	6.422836	AAACTG	0.30518	0.3056
cg1346255	INADL	TCF-4E [T	142	148	6.302385	AACAAA	0.61035	0.61344
cg1346255	INADL	PPAR-alp	1646	1656	6.299891	CACTGG	0.03719	0.03639
cg1346255	INADL	c-Ets-1 [T	1267	1273	6.295602	ATGGAA	0.48828	0.48798
cg1346255	INADL	c-Ets-1 [T	1677	1683	6.295602	ATGGAA	0.48828	0.48798
cg1346255	INADL	GR-alpha [	374	378	6.263098	CCTCA	3.90625	3.91061
cg1346255	INADL	GR-alpha [	453	457	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	619	623	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	884	888	6.263098	CCTCA	3.90625	3.91061
cg1346255	INADL	GR-alpha [	916	920	6.263098	TAAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1085	1089	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1120	1124	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1207	1211	6.263098	CCTTA	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1214	1218	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1255	1259	6.263098	CCTCA	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1324	1328	6.263098	CCTTA	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1495	1499	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1541	1545	6.263098	CCTTA	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1641	1645	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1758	1762	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1769	1773	6.263098	CCTCA	3.90625	3.91061
cg1346255	INADL	GR-alpha [	1875	1879	6.263098	TGAGG	3.90625	3.91061
cg1346255	INADL	c-Ets-1 [T	180	186	6.167515	TTTCCA	0.36621	0.36731
cg1346255	INADL	p53 [T006	1155	1161	6.095267	TTGGCC	0.61035	0.594
cg1346255	INADL	HNF-1B [	761	769	6.086797	TGTTAA	0.09918	0.10196
cg1346255	INADL	GR-alpha [	160	164	6.055408	TCAGG	3.90625	3.9065
cg1346255	INADL	GR-alpha [	490	494	6.055408	CCTGA	3.90625	3.9065
cg1346255	INADL	GR-alpha [	640	644	6.055408	TCAGG	3.90625	3.9065
cg1346255	INADL	GR-alpha [	1024	1028	6.055408	CCTGA	3.90625	3.9065
cg1346255	INADL	GR-alpha [	1624	1628	6.055408	CCTGA	3.90625	3.9065
cg1346255	INADL	GR-alpha [	1654	1658	6.055408	CCTAA	3.90625	3.9065
cg1346255	INADL	GR-alpha [	1664	1668	6.055408	TTAGG	3.90625	3.9065
cg1346255	INADL	c-Ets-1 [T	1523	1529	6.039428	CTGGAA	0.36621	0.36731
cg1346255	INADL	C/EBPalp	119	125	5.996794	ACCAAT	0.97656	0.99
cg1346255	INADL	RXR-alph	320	326	5.937582	GGGTAA	0.73242	0.72249
cg1346255	INADL	HNF-1A [	1051	1058	5.898157	GTTAAG	0.24414	0.24409
cg1346255	INADL	p53 [T006	1651	1657	5.883561	GGGCCT	0.61035	0.594
cg1346255	INADL	STAT4 [T	435	440	5.882353	GGAAGG	0.48828	0.48408
cg1346255	INADL	PXR-1:RX	972	979	5.850108	TGAACC	0.06104	0.06035
cg1346255	INADL	USF1 [T0	571	580	5.845905	TTGACA	0.01526	0.01523
cg1346255	INADL	SRF [T007	635	647	5.741643	CCATAT	0.00453	0.00452

cg1346255	INADL	RXR-alph	1601	1607	5.715466	AACACC	0.61035	0.6044
cg1346255	INADL	HNF-1C [	762	770	5.695506	GTTAAA	0.07629	0.07817
cg1346255	INADL	AR [T000	1188	1196	5.644986	GGACAC	0.05341	0.05229
cg1346255	INADL	C/EBPalph	1109	1115	5.565669	TCCAAT	0.73242	0.74391
cg1346255	INADL	IRF-1 [T0	1265	1273	5.564062	TCATGG	0.22888	0.23087
cg1346255	INADL	IRF-1 [T0	1296	1304	5.564062	TTTCCG	0.22888	0.23087
cg1346255	INADL	c-Ets-1 [T	402	408	5.558311	GGGGAA	0.36621	0.3623
cg1346255	INADL	GATA-2 [	1103	1111	5.555555	CCTTTA	0.18311	0.1835
cg1346255	INADL	Pax-5 [T0	1202	1208	5.544826	ATGGCC	0.73242	0.72046
cg1346255	INADL	Pax-5 [T0	1290	1296	5.544826	GGGCGG	0.73242	0.72046
cg1346255	INADL	TFIID [T0	116	122	5.544826	TTTACC	0.73242	0.75085
cg1346255	INADL	TFIID [T0	761	767	5.544826	TGTTAA	0.73242	0.75085
cg1346255	INADL	TFIID [T0	1043	1049	5.544826	TTCTAA	0.73242	0.75085
cg1346255	INADL	TFIID [T0	1468	1474	5.544826	TTTAAC	0.73242	0.75085
cg1346255	INADL	TFIID [T0	1809	1815	5.544826	TACTAA	0.73242	0.75085
cg1346255	INADL	C/EBPalph	1490	1496	5.455853	AGCAAT	0.73242	0.74391
cg1346255	INADL	RAR-beta	970	979	5.389083	TCTGAA	0.15259	0.15189
cg1346255	INADL	C/EBPalph	1611	1617	5.38654	AACAAT	0.73242	0.74391
cg1346255	INADL	AP-2alpha	711	716	5.100982	AAAGGC	0.97656	0.97567
cg1346255	INADL	SRY [T00	706	714	5.086565	TCATCA	0.06104	0.06209
cg1346255	INADL	SRY [T00	822	830	5.086565	CAATCA	0.06104	0.06209
cg1346255	INADL	GR-beta [	227	231	5.042296	GTATT	3.90625	3.95351
cg1346255	INADL	GR-beta [	279	283	5.042296	GTATT	3.90625	3.95351
cg1346255	INADL	GR-beta [	308	312	5.042296	AATAC	3.90625	3.95351
cg1346255	INADL	GR-beta [	582	586	5.042296	GGATT	3.90625	3.95351
cg1346255	INADL	GR-beta [	644	648	5.042296	GTATT	3.90625	3.95351
cg1346255	INADL	GR-beta [	864	868	5.042296	GTATT	3.90625	3.95351
cg1346255	INADL	GR-beta [	1221	1225	5.042296	AATAC	3.90625	3.95351
cg1346255	INADL	GR-beta [	1719	1723	5.042296	AATCC	3.90625	3.95351
cg1346255	INADL	GR-beta [	1816	1820	5.042296	AATAC	3.90625	3.95351
cg1346255	INADL	c-Ets-1 [T	33	39	4.910652	ATGGAA	0.48828	0.49031
cg1346255	INADL	XBP-1 [T	881	886	4.894955	ATGCCT	0.97656	0.96979
cg1346255	INADL	XBP-1 [T	1091	1096	4.894955	AGGCAT	0.97656	0.96979
cg1346255	INADL	AR [T000	622	630	4.890444	GGACAC	0.11444	0.11247
cg1346255	INADL	AP-2alpha	1653	1658	4.890408	GCCTAA	0.97656	0.97567
cg1346255	INADL	AP-2alpha	1664	1669	4.890408	TTAGGC	0.97656	0.97567
cg1346255	INADL	HNF-1C [	1256	1264	4.875677	CTCACT	0.04578	0.04693
cg1346255	INADL	GCF [T00	391	399	4.846987	TCACGG	0.27466	0.26486
cg1346255	INADL	C/EBPalph	695	701	4.845599	AATTGC	0.97656	0.99332
cg1346255	INADL	HNF-3alph	1465	1472	4.842999	AATTTT	0.09155	0.09582
cg1346255	INADL	TFII-I [T0	994	999	4.756447	CATTCC	2.92969	2.93695
cg1346255	INADL	FOXP3 [T	178	183	4.756447	GTTTTC	2.92969	2.96063
cg1346255	INADL	FOXP3 [T	250	255	4.756447	AAAAAC	2.92969	2.96063
cg1346255	INADL	FOXP3 [T	809	814	4.756447	GTTGAG	2.92969	2.96063
cg1346255	INADL	FOXP3 [T	1449	1454	4.756447	AAAAAC	2.92969	2.96063
cg1346255	INADL	FOXP3 [T	1526	1531	4.756447	GAAAAC	2.92969	2.96063
cg1346255	INADL	FOXP3 [T	1598	1603	4.756447	AAAAAC	2.92969	2.96063
cg1346255	INADL	c-Myb [T0	345	352	4.754782	TAACTG	0.30518	0.30568

cg1346255	INADL	c-Myb [T0	350	357	4.754782	GACAGT	0.30518	0.30568
cg1346255	INADL	Ik-1 [T027	1856	1868	4.748597	TCCCAG	0.00313	0.00308
cg1346255	INADL	c-Ets-1 [T	1296	1302	4.74411	TTTCCG	0.85449	0.85764
cg1346255	INADL	PPAR-alp	1074	1084	4.727619	TTGCCC	0.03242	0.03183
cg1346255	INADL	VDR [T00	354	362	4.617121	GTTCAG	0.37384	0.37445
cg1346255	INADL	GATA-2 [	1560	1568	4.444445	CCGTTA	0.24414	0.24541
cg1346255	INADL	AP-2alpha	916	921	4.422424	TAAGGC	0.97656	0.96979
cg1346255	INADL	AP-2alpha	1323	1328	4.422424	GCCTTA	0.97656	0.96979
cg1346255	INADL	TCF-4 [T0	568	577	4.412902	CCTTTG	0.04196	0.04202
cg1346255	INADL	STAT4 [T	404	409	4.411765	GGAAGC	1.95312	1.94235
cg1346255	INADL	STAT4 [T	994	999	4.411765	CATTCC	1.95312	1.94235
cg1346255	INADL	HOXD9 [	789	798	4.321431	AATAAA	0.03433	0.03596
cg1346255	INADL	HOXD10 [	789	798	4.321431	AATAAA	0.03433	0.03596
cg1346255	INADL	Sp1 [T007	1289	1298	4.309123	GGGGCG	0.08583	0.08339
cg1346255	INADL	c-Ets-1 [T	1166	1172	4.282938	GAGGAA	0.85449	0.85764
cg1346255	INADL	HNF-1B [	1257	1265	4.252262	TCACTA	0.05341	0.0549
cg1346255	INADL	GR-beta [	111	115	4.201913	TGATT	7.8125	7.94607
cg1346255	INADL	GR-beta [	158	162	4.201913	AATCA	7.8125	7.94607
cg1346255	INADL	GR-beta [	389	393	4.201913	AATCA	7.8125	7.94607
cg1346255	INADL	GR-beta [	541	545	4.201913	TGATT	7.8125	7.94607
cg1346255	INADL	GR-beta [	597	601	4.201913	CGATT	7.8125	7.94607
cg1346255	INADL	GR-beta [	766	770	4.201913	AATAA	7.8125	7.94607
cg1346255	INADL	GR-beta [	789	793	4.201913	AATAA	7.8125	7.94607
cg1346255	INADL	GR-beta [	794	798	4.201913	AATCA	7.8125	7.94607
cg1346255	INADL	GR-beta [	823	827	4.201913	AATCA	7.8125	7.94607
cg1346255	INADL	GR-beta [	914	918	4.201913	AATAA	7.8125	7.94607
cg1346255	INADL	GR-beta [	1170	1174	4.201913	AATCA	7.8125	7.94607
cg1346255	INADL	GR-beta [	1326	1330	4.201913	TTATT	7.8125	7.94607
cg1346255	INADL	GR-beta [	1416	1420	4.201913	AATAA	7.8125	7.94607
cg1346255	INADL	c-Ets-1 [T	64	70	4.154851	CAGGAA	0.24414	0.24526
cg1346255	INADL	c-Ets-1 [T	1621	1627	4.154851	ATTCCT	0.24414	0.24526
cg1346255	INADL	NF-AT1 [	1524	1533	4.134416	TGGAAA	0.08392	0.08485
cg1346255	INADL	SRY [T00	793	801	4.087393	AAATCA	0.12207	0.12407
cg1346255	INADL	c-Ets-2 [T	329	337	4.017001	ATAAAG	0.16022	0.16243
cg1346255	INADL	c-Ets-2 [T	1679	1687	4.017001	GGAAAG	0.16022	0.16243
cg1346255	INADL	Pax-5 [T0	531	537	4.007279	ACTGCC	1.09863	1.07975
cg1346255	INADL	Pax-5 [T0	1128	1134	4.007279	GGGCTG	1.09863	1.07975
cg1346255	INADL	TFIID [T0	137	143	4.007279	TTTATA	1.09863	1.13456
cg1346255	INADL	TFIID [T0	326	332	4.007279	TTTATA	1.09863	1.13456
cg1346255	INADL	TFIID [T0	327	333	4.007279	TTATAA	1.09863	1.13456
cg1346255	INADL	TFIID [T0	471	477	4.007279	TTATAA	1.09863	1.13456
cg1346255	INADL	TFIID [T0	894	900	4.007279	TCTTAA	1.09863	1.13456
cg1346255	INADL	TFIID [T0	1582	1588	4.007279	TCTTAA	1.09863	1.13456
cg1346255	INADL	TFIID [T0	1594	1600	4.007279	TTATAA	1.09863	1.13456
cg1346255	INADL	AP-2alpha	425	430	3.970052	CAAGGC	0.97656	0.96469
cg1346255	INADL	AP-2alpha	1740	1745	3.970052	CAAGGC	0.97656	0.96469
cg1346255	INADL	GR [T050	1636	1642	3.763516	CTCTTT	0.73242	0.74251
cg1346255	INADL	PEA3 [T0	1423	1431	3.710864	TCTCAT	0.09155	0.09258

cg1346255	INADL	IRF-1 [T0	330	338	3.692688	TAAAGG	0.06866	0.06927
cg1346255	INADL	IRF-1 [T0	1680	1688	3.692688	GAAAGG	0.06866	0.06927
cg1346255	INADL	c-Ets-1 [T	454	460	3.590463	GAGGAA	0.61035	0.60765
cg1346255	INADL	p53 [T006	1950	1956	3.586914	GGGCGA	0.73242	0.7189
cg1346255	INADL	C/EBPalp	820	826	3.555778	ACCAAT	0.24414	0.24752
cg1346255	INADL	p53 [T006	531	537	3.516613	ACTGCC	0.73242	0.7189
cg1346255	INADL	HNF-3alp	751	758	3.500065	TATAAA	0.27466	0.28532
cg1346255	INADL	VDR [T00	1343	1351	3.462841	GTTCAA	0.21362	0.21341
cg1346255	INADL	NF-AT1 [	176	185	3.445347	GTGTTT	0.07629	0.07722
cg1346255	INADL	NF-AT1 [	1268	1277	3.445347	TGGAAA	0.07629	0.07722
cg1346255	INADL	RXR-alpha	616	622	3.392904	GGGTGA	1.09863	1.08572
cg1346255	INADL	RXR-alpha	1536	1542	3.392904	CTCACC	1.09863	1.08572
cg1346255	INADL	GR-beta [	194	198	3.361531	AATAT	3.90625	3.99611
cg1346255	INADL	GR-beta [	197	201	3.361531	ATATT	3.90625	3.99611
cg1346255	INADL	GR-beta [	340	344	3.361531	AGATT	3.90625	3.99611
cg1346255	INADL	GR-beta [	609	613	3.361531	AGATT	3.90625	3.99611
cg1346255	INADL	GR-beta [	702	706	3.361531	AATAT	3.90625	3.99611
cg1346255	INADL	GR-beta [	755	759	3.361531	AATAT	3.90625	3.99611
cg1346255	INADL	GR-beta [	756	760	3.361531	ATATT	3.90625	3.99611
cg1346255	INADL	GR-beta [	781	785	3.361531	ATATT	3.90625	3.99611
cg1346255	INADL	GR-beta [	1112	1116	3.361531	AATCT	3.90625	3.99611
cg1346255	INADL	PR B [T00	1047	1053	3.29756	AAATGT	0.24414	0.25122
cg1346255	INADL	PR B [T00	1611	1617	3.29756	AACAAT	0.24414	0.25122
cg1346255	INADL	PR A [T01	1047	1053	3.29756	AAATGT	0.24414	0.25122
cg1346255	INADL	PR A [T01	1611	1617	3.29756	AACAAT	0.24414	0.25122
cg1346255	INADL	AP-2alpha	1056	1061	3.229049	GCCTCT	0.48828	0.48238
cg1346255	INADL	TCF-4E [T	708	714	3.151193	ATCAAA	0.24414	0.24672
cg1346255	INADL	TCF-4E [T	795	801	3.151193	ATCAAA	0.24414	0.24672
cg1346255	INADL	TCF-4E [T	824	830	3.151193	ATCAAA	0.24414	0.24672
cg1346255	INADL	IRF-1 [T0	1675	1683	3.145547	ATATGG	0.07629	0.07756
cg1346255	INADL	POU2F2 (	217	227	3.116744	TGAATT	0.02575	0.0265
cg1346255	INADL	Pax-5 [T0	1950	1956	3.075094	GGGCGA	0.12207	0.11895
cg1346255	INADL	NF-Y [T0	1107	1114	3.051543	TATCCA	0.06104	0.06218
cg1346255	INADL	STAT4 [T	35	40	2.941176	GGAAGT	2.92969	2.929
cg1346255	INADL	STAT4 [T	334	339	2.941176	GGAAAG	2.92969	2.929
cg1346255	INADL	STAT4 [T	931	936	2.941176	GGAACC	2.92969	2.929
cg1346255	INADL	STAT4 [T	1168	1173	2.941176	GGAATC	2.92969	2.929
cg1346255	INADL	STAT4 [T	1512	1517	2.941176	TGTTCC	2.92969	2.929
cg1346255	INADL	STAT4 [T	1679	1684	2.941176	GGAAAG	2.92969	2.929
cg1346255	INADL	STAT4 [T	1684	1689	2.941176	GGAAAG	2.92969	2.929
cg1346255	INADL	p53 [T006	938	944	2.813291	GGGCAG	0.48828	0.47786
cg1346255	INADL	TBP [T00	137	146	2.807313	TTTATA	0.12207	0.12635
cg1346255	INADL	TBP [T00	326	335	2.807313	TTTATA	0.12207	0.12635
cg1346255	INADL	TBP [T00	468	477	2.807313	CACTTA	0.12207	0.12635
cg1346255	INADL	TBP [T00	1591	1600	2.807313	TAATTA	0.12207	0.12635
cg1346255	INADL	NF-AT1 [	1684	1692	2.619709	GGAAAG	0.09155	0.0926
cg1346255	INADL	c-Myb [T0	529	536	2.570796	AAACTG	0.06104	0.06117
cg1346255	INADL	AP-2alpha	373	378	2.550491	GCCTCA	0.48828	0.48266

cg1346255	INADL	AP-2alpha	883	888	2.550491	GCCTCA	0.48828	0.48266
cg1346255	INADL	AP-2alpha	1085	1090	2.550491	TGAGGC	0.48828	0.48266
cg1346255	INADL	AP-2alpha	1254	1259	2.550491	GCCTCA	0.48828	0.48266
cg1346255	INADL	AP-2alpha	1641	1646	2.550491	TGAGGC	0.48828	0.48266
cg1346255	INADL	AP-2alpha	1758	1763	2.550491	TGAGGC	0.48828	0.48266
cg1346255	INADL	AP-2alpha	1875	1880	2.550491	TGAGGC	0.48828	0.48266
cg1346255	INADL	RXR-alph	1691	1697	2.544678	TTCACC	0.85449	0.84796
cg1346255	INADL	c-Jun [T00	11	17	2.538231	TGACTT	0.48828	0.48929
cg1346255	INADL	NF-AT2 [	1684	1693	2.430885	GGAAAG	0.01144	0.01167
cg1346255	INADL	Ik-1 [T027	1721	1733	2.374299	TCCCAG	0.00063	0.00061
cg1346255	INADL	C/EBPalp	654	660	2.371703	CACAAT	0.48828	0.49114
cg1346255	INADL	GATA-2 [	1540	1548	2.222222	CCCTTA	0.22888	0.23091
cg1346255	INADL	c-Ets-2 [T	451	459	2.217136	CATGAG	0.16785	0.16856
cg1346255	INADL	c-Ets-2 [T	1163	1171	2.217136	TCCGAG	0.16785	0.16856
cg1346255	INADL	GATA-1 [	730	735	2.176375	TATCCA	3.90625	3.92756
cg1346255	INADL	GATA-1 [	984	989	2.176375	TATCCT	3.90625	3.92756
cg1346255	INADL	GATA-1 [	1107	1112	2.176375	TATCCA	3.90625	3.92756
cg1346255	INADL	NF-1 [T00	1839	1846	2.067686	TTGGCA	0.12207	0.12133
cg1346255	INADL	LEF-1 [T0	141	148	2.004405	TAACAA	0.18311	0.18582
cg1346255	INADL	LEF-1 [T0	406	413	2.004405	AAGCAA	0.18311	0.18582
cg1346255	INADL	p53 [T006	1073	1079	1.970013	TTTGCC	0.36621	0.36261
cg1346255	INADL	AP-2alpha	1734	1739	1.871933	GGAGGC	0.97656	0.95407
cg1346255	INADL	AP-2alpha	1907	1912	1.871933	GGAGGC	0.97656	0.95407
cg1346255	INADL	TBP [T00	747	756	1.871542	ATAGTA	0.18311	0.18942
cg1346255	INADL	USF1 [T0	575	584	1.858812	CACGTG	0.03624	0.03558
cg1346255	INADL	C/EBPalp	258	264	1.830762	AATTGA	0.48828	0.49438
cg1346255	INADL	TFII-I [T0	486	491	1.824994	CTCTCC	0.48828	0.48408
cg1346255	INADL	TFII-I [T0	564	569	1.824994	CTCTCC	0.48828	0.48408
cg1346255	INADL	TFII-I [T0	1063	1068	1.824994	GGAGAG	0.48828	0.48408
cg1346255	INADL	TFII-I [T0	1569	1574	1.824994	CTCTCC	0.48828	0.48408
cg1346255	INADL	PXR-1:RX	351	358	1.759733	ACAGTT	0.06104	0.06168
cg1346255	INADL	p53 [T006	1096	1102	1.758307	TCTGCC	0.36621	0.36261
cg1346255	INADL	p53 [T006	1746	1752	1.758307	GGGCAG	0.36621	0.36261
cg1346255	INADL	LEF-1 [T0	707	714	1.703176	CATCAA	0.09155	0.09326
cg1346255	INADL	GR-beta [	67	71	1.680765	GAATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	87	91	1.680765	GCATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	151	155	1.680765	GAATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	152	156	1.680765	AATTC	3.90625	3.94936
cg1346255	INADL	GR-beta [	218	222	1.680765	GAATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	447	451	1.680765	AATGC	3.90625	3.94936
cg1346255	INADL	GR-beta [	649	653	1.680765	AATGC	3.90625	3.94936
cg1346255	INADL	GR-beta [	683	687	1.680765	GCATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	966	970	1.680765	GAATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	967	971	1.680765	AATTC	3.90625	3.94936
cg1346255	INADL	GR-beta [	993	997	1.680765	GCATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	1070	1074	1.680765	GAATT	3.90625	3.94936
cg1346255	INADL	GR-beta [	1303	1307	1.680765	AATTC	3.90625	3.94936
cg1346255	INADL	GR-beta [	1620	1624	1.680765	AATTC	3.90625	3.94936

cg1346255	INADL	c-Ets-1 [T(	332	338	1.641124	AAGGAA	0.36621	0.36952
cg1346255	INADL	c-Ets-1 [T(	1682	1688	1.641124	AAGGAA	0.36621	0.36952
cg1346255	INADL	C/EBPbeta	72	75	1.639871	TTGG	15.625	15.72563
cg1346255	INADL	C/EBPbeta	120	123	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	244	247	1.639871	TTGG	15.625	15.72563
cg1346255	INADL	C/EBPbeta	614	617	1.639871	TTGG	15.625	15.72563
cg1346255	INADL	C/EBPbeta	630	633	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	821	824	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1002	1005	1.639871	TTGG	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1110	1113	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1155	1158	1.639871	TTGG	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1195	1198	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1731	1734	1.639871	TTGG	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1739	1742	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1786	1789	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1820	1823	1.639871	CCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1839	1842	1.639871	TTGG	15.625	15.72563
cg1346255	INADL	TCF-4 [T0	822	831	1.623895	CAATCA	0.04578	0.04635
cg1346255	INADL	TFIID [T0	179	185	1.537547	TTTTCCA	0.73242	0.75096
cg1346255	INADL	TFIID [T0	242	248	1.537547	TTTTGG	0.73242	0.75096
cg1346255	INADL	TFIID [T0	784	790	1.537547	TTCAAA	0.73242	0.75096
cg1346255	INADL	TFIID [T0	1524	1530	1.537547	TGGAAA	0.73242	0.75096
cg1346255	INADL	NF-Y [T0(	117	124	1.51343	TTACCA	0.18311	0.18459
cg1346255	INADL	STAT4 [T(	66	71	1.470588	GGAATT	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	179	184	1.470588	TTTTCC	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	456	461	1.470588	GGAACT	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	527	532	1.470588	GGAAAC	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	965	970	1.470588	GGAATT	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	1269	1274	1.470588	GGAAAC	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	1295	1300	1.470588	GTTTCC	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	1525	1530	1.470588	GGAAAA	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	1552	1557	1.470588	GGAAAA	1.95312	1.96333
cg1346255	INADL	STAT4 [T(	1620	1625	1.470588	AATTCC	1.95312	1.96333
cg1346255	INADL	TCF-4 [T0	793	802	1.461318	AAATCA	0.04578	0.04635
cg1346255	INADL	PR B [T00	1509	1515	1.404665	CAGTGT	0.36621	0.37023
cg1346255	INADL	PR A [T01	1509	1515	1.404665	CAGTGT	0.36621	0.37023
cg1346255	INADL	C/EBPbeta	155	158	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	260	263	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	270	273	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	376	379	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	571	574	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	601	604	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	709	712	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	785	788	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	796	799	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	810	813	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	817	820	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	825	828	1.366559	TCAA	15.625	15.72563

cg1346255	INADL	C/EBPbeta	989	992	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1119	1122	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1345	1348	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1640	1643	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1701	1704	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1757	1760	1.366559	TTGA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1771	1774	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	C/EBPbeta	1973	1976	1.366559	TCAA	15.625	15.72563
cg1346255	INADL	LEF-1 [T0	794	801	1.362541	AATCAA	0.09155	0.09326
cg1346255	INADL	LEF-1 [T0	823	830	1.362541	AATCAA	0.09155	0.09326
cg1346255	INADL	AP-2alpha	1242	1247	1.357116	ACAGGC	0.48828	0.48203
cg1346255	INADL	AP-2alpha	1848	1853	1.357116	GCCTGT	0.48828	0.48203
cg1346255	INADL	NF-Y [T0	818	825	1.285795	CAACCA	0.18311	0.18459
cg1346255	INADL	GATA-1 [	16	21	1.038567	TATCAT	1.95312	1.98662
cg1346255	INADL	GATA-1 [	704	709	1.038567	TATCAT	1.95312	1.98662
cg1346255	INADL	TCF-4 [T0	706	715	0.98855	TCATCA	0.05722	0.05784
cg1346255	INADL	TBP [T007	324	333	0.935771	AATTTAT	0.12207	0.12628
cg1346255	INADL	TBP [T007	1031	1040	0.935771	TTTATAT	0.12207	0.12628
cg1346255	INADL	HNF-1A [	341	348	0.925521	GATTTA	0.48828	0.49664
cg1346255	INADL	GATA-1 [	1794	1799	0.863549	GTGATA	1.95312	1.98662
cg1346255	INADL	GR-beta [T	28	32	0.840383	TAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	29	33	0.840383	AATTA	7.8125	7.94706
cg1346255	INADL	GR-beta [T	132	136	0.840383	TCATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	219	223	0.840383	AATTA	7.8125	7.94706
cg1346255	INADL	GR-beta [T	258	262	0.840383	AATTG	7.8125	7.94706
cg1346255	INADL	GR-beta [T	323	327	0.840383	TAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	443	447	0.840383	AATGA	7.8125	7.94706
cg1346255	INADL	GR-beta [T	656	660	0.840383	CAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	657	661	0.840383	AATTG	7.8125	7.94706
cg1346255	INADL	GR-beta [T	669	673	0.840383	TCATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	694	698	0.840383	TAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	695	699	0.840383	AATTG	7.8125	7.94706
cg1346255	INADL	GR-beta [T	720	724	0.840383	AATGG	7.8125	7.94706
cg1346255	INADL	GR-beta [T	733	737	0.840383	CCATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1201	1205	0.840383	AATGG	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1302	1306	0.840383	TAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1464	1468	0.840383	TAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1493	1497	0.840383	AATGA	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1591	1595	0.840383	TAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1592	1596	0.840383	AATTA	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1613	1617	0.840383	CAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1614	1618	0.840383	AATTA	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1619	1623	0.840383	CAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1670	1674	0.840383	TAATT	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1671	1675	0.840383	AATTA	7.8125	7.94706
cg1346255	INADL	GR-beta [T	1824	1828	0.840383	AATTA	7.8125	7.94706
cg1346255	INADL	GATA-1 [	638	643	0.758539	TATCAG	1.95312	1.98662
cg1346255	INADL	GATA-1 [	1225	1230	0.758539	CTGATA	1.95312	1.98662

cg1346255	INADL	GATA-1 [	1587	1592	0.280028	AAGATA	0.97656	0.99875
cg1346255	INADL	AP-2alpha	1946	1951	0.226186	GCCTGG	0.97656	0.95305
cg1346255	INADL	GR-alpha [	223	227	0.207689	AGAGG	7.8125	7.81264
cg1346255	INADL	GR-alpha [	331	335	0.207689	AAAGG	7.8125	7.81264
cg1346255	INADL	GR-alpha [	568	572	0.207689	CCTTT	7.8125	7.81264
cg1346255	INADL	GR-alpha [	711	715	0.207689	AAAGG	7.8125	7.81264
cg1346255	INADL	GR-alpha [	854	858	0.207689	AAAGG	7.8125	7.81264
cg1346255	INADL	GR-alpha [	901	905	0.207689	AAAGG	7.8125	7.81264
cg1346255	INADL	GR-alpha [	1057	1061	0.207689	CCTCT	7.8125	7.81264
cg1346255	INADL	GR-alpha [	1103	1107	0.207689	CCTTT	7.8125	7.81264
cg1346255	INADL	GR-alpha [	1681	1685	0.207689	AAAGG	7.8125	7.81264
cg1346255	INADL	HNF-1A [	762	769	0.143882	GTTAAA	0.24414	0.25261
cg1346255	INADL	Elk-1 [T00	431	439	0.134348	AGCAGG	0.06104	0.06047
cg1346255	INADL	GATA-1 [	1404	1409	0.105011	GAGATA	0.97656	0.98738
cg1346255	INADL	GATA-1 [	1564	1569	0.105011	TATCTC	0.97656	0.98738
cg1346255	INADL	GR-alpha [	978	982	0	CCTGT	7.8125	7.81264
cg1346255	INADL	GR-alpha [	1242	1246	0	ACAGG	7.8125	7.81264
cg1346255	INADL	GR-alpha [	1530	1534	0	ACAGG	7.8125	7.81264
cg1346255	INADL	GR-alpha [	1714	1718	0	CCTGT	7.8125	7.81264
cg1346255	INADL	GR-alpha [	1849	1853	0	CCTGT	7.8125	7.81264
cg1346255	INADL	AP-2alpha	1089	1094	0	GCAGGC	0.97656	0.95305
cg1346255	INADL	RXR-alpha	972	978	0	TGAACC	0.24414	0.2444
cg1346255	INADL	Pax-5 [T0	61	67	0	GGGCAG	1.09863	1.06846
cg1346255	INADL	Pax-5 [T0	1123	1129	0	GGGCAG	1.09863	1.06846
cg1346255	INADL	p53 [T006	61	67	0	GGGCAG	0.36621	0.35912
cg1346255	INADL	p53 [T006	1123	1129	0	GGGCAG	0.36621	0.35912
cg1346255	INADL	TFII-I [T0	334	339	0	GGAAAG	1.46484	1.45997
cg1346255	INADL	TFII-I [T0	1679	1684	0	GGAAAG	1.46484	1.45997
cg1346255	INADL	TFII-I [T0	1684	1689	0	GGAAAG	1.46484	1.45997
cg1346255	INADL	c-Ets-1 [T	433	439	0	CAGGAA	0.24414	0.2429
cg1346255	INADL	YY1 [T00	33	36	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	479	482	0	CCAT	7.8125	7.81711
cg1346255	INADL	YY1 [T00	522	525	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	538	541	0	CCAT	7.8125	7.81711
cg1346255	INADL	YY1 [T00	587	590	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	635	638	0	CCAT	7.8125	7.81711
cg1346255	INADL	YY1 [T00	721	724	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	733	736	0	CCAT	7.8125	7.81711
cg1346255	INADL	YY1 [T00	888	891	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	908	911	0	CCAT	7.8125	7.81711
cg1346255	INADL	YY1 [T00	929	932	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1160	1163	0	CCAT	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1202	1205	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1267	1270	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1287	1290	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1479	1482	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1677	1680	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1704	1707	0	ATGG	7.8125	7.81711

cg1346255	INADL	YY1 [T00	1782	1785	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1791	1794	0	ATGG	7.8125	7.81711
cg1346255	INADL	YY1 [T00	1802	1805	0	CCAT	7.8125	7.81711
cg1346255	INADL	GATA-1 [	1544	1549	0	TATCTG	0.97656	0.98738
cg1346255	INADL	C/EBPbeta	46	49	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	81	84	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	92	95	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	101	104	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	143	146	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	185	188	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	204	207	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	208	211	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	398	401	0	GCAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	408	411	0	GCAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	424	427	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	511	514	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	655	658	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	659	662	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	665	668	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	697	700	0	TTGC	15.625	15.71349
cg1346255	INADL	C/EBPbeta	715	718	0	GCAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	739	742	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	760	763	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	867	870	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	912	915	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1017	1020	0	TTGC	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1074	1077	0	TTGC	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1341	1344	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1396	1399	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1431	1434	0	TTGT	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1459	1462	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1482	1485	0	GCAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1491	1494	0	GCAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1608	1611	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1612	1615	0	ACAA	15.625	15.71349
cg1346255	INADL	C/EBPbeta	1618	1621	0	ACAA	15.625	15.71349
cg1346255	INADL	NF-1 [T00	1155	1162	0	TTGGCC	0.12207	0.11983
cg1346255	INADL	TFIID [T0	136	142	0	TTTTATA	1.09863	1.13474
cg1346255	INADL	TFIID [T0	472	478	0	TATAAA	1.09863	1.13474
cg1346255	INADL	TFIID [T0	896	902	0	TTAAAA	1.09863	1.13474
cg1346255	INADL	TFIID [T0	897	903	0	TAAAAA	1.09863	1.13474
cg1346255	INADL	TFIID [T0	1595	1601	0	TATAAA	1.09863	1.13474
cg1346255	INADL	TFIID [T0	1973	1979	0	TCAAAA	1.09863	1.13474
cg1346255	INADL	FOXP3 [T	664	669	0	GTTGTT	1.46484	1.47315
cg1346255	INADL	GR-beta [	42	46	0	AAATT	3.90625	3.99611
cg1346255	INADL	GR-beta [	43	47	0	AATTT	3.90625	3.99611
cg1346255	INADL	GR-beta [	68	72	0	AATTT	3.90625	3.99611
cg1346255	INADL	GR-beta [	122	126	0	AATGT	3.90625	3.99611

cg1346255	INADL	GR-beta [T	171	175	0	AATGT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	257	261	0	AAATT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	324	328	0	AATTT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	774	778	0	AATGT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	861	865	0	AATGT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	1014	1018	0	ACATT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	1048	1052	0	AATGT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	1071	1075	0	AATTT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	1150	1154	0	ACATT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	1352	1356	0	ACATT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	1465	1469	0	AATTT	3.90625	3.99611
cg1346255	INADL	GR-beta [T	1823	1827	0	AAATT	3.90625	3.99611
cg1346255	INADL	GR [T0507	735	741	0	ATTTTTC	0.36621	0.37562
cg1346255	INADL	GR [T0507	1974	1980	0	CAAAAA	0.36621	0.37562
cg1346255	INADL	HNF-3alph	304	311	0	TGAAAAT	0.09155	0.09511
cg1346255	INADL	HNF-3alph	785	792	0	TCAAAAT	0.09155	0.09511
cg1346255	INADL	HNF-3alph	1812	1819	0	TAAAAAT	0.09155	0.09511
cg1346255	INADL	SRY [T009	140	148	0	ATAACA	0.03052	0.03101
cg1346255	INADL	TCF-4E [T	407	413	0	AGCAAA	0.12207	0.12262
cg1346255	INADL	HNF-1A [	1466	1473	0	ATTTTAA	0.24414	0.25261
cg1346255	INADL	IRF-2 [T01	37	42	0	AAGTGA	0.48828	0.49387
cg1346255	INADL	IRF-2 [T01	1335	1340	0	TCACTT	0.48828	0.49387
cg1346255	INADL	IRF-2 [T01	1753	1758	0	TCACTT	0.48828	0.49387
cg1346255	INADL	c-Myc [T0	575	580	0	CACGTG	0.48828	0.48199
cg2169045	ITGBL1	Elk-1 [T00	1476	1484	9.979803	CTTCCGC	0.10681	0.11027
cg2169045	ITGBL1	Elk-1 [T00	1477	1485	9.979803	TTCCGGA	0.10681	0.11027
cg2169045	ITGBL1	c-Ets-1 [T0	1456	1462	9.841249	ATTCCCT	0.24414	0.23698
cg1024334	ITGBL1	c-Ets-1 [T0	593	599	9.841249	ATTCCCT	0.24414	0.23698
cg2169045	ITGBL1	STAT1beta	1664	1673	9.807397	CTTTCCA	0.14877	0.14533
cg2169045	ITGBL1	XBP-1 [T0	264	269	9.789909	ATGGCT	1.95312	1.94901
cg2169045	ITGBL1	XBP-1 [T0	1798	1803	9.789909	AGACAT	1.95312	1.94901
cg1024334	ITGBL1	XBP-1 [T0	65	70	9.789909	ATGTCT	1.95312	1.94901
cg1024334	ITGBL1	XBP-1 [T0	105	110	9.789909	ATGTCT	1.95312	1.94901
cg1024334	ITGBL1	XBP-1 [T0	959	964	9.789909	AGCCAT	1.95312	1.94901
cg1024334	ITGBL1	XBP-1 [T0	1141	1146	9.789909	CGCCAT	1.95312	1.94901
cg1024334	ITGBL1	XBP-1 [T0	1222	1227	9.789909	ATGGCT	1.95312	1.94901
cg1024334	ITGBL1	XBP-1 [T0	1324	1329	9.789909	ATGTCT	1.95312	1.94901
cg1024334	ITGBL1	XBP-1 [T0	1632	1637	9.789909	ATGTCT	1.95312	1.94901
cg2169045	ITGBL1	PR B [T00	1008	1014	9.743489	AACACC	1.09863	1.0981
cg2169045	ITGBL1	PR A [T01	1008	1014	9.743489	AACACC	1.09863	1.0981
cg1024334	ITGBL1	PR B [T00	53	59	9.743489	TTGTGTT	1.09863	1.0981
cg1024334	ITGBL1	PR B [T00	511	517	9.743489	TTGTGTT	1.09863	1.0981
cg1024334	ITGBL1	PR B [T00	1505	1511	9.743489	CTGTGTT	1.09863	1.0981
cg1024334	ITGBL1	PR A [T01	53	59	9.743489	TTGTGTT	1.09863	1.0981
cg1024334	ITGBL1	PR A [T01	511	517	9.743489	TTGTGTT	1.09863	1.0981
cg1024334	ITGBL1	PR A [T01	1505	1511	9.743489	CTGTGTT	1.09863	1.0981
cg1024334	ITGBL1	c-Myb [T0	1723	1730	9.729271	GAACTG	0.36621	0.34746
cg2169045	ITGBL1	LEF-1 [T0	1764	1771	9.72404	AGGCAA	0.21362	0.21229

cg2169045	ITGBL1	c-Jun [T00	1218	1224	9.717135	TGACCT	0.73242	0.7366
cg1024334	ITGBL1	c-Jun [T00	1863	1869	9.717135	CAGGTC	0.73242	0.7366
cg1024334	ITGBL1	c-Myb [T0	902	909	9.704537	CAACTC	0.36621	0.34746
cg2169045	ITGBL1	HNF-1C [	460	468	9.639597	ACAATT	0.19836	0.18179
cg2169045	ITGBL1	TFIID [T0	85	91	9.552105	TGTGAA	1.46484	1.37777
cg2169045	ITGBL1	TFIID [T0	934	940	9.552105	TTTGGA	1.46484	1.37777
cg2169045	ITGBL1	TFIID [T0	980	986	9.552105	TGTGAA	1.46484	1.37777
cg2169045	ITGBL1	TFIID [T0	1160	1166	9.552105	TTCCAA	1.46484	1.37777
cg2169045	ITGBL1	TFIID [T0	1521	1527	9.552105	TTCCAA	1.46484	1.37777
cg2169045	ITGBL1	TFIID [T0	1568	1574	9.552105	TTTCGTA	1.46484	1.37777
cg2169045	ITGBL1	TFIID [T0	1634	1640	9.552105	TACCAA	1.46484	1.37777
cg2169045	ITGBL1	Pax-5 [T0	881	887	9.552105	GGGCAA	1.46484	1.61918
cg1024334	ITGBL1	TFIID [T0	321	327	9.552105	TTTCTCA	1.46484	1.37777
cg1024334	ITGBL1	TFIID [T0	516	522	9.552105	TTTGTCA	1.46484	1.37777
cg1024334	ITGBL1	TFIID [T0	699	705	9.552105	TGTCAA	1.46484	1.37777
cg1024334	ITGBL1	TFIID [T0	761	767	9.552105	TGTCAA	1.46484	1.37777
cg1024334	ITGBL1	TFIID [T0	1346	1352	9.552105	TTTGGA	1.46484	1.37777
cg1024334	ITGBL1	TFIID [T0	1480	1486	9.552105	TTTCCCA	1.46484	1.37777
cg1024334	ITGBL1	TFIID [T0	1804	1810	9.552105	TACCAA	1.46484	1.37777
cg1024334	ITGBL1	TFIID [T0	1925	1931	9.552105	TGGGAA	1.46484	1.37777
cg1024334	ITGBL1	Pax-5 [T0	713	719	9.552105	GTGGCC	1.46484	1.61918
cg1024334	ITGBL1	NF-1 [T00	379	386	9.535536	CTGTCC	0.73242	0.74634
cg1024334	ITGBL1	NF-1 [T00	1254	1261	9.535536	TTGGAC	0.73242	0.74634
cg1024334	ITGBL1	NF-1 [T00	1686	1693	9.535536	TTGGCC	0.73242	0.74634
cg2169045	ITGBL1	HNF-1B [	148	156	9.513548	TATCTA	0.09155	0.08192
cg1024334	ITGBL1	NF-1 [T00	542	549	9.513281	CAACCC	0.73242	0.74634
cg1024334	ITGBL1	NF-1 [T00	1232	1239	9.513281	TAAGCC	0.73242	0.74634
cg2169045	ITGBL1	FOXP3 [T	172	177	9.512894	GTTATG	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	655	660	9.512894	AAGAAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	689	694	9.512894	CTAAAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	710	715	9.512894	GTTTAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	804	809	9.512894	GTTTAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	813	818	9.512894	GTTGCT	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	967	972	9.512894	GTTCTT	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	1058	1063	9.512894	ATAAAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	1082	1087	9.512894	AATAAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	1227	1232	9.512894	GTTGCT	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	1492	1497	9.512894	GAGAAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	1716	1721	9.512894	CAGAAC	7.32422	7.22156
cg2169045	ITGBL1	FOXP3 [T	1957	1962	9.512894	GTAAAC	7.32422	7.22156
cg2169045	ITGBL1	TFII-I [T0	458	463	9.512894	GGACAA	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	615	620	9.512894	AAATCC	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1102	1107	9.512894	TTTTCC	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1158	1163	9.512894	AATTCC	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1180	1185	9.512894	TTGTCC	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1188	1193	9.512894	GGAAGG	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1208	1213	9.512894	GGATAC	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1353	1358	9.512894	TTATCC	7.32422	7.44385

cg2169045	ITGBL1	TFII-I [T0	1384	1389	9.512894	GGAAGG	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1401	1406	9.512894	GGATTT	7.32422	7.44385
cg2169045	ITGBL1	TFII-I [T0	1481	1486	9.512894	GGAAGG	7.32422	7.44385
cg1024334	ITGBL1	FOXP3 [T	34	39	9.512894	GTTCTT	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	116	121	9.512894	GTTCTC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	303	308	9.512894	ATAAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	390	395	9.512894	ACCAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	422	427	9.512894	CTAAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	540	545	9.512894	CCCAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	768	773	9.512894	ATAAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1167	1172	9.512894	GTTATT	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1245	1250	9.512894	GTTATT	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1265	1270	9.512894	ATAAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1492	1497	9.512894	AGCAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1565	1570	9.512894	CTAAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1721	1726	9.512894	GAGAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1798	1803	9.512894	ATAAAC	7.32422	7.22156
cg1024334	ITGBL1	FOXP3 [T	1989	1994	9.512894	GTTCTT	7.32422	7.22156
cg1024334	ITGBL1	TFII-I [T0	170	175	9.512894	AAATCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	489	494	9.512894	GGATAA	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	592	597	9.512894	AATTCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	740	745	9.512894	GGACAC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	870	875	9.512894	AAATCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	937	942	9.512894	GTGTCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1220	1225	9.512894	GGATGG	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1256	1261	9.512894	GGACAA	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1263	1268	9.512894	GGATAA	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1288	1293	9.512894	TTTTCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1340	1345	9.512894	TTTTCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1349	1354	9.512894	GGAAAA	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1408	1413	9.512894	GGAATT	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1410	1415	9.512894	AATTCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1479	1484	9.512894	GTTTCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1842	1847	9.512894	GGAAGG	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1852	1857	9.512894	GTGTCC	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1927	1932	9.512894	GGAAAA	7.32422	7.44385
cg1024334	ITGBL1	TFII-I [T0	1939	1944	9.512894	CCTTCC	7.32422	7.44385
cg1024334	ITGBL1	CTF [T001	1681	1692	9.45549	GCCCAT	0.01717	0.01814
cg2169045	ITGBL1	TCF-4E [T	817	823	9.453578	CTTTGG	0.48828	0.46934
cg2169045	ITGBL1	TCF-4E [T	1161	1167	9.453578	TCCAAA	0.48828	0.46934
cg1024334	ITGBL1	TCF-4E [T	552	558	9.453578	TCCAAA	0.48828	0.46934
cg1024334	ITGBL1	TCF-4E [T	1129	1135	9.453578	CTCAAA	0.48828	0.46934
cg1024334	ITGBL1	TCF-4E [T	1345	1351	9.453578	CTTTGG	0.48828	0.46934
cg1024334	ITGBL1	TCF-4E [T	1760	1766	9.453578	CTTTGT	0.48828	0.46934
cg2169045	ITGBL1	c-Jun [T00	1924	1930	9.442241	TGACAG	0.73242	0.7366
cg2169045	ITGBL1	PPAR-alp	1386	1396	9.39865	AAGGCC	0.00286	0.00313
cg2169045	ITGBL1	c-Jun [T00	161	167	9.397655	ATTGTC	0.73242	0.7366
cg2169045	ITGBL1	c-Jun [T00	1722	1728	9.397655	ATTGTC	0.73242	0.7366

cg1024334	ITGBL1	c-Jun [T00	208	214	9.397655	ATTGTC	0.73242	0.7366
cg2169045	ITGBL1	HOXD9 [	728	737	9.356547	CTCTTA	0.02289	0.02088
cg2169045	ITGBL1	HOXD10 [	728	737	9.356547	CTCTTA	0.02289	0.02088
cg2169045	ITGBL1	LEF-1 [T0	817	824	9.313676	CTTTGG	0.21362	0.21229
cg1024334	ITGBL1	LEF-1 [T0	551	558	9.313676	CTCCAA	0.21362	0.21229
cg1024334	ITGBL1	c-Myb [T0	1800	1807	9.29064	AAACTA	0.36621	0.34746
cg1024334	ITGBL1	c-Ets-1 [T	608	614	9.276861	GTTCCC	0.36621	0.37402
cg2169045	ITGBL1	SRY [T00	1159	1167	9.264664	ATTCCA	0.12207	0.11857
cg2169045	ITGBL1	ATF [T00	1539	1550	9.257019	TTCATG	0.07725	0.07678
cg1024334	ITGBL1	HNF-1B [	1633	1641	9.205329	TGTCTA	0.08392	0.07596
cg2169045	ITGBL1	c-Ets-1 [T	935	941	9.19359	TTGGAA	0.85449	0.84987
cg2169045	ITGBL1	c-Ets-1 [T	1159	1165	9.19359	ATTCCA	0.85449	0.84987
cg1024334	ITGBL1	NF-AT1 [	1476	1484	9.158155	TCTGTT	0.22888	0.22581
cg2169045	ITGBL1	c-Ets-1 [T	1739	1745	9.148774	GTTCCC	0.85449	0.84987
cg1024334	ITGBL1	STAT5A [	1383	1395	9.080962	TCTTTTC	0.02816	0.02551
cg2169045	ITGBL1	c-Ets-1 [T	674	680	9.065503	ATTCCA	0.85449	0.84987
cg2169045	ITGBL1	NF-AT1 [	1167	1175	9.042733	GGAAAT	0.22888	0.22581
cg1024334	ITGBL1	NF-AT1 [	521	529	9.042733	CAGATT	0.22888	0.22581
cg2169045	ITGBL1	c-Jun [T00	1543	1549	9.013496	TGACGT	0.61035	0.60549
cg2169045	ITGBL1	MEF-2A [	1590	1600	9.003254	TATTTTT	0.07343	0.06466
cg2169045	ITGBL1	PXR-1:RX	1293	1300	8.998824	TGAACA	0.24414	0.24356
cg2169045	ITGBL1	LEF-1 [T0	1160	1167	8.973041	TTCCAA	0.54932	0.53171
cg1024334	ITGBL1	LEF-1 [T0	1345	1352	8.973041	CTTTGG	0.54932	0.53171
cg2169045	ITGBL1	GR [T050	1006	1012	8.971049	CAAACA	0.61035	0.5928
cg1024334	ITGBL1	GR [T050	513	519	8.971049	GTGTTT	0.61035	0.5928
cg1024334	ITGBL1	GR [T050	1392	1398	8.971049	CAAATA	0.61035	0.5928
cg2169045	ITGBL1	c-Myb [T0	1991	1998	8.947824	GAACTT	0.39673	0.37851
cg1024334	ITGBL1	c-Myb [T0	6	13	8.947824	TAACTT	0.39673	0.37851
cg1024334	ITGBL1	c-Myb [T0	1076	1083	8.947824	GAACTT	0.39673	0.37851
cg1024334	ITGBL1	Elk-1 [T00	428	436	8.931691	AGCTGG	0.24414	0.26271
cg1024334	ITGBL1	T3R-beta1	1867	1875	8.924046	TCACCC	0.2594	0.2685
cg2169045	ITGBL1	c-Ets-2 [T	783	791	8.912323	TTCCTG	0.27466	0.27171
cg2169045	ITGBL1	c-Ets-2 [T	1019	1027	8.912323	TTCCTG	0.27466	0.27171
cg1024334	ITGBL1	c-Ets-2 [T	1070	1078	8.912323	CTTCAG	0.27466	0.27171
cg1024334	ITGBL1	c-Ets-2 [T	1586	1594	8.912323	TTCCTA	0.27466	0.27171
cg1024334	ITGBL1	p53 [T006	1885	1891	8.912104	GGGCCC	0.12207	0.13824
cg2169045	ITGBL1	GATA-2 [	1208	1216	8.888889	GGATAC	0.22888	0.22339
cg2169045	ITGBL1	AP-1 [T00	1950	1958	8.862731	TGACTT	0.24414	0.23028
cg2169045	ITGBL1	ELF-1 [T0	1089	1101	8.840217	ACACTT	0.01085	0.01047
cg2169045	ITGBL1	c-Jun [T00	472	478	8.832178	TGACCT	0.61035	0.60549
cg2169045	ITGBL1	PR B [T00	392	398	8.827054	ATCTGT	0.36621	0.35051
cg2169045	ITGBL1	PR B [T00	646	652	8.827054	AACAGC	0.36621	0.35051
cg2169045	ITGBL1	PR B [T00	917	923	8.827054	ATCTGT	0.36621	0.35051
cg2169045	ITGBL1	PR B [T00	1682	1688	8.827054	AACAGG	0.36621	0.35051
cg2169045	ITGBL1	PR A [T01	392	398	8.827054	ATCTGT	0.36621	0.35051
cg2169045	ITGBL1	PR A [T01	646	652	8.827054	AACAGC	0.36621	0.35051
cg2169045	ITGBL1	PR A [T01	917	923	8.827054	ATCTGT	0.36621	0.35051
cg2169045	ITGBL1	PR A [T01	1682	1688	8.827054	AACAGG	0.36621	0.35051

cg1024334	ITGBL1	PR B [T00	425	431	8.827054	AACAGC	0.36621	0.35051
cg1024334	ITGBL1	PR B [T00	1121	1127	8.827054	AGCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR B [T00	1241	1247	8.827054	AGCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR B [T00	1279	1285	8.827054	ACCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR B [T00	1475	1481	8.827054	ATCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR B [T00	1914	1920	8.827054	ACCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR A [T01	425	431	8.827054	AACAGC	0.36621	0.35051
cg1024334	ITGBL1	PR A [T01	1121	1127	8.827054	AGCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR A [T01	1241	1247	8.827054	AGCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR A [T01	1279	1285	8.827054	ACCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR A [T01	1475	1481	8.827054	ATCTGT	0.36621	0.35051
cg1024334	ITGBL1	PR A [T01	1914	1920	8.827054	ACCTGT	0.36621	0.35051
cg2169045	ITGBL1	NFI/CTF [	931	938	8.814757	TCATTTC	0.48828	0.48845
cg2169045	ITGBL1	NFI/CTF [	1245	1252	8.814757	CCAAAA	0.48828	0.48845
cg2169045	ITGBL1	NFI/CTF [	1365	1372	8.814757	CCATTTC	0.48828	0.48845
cg1024334	ITGBL1	c-Jun [T00	1115	1121	8.807683	GTTGTC	0.61035	0.60549
cg1024334	ITGBL1	NF-1 [T00	1480	1487	8.790071	TTTCCC	0.24414	0.24339
cg1024334	ITGBL1	NF-1 [T00	1924	1931	8.790071	TTGGGA	0.24414	0.24339
cg2169045	ITGBL1	LEF-1 [T0	110	117	8.759086	CTTTGTC	0.54932	0.53171
cg2169045	ITGBL1	LEF-1 [T0	1898	1905	8.759086	TCACAA	0.54932	0.53171
cg1024334	ITGBL1	LEF-1 [T0	1760	1767	8.759086	CTTTGTA	0.54932	0.53171
cg2169045	ITGBL1	XBP-1 [T0	102	107	8.75604	TTTCAT	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	175	180	8.75604	ATGAGA	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	191	196	8.75604	TCTCAT	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	331	336	8.75604	TTTCAT	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	498	503	8.75604	GATCAT	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	549	554	8.75604	ATGAAA	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	929	934	8.75604	TTTCAT	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	940	945	8.75604	ATGAAA	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	1230	1235	8.75604	GCTCAT	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	1272	1277	8.75604	ATGAAA	2.92969	2.75329
cg2169045	ITGBL1	XBP-1 [T0	1852	1857	8.75604	ATGAAA	2.92969	2.75329
cg1024334	ITGBL1	XBP-1 [T0	76	81	8.75604	GCTCAT	2.92969	2.75329
cg1024334	ITGBL1	XBP-1 [T0	101	106	8.75604	GATCAT	2.92969	2.75329
cg1024334	ITGBL1	XBP-1 [T0	465	470	8.75604	ATGAAA	2.92969	2.75329
cg1024334	ITGBL1	XBP-1 [T0	885	890	8.75604	GCTCAT	2.92969	2.75329
cg1024334	ITGBL1	XBP-1 [T0	1472	1477	8.75604	ATGATC	2.92969	2.75329
cg1024334	ITGBL1	XBP-1 [T0	1520	1525	8.75604	TATCAT	2.92969	2.75329
cg1024334	ITGBL1	XBP-1 [T0	1623	1628	8.75604	TATCAT	2.92969	2.75329
cg2169045	ITGBL1	c-Myb [T0	551	558	8.728118	GAAAGT	0.30518	0.28602
cg1024334	ITGBL1	c-Myb [T0	1154	1161	8.728118	GTAAGT	0.30518	0.28602
cg1024334	ITGBL1	c-Jun [T00	237	243	8.571705	TGACTG	0.12207	0.1249
cg1024334	ITGBL1	RAR-beta	539	548	8.55975	CCCCAA	0.26703	0.27434
cg2169045	ITGBL1	RAR-beta	627	636	8.541284	TAAAAA	0.26703	0.27434
cg1024334	ITGBL1	NF-AT1 [	1285	1293	8.532897	TCCTTTT	0.10681	0.10494
cg1024334	ITGBL1	USF2 [T0	1830	1839	8.532138	TGTCCA	0.103	0.10815
cg2169045	ITGBL1	c-Ets-1 [T	1520	1526	8.501115	GTTCCA	0.24414	0.23702
cg1024334	ITGBL1	LEF-1 [T0	1128	1135	8.457856	CCTCAA	0.15259	0.154

cg2169045	ITGBL1	c-Myb [T0	245	252	8.443873	TACAGT	0.30518	0.28602
cg1024334	ITGBL1	c-Myb [T0	786	793	8.443873	CAACTG	0.30518	0.28602
cg1024334	ITGBL1	c-Myb [T0	473	480	8.412632	TCCAGT	0.30518	0.28602
cg1024334	ITGBL1	HOXD9 [	1241	1250	8.402327	AGCTGT	0.02289	0.01984
cg1024334	ITGBL1	HOXD10 [	1241	1250	8.402327	AGCTGT	0.02289	0.01984
cg2169045	ITGBL1	PPAR-alph	580	590	8.384593	TTCTGG	0.02003	0.02186
cg2169045	ITGBL1	HNF-3alph	299	306	8.343064	ATAAAA	0.27466	0.23078
cg2169045	ITGBL1	HNF-3alph	428	435	8.343064	AATTTA	0.27466	0.23078
cg2169045	ITGBL1	HNF-3alph	1140	1147	8.343064	CATTTTA	0.27466	0.23078
cg1024334	ITGBL1	HNF-3alph	371	378	8.343064	AATTTA	0.27466	0.23078
cg1024334	ITGBL1	HNF-3alph	1425	1432	8.343064	TTAAAA	0.27466	0.23078
cg1024334	ITGBL1	HNF-3alph	1765	1772	8.343064	TATTTA	0.27466	0.23078
cg2169045	ITGBL1	c-Ets-2 [T	136	144	8.339336	TTCCTAC	0.13733	0.13927
cg2169045	ITGBL1	c-Ets-2 [T	1379	1387	8.339336	AGGCAG	0.13733	0.13927
cg2169045	ITGBL1	PR B [T00	321	327	8.338824	TCCTGTT	1.09863	1.09384
cg2169045	ITGBL1	PR B [T00	586	592	8.338824	GCCTGT	1.09863	1.09384
cg2169045	ITGBL1	PR B [T00	606	612	8.338824	CCCTGT	1.09863	1.09384
cg2169045	ITGBL1	PR B [T00	963	969	8.338824	TTCTGTT	1.09863	1.09384
cg2169045	ITGBL1	PR B [T00	1255	1261	8.338824	AACAGA	1.09863	1.09384
cg2169045	ITGBL1	PR B [T00	1714	1720	8.338824	AACAGA	1.09863	1.09384
cg2169045	ITGBL1	PR B [T00	1838	1844	8.338824	TCCTGTT	1.09863	1.09384
cg2169045	ITGBL1	PR A [T01	321	327	8.338824	TCCTGTT	1.09863	1.09384
cg2169045	ITGBL1	PR A [T01	586	592	8.338824	GCCTGT	1.09863	1.09384
cg2169045	ITGBL1	PR A [T01	606	612	8.338824	CCCTGT	1.09863	1.09384
cg2169045	ITGBL1	PR A [T01	963	969	8.338824	TTCTGTT	1.09863	1.09384
cg2169045	ITGBL1	PR A [T01	1255	1261	8.338824	AACAGA	1.09863	1.09384
cg2169045	ITGBL1	PR A [T01	1714	1720	8.338824	AACAGA	1.09863	1.09384
cg2169045	ITGBL1	PR A [T01	1838	1844	8.338824	TCCTGTT	1.09863	1.09384
cg1024334	ITGBL1	PR B [T00	119	125	8.338824	CTCTGTT	1.09863	1.09384
cg1024334	ITGBL1	PR B [T00	736	742	8.338824	AACAGG	1.09863	1.09384
cg1024334	ITGBL1	PR B [T00	1495	1501	8.338824	AACAGG	1.09863	1.09384
cg1024334	ITGBL1	PR B [T00	1985	1991	8.338824	TCCTGTT	1.09863	1.09384
cg1024334	ITGBL1	PR A [T01	119	125	8.338824	CTCTGTT	1.09863	1.09384
cg1024334	ITGBL1	PR A [T01	736	742	8.338824	AACAGG	1.09863	1.09384
cg1024334	ITGBL1	PR A [T01	1495	1501	8.338824	AACAGG	1.09863	1.09384
cg1024334	ITGBL1	PR A [T01	1985	1991	8.338824	TCCTGTT	1.09863	1.09384
cg2169045	ITGBL1	PXR-1:RX	1124	1131	8.304332	AGTGTT	0.12207	0.11843
cg2169045	ITGBL1	GR-alpha [	255	259	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	413	417	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	482	486	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	570	574	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	578	582	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	598	602	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1036	1040	8.281568	CCTCC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1118	1122	8.281568	CCTTG	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1189	1193	8.281568	GAAGG	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1193	1197	8.281568	GGAGG	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1385	1389	8.281568	GAAGG	7.8125	8.20394

cg2169045	ITGBL1	GR-alpha [	1413	1417	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1482	1486	8.281568	GAAGG	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1488	1492	8.281568	GAAGG	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1497	1501	8.281568	CCTCC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1561	1565	8.281568	CCTTC	7.8125	8.20394
cg2169045	ITGBL1	GR-alpha [	1677	1681	8.281568	CAAGG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	528	532	8.281568	CCTTG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	634	638	8.281568	CCTTC	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	874	878	8.281568	CCTCG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	983	987	8.281568	CCTCC	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	993	997	8.281568	CCTCC	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	997	1001	8.281568	CCTCG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1012	1016	8.281568	CCTTG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1096	1100	8.281568	CCTCC	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1100	1104	8.281568	CCTTC	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1259	1263	8.281568	CAAGG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1405	1409	8.281568	GGAGG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1485	1489	8.281568	CAAGG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1499	1503	8.281568	GGAGG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1750	1754	8.281568	CCTTG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1839	1843	8.281568	GGAGG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1843	1847	8.281568	GAAGG	7.8125	8.20394
cg1024334	ITGBL1	GR-alpha [	1939	1943	8.281568	CCTTC	7.8125	8.20394
cg1024334	ITGBL1	NF-AT2 [T	1349	1358	8.245775	GGAAAA	0.08965	0.08482
cg1024334	ITGBL1	NFI/CTF [	541	548	8.241664	CCAACC	0.18311	0.1922
cg1024334	ITGBL1	HOXD9 [T	121	130	8.224939	CTGTTAT	0.08774	0.0777
cg1024334	ITGBL1	HOXD9 [T	1163	1172	8.224939	GTTTGTT	0.08774	0.0777
cg1024334	ITGBL1	HOXD10 [	121	130	8.224939	CTGTTAT	0.08774	0.0777
cg1024334	ITGBL1	HOXD10 [	1163	1172	8.224939	GTTTGTT	0.08774	0.0777
cg1024334	ITGBL1	ENKTF-1	956	963	8.19852	CCCAGC	0.73242	0.80254
cg1024334	ITGBL1	ENKTF-1	1138	1145	8.19852	TCTCGC	0.73242	0.80254
cg1024334	ITGBL1	ENKTF-1	1200	1207	8.19852	TGGCAG	0.73242	0.80254
cg2169045	ITGBL1	NF-1 [T00	594	601	8.191058	TTGGCCT	0.24414	0.24485
cg1024334	ITGBL1	NF-1 [T00	682	689	8.191058	CAGTCCA	0.24414	0.24485
cg2169045	ITGBL1	PXR-1:RX	9	16	8.180749	AATGTT	0.12207	0.11255
cg2169045	ITGBL1	SRY [T00	110	118	8.174786	CTTTGTC	0.15259	0.14791
cg1024334	ITGBL1	SRY [T00	1106	1114	8.174786	CTTTGCT	0.15259	0.14791
cg1024334	ITGBL1	IRF-1 [T0	1345	1353	8.151819	CTTTGGA	0.25177	0.2462
cg1024334	ITGBL1	c-Jun [T00	759	765	8.128539	AATGTCA	0.48828	0.47447
cg1024334	ITGBL1	NF-AT1 [T	1927	1935	8.12076	GGAAAA	0.1297	0.12846
cg2169045	ITGBL1	VDR [T00	12	20	8.079962	GTTCAGA	0.24414	0.22992
cg2169045	ITGBL1	GR-alpha [	138	142	8.073878	CCTAC	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	282	286	8.073878	CCTGG	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	777	781	8.073878	CCAGG	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	785	789	8.073878	CCTGG	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	809	813	8.073878	CTAGG	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	857	861	8.073878	CCTAC	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	862	866	8.073878	CCTAC	7.8125	8.20289

cg2169045	ITGBL1	GR-alpha [	866	870	8.073878	CCTAC	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	1107	1111	8.073878	CCTGC	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	1221	1225	8.073878	CCTGG	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	1381	1385	8.073878	GCAGG	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	1429	1433	8.073878	CCTGC	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	1572	1576	8.073878	GTAGG	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	1743	1747	8.073878	CCTGC	7.8125	8.20289
cg2169045	ITGBL1	GR-alpha [	1934	1938	8.073878	CCTGC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	96	100	8.073878	GCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	150	154	8.073878	CCTGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	250	254	8.073878	GTAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	597	601	8.073878	CCTAC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	806	810	8.073878	CCTGC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	810	814	8.073878	CCTAG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	878	882	8.073878	GCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	924	928	8.073878	CCTGC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	932	936	8.073878	CCTGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	986	990	8.073878	CCTGC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1043	1047	8.073878	CCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1065	1069	8.073878	CCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1185	1189	8.073878	CCTGC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1190	1194	8.073878	CCTGC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1202	1206	8.073878	GCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1217	1221	8.073878	GCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1414	1418	8.073878	CCTGC	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1813	1817	8.073878	GCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1836	1840	8.073878	CCTGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1862	1866	8.073878	GCAGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1889	1893	8.073878	CCTGG	7.8125	8.20289
cg1024334	ITGBL1	GR-alpha [	1943	1947	8.073878	CCAGG	7.8125	8.20289
cg2169045	ITGBL1	HNF-1C [	147	155	8.067744	TTATCTA	0.19836	0.18126
cg2169045	ITGBL1	HNF-1C [	305	313	8.067744	TTATATA	0.19836	0.18126
cg2169045	ITGBL1	TFIID [T0	83	89	8.014558	TTTGTGA	2.19727	1.99811
cg2169045	ITGBL1	TFIID [T0	102	108	8.014558	TTTCATA	2.19727	1.99811
cg2169045	ITGBL1	TFIID [T0	129	135	8.014558	TTTCTTA	2.19727	1.99811
cg2169045	ITGBL1	TFIID [T0	169	175	8.014558	TTTGTTA	2.19727	1.99811
cg2169045	ITGBL1	TFIID [T0	465	471	8.014558	TAACAA	2.19727	1.99811
cg2169045	ITGBL1	TFIID [T0	665	671	8.014558	TTTGTAA	2.19727	1.99811
cg2169045	ITGBL1	TFIID [T0	1709	1715	8.014558	TCTGAA	2.19727	1.99811
cg2169045	ITGBL1	TFIID [T0	1898	1904	8.014558	TCACAA	2.19727	1.99811
cg2169045	ITGBL1	Pax-5 [T0	1074	1080	8.014558	TATGCC	2.19727	2.42766
cg2169045	ITGBL1	Pax-5 [T0	1510	1516	8.014558	GGGCTG	2.19727	2.42766
cg2169045	ITGBL1	Pax-5 [T0	1915	1921	8.014558	TAAGCC	2.19727	2.42766
cg2169045	ITGBL1	Pax-5 [T0	1929	1935	8.014558	GCAGCC	2.19727	2.42766
cg1024334	ITGBL1	TFIID [T0	179	185	8.014558	TTTGCTA	2.19727	1.99811
cg1024334	ITGBL1	TFIID [T0	330	336	8.014558	TTTGATA	2.19727	1.99811
cg1024334	ITGBL1	TFIID [T0	357	363	8.014558	TTTGAGA	2.19727	1.99811
cg1024334	ITGBL1	TFIID [T0	792	798	8.014558	TTTCTAA	2.19727	1.99811

cg1024334	ITGBL1	TFIID [T0	1164	1170	8.014558	TTTGTTA	2.19727	1.99811
cg1024334	ITGBL1	TFIID [T0	1347	1353	8.014558	TTGGAA	2.19727	1.99811
cg1024334	ITGBL1	Pax-5 [T0	863	869	8.014558	GCTGCC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	913	919	8.014558	GGAGCC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	952	958	8.014558	TCTGCC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	1038	1044	8.014558	GCAGCC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	1205	1211	8.014558	GGGCTC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	1225	1231	8.014558	GCTGCC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	1488	1494	8.014558	GGGCAG	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	1611	1617	8.014558	TATGCC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	1884	1890	8.014558	TGGGCC	2.19727	2.42766
cg1024334	ITGBL1	Pax-5 [T0	1973	1979	8.014558	GGGCCT	2.19727	2.42766
cg2169045	ITGBL1	C/EBPalph	713	719	8.006685	TACAAT	0.24414	0.23098
cg1024334	ITGBL1	C/EBPalph	79	85	8.006685	CATTGG	0.24414	0.23098
cg1024334	ITGBL1	ETF [T002	532	542	7.870358	GCCCCG	0.07153	0.08737
cg1024334	ITGBL1	HNF-1B [	1244	1252	7.862525	TGTTATT	0.06866	0.0616
cg1024334	ITGBL1	POU2F2 (	1506	1516	7.84518	TGTGTT	0.01717	0.01535
cg1024334	ITGBL1	p53 [T006	913	919	7.833758	GGAGCC	0.48828	0.55336
cg2169045	ITGBL1	RXR-alph	1337	1343	7.815913	ACTACC	0.24414	0.26389
cg2169045	ITGBL1	RXR-alph	1445	1451	7.815913	GCCACC	0.24414	0.26389
cg1024334	ITGBL1	T3R-beta1	347	355	7.813363	ATGGGG	0.27466	0.28753
cg1024334	ITGBL1	T3R-beta1	1904	1912	7.813363	GGTGGG	0.27466	0.28753
cg1024334	ITGBL1	GATA-2 [	1442	1450	7.777778	CCAGTA	0.30518	0.29346
cg1024334	ITGBL1	T3R-beta1	997	1005	7.774776	CCTCGG	0.27466	0.28753
cg1024334	ITGBL1	AR [T000	1256	1264	7.756626	GGACAA	0.19836	0.20641
cg2169045	ITGBL1	NF-AT1 [	1661	1669	7.744746	CAGCTT	0.19836	0.19379
cg2169045	ITGBL1	NF-AT1 [	1832	1840	7.744746	TACCTT	0.19836	0.19379
cg2169045	ITGBL1	POU2F2 (	1785	1795	7.738542	TTTTTAA	0.00715	0.00609
cg2169045	ITGBL1	c-Jun [T00	526	532	7.686747	TGACTG	0.48828	0.48672
cg2169045	ITGBL1	p53 [T006	30	36	7.641867	AAGGCC	0.73242	0.79826
cg2169045	ITGBL1	p53 [T006	1386	1392	7.641867	AAGGCC	0.73242	0.79826
cg2169045	ITGBL1	ELF-1 [T0	1015	1027	7.634825	TTACTT	0.00846	0.00821
cg2169045	ITGBL1	NFI/CTF [	1963	1970	7.587343	ACTCTT	0.36621	0.36269
cg1024334	ITGBL1	NFI/CTF [	271	278	7.587343	CCAATT	0.36621	0.36269
cg1024334	ITGBL1	NFI/CTF [	602	609	7.587343	CCAAGT	0.36621	0.36269
cg1024334	ITGBL1	NFI/CTF [	1236	1243	7.587343	CCAAGA	0.36621	0.36269
cg1024334	ITGBL1	NF-AT1 [	1337	1345	7.574801	TGCTTT	0.19836	0.19379
cg2169045	ITGBL1	c-Myb [T0	1525	1532	7.545286	AAACTG	0.42725	0.40917
cg2169045	ITGBL1	GR [T050	80	86	7.527031	ATGTTT	1.83105	1.71535
cg2169045	ITGBL1	GR [T050	166	172	7.527031	CATTTT	1.83105	1.71535
cg2169045	ITGBL1	GR [T050	662	668	7.527031	AATTTT	1.83105	1.71535
cg2169045	ITGBL1	GR [T050	815	821	7.527031	TGCTTT	1.83105	1.71535
cg2169045	ITGBL1	GR [T050	1246	1252	7.527031	CAAAAG	1.83105	1.71535
cg1024334	ITGBL1	GR [T050	687	693	7.527031	CAAATA	1.83105	1.71535
cg1024334	ITGBL1	GR [T050	702	708	7.527031	CAAATA	1.83105	1.71535
cg1024334	ITGBL1	GR [T050	764	770	7.527031	CAAAAT	1.83105	1.71535
cg1024334	ITGBL1	GR [T050	1131	1137	7.527031	CAAAGC	1.83105	1.71535
cg1024334	ITGBL1	GR [T050	1332	1338	7.527031	CCTTTT	1.83105	1.71535

cg1024334	ITGBL1	GR [T050	1513	1519	7.527031	CATTTTC	1.83105	1.71535
cg1024334	ITGBL1	GR [T050	1879	1885	7.527031	CATTTTC	1.83105	1.71535
cg1024334	ITGBL1	GR [T050	1916	1922	7.527031	CTGTTTC	1.83105	1.71535
cg1024334	ITGBL1	PXR-1:RX	734	741	7.486257	TGAACA	0.24414	0.24326
cg2169045	ITGBL1	C/EBPalp	1514	1520	7.465744	TGCAAT	0.48828	0.45033
cg1024334	ITGBL1	C/EBPalp	1362	1368	7.465744	CATTGA	0.48828	0.45033
cg1024334	ITGBL1	PEA3 [T0	1219	1227	7.421728	AGGATG	0.34332	0.35389
cg2169045	ITGBL1	C/EBPalp	157	163	7.396431	TACAAT	0.48828	0.45033
cg1024334	ITGBL1	C/EBPalp	368	374	7.396431	TACAAT	0.48828	0.45033
cg1024334	ITGBL1	C/EBPalp	1252	1258	7.396431	AATTGG	0.48828	0.45033
cg1024334	ITGBL1	E2F-1 [T0	986	993	7.336545	CCTGCC	0.45776	0.49661
cg1024334	ITGBL1	c-Ets-2 [T	1412	1420	7.268173	TTCCTGC	0.09155	0.08977
cg1024334	ITGBL1	p53 [T006	1934	1940	7.266844	ACAGCC	0.73242	0.79826
cg1024334	ITGBL1	POU2F2 (	1421	1431	7.236857	TGAGTT	0.00238	0.00196
cg1024334	ITGBL1	c-Ets-1 [T	1480	1486	7.199436	TTTCCC	0.73242	0.73732
cg1024334	ITGBL1	c-Ets-1 [T	1925	1931	7.199436	TGGGAA	0.73242	0.73732
cg1024334	ITGBL1	SRY [T00	1803	1811	7.175614	CTACCA	0.30518	0.29547
cg2169045	ITGBL1	XBP-1 [T	256	261	7.172312	CTTCAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	291	296	7.172312	ATGATT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	441	446	7.172312	ACTCAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	445	450	7.172312	ATGATT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	735	740	7.172312	ATTCAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1171	1176	7.172312	ATGAAG	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1234	1239	7.172312	ATGAAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1469	1474	7.172312	ATGAGT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1534	1539	7.172312	CATCAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1538	1543	7.172312	ATTCAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1562	1567	7.172312	CTTCAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1870	1875	7.172312	AATCAT	2.92969	2.7512
cg2169045	ITGBL1	XBP-1 [T	1873	1878	7.172312	CATCAT	2.92969	2.7512
cg1024334	ITGBL1	XBP-1 [T	128	133	7.172312	ATTCAT	2.92969	2.7512
cg1024334	ITGBL1	XBP-1 [T	1320	1325	7.172312	CCTCAT	2.92969	2.7512
cg1024334	ITGBL1	XBP-1 [T	1359	1364	7.172312	AATCAT	2.92969	2.7512
cg1024334	ITGBL1	p53 [T006	1884	1890	7.153797	TGGGCC	1.09863	1.22478
cg1024334	ITGBL1	p53 [T006	713	719	7.150251	GTGGCC	1.09863	1.22478
cg2169045	ITGBL1	NF-AT1 [	1099	1107	7.095752	TTATTTT	0.15259	0.14325
cg2169045	ITGBL1	TFIID [T0	907	913	7.082373	TTTAGC	0.12207	0.11255
cg1024334	ITGBL1	TFIID [T0	166	172	7.082373	TGCTAA	0.12207	0.11255
cg2169045	ITGBL1	c-Ets-1 [T	1103	1109	7.071349	TTTCCCT	0.73242	0.73732
cg1024334	ITGBL1	AR [T000	1849	1857	7.049779	CCTGTG	0.23651	0.23986
cg2169045	ITGBL1	IRF-1 [T0	1404	1412	7.044985	TTTCCTC	0.1297	0.12685
cg1024334	ITGBL1	IRF-1 [T0	1289	1297	7.044985	TTTCCTC	0.1297	0.12685
cg1024334	ITGBL1	HNF-1C [	1245	1253	7.028835	GTTATT	0.08392	0.07499
cg2169045	ITGBL1	C/EBPalp	1721	1727	7.00174	CATTGT	0.73242	0.68282
cg1024334	ITGBL1	C/EBPalp	1684	1690	7.00174	CATTGG	0.73242	0.68282
cg2169045	ITGBL1	HNF-3alp	75	82	7.000129	TAAAAA	0.82397	0.71909
cg2169045	ITGBL1	HNF-3alp	621	628	7.000129	CATTTTT	0.82397	0.71909
cg2169045	ITGBL1	HNF-3alp	662	669	7.000129	AATTTTC	0.82397	0.71909

cg2169045	ITGBL1	HNF-3alph	1100	1107	7.000129	TATTTC	0.82397	0.71909
cg2169045	ITGBL1	HNF-3alph	1778	1785	7.000129	TATTTAT	0.82397	0.71909
cg1024334	ITGBL1	HNF-3alph	313	320	7.000129	AATTTC	0.82397	0.71909
cg1024334	ITGBL1	HNF-3alph	685	692	7.000129	TCCAAA	0.82397	0.71909
cg1024334	ITGBL1	HNF-3alph	1378	1385	7.000129	AATTTC	0.82397	0.71909
cg1024334	ITGBL1	HNF-3alph	1390	1397	7.000129	TGCAAA	0.82397	0.71909
cg1024334	ITGBL1	HNF-3alph	1927	1934	7.000129	GGAAAA	0.82397	0.71909
cg1024334	ITGBL1	NF-1 [T00	537	544	6.948522	GGCCCC	0.48828	0.50205
cg1024334	ITGBL1	ENKTF-1	1090	1097	6.942764	TGGCGT	1.46484	1.56616
cg1024334	ITGBL1	p53 [T006	1973	1979	6.938545	GGGCCT	1.09863	1.22478
cg2169045	ITGBL1	VDR [T00	374	382	6.925682	GTTCAA	0.42725	0.41
cg1024334	ITGBL1	STAT1bet	524	533	6.908963	ATTTCCT	0.103	0.09938
cg2169045	ITGBL1	C/EBPalph	1811	1817	6.85549	TGCAAT	0.73242	0.68282
cg2169045	ITGBL1	C/EBPalph	1814	1820	6.85549	AATTGC	0.73242	0.68282
cg1024334	ITGBL1	C/EBPalph	286	292	6.85549	TGCAAT	0.73242	0.68282
cg1024334	ITGBL1	C/EBPalph	897	903	6.85549	AATTGC	0.73242	0.68282
cg1024334	ITGBL1	E2F-1 [T0	857	864	6.839754	AGTGCC	0.30518	0.33862
cg2169045	ITGBL1	PU.1 [T02	1089	1101	6.801739	ACACTT	0.00337	0.00315
cg2169045	ITGBL1	c-Jun [T00	1906	1912	6.787369	TGACAG	0.73242	0.73062
cg2169045	ITGBL1	NFI/CTF [	1039	1046	6.786076	CCAAAC	0.73242	0.74795
cg2169045	ITGBL1	NFI/CTF [	1523	1530	6.786076	CCAAAC	0.73242	0.74795
cg1024334	ITGBL1	NFI/CTF [	1920	1927	6.786076	TTGCTTC	0.73242	0.74795
cg1024334	ITGBL1	p53 [T006	1205	1211	6.778774	GGGCTC	1.09863	1.22478
cg2169045	ITGBL1	c-Ets-2 [T	280	288	6.769996	TTCCTGC	0.03052	0.02816
cg2169045	ITGBL1	LEF-1 [T0	374	381	6.75468	GTTCAA	0.06104	0.05927
cg2169045	ITGBL1	ATF3 [T01	764	771	6.744803	TGACCT	0.27466	0.26471
cg2169045	ITGBL1	HNF-1B [	306	314	6.728796	TATATA	0.04578	0.04078
cg1024334	ITGBL1	NF-1 [T00	864	871	6.722386	CTGCCC	0.24414	0.2565
cg2169045	ITGBL1	c-Ets-2 [T	1837	1845	6.695187	TTCCTGT	0.09155	0.08559
cg1024334	ITGBL1	c-Jun [T00	384	390	6.668031	CAAGTC	0.61035	0.6179
cg1024334	ITGBL1	IRF-1 [T0	1480	1488	6.622811	TTTCCCA	0.19073	0.1875
cg1024334	ITGBL1	IRF-1 [T0	1923	1931	6.622811	CTTGGG	0.19073	0.1875
cg2169045	ITGBL1	FOXP3 [T	44	49	6.581441	TAAAAC	0.97656	0.904
cg2169045	ITGBL1	FOXP3 [T	610	615	6.581441	GTTTTA	0.97656	0.904
cg2169045	ITGBL1	FOXP3 [T	643	648	6.581441	TAAAAC	0.97656	0.904
cg2169045	ITGBL1	FOXP3 [T	901	906	6.581441	GTTTTA	0.97656	0.904
cg2169045	ITGBL1	FOXP3 [T	1070	1075	6.581441	GTTTTA	0.97656	0.904
cg2169045	ITGBL1	FOXP3 [T	1842	1847	6.581441	GTTTTA	0.97656	0.904
cg2169045	ITGBL1	TFII-I [T0	318	323	6.581441	ATCTCC	0.97656	0.9991
cg2169045	ITGBL1	TFII-I [T0	695	700	6.581441	ATCTCC	0.97656	0.9991
cg2169045	ITGBL1	TFII-I [T0	788	793	6.581441	GGAGAT	0.97656	0.9991
cg2169045	ITGBL1	TFII-I [T0	1045	1050	6.581441	CACTCC	0.97656	0.9991
cg1024334	ITGBL1	FOXP3 [T	1275	1280	6.581441	TTCAAC	0.97656	0.904
cg2169045	ITGBL1	AR [T000	341	349	6.566205	GGACAG	0.19836	0.20813
cg1024334	ITGBL1	RXR-alph	935	941	6.563693	GGGTGT	0.24414	0.25119
cg2169045	ITGBL1	p53 [T006	1510	1516	6.563521	GGGCTG	0.48828	0.54643
cg2169045	ITGBL1	p53 [T006	1929	1935	6.563521	GCAGCC	0.48828	0.54643
cg1024334	ITGBL1	p53 [T006	1038	1044	6.563521	GCAGCC	0.48828	0.54643

cg1024334	ITGBL1	MEF-2A [	295	305	6.559479	TGCTAT	0.02384	0.02083
cg1024334	ITGBL1	AR [T000	934	942	6.50872	TGGGTG	0.19836	0.20813
cg2169045	ITGBL1	XBP-1 [T	1075	1080	6.478682	ATGCCC	0.97656	0.99906
cg1024334	ITGBL1	XBP-1 [T	1612	1617	6.478682	ATGCCC	0.97656	0.99906
cg1024334	ITGBL1	c-Jun [T00	439	445	6.475265	TGACAC	0.61035	0.6179
cg1024334	ITGBL1	c-Ets-1 [T	1347	1353	6.423689	TTGGAA	0.48828	0.48842
cg2169045	ITGBL1	c-Myb [T0	706	713	6.422836	CCCAGT	0.30518	0.30272
cg1024334	ITGBL1	AR [T000	1826	1834	6.400417	CCTCTGT	0.19836	0.20813
cg2169045	ITGBL1	C/EBPalp	160	166	6.391486	AATTGT	0.48828	0.47407
cg2169045	ITGBL1	C/EBPalp	459	465	6.391486	GACAAT	0.48828	0.47407
cg2169045	ITGBL1	C/EBPalp	1178	1184	6.391486	AATTGT	0.48828	0.47407
cg2169045	ITGBL1	TCF-4E [	375	381	6.302385	TTCAAA	0.61035	0.59686
cg2169045	ITGBL1	TCF-4E [	1311	1317	6.302385	CTTTGC	0.61035	0.59686
cg2169045	ITGBL1	TCF-4E [	1461	1467	6.302385	CTTTGTT	0.61035	0.59686
cg2169045	ITGBL1	TCF-4E [	1765	1771	6.302385	GGCAAA	0.61035	0.59686
cg1024334	ITGBL1	TCF-4E [	30	36	6.302385	CTTTGTT	0.61035	0.59686
cg1024334	ITGBL1	TCF-4E [	1805	1811	6.302385	ACCAAA	0.61035	0.59686
cg2169045	ITGBL1	c-Ets-1 [T	1665	1671	6.295602	TTTCCAT	0.48828	0.48842
cg2169045	ITGBL1	NF-kappa	1493	1503	6.280642	AGAACC	0.03052	0.03409
cg2169045	ITGBL1	GR-alpha [	29	33	6.263098	TAAGG	3.90625	3.89624
cg2169045	ITGBL1	GR-alpha [	338	342	6.263098	TGAGG	3.90625	3.89624
cg2169045	ITGBL1	GR-alpha [	1198	1202	6.263098	TGAGG	3.90625	3.89624
cg2169045	ITGBL1	GR-alpha [	1987	1991	6.263098	TGAGG	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	111	115	6.263098	CCTTA	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	628	632	6.263098	CCTCA	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	824	828	6.263098	TGAGG	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	1128	1132	6.263098	CCTCA	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	1150	1154	6.263098	TGAGG	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	1297	1301	6.263098	CCTTA	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	1320	1324	6.263098	CCTCA	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	1542	1546	6.263098	TGAGG	3.90625	3.89624
cg1024334	ITGBL1	GR-alpha [	1976	1980	6.263098	CCTCA	3.90625	3.89624
cg1024334	ITGBL1	C/EBPalp	1552	1558	6.245236	TGCAAT	0.97656	0.91422
cg2169045	ITGBL1	ATF-2 [T0	1542	1551	6.203442	ATGACG	0.11826	0.11557
cg2169045	ITGBL1	SRY [T00	373	381	6.176442	AGTTCA	0.15259	0.14742
cg2169045	ITGBL1	SRY [T00	1897	1905	6.176442	GTCACA	0.15259	0.14742
cg1024334	ITGBL1	c-Jun [T00	516	522	6.152811	TTTGTCA	0.36621	0.34478
cg2169045	ITGBL1	RXR-alph	138	144	6.119461	CCTACC	0.73242	0.78318
cg2169045	ITGBL1	RXR-alph	857	863	6.119461	CCTACC	0.73242	0.78318
cg1024334	ITGBL1	RXR-alph	597	603	6.119461	CCTACC	0.73242	0.78318
cg1024334	ITGBL1	HNF-1C [	1632	1640	6.115467	ATGTCT	0.14496	0.13124
cg2169045	ITGBL1	c-Fos [T00	363	372	6.103724	GAGTCA	0.09155	0.09198
cg2169045	ITGBL1	GR-alpha [	490	494	6.055408	TTAGG	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	503	507	6.055408	TCAGG	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	767	771	6.055408	CCTAA	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	1021	1025	6.055408	CCTGA	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	1132	1136	6.055408	CCTGA	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	1205	1209	6.055408	TCAGG	3.90625	3.89835

cg2169045	ITGBL1	GR-alpha [	1322	1326	6.055408	CCTGA	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	1377	1381	6.055408	TCAGG	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	1397	1401	6.055408	TCAGG	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	1505	1509	6.055408	TCAGG	3.90625	3.89835
cg2169045	ITGBL1	GR-alpha [	1880	1884	6.055408	CCTGA	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	157	161	6.055408	CCTGA	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	421	425	6.055408	CCTAA	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	647	651	6.055408	TCAGG	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	1072	1076	6.055408	TCAGG	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	1230	1234	6.055408	CCTAA	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	1402	1406	6.055408	TCAGG	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	1526	1530	6.055408	CCTGA	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	1588	1592	6.055408	CCTAA	3.90625	3.89835
cg1024334	ITGBL1	GR-alpha [	1978	1982	6.055408	TCAGG	3.90625	3.89835
cg1024334	ITGBL1	c-Myb [T0	376	383	6.04018	AAACTG	0.21362	0.2053
cg1024334	ITGBL1	RXR-alph	1866	1872	5.937582	GTCACC	0.73242	0.78318
cg2169045	ITGBL1	GCF [T00	1326	1334	5.917256	ACACAG	0.64087	0.72542
cg1024334	ITGBL1	GCF [T00	1945	1953	5.917256	AGGCAG	0.64087	0.72542
cg2169045	ITGBL1	STAT4 [T	1188	1193	5.882353	GGAAGG	0.48828	0.51201
cg2169045	ITGBL1	STAT4 [T	1384	1389	5.882353	GGAAGG	0.48828	0.51201
cg2169045	ITGBL1	STAT4 [T	1481	1486	5.882353	GGAAGG	0.48828	0.51201
cg1024334	ITGBL1	STAT4 [T	1842	1847	5.882353	GGAAGG	0.48828	0.51201
cg1024334	ITGBL1	STAT4 [T	1939	1944	5.882353	CCTTCC	0.48828	0.51201
cg1024334	ITGBL1	AR [T000	1325	1333	5.859358	TGTCTG	0.24414	0.25115
cg1024334	ITGBL1	PXR-1:RX	1003	1010	5.850108	TGAACC	0.06104	0.06404
cg2169045	ITGBL1	c-Jun [T00	68	74	5.783074	AAAGTC	0.36621	0.34478
cg2169045	ITGBL1	c-Jun [T00	327	333	5.783074	TGACTT	0.36621	0.34478
cg1024334	ITGBL1	c-Jun [T00	1730	1736	5.783074	AAAGTC	0.36621	0.34478
cg1024334	ITGBL1	C/EBPalph	207	213	5.781231	TATTGT	0.97656	0.91422
cg1024334	ITGBL1	VDR [T00	730	738	5.771401	TCTGTG	0.42725	0.41266
cg2169045	ITGBL1	POU2F2 (	306	316	5.731804	TATATA	0.06437	0.05879
cg1024334	ITGBL1	POU2F2 (	1459	1469	5.731804	CATGTA	0.06437	0.05879
cg2169045	ITGBL1	ENKTF-1	603	610	5.687009	TGGCCC	0.73242	0.76357
cg2169045	ITGBL1	ENKTF-1	742	749	5.687009	TGGCTT	0.73242	0.76357
cg2169045	ITGBL1	ENKTF-1	1968	1975	5.687009	TGGCAC	0.73242	0.76357
cg1024334	ITGBL1	ENKTF-1	1231	1238	5.687009	CTAAGC	0.73242	0.76357
cg1024334	ITGBL1	c-Ets-1 [T	802	808	5.686398	CTTCCC	0.36621	0.38732
cg1024334	ITGBL1	NF-1 [T00	1954	1961	5.626299	TTGGAC	0.24414	0.25051
cg1024334	ITGBL1	RBP-Jkapp	607	618	5.616685	TGTTCC	0.00715	0.00686
cg2169045	ITGBL1	HNF-1A [	406	413	5.610392	CACTTA	0.24414	0.23087
cg2169045	ITGBL1	T3R-beta1	1362	1370	5.591999	TCACCA	0.21362	0.21789
cg2169045	ITGBL1	c-Jun [T00	764	770	5.587335	TGACCT	0.48828	0.49294
cg2169045	ITGBL1	C/EBPalph	722	728	5.565669	TACAAT	0.73242	0.68229
cg2169045	ITGBL1	C/EBPalph	1611	1617	5.565669	TACAAT	0.73242	0.68229
cg1024334	ITGBL1	TCF-4 [T0	1127	1136	5.564029	TCCTCA	0.04959	0.04908
cg1024334	ITGBL1	NFI/CTF [	546	553	5.558661	CCAAAC	0.54932	0.55504
cg1024334	ITGBL1	NFI/CTF [	828	835	5.558661	GGGTTT	0.54932	0.55504
cg1024334	ITGBL1	NFI/CTF [	1156	1163	5.558661	AAGTTT	0.54932	0.55504

cg2169045	ITGBL1	TFIID [T0	238	244	5.544826	TGATAA	0.73242	0.65314
cg2169045	ITGBL1	TFIID [T0	1844	1850	5.544826	TTTACC	0.73242	0.65314
cg1024334	ITGBL1	TFIID [T0	230	236	5.544826	TACTAA	0.73242	0.65314
cg1024334	ITGBL1	TFIID [T0	1587	1593	5.544826	TCCTAA	0.73242	0.65314
cg1024334	ITGBL1	TFIID [T0	1796	1802	5.544826	TGATAA	0.73242	0.65314
cg2169045	ITGBL1	p53 [T006	1915	1921	5.508538	TAAGCC	0.61035	0.65765
cg2169045	ITGBL1	HOXD9 [	1094	1103	5.453039	TCCTTTT	0.04578	0.03952
cg2169045	ITGBL1	HOXD10	1094	1103	5.453039	TCCTTTT	0.04578	0.03952
cg1024334	ITGBL1	C/EBPalp	270	276	5.38654	ACCAAT	0.73242	0.68229
cg1024334	ITGBL1	C/EBPalp	273	279	5.38654	AATTGT	0.73242	0.68229
cg1024334	ITGBL1	IRF-1 [T0	525	533	5.309227	TTTCCTT	0.22888	0.21959
cg2169045	ITGBL1	HOXD9 [	1604	1613	5.275652	AATAAA	0.04578	0.03952
cg2169045	ITGBL1	HOXD10	1604	1613	5.275652	AATAAA	0.04578	0.03952
cg2169045	ITGBL1	RXR-alph	702	708	5.271235	CCCACC	0.61035	0.65415
cg2169045	ITGBL1	RXR-alph	1225	1231	5.271235	GGGTTG	0.61035	0.65415
cg1024334	ITGBL1	RXR-alph	24	30	5.271235	GCAACC	0.61035	0.65415
cg1024334	ITGBL1	C/EBPalp	1315	1321	5.240291	TATTGC	0.97656	0.90302
cg2169045	ITGBL1	IRF-1 [T0	1665	1673	5.21856	TTTCCA	0.1297	0.12724
cg2169045	ITGBL1	GR [T050	1649	1655	5.207533	GGTTTT	0.24414	0.24013
cg2169045	ITGBL1	GR [T050	1767	1773	5.207533	CAAAGA	0.24414	0.24013
cg1024334	ITGBL1	GR [T050	49	55	5.207533	GGTTTT	0.24414	0.24013
cg1024334	ITGBL1	GR [T050	145	151	5.207533	CAAAAC	0.24414	0.24013
cg1024334	ITGBL1	c-Ets-2 [T	526	534	5.162974	TTCCTT	0.13733	0.13279
cg1024334	ITGBL1	NF-AT1 [	1349	1357	5.125037	GGAAAA	0.05341	0.05073
cg2169045	ITGBL1	AP-2alpha	232	237	5.100982	AAAGGC	0.97656	0.97517
cg1024334	ITGBL1	RXR-alph	840	846	5.089356	AGCACC	0.48828	0.51407
cg1024334	ITGBL1	RXR-alph	1907	1913	5.089356	GGGTGA	0.48828	0.51407
cg1024334	ITGBL1	USF2 [T0	151	160	5.052423	CTGGCA	0.103	0.10797
cg2169045	ITGBL1	GR-beta [	243	247	5.042296	AATAC	3.90625	3.7093
cg2169045	ITGBL1	GR-beta [	616	620	5.042296	AATCC	3.90625	3.7093
cg2169045	ITGBL1	GR-beta [	780	784	5.042296	GGATT	3.90625	3.7093
cg2169045	ITGBL1	GR-beta [	924	928	5.042296	AATAC	3.90625	3.7093
cg2169045	ITGBL1	GR-beta [	1401	1405	5.042296	GGATT	3.90625	3.7093
cg2169045	ITGBL1	GR-beta [	1589	1593	5.042296	GTATT	3.90625	3.7093
cg2169045	ITGBL1	GR-beta [	1609	1613	5.042296	AATAC	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	171	175	5.042296	AATCC	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	651	655	5.042296	GGATT	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	871	875	5.042296	AATCC	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	1314	1318	5.042296	GTATT	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	1394	1398	5.042296	AATAC	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	1754	1758	5.042296	GGATT	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	1764	1768	5.042296	GTATT	3.90625	3.7093
cg1024334	ITGBL1	GR-beta [	1931	1935	5.042296	AATAC	3.90625	3.7093
cg1024334	ITGBL1	HOXD9 [	1672	1681	5.035116	AATATA	0.00763	0.00669
cg1024334	ITGBL1	HOXD10	1672	1681	5.035116	AATATA	0.00763	0.00669
cg1024334	ITGBL1	C/EBPalp	1356	1362	5.024728	TGCAAT	0.97656	0.90302
cg2169045	ITGBL1	NFI/CTF	1162	1169	5.021086	CCAAAG	0.24414	0.25666
cg1024334	ITGBL1	NFI/CTF	1343	1350	5.021086	TCCTTT	0.24414	0.25666

cg1024334	ITGBL1	NFI/CTF [	1682	1689	5.021086	CCCATT	0.24414	0.25666
cg2169045	ITGBL1	c-Jun [T00	1894	1900	5.000337	GGTGTC	0.61035	0.60573
cg1024334	ITGBL1	c-Jun [T00	266	272	5.000337	TGACAC	0.61035	0.60573
cg2169045	ITGBL1	c-Ets-1 [T	1186	1192	4.910652	ATGGAA	0.48828	0.48026
cg2169045	ITGBL1	XBP-1 [T	1877	1882	4.894955	ATGCCT	0.97656	0.99839
cg1024334	ITGBL1	AP-2alpha	420	425	4.890408	GCCTAA	0.97656	0.97517
cg2169045	ITGBL1	c-Jun [T00	214	220	4.883696	TATGTC	0.61035	0.60573
cg2169045	ITGBL1	NF-1 [T00	1519	1526	4.880836	TGTTCC	0.24414	0.24345
cg1024334	ITGBL1	NF-1 [T00	832	839	4.880836	TTGGCA	0.24414	0.24345
cg2169045	ITGBL1	NF-Y [T0	1077	1084	4.867193	GCCCCA	0.36621	0.35921
cg2169045	ITGBL1	HNF-3alp	1605	1612	4.842999	ATAAAA	0.09155	0.07438
cg1024334	ITGBL1	p53 [T006	1678	1684	4.786849	AGTGCC	0.48828	0.53921
cg2169045	ITGBL1	FOXP3 [T	325	330	4.756447	GTTGAC	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	555	560	4.756447	GTTTTT	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	590	595	4.756447	GTTTTT	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	628	633	4.756447	AAAAAC	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	846	851	4.756447	GTTGAG	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	983	988	4.756447	GAAAAC	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	1252	1257	4.756447	AAAAAC	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	1465	1470	4.756447	GTTGAT	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	1650	1655	4.756447	GTTTTG	2.92969	2.82
cg2169045	ITGBL1	FOXP3 [T	1985	1990	4.756447	GTTGAG	2.92969	2.82
cg2169045	ITGBL1	TFII-I [T0	546	551	4.756447	GGAATG	2.92969	2.89715
cg2169045	ITGBL1	TFII-I [T0	673	678	4.756447	CATTCC	2.92969	2.89715
cg2169045	ITGBL1	TFII-I [T0	937	942	4.756447	GGAATG	2.92969	2.89715
cg2169045	ITGBL1	TFII-I [T0	1167	1172	4.756447	GGAAAT	2.92969	2.89715
cg2169045	ITGBL1	TFII-I [T0	1403	1408	4.756447	ATTTCC	2.92969	2.89715
cg1024334	ITGBL1	FOXP3 [T	50	55	4.756447	GTTTTG	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	57	62	4.756447	GTTGAT	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	145	150	4.756447	CAAAAC	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	223	228	4.756447	GAAAAC	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	277	282	4.756447	GTTTTT	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	889	894	4.756447	ATCAAC	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	1272	1277	4.756447	GTTTTC	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	1658	1663	4.756447	GTTTTC	2.92969	2.82
cg1024334	ITGBL1	FOXP3 [T	1710	1715	4.756447	GTTTTT	2.92969	2.82
cg1024334	ITGBL1	TFII-I [T0	470	475	4.756447	ATATCC	2.92969	2.89715
cg1024334	ITGBL1	TFII-I [T0	524	529	4.756447	ATTTCC	2.92969	2.89715
cg1024334	ITGBL1	TFII-I [T0	682	687	4.756447	CAGTCC	2.92969	2.89715
cg1024334	ITGBL1	c-Ets-1 [T	430	436	4.654478	CTGGAA	0.85449	0.8381
cg1024334	ITGBL1	c-Ets-1 [T	1940	1946	4.654478	CTTCCA	0.85449	0.8381
cg2169045	ITGBL1	VDR [T00	1289	1297	4.617121	TCAGTG	0.37384	0.36855
cg1024334	ITGBL1	VDR [T00	1821	1829	4.617121	GTTCAC	0.37384	0.36855
cg2169045	ITGBL1	c-Ets-2 [T	253	261	4.589988	TTCCTTC	0.06866	0.06805
cg2169045	ITGBL1	c-Ets-1 [T	135	141	4.539113	ATTCCT	0.85449	0.8381
cg2169045	ITGBL1	USF2 [T0	1126	1135	4.528187	TGTTCA	0.06866	0.07203
cg2169045	ITGBL1	T3R-beta1	489	497	4.481316	ATTAGG	0.27466	0.27245
cg2169045	ITGBL1	T3R-beta1	1481	1489	4.481316	GGAAGG	0.27466	0.27245

cg1024334	ITGBL1	AP-2alpha	809	814	4.438035	GCCTAG	0.97656	0.99839
cg2169045	ITGBL1	RXR-alph	1577	1583	4.423008	GGGTGG	0.24414	0.25781
cg1024334	ITGBL1	RXR-alph	1113	1119	4.423008	GGGTTG	0.24414	0.25781
cg2169045	ITGBL1	AP-2alpha	29	34	4.422424	TAAGGC	0.97656	0.99839
cg2169045	ITGBL1	STAT4 [T	546	551	4.411765	GGAATG	1.95312	1.99838
cg2169045	ITGBL1	STAT4 [T	673	678	4.411765	CATTCC	1.95312	1.99838
cg2169045	ITGBL1	STAT4 [T	937	942	4.411765	GGAATG	1.95312	1.99838
cg2169045	ITGBL1	STAT4 [T	1475	1480	4.411765	GCTTCC	1.95312	1.99838
cg1024334	ITGBL1	STAT4 [T	432	437	4.411765	GGAAGC	1.95312	1.99838
cg2169045	ITGBL1	c-Ets-1 [T	544	550	4.411026	AAGGAA	0.85449	0.8381
cg2169045	ITGBL1	p53 [T006	602	608	4.33696	CTGGCC	0.24414	0.28373
cg2169045	ITGBL1	HOXD9 [	90	99	4.321431	AATAAA	0.03433	0.02831
cg2169045	ITGBL1	HOXD9 [	899	908	4.321431	ATGTTT	0.03433	0.02831
cg2169045	ITGBL1	HOXD9 [	1266	1275	4.321431	AATAAA	0.03433	0.02831
cg2169045	ITGBL1	HOXD10 [	90	99	4.321431	AATAAA	0.03433	0.02831
cg2169045	ITGBL1	HOXD10 [	899	908	4.321431	ATGTTT	0.03433	0.02831
cg2169045	ITGBL1	HOXD10 [	1266	1275	4.321431	AATAAA	0.03433	0.02831
cg2169045	ITGBL1	PEA3 [T0	760	768	4.30818	AGGATG	0.13733	0.13607
cg1024334	ITGBL1	c-Ets-1 [T	1406	1412	4.282938	GAGGAA	0.85449	0.8381
cg2169045	ITGBL1	CREB [T0	1543	1551	4.261795	TGACGT	0.04578	0.0464
cg2169045	ITGBL1	C/EBPalp	636	642	4.235345	TATTGC	0.48828	0.46347
cg2169045	ITGBL1	C/EBPalp	989	995	4.235345	TATTGC	0.48828	0.46347
cg2169045	ITGBL1	GR-beta [	42	46	4.201913	AATAA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	90	94	4.201913	AATAA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	95	99	4.201913	AATCA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	133	137	4.201913	TTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	221	225	4.201913	TTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	292	296	4.201913	TGATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	401	405	4.201913	AATCA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	446	450	4.201913	TGATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	635	639	4.201913	CTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	750	754	4.201913	TGATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	904	908	4.201913	TTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	988	992	4.201913	CTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1025	1029	4.201913	AATCA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1082	1086	4.201913	AATAA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1099	1103	4.201913	TTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1148	1152	4.201913	AATAG	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1266	1270	4.201913	AATAA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1375	1379	4.201913	AATCA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1604	1608	4.201913	AATAA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1691	1695	4.201913	TTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1781	1785	4.201913	TTATT	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1870	1874	4.201913	AATCA	7.8125	7.23274
cg2169045	ITGBL1	GR-beta [	1913	1917	4.201913	AATAA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	59	63	4.201913	TGATT	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	193	197	4.201913	AATAA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	203	207	4.201913	TGATT	7.8125	7.23274

cg1024334	ITGBL1	GR-beta [	206	210	4.201913	TTATT	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	302	306	4.201913	AATAA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	482	486	4.201913	AATCA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	493	497	4.201913	AATAA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	654	658	4.201913	TTATT	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	767	771	4.201913	AATAA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	1168	1172	4.201913	TTATT	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	1246	1250	4.201913	TTATT	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	1359	1363	4.201913	AATCA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	1367	1371	4.201913	AATAA	7.8125	7.23274
cg1024334	ITGBL1	GR-beta [	1555	1559	4.201913	AATAG	7.8125	7.23274
cg2169045	ITGBL1	c-Ets-1 [T	279	285	4.154851	ATTCCT	0.24414	0.23719
cg2169045	ITGBL1	c-Ets-1 [T	782	788	4.154851	ATTCCT	0.24414	0.23719
cg1024334	ITGBL1	c-Ets-1 [T	1411	1417	4.154851	ATTCCT	0.24414	0.23719
cg2169045	ITGBL1	NF-1 [T00	1076	1083	4.135372	TGCCCC	0.24414	0.25714
cg2169045	ITGBL1	p53 [T006	584	590	4.125254	GGGCCT	0.73242	0.82434
cg1024334	ITGBL1	p53 [T006	535	541	4.125254	CCGGCC	0.73242	0.82434
cg2169045	ITGBL1	POU2F2 (	609	619	4.120113	TGTTTTA	0.01717	0.01453
cg2169045	ITGBL1	c-Ets-2 [T	1675	1683	4.091811	GACAAG	0.16022	0.15061
cg1024334	ITGBL1	SRY [T00	481	489	4.087393	AAATCA	0.12207	0.11312
cg1024334	ITGBL1	SRY [T00	1760	1768	4.087393	CTTTGTA	0.12207	0.11312
cg2169045	ITGBL1	E2F-1 [T0	1655	1662	4.052917	GCGGTA	0.15259	0.15999
cg2169045	ITGBL1	IRF-1 [T0	1103	1111	4.035054	TTTCCCT	0.1297	0.12468
cg2169045	ITGBL1	C/EBPalp	1215	1221	4.019783	GATTGA	0.48828	0.46347
cg2169045	ITGBL1	C/EBPalp	1947	1953	4.019783	GATTGA	0.48828	0.46347
cg2169045	ITGBL1	RXR-alpha	563	569	4.019014	GGGTAT	0.97656	1.02803
cg2169045	ITGBL1	c-Ets-2 [T	1162	1170	4.017001	CCAAAG	0.16022	0.15061
cg1024334	ITGBL1	c-Ets-2 [T	1342	1350	4.017001	TTCCTTT	0.16022	0.15061
cg2169045	ITGBL1	TFIID [T	1	7	4.007279	TTGTAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	41	47	4.007279	TAATAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	72	78	4.007279	TCATAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	226	232	4.007279	TTTATA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	227	233	4.007279	TTATAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	539	545	4.007279	TTTTAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	611	617	4.007279	TTTTAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	624	630	4.007279	TTTTAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	711	717	4.007279	TTTACA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	805	811	4.007279	TTTACT	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	1142	1148	4.007279	TTTTAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	1603	1609	4.007279	TAATAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	1786	1792	4.007279	TTTTAA	1.09863	0.94722
cg2169045	ITGBL1	TFIID [T	1955	1961	4.007279	TAGTAA	1.09863	0.94722
cg2169045	ITGBL1	Pax-5 [T0	30	36	4.007279	AAGGCC	1.09863	1.18533
cg2169045	ITGBL1	Pax-5 [T0	506	512	4.007279	GGGCAG	1.09863	1.18533
cg2169045	ITGBL1	Pax-5 [T0	1386	1392	4.007279	AAGGCC	1.09863	1.18533
cg1024334	ITGBL1	TFIID [T	259	265	4.007279	TAGTAA	1.09863	0.94722
cg1024334	ITGBL1	TFIID [T	448	454	4.007279	TTTTAA	1.09863	0.94722
cg1024334	ITGBL1	TFIID [T	492	498	4.007279	TAATAA	1.09863	0.94722

cg1024334	ITGBL1	TFIID [T0	657	663	4.007279	TTTTAA	1.09863	0.94722
cg1024334	ITGBL1	TFIID [T0	670	676	4.007279	TTTAAT	1.09863	0.94722
cg1024334	ITGBL1	TFIID [T0	1247	1253	4.007279	TATTAA	1.09863	0.94722
cg1024334	ITGBL1	TFIID [T0	1572	1578	4.007279	TTTTAA	1.09863	0.94722
cg1024334	ITGBL1	TFIID [T0	1713	1719	4.007279	TTTTAA	1.09863	0.94722
cg1024334	ITGBL1	Pax-5 [T0	1678	1684	4.007279	AGTGCC	1.09863	1.18533
cg1024334	ITGBL1	Pax-5 [T0	1816	1822	4.007279	GGGCAG	1.09863	1.18533
cg1024334	ITGBL1	Pax-5 [T0	1885	1891	4.007279	GGGCCC	1.09863	1.18533
cg1024334	ITGBL1	Pax-5 [T0	1934	1940	4.007279	ACAGCC	1.09863	1.18533
cg2169045	ITGBL1	AP-2alpha	1117	1122	3.970052	GCCTTG	0.97656	1.02535
cg1024334	ITGBL1	c-Ets-1 [T	1585	1591	3.846637	GTTCCT	0.24414	0.23719
cg1024334	ITGBL1	NFI/CTF [	1484	1491	3.793671	CCAAGG	0.18311	0.19063
cg2169045	ITGBL1	IRF-1 [T0	1836	1844	3.788396	TTTCCT	0.1297	0.12468
cg2169045	ITGBL1	GR [T050	108	114	3.763516	ATCTTT	0.73242	0.6946
cg2169045	ITGBL1	GR [T050	377	383	3.763516	CAAAGA	0.73242	0.6946
cg2169045	ITGBL1	GR [T050	1309	1315	3.763516	CTCTTT	0.73242	0.6946
cg1024334	ITGBL1	GR [T050	554	560	3.763516	CAAAGA	0.73242	0.6946
cg1024334	ITGBL1	GR [T050	1104	1110	3.763516	CTCTTT	0.73242	0.6946
cg1024334	ITGBL1	GR [T050	1807	1813	3.763516	CAAAGA	0.73242	0.6946
cg2169045	ITGBL1	p53 [T006	840	846	3.750231	GGGCTT	0.73242	0.82434
cg2169045	ITGBL1	AP-2alpha	577	582	3.743866	GCCTTC	0.48828	0.5124
cg2169045	ITGBL1	AP-2alpha	597	602	3.743866	GCCTTC	0.48828	0.5124
cg2169045	ITGBL1	AP-2alpha	1385	1390	3.743866	GAAGGC	0.48828	0.5124
cg2169045	ITGBL1	TBP [T007	1596	1605	3.743085	TTTATA	0.03052	0.02609
cg2169045	ITGBL1	c-Ets-1 [T	252	258	3.71855	GTTCCT	0.61035	0.61936
cg2169045	ITGBL1	c-Ets-1 [T	1678	1684	3.71855	AAGGAA	0.61035	0.61936
cg1024334	ITGBL1	c-Ets-1 [T	1283	1289	3.71855	GTTCCT	0.61035	0.61936
cg1024334	ITGBL1	PEA3 [T0	1520	1528	3.710864	TATCAT	0.09155	0.08745
cg2169045	ITGBL1	c-Ets-1 [T	1988	1994	3.590463	GAGGAA	0.61035	0.61936
cg1024334	ITGBL1	c-Ets-1 [T	1125	1131	3.590463	GTTCCT	0.61035	0.61936
cg1024334	ITGBL1	p53 [T006	1028	1034	3.586914	CTCGCC	0.73242	0.80362
cg2169045	ITGBL1	p53 [T006	506	512	3.516613	GGGCAG	0.73242	0.80362
cg1024334	ITGBL1	p53 [T006	1816	1822	3.516613	GGGCAG	0.73242	0.80362
cg2169045	ITGBL1	HNF-3alph	1590	1597	3.500065	TATTTT	0.27466	0.23175
cg2169045	ITGBL1	HNF-3alph	1782	1789	3.500065	TATTTT	0.27466	0.23175
cg1024334	ITGBL1	HNF-3alph	298	305	3.500065	TATAAA	0.27466	0.23175
cg1024334	ITGBL1	VDR [T00	999	1007	3.462841	TCGGTG	0.21362	0.21283
cg1024334	ITGBL1	c-Ets-1 [T	1073	1079	3.462376	CAGGAA	0.61035	0.61936
cg2169045	ITGBL1	NF-AT1 [	1661	1670	3.445347	CAGCTT	0.07629	0.07204
cg2169045	ITGBL1	PXR-1:RX	351	358	3.395883	TGGGTT	0.12207	0.11883
cg1024334	ITGBL1	RXR-alph	629	635	3.392904	CTCACC	1.09863	1.1653
cg1024334	ITGBL1	AR [T000	740	748	3.382886	GGACAC	0.06866	0.06629
cg2169045	ITGBL1	Elk-1 [T00	1018	1026	3.381796	CTTCCT	0.04578	0.04517
cg1024334	ITGBL1	p53 [T006	845	851	3.375208	CCCGCC	0.73242	0.80362
cg2169045	ITGBL1	ATF3 [T0	213	220	3.372402	TTATGT	0.09155	0.08824
cg1024334	ITGBL1	T3R-beta1	579	587	3.370634	GTGTGG	0.27466	0.27326
cg2169045	ITGBL1	GR-beta [	18	22	3.361531	AGATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [	277	281	3.361531	AGATT	3.90625	3.51525

cg2169045	ITGBL1	GR-beta [T	317	321	3.361531	AATCT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	391	395	3.361531	AATCT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	535	539	3.361531	AATAT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	536	540	3.361531	ATATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	725	729	3.361531	AATCT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	733	737	3.361531	ATATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	835	839	3.361531	AATCT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1214	1218	3.361531	AGATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1454	1458	3.361531	AGATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1614	1618	3.361531	AATCT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1777	1781	3.361531	ATATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1864	1868	3.361531	AGATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1946	1950	3.361531	AGATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	126	130	3.361531	ATATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	469	473	3.361531	AATAT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	522	526	3.361531	AGATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	673	677	3.361531	AATAT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	689	693	3.361531	AATAT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	690	694	3.361531	ATATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	704	708	3.361531	AATAT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	705	709	3.361531	ATATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	728	732	3.361531	AATCT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	1373	1377	3.361531	AATAT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	1650	1654	3.361531	AGATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	1672	1676	3.361531	AATAT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	1770	1774	3.361531	AATCT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [T	1788	1792	3.361531	AGATT	3.90625	3.51525
cg1024334	ITGBL1	NF-Y [T0	80	87	3.353763	ATTGGA	0.48828	0.48427
cg2169045	ITGBL1	T3R-beta1	1129	1137	3.351341	TCACCT	0.27466	0.27326
cg2169045	ITGBL1	IRF-1 [T0	1163	1171	3.347186	CAAAGG	0.06866	0.0661
cg1024334	ITGBL1	IRF-1 [T0	1341	1349	3.347186	TTTCCTT	0.06866	0.0661
cg2169045	ITGBL1	PR B [T00	8	14	3.29756	AAATGT	0.24414	0.21408
cg2169045	ITGBL1	PR B [T00	78	84	3.29756	AAATGT	0.24414	0.21408
cg2169045	ITGBL1	PR B [T00	943	949	3.29756	AAATGT	0.24414	0.21408
cg2169045	ITGBL1	PR B [T00	1061	1067	3.29756	AACATT	0.24414	0.21408
cg2169045	ITGBL1	PR B [T00	1553	1559	3.29756	AACATT	0.24414	0.21408
cg2169045	ITGBL1	PR A [T01	8	14	3.29756	AAATGT	0.24414	0.21408
cg2169045	ITGBL1	PR A [T01	78	84	3.29756	AAATGT	0.24414	0.21408
cg2169045	ITGBL1	PR A [T01	943	949	3.29756	AAATGT	0.24414	0.21408
cg2169045	ITGBL1	PR A [T01	1061	1067	3.29756	AACATT	0.24414	0.21408
cg2169045	ITGBL1	PR A [T01	1553	1559	3.29756	AACATT	0.24414	0.21408
cg1024334	ITGBL1	PR B [T00	273	279	3.29756	AATTGT	0.24414	0.21408
cg1024334	ITGBL1	PR B [T00	306	312	3.29756	AACATT	0.24414	0.21408
cg1024334	ITGBL1	PR A [T01	273	279	3.29756	AATTGT	0.24414	0.21408
cg1024334	ITGBL1	PR A [T01	306	312	3.29756	AACATT	0.24414	0.21408
cg2169045	ITGBL1	c-Ets-2 [T	1985	1993	3.2883	GTTGAG	0.18311	0.18314
cg2169045	ITGBL1	AP-2alpha	1762	1767	3.229049	AGAGGC	0.48828	0.5124
cg1024334	ITGBL1	RAR-beta	827	836	3.226064	GGGGTT	0.12207	0.12558

cg1024334	ITGBL1	RAR-beta	1001	1010	3.226064	GGTGAA	0.12207	0.12558
cg2169045	ITGBL1	RXR-alpha	629	635	3.170788	AAAACC	0.24414	0.24551
cg1024334	ITGBL1	TCF-4E [T	483	489	3.151193	ATCAAA	0.24414	0.23169
cg2169045	ITGBL1	Elk-1 [T00	1092	1100	3.121991	CTTCCTT	0.07629	0.07518
cg2169045	ITGBL1	c-Ets-1 [T	1476	1482	3.102985	CTTCCG	0.24414	0.26272
cg2169045	ITGBL1	c-Ets-1 [T	1479	1485	3.102985	CCGGAA	0.24414	0.26272
cg1024334	ITGBL1	Pax-5 [T0	1028	1034	3.075094	CTCGCC	0.12207	0.13819
cg2169045	ITGBL1	NF-Y [T0	140	147	3.051543	TACCCA	0.06104	0.05632
cg1024334	ITGBL1	HOXD9 [T	1373	1382	2.949288	AATATA	0.02289	0.01848
cg1024334	ITGBL1	HOXD10 [	1373	1382	2.949288	AATATA	0.02289	0.01848
cg2169045	ITGBL1	c-Ets-2 [T	541	549	2.945838	TTAAAG	0.06104	0.05567
cg1024334	ITGBL1	c-Ets-2 [T	1284	1292	2.945838	TTCCTTT	0.06104	0.05567
cg2169045	ITGBL1	STAT4 [T	134	139	2.941176	TATTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	251	256	2.941176	TGTTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	278	283	2.941176	GATTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	781	786	2.941176	GATTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1017	1022	2.941176	ACTTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1091	1096	2.941176	ACTTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1455	1460	2.941176	GATTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1519	1524	2.941176	TGTTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1664	1669	2.941176	CTTTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1680	1685	2.941176	GGAACA	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1738	1743	2.941176	GGTTCC	2.92969	2.92382
cg2169045	ITGBL1	STAT4 [T	1835	1840	2.941176	CTTTCC	2.92969	2.92382
cg1024334	ITGBL1	STAT4 [T	1	6	2.941176	GGAAGT	2.92969	2.92382
cg1024334	ITGBL1	STAT4 [T	607	612	2.941176	TGTTCC	2.92969	2.92382
cg1024334	ITGBL1	STAT4 [T	801	806	2.941176	ACTTCC	2.92969	2.92382
cg1024334	ITGBL1	STAT4 [T	1124	1129	2.941176	TGTTCC	2.92969	2.92382
cg1024334	ITGBL1	STAT4 [T	1282	1287	2.941176	TGTTCC	2.92969	2.92382
cg2169045	ITGBL1	TCF-4 [T0	373	382	2.859093	AGTTCA	0.03433	0.03101
cg1024334	ITGBL1	p53 [T006	863	869	2.813291	GCTGCC	0.48828	0.53227
cg1024334	ITGBL1	p53 [T006	1225	1231	2.813291	GCTGCC	0.48828	0.53227
cg1024334	ITGBL1	p53 [T006	1488	1494	2.813291	GGGCAG	0.48828	0.53227
cg1024334	ITGBL1	NF-1 [T00	1883	1890	2.813149	TTGGGC	0.24414	0.2566
cg2169045	ITGBL1	PR B [T00	1516	1522	2.80933	CAATGT	0.73242	0.66711
cg2169045	ITGBL1	PR B [T00	1719	1725	2.80933	AACATT	0.73242	0.66711
cg2169045	ITGBL1	PR A [T01	1516	1522	2.80933	CAATGT	0.73242	0.66711
cg2169045	ITGBL1	PR A [T01	1719	1725	2.80933	AACATT	0.73242	0.66711
cg2169045	ITGBL1	TBP [T00	224	233	2.807313	TTTTTAT	0.12207	0.10444
cg2169045	ITGBL1	TBP [T00	226	235	2.807313	TTTATAA	0.12207	0.10444
cg1024334	ITGBL1	AR [T000	376	384	2.733525	AAACTG	0.11444	0.11078
cg1024334	ITGBL1	RXR-alpha	541	547	2.726556	CCAACC	0.85449	0.89683
cg1024334	ITGBL1	c-Ets-2 [T	1837	1845	2.715313	CTGGAG	0.07629	0.07844
cg1024334	ITGBL1	NF-Y [T0	1253	1260	2.673185	ATTGGA	0.21362	0.20842
cg1024334	ITGBL1	PXR-1:RX	1818	1825	2.577808	GCAGTT	0.12207	0.11843
cg1024334	ITGBL1	AP-2alpha	627	632	2.550491	GCCTCA	0.48828	0.51216
cg1024334	ITGBL1	AP-2alpha	1319	1324	2.550491	GCCTCA	0.48828	0.51216
cg1024334	ITGBL1	AP-2alpha	1542	1547	2.550491	TGAGGC	0.48828	0.51216

cg1024334	ITGBL1	AP-2alpha	1975	1980	2.550491	GCCTCA	0.48828	0.51216
cg1024334	ITGBL1	RXR-alpha	350	356	2.544678	GGGTGA	0.85449	0.89683
cg2169045	ITGBL1	c-Jun [T00	1950	1956	2.538231	TGACTTA	0.48828	0.48077
cg2169045	ITGBL1	AR [T0004	458	466	2.519152	GGACAA	0.11444	0.11078
cg2169045	ITGBL1	AR [T0004	1177	1185	2.519152	TAATTGT	0.11444	0.11078
cg2169045	ITGBL1	POU2F2 (	446	456	2.508421	TGATTTA	0.01001	0.00847
cg2169045	ITGBL1	PXR-1:RX	371	378	2.454225	GTAGTTC	0.12207	0.11843
cg2169045	ITGBL1	C/EBPalph	142	148	2.371703	CCCAATT	0.48828	0.47439
cg1024334	ITGBL1	C/EBPalph	397	403	2.371703	AATTGTC	0.48828	0.47439
cg2169045	ITGBL1	c-Jun [T00	1324	1330	2.345465	TGACACA	0.48828	0.48077
cg2169045	ITGBL1	LEF-1 [T0	1461	1468	2.345041	CTTTGTT	0.09155	0.09076
cg1024334	ITGBL1	LEF-1 [T0	1106	1113	2.345041	CTTTGCT	0.09155	0.09076
cg2169045	ITGBL1	VDR [T00	354	362	2.308561	GTTCACC	0.10681	0.1091
cg2169045	ITGBL1	VDR [T00	1127	1135	2.308561	GTTCACC	0.10681	0.1091
cg2169045	ITGBL1	T3R-beta1	1192	1200	2.259951	GGGAGG	0.03052	0.03203
cg1024334	ITGBL1	T3R-beta1	388	396	2.240658	TCACCAA	0.15259	0.15303
cg1024334	ITGBL1	LEF-1 [T0	1804	1811	2.21836	TACCAAA	0.18311	0.17215
cg1024334	ITGBL1	c-Ets-2 [T	1126	1134	2.217136	TTCCTCA	0.16785	0.16456
cg1024334	ITGBL1	NF-Y [T0	268	275	2.194008	ACACCA	0.21362	0.20748
cg2169045	ITGBL1	GATA-1 [	1207	1212	2.176375	AGGATA	3.90625	3.79558
cg1024334	ITGBL1	GATA-1 [	471	476	2.176375	TATCCA	3.90625	3.79558
cg1024334	ITGBL1	GATA-1 [	488	493	2.176375	AGGATA	3.90625	3.79558
cg2169045	ITGBL1	RAR-beta	351	360	2.144554	TGGGTTC	0.07629	0.07711
cg2169045	ITGBL1	c-Ets-2 [T	1405	1413	2.142327	TTCCTCT	0.16785	0.16456
cg1024334	ITGBL1	c-Ets-2 [T	1290	1298	2.142327	TTCCTCT	0.16785	0.16456
cg2169045	ITGBL1	NF-1 [T00	1967	1974	2.067686	TTGGCAC	0.12207	0.12476
cg2169045	ITGBL1	GATA-1 [	1354	1359	2.001358	TATCCC	3.90625	3.79558
cg1024334	ITGBL1	GATA-1 [	1262	1267	2.001358	GGGATA	3.90625	3.79558
cg2169045	ITGBL1	SRY [T00	1461	1469	1.998343	CTTTGTT	0.03052	0.02861
cg2169045	ITGBL1	p53 [T006	881	887	1.970013	GGGCAA	0.36621	0.38097
cg1024334	ITGBL1	GATA-1 [	675	680	1.896347	TATCGG	3.90625	3.79558
cg2169045	ITGBL1	PR B [T00	1123	1129	1.892895	AAGTGT	0.12207	0.1127
cg2169045	ITGBL1	PR A [T01	1123	1129	1.892895	AAGTGT	0.12207	0.1127
cg1024334	ITGBL1	PR B [T00	604	610	1.892895	AAGTGT	0.12207	0.1127
cg1024334	ITGBL1	PR A [T01	604	610	1.892895	AAGTGT	0.12207	0.1127
cg2169045	ITGBL1	c-Ets-2 [T	1093	1101	1.874674	TTCCTTT	0.16785	0.16456
cg1024334	ITGBL1	AP-2alpha	992	997	1.871933	GCCTCC	0.97656	1.07805
cg2169045	ITGBL1	TBP [T007	294	303	1.871542	ATTCTAT	0.18311	0.15671
cg1024334	ITGBL1	TBP [T007	294	303	1.871542	GTGCTAT	0.18311	0.15671
cg2169045	ITGBL1	C/EBPalph	1237	1243	1.830762	AATTGAC	0.48828	0.46352
cg1024334	ITGBL1	C/EBPalph	894	900	1.830762	CGCAAT	0.48828	0.46352
cg2169045	ITGBL1	FOXP3 [T	396	401	1.824994	GTTGTA	0.48828	0.46414
cg2169045	ITGBL1	FOXP3 [T	1859	1864	1.824994	GTTGTA	0.48828	0.46414
cg2169045	ITGBL1	TFII-I [T0	821	826	1.824994	GGAGAG	0.48828	0.51201
cg2169045	ITGBL1	TFII-I [T0	1050	1055	1.824994	CTCTCC	0.48828	0.51201
cg2169045	ITGBL1	TFII-I [T0	1408	1413	1.824994	CTCTCC	0.48828	0.51201
cg1024334	ITGBL1	FOXP3 [T	784	789	1.824994	TACAAC	0.48828	0.46414
cg1024334	ITGBL1	TFII-I [T0	816	821	1.824994	CTCTCC	0.48828	0.51201

cg1024334	ITGBL1	TFII-I [T0	978	983	1.824994	CTCTCC	0.48828	0.51201
cg1024334	ITGBL1	TFII-I [T0	1293	1298	1.824994	CTCTCC	0.48828	0.51201
cg2169045	ITGBL1	C/EBPalph	1079	1085	1.761449	CCCAAT	0.48828	0.46352
cg2169045	ITGBL1	p53 [T006	1074	1080	1.758307	TATGCC	0.36621	0.38097
cg1024334	ITGBL1	p53 [T006	952	958	1.758307	TCTGCC	0.36621	0.38097
cg1024334	ITGBL1	p53 [T006	1611	1617	1.758307	TATGCC	0.36621	0.38097
cg1024334	ITGBL1	RXR-alpha	945	951	1.696452	GGGTCC	0.48828	0.52093
cg2169045	ITGBL1	GR-beta [T	210	214	1.680765	GCATT	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	672	676	1.680765	GCATT	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	886	890	1.680765	AATTC	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1139	1143	1.680765	GCATT	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1158	1162	1.680765	AATTC	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1236	1240	1.680765	GAATT	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1348	1352	1.680765	GCATT	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1419	1423	1.680765	AATTC	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1621	1625	1.680765	GAATT	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1622	1626	1.680765	AATTC	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1703	1707	1.680765	AATGC	3.90625	3.70067
cg2169045	ITGBL1	GR-beta [T	1757	1761	1.680765	AATGC	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	185	189	1.680765	AATGC	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	354	358	1.680765	GAATT	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	497	501	1.680765	AATGC	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	592	596	1.680765	AATTC	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	1354	1358	1.680765	AATGC	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	1409	1413	1.680765	GAATT	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	1410	1414	1.680765	AATTC	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	1429	1433	1.680765	AATGC	3.90625	3.70067
cg1024334	ITGBL1	GR-beta [T	1602	1606	1.680765	AATGC	3.90625	3.70067
cg1024334	ITGBL1	c-Ets-2 [T	1403	1411	1.64415	CAGGAG	0.04578	0.04602
cg2169045	ITGBL1	c-Ets-1 [T	1165	1171	1.641124	AAGGAA	0.36621	0.35197
cg1024334	ITGBL1	c-Ets-1 [T	525	531	1.641124	TTTCCTT	0.36621	0.35197
cg1024334	ITGBL1	c-Ets-1 [T	1341	1347	1.641124	TTTCCTT	0.36621	0.35197
cg2169045	ITGBL1	C/EBPbeta	143	146	1.639871	CCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	561	564	1.639871	TTGG	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	594	597	1.639871	TTGG	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	819	822	1.639871	TTGG	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	935	938	1.639871	TTGG	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1039	1042	1.639871	CCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1080	1083	1.639871	CCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1162	1165	1.639871	CCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1245	1248	1.639871	CCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1369	1372	1.639871	TTGG	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1523	1526	1.639871	CCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1636	1639	1.639871	CCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1967	1970	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	81	84	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	271	274	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	383	386	1.639871	CCAA	15.625	15.23827

cg1024334	ITGBL1	C/EBPbeta	391	394	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	541	544	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	546	549	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	553	556	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	602	605	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	686	689	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	832	835	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	868	871	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1160	1163	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1236	1239	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1254	1257	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1347	1350	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1484	1487	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1686	1689	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1752	1755	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1806	1809	1.639871	CCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1883	1886	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1924	1927	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1954	1957	1.639871	TTGG	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1993	1996	1.639871	TTGG	15.625	15.23827
cg2169045	ITGBL1	XBP-1 [T	163	168	1.583727	TGTCAT	0.97656	0.94995
cg2169045	ITGBL1	XBP-1 [T	216	221	1.583727	TGTCAT	0.97656	0.94995
cg2169045	ITGBL1	XBP-1 [T	471	476	1.583727	ATGACC	0.97656	0.94995
cg2169045	ITGBL1	XBP-1 [T	763	768	1.583727	ATGACC	0.97656	0.94995
cg1024334	ITGBL1	XBP-1 [T	210	215	1.583727	TGTCAT	0.97656	0.94995
cg1024334	ITGBL1	XBP-1 [T	265	270	1.583727	ATGACA	0.97656	0.94995
cg1024334	ITGBL1	XBP-1 [T	438	443	1.583727	ATGACA	0.97656	0.94995
cg1024334	ITGBL1	XBP-1 [T	1892	1897	1.583727	GGTCAT	0.97656	0.94995
cg2169045	ITGBL1	TFIID [T0	2	8	1.537547	TGTAAA	0.73242	0.65627
cg2169045	ITGBL1	TFIID [T0	664	670	1.537547	TTTTGTA	0.73242	0.65627
cg2169045	ITGBL1	Pax-5 [T0	602	608	1.537547	CTGGCC	0.73242	0.83087
cg1024334	ITGBL1	TFIID [T0	278	284	1.537547	TTTTTCA	0.73242	0.65627
cg1024334	ITGBL1	TFIID [T0	1348	1354	1.537547	TGGAAA	0.73242	0.65627
cg1024334	ITGBL1	TFIID [T0	1515	1521	1.537547	TTTTGTA	0.73242	0.65627
cg1024334	ITGBL1	Pax-5 [T0	529	535	1.537547	CTTGCC	0.73242	0.83087
cg1024334	ITGBL1	Pax-5 [T0	845	851	1.537547	CCCGCC	0.73242	0.83087
cg1024334	ITGBL1	Sp1 [T007	843	852	1.523913	ACCCCG	0.03242	0.03924
cg2169045	ITGBL1	c-Ets-1 [T	1404	1410	1.513038	TTTCCTC	0.36621	0.35197
cg1024334	ITGBL1	c-Ets-1 [T	1289	1295	1.513038	TTTCCTC	0.36621	0.35197
cg1024334	ITGBL1	RXR-alpha	828	834	1.474336	GGGTTT	0.48828	0.52093
cg2169045	ITGBL1	STAT4 [T	1102	1107	1.470588	TTTTCC	1.95312	1.90161
cg2169045	ITGBL1	STAT4 [T	1158	1163	1.470588	AATTCC	1.95312	1.90161
cg2169045	ITGBL1	STAT4 [T	1990	1995	1.470588	GGAACT	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	592	597	1.470588	AATTCC	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1075	1080	1.470588	GGAACT	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1288	1293	1.470588	TTTTCC	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1340	1345	1.470588	TTTTCC	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1349	1354	1.470588	GGAAAA	1.95312	1.90161

cg1024334	ITGBL1	STAT4 [T	1408	1413	1.470588	GGAATT	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1410	1415	1.470588	AATTCC	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1479	1484	1.470588	GTTTCC	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1584	1589	1.470588	AGTTCC	1.95312	1.90161
cg1024334	ITGBL1	STAT4 [T	1927	1932	1.470588	GGAAAA	1.95312	1.90161
cg2169045	ITGBL1	GR [T050	590	596	1.444018	GTTTTTC	0.12207	0.11476
cg2169045	ITGBL1	PR B [T00	1960	1966	1.404665	AACACT	0.36621	0.35143
cg2169045	ITGBL1	PR A [T01	1960	1966	1.404665	AACACT	0.36621	0.35143
cg2169045	ITGBL1	c-Ets-1 [T	1836	1842	1.384951	TTTCCTC	0.36621	0.35197
cg1024334	ITGBL1	NF-AT1 [	1348	1357	1.378139	TGGAAA	0.01907	0.01758
cg2169045	ITGBL1	C/EBPbeta	97	100	1.366559	TCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	314	317	1.366559	TCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	326	329	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	376	379	1.366559	TCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	847	850	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1120	1123	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1217	1220	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1239	1242	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1416	1419	1.366559	TCAA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1466	1469	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1825	1828	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1949	1952	1.366559	TTGA	15.625	15.23827
cg2169045	ITGBL1	C/EBPbeta	1986	1989	1.366559	TTGA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	58	61	1.366559	TTGA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	331	334	1.366559	TTGA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	358	361	1.366559	TTGA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	484	487	1.366559	TCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	701	704	1.366559	TCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	724	727	1.366559	TTGA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	763	766	1.366559	TCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	890	893	1.366559	TCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1130	1133	1.366559	TCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1209	1212	1.366559	TCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1276	1279	1.366559	TCAA	15.625	15.23827
cg1024334	ITGBL1	C/EBPbeta	1364	1367	1.366559	TTGA	15.625	15.23827
cg1024334	ITGBL1	LEF-1 [T0	482	489	1.362541	AATCAA	0.09155	0.08414
cg2169045	ITGBL1	AP-2alpha	343	348	1.357116	ACAGGC	0.48828	0.51319
cg2169045	ITGBL1	AP-2alpha	586	591	1.357116	GCCTGT	0.48828	0.51319
cg2169045	ITGBL1	HNF-3alph	537	544	1.342935	TATTTA	0.03052	0.02477
cg2169045	ITGBL1	HNF-3alph	1144	1151	1.342935	TTAAAA	0.03052	0.02477
cg1024334	ITGBL1	HNF-3alph	655	662	1.342935	TATTTA	0.03052	0.02477
cg1024334	ITGBL1	c-Myb [T0	1817	1824	1.285398	GGCAGT	0.06104	0.06236
cg2169045	ITGBL1	GATA-2 [	1699	1707	1.111111	AGATAA	0.09155	0.08894
cg1024334	ITGBL1	T3R-beta1	1823	1831	1.110682	TCACCTC	0.07629	0.07886
cg1024334	ITGBL1	NF-Y [T0	1685	1692	1.069274	ATTGGC	0.12207	0.11765
cg1024334	ITGBL1	GATA-1 [	331	336	1.038567	TTGATA	1.95312	1.80234
cg1024334	ITGBL1	GATA-1 [	1520	1525	1.038567	TATCAT	1.95312	1.80234
cg1024334	ITGBL1	GATA-1 [	1623	1628	1.038567	TATCAT	1.95312	1.80234

cg1024334	ITGBL1	POU2F2 (	476	486	1.003369	AGTTTA	0.00286	0.00234
cg1024334	ITGBL1	POU2F1 [	1600	1610	0.998383	TTAATG	0.01383	0.01245
cg2169045	ITGBL1	HNF-1A [	461	468	0.925521	CAATTA	0.48828	0.45029
cg1024334	ITGBL1	GATA-1 [	406	411	0.863549	GTGATA	1.95312	1.80234
cg1024334	ITGBL1	GATA-1 [	1795	1800	0.863549	GTGATA	1.95312	1.80234
cg1024334	ITGBL1	GATA-1 [	1909	1914	0.863549	GTGATA	1.95312	1.80234
cg1024334	ITGBL1	RXR-alpha	1955	1961	0.848226	TGGACC	0.48828	0.51313
cg2169045	ITGBL1	GR-beta [T	123	127	0.840383	AATTA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	144	148	0.840383	CAATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	145	149	0.840383	AATTA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	159	163	0.840383	CAATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	160	164	0.840383	AATTG	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	165	169	0.840383	TCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	193	197	0.840383	TCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	218	222	0.840383	TCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	303	307	0.840383	AATTA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	461	465	0.840383	CAATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	462	466	0.840383	AATTA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	470	474	0.840383	AATGA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	548	552	0.840383	AATGA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	620	624	0.840383	CCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	677	681	0.840383	CCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	931	935	0.840383	TCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	939	943	0.840383	AATGA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1157	1161	0.840383	TAATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1170	1174	0.840383	AATGA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1177	1181	0.840383	TAATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1178	1182	0.840383	AATTG	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1237	1241	0.840383	AATTG	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1271	1275	0.840383	AATGA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1365	1369	0.840383	CCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1536	1540	0.840383	TCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1564	1568	0.840383	TCATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1639	1643	0.840383	AATTA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1688	1692	0.840383	TAATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1689	1693	0.840383	AATTA	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1735	1739	0.840383	AATGG	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1813	1817	0.840383	CAATT	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1814	1818	0.840383	AATTG	7.8125	7.2174
cg2169045	ITGBL1	GR-beta [T	1829	1833	0.840383	AATTA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	78	82	0.840383	TCATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	130	134	0.840383	TCATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	176	180	0.840383	CCATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	215	219	0.840383	TAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	216	220	0.840383	AATTA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	235	239	0.840383	AATGA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	264	268	0.840383	AATGA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	272	276	0.840383	CAATT	7.8125	7.2174

cg1024334	ITGBL1	GR-beta [T	273	277	0.840383	AATTG	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	288	292	0.840383	CAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	312	316	0.840383	TAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	346	350	0.840383	AATGG	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	370	374	0.840383	CAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	397	401	0.840383	AATTG	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	464	468	0.840383	AATGA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	591	595	0.840383	TAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	796	800	0.840383	TAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	797	801	0.840383	AATTA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	896	900	0.840383	CAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	897	901	0.840383	AATTG	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1252	1256	0.840383	AATTG	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1361	1365	0.840383	TCATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1377	1381	0.840383	TAATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1471	1475	0.840383	AATGA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1608	1612	0.840383	AATTA	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1683	1687	0.840383	CCATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1871	1875	0.840383	CCATT	7.8125	7.2174
cg1024334	ITGBL1	GR-beta [T	1894	1898	0.840383	TCATT	7.8125	7.2174
cg2169045	ITGBL1	HNF-1A [	921	928	0.781639	GTTAAT	0.48828	0.45029
cg1024334	ITGBL1	TCF-4 [T0	481	490	0.76243	AAATCA	0.05722	0.05422
cg2169045	ITGBL1	GATA-1 [	237	242	0.758539	CTGATA	1.95312	1.80234
cg1024334	ITGBL1	GATA-1 [	158	163	0.758539	CTGATA	1.95312	1.80234
cg1024334	ITGBL1	GATA-1 [	1400	1405	0.758539	TATCAG	1.95312	1.80234
cg2169045	ITGBL1	AP-2alpha	1377	1382	0.678558	TCAGGC	0.48828	0.51196
cg2169045	ITGBL1	AP-2alpha	1879	1884	0.678558	GCCTGA	0.48828	0.51196
cg1024334	ITGBL1	AP-2alpha	1978	1983	0.678558	TCAGGC	0.48828	0.51196
cg1024334	ITGBL1	LEF-1 [T0	30	37	0.641865	CTTTGTT	0.06104	0.05974
cg1024334	ITGBL1	PR B [T00	787	793	0.48823	AACTGT	0.12207	0.11255
cg1024334	ITGBL1	PR B [T00	1268	1274	0.48823	AACTGT	0.12207	0.11255
cg1024334	ITGBL1	PR A [T01	787	793	0.48823	AACTGT	0.12207	0.11255
cg1024334	ITGBL1	PR A [T01	1268	1274	0.48823	AACTGT	0.12207	0.11255
cg2169045	ITGBL1	AP-1 [T00	360	368	0.314596	CGTGAG	0.09155	0.08806
cg2169045	ITGBL1	GATA-1 [	50	55	0.280028	TATCTA	0.97656	0.8795
cg2169045	ITGBL1	GATA-1 [	107	112	0.280028	TATCTT	0.97656	0.8795
cg2169045	ITGBL1	GATA-1 [	148	153	0.280028	TATCTA	0.97656	0.8795
cg2169045	ITGBL1	GATA-1 [	1751	1756	0.280028	TAGATA	0.97656	0.8795
cg1024334	ITGBL1	GATA-1 [	1302	1307	0.280028	TATCTA	0.97656	0.8795
cg1024334	ITGBL1	GATA-1 [	1446	1451	0.280028	TATCTT	0.97656	0.8795
cg2169045	ITGBL1	c-Ets-1 [T	1092	1098	0.256174	CTTCCTT	0.24414	0.23743
cg1024334	ITGBL1	AP-2alpha	931	936	0.226186	GCCTGG	0.97656	1.07867
cg1024334	ITGBL1	AP-2alpha	1065	1070	0.226186	CCAGGC	0.97656	1.07867
cg1024334	ITGBL1	AP-2alpha	1943	1948	0.226186	CCAGGC	0.97656	1.07867
cg1024334	ITGBL1	p53 [T006	529	535	0.211706	CTTGCC	0.36621	0.40082
cg2169045	ITGBL1	GR-alpha [	24	28	0.207689	CCTCT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	232	236	0.207689	AAAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	433	437	0.207689	AAAGG	7.8125	7.79817

cg2169045	ITGBL1	GR-alpha [	475	479	0.207689	CCTTT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	543	547	0.207689	AAAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1049	1053	0.207689	CCTCT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1095	1099	0.207689	CCTTT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1164	1168	0.207689	AAAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1258	1262	0.207689	AGAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1275	1279	0.207689	AAAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1343	1347	0.207689	CCTCT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1407	1411	0.207689	CCTCT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1460	1464	0.207689	CCTTT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1585	1589	0.207689	AAAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1646	1650	0.207689	AGAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1762	1766	0.207689	AGAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1834	1838	0.207689	CCTTT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1855	1859	0.207689	AAAGG	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	29	33	0.207689	CCTTT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	486	490	0.207689	AAAGG	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	661	665	0.207689	AAAGG	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	977	981	0.207689	CCTCT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1286	1290	0.207689	CCTTT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1292	1296	0.207689	CCTCT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1332	1336	0.207689	CCTTT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1344	1348	0.207689	CCTTT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1717	1721	0.207689	AAAGG	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1826	1830	0.207689	CCTCT	7.8125	7.79817
cg1024334	ITGBL1	Elk-1 [T00	1838	1846	0.134348	TGGAGG	0.06104	0.06399
cg1024334	ITGBL1	c-Ets-1 [T	1840	1846	0.128087	GAGGAA	0.24414	0.24982
cg2169045	ITGBL1	GATA-1 [	177	182	0.105011	GAGATA	0.97656	0.92541
cg2169045	ITGBL1	GATA-1 [	789	794	0.105011	GAGATA	0.97656	0.92541
cg2169045	ITGBL1	GATA-1 [	1698	1703	0.105011	GAGATA	0.97656	0.92541
cg2169045	ITGBL1	GR-beta [T	9	13	0	AATGT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	79	83	0	AATGT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	122	126	0	AAATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	302	306	0	AAATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	427	431	0	AAATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	428	432	0	AATTT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	487	491	0	ACATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	661	665	0	AAATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	662	666	0	AATTT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	716	720	0	AATGT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	885	889	0	AAATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	944	948	0	AATGT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	978	982	0	AATGT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1062	1066	0	ACATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1418	1422	0	AAATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1517	1521	0	AATGT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1554	1558	0	ACATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1638	1642	0	AAATT	3.90625	3.51525

cg2169045	ITGBL1	GR-beta [T	1720	1724	0	ACATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1800	1804	0	ACATT	3.90625	3.51525
cg2169045	ITGBL1	GR-beta [T	1828	1832	0	AAATT	3.90625	3.51525
cg2169045	ITGBL1	XBP-1 [T0	70	75	0	AGTCAT	0.97656	0.94838
cg2169045	ITGBL1	XBP-1 [T0	1542	1547	0	ATGACG	0.97656	0.94838
cg2169045	ITGBL1	TFIID [T0	4	10	0	TAAAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	64	70	0	TCTAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	225	231	0	TTTTATA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	228	234	0	TATAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	298	304	0	TATAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	449	455	0	TTTAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	623	629	0	TTTTTAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	625	631	0	TTTAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	626	632	0	TTAAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	1143	1149	0	TTTAAA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	1593	1599	0	TTTTTTA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	1595	1601	0	TTTTATA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	1784	1790	0	TTTTTTA	1.09863	0.95175
cg2169045	ITGBL1	TFIID [T0	1785	1791	0	TTTTTAA	1.09863	0.95175
cg2169045	ITGBL1	c-Jun [T00	362	368	0	TGAGTC	0.12207	0.11843
cg2169045	ITGBL1	GR-alpha [	322	326	0	CCTGT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	343	347	0	ACAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	587	591	0	CCTGT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	607	611	0	CCTGT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	634	638	0	CCTAT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	758	762	0	ACAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1358	1362	0	CCTGT	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1683	1687	0	ACAGG	7.8125	7.79817
cg2169045	ITGBL1	GR-alpha [	1839	1843	0	CCTGT	7.8125	7.79817
cg2169045	ITGBL1	FOXP3 [T	249	254	0	GTTGTT	1.46484	1.44953
cg2169045	ITGBL1	HNF-3alph	222	229	0	TATTTTT	0.09155	0.07727
cg2169045	ITGBL1	C/EBPbeta	1	4	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	84	87	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	112	115	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	158	161	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	162	165	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	170	173	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	250	253	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	397	400	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	425	428	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	460	463	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	467	470	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	638	641	0	TTGC	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	659	662	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	666	669	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	714	717	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	723	726	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	754	757	0	TTGT	15.625	15.26275

cg2169045	ITGBL1	C/EBPbeta	814	817	0	TTGC	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	844	847	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	883	886	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	971	974	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	975	978	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	991	994	0	TTGC	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1005	1008	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1180	1183	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1228	1231	0	TTGC	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1313	1316	0	TTGC	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1432	1435	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1463	1466	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1515	1518	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1612	1615	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1653	1656	0	TTGC	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1676	1679	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1723	1726	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1766	1769	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1793	1796	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1812	1815	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1816	1819	0	TTGC	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1818	1821	0	GCAA	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1860	1863	0	TTGT	15.625	15.26275
cg2169045	ITGBL1	C/EBPbeta	1900	1903	0	ACAA	15.625	15.26275
cg2169045	ITGBL1	YY1 [T00	202	205	0	ATGG	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	264	267	0	ATGG	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	271	274	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	620	623	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	677	680	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	913	916	0	ATGG	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1184	1187	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1186	1189	0	ATGG	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1365	1368	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1502	1505	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1629	1632	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1668	1671	0	CCAT	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1670	1673	0	ATGG	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1736	1739	0	ATGG	7.8125	7.79459
cg2169045	ITGBL1	YY1 [T00	1884	1887	0	ATGG	7.8125	7.79459
cg2169045	ITGBL1	TFII-I [T0	341	346	0	GGACAG	1.46484	1.48598
cg2169045	ITGBL1	TFII-I [T0	1664	1669	0	CTTTCC	1.46484	1.48598
cg2169045	ITGBL1	TFII-I [T0	1835	1840	0	CTTTCC	1.46484	1.48598
cg2169045	ITGBL1	STAT4 [T	1167	1172	0	GGAAAT	0.48828	0.46235
cg2169045	ITGBL1	STAT4 [T	1403	1408	0	ATTTCC	0.48828	0.46235
cg2169045	ITGBL1	c-Ets-1 [T	1018	1024	0	CTTCCTC	0.24414	0.24982
cg2169045	ITGBL1	c-Ets-1 [T	1382	1388	0	CAGGAA	0.24414	0.24982
cg2169045	ITGBL1	HOXD9 [T	42	51	0	AATAAA	0.01144	0.00905
cg2169045	ITGBL1	HOXD10 [	42	51	0	AATAAA	0.01144	0.00905

cg2169045	ITGBL1	ER-alpha [	472	476	0	TGACC	1.95312	1.99744
cg2169045	ITGBL1	ER-alpha [	764	768	0	TGACC	1.95312	1.99744
cg2169045	ITGBL1	ER-alpha [	1218	1222	0	TGACC	1.95312	1.99744
cg2169045	ITGBL1	RXR-alpha	352	358	0	GGGTTC	0.24414	0.24342
cg2169045	ITGBL1	GR [T050	557	563	0	TTTTTTG	0.36621	0.33174
cg2169045	ITGBL1	GATA-1 [	1055	1060	0	CAGATA	0.97656	0.92541
cg2169045	ITGBL1	Pax-5 [T0	584	590	0	GGGCCT	1.09863	1.24633
cg2169045	ITGBL1	Pax-5 [T0	840	846	0	GGGCTT	1.09863	1.24633
cg2169045	ITGBL1	Elk-1 [T00	1380	1388	0	GGCAGG	0.06104	0.06399
cg2169045	ITGBL1	IRF-2 [T0	889	894	0	TCACTT	0.48828	0.46235
cg2169045	ITGBL1	IRF-2 [T0	1903	1908	0	AAGTGA	0.48828	0.46235
cg1024334	ITGBL1	GR-beta [	64	68	0	AATGT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	197	201	0	AATGT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	289	293	0	AATTT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	307	311	0	ACATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	313	317	0	AATTT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	327	331	0	ACATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	355	359	0	AATTT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	371	375	0	AATTT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	396	400	0	AAATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	759	763	0	AATGT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	1251	1255	0	AAATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	1378	1382	0	AATTT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	1512	1516	0	ACATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	1607	1611	0	AAATT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	1776	1780	0	AATGT	3.90625	3.51525
cg1024334	ITGBL1	GR-beta [	1878	1882	0	ACATT	3.90625	3.51525
cg1024334	ITGBL1	XBP-1 [T	236	241	0	ATGACT	0.97656	0.94838
cg1024334	ITGBL1	TFIID [T0	447	453	0	TTTTTAA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	570	576	0	TTTAAA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	753	759	0	TTTTTTA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	754	760	0	TTTTTAA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	1273	1279	0	TTTTCAA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	1571	1577	0	TTTTTAA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	1573	1579	0	TTTAAA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	1711	1717	0	TTTTTTA	1.09863	0.95175
cg1024334	ITGBL1	TFIID [T0	1712	1718	0	TTTTTAA	1.09863	0.95175
cg1024334	ITGBL1	GR-alpha [	737	741	0	ACAGG	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1280	1284	0	CCTGT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1496	1500	0	ACAGG	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1849	1853	0	CCTGT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1915	1919	0	CCTGT	7.8125	7.79817
cg1024334	ITGBL1	GR-alpha [	1986	1990	0	CCTGT	7.8125	7.79817
cg1024334	ITGBL1	FOXP3 [T	362	367	0	GACAAC	1.46484	1.44953
cg1024334	ITGBL1	FOXP3 [T	510	515	0	GTTGTG	1.46484	1.44953
cg1024334	ITGBL1	FOXP3 [T	641	646	0	CACAAC	1.46484	1.44953
cg1024334	ITGBL1	FOXP3 [T	1115	1120	0	GTTGTC	1.46484	1.44953
cg1024334	ITGBL1	FOXP3 [T	1454	1459	0	CACAAC	1.46484	1.44953

cg1024334	ITGBL1	HNF-3alpl	763	770	0	TCAAAA'	0.09155	0.07727
cg1024334	ITGBL1	HNF-3alpl	1369	1376	0	TAAAAA'	0.09155	0.07727
cg1024334	ITGBL1	C/EBPbeta	22	25	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	24	27	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	32	35	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	45	48	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	53	56	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	140	143	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	144	147	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	180	183	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	209	212	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	275	278	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	287	290	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	292	295	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	363	366	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	369	372	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	394	397	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	399	402	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	500	503	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	511	514	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	517	520	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	530	533	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	642	645	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	698	701	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	781	784	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	785	788	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	895	898	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	899	902	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	901	904	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	927	930	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1014	1017	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1083	1086	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1108	1111	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1116	1119	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1165	1168	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1215	1218	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1258	1261	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1317	1320	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1336	1339	0	TTGC	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1357	1360	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1391	1394	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1455	1458	0	ACAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1493	1496	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1517	1520	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1553	1556	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1605	1608	0	GCAA	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1762	1765	0	TTGT	15.625	15.26275
cg1024334	ITGBL1	C/EBPbeta	1920	1923	0	TTGC	15.625	15.26275

cg1024334	ITGBL1	YY1 [T00	176	179	0	CCAT	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	338	341	0	ATGG	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	347	350	0	ATGG	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	773	776	0	CCAT	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	961	964	0	CCAT	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	1143	1146	0	CCAT	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	1222	1225	0	ATGG	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	1683	1686	0	CCAT	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	1690	1693	0	CCAT	7.8125	7.79459
cg1024334	ITGBL1	YY1 [T00	1871	1874	0	CCAT	7.8125	7.79459
cg1024334	ITGBL1	TFII-I [T0	379	384	0	CTGTCC	1.46484	1.48598
cg1024334	ITGBL1	TFII-I [T0	1328	1333	0	CTGTCC	1.46484	1.48598
cg1024334	ITGBL1	TFII-I [T0	1829	1834	0	CTGTCC	1.46484	1.48598
cg1024334	ITGBL1	STAT4 [T	524	529	0	ATTTCC	0.48828	0.46235
cg1024334	ITGBL1	HOXD9 [T	1367	1376	0	AATAAA	0.01144	0.00905
cg1024334	ITGBL1	HOXD10 [	1367	1376	0	AATAAA	0.01144	0.00905
cg1024334	ITGBL1	ER-alpha [	1865	1869	0	GGTCA	1.95312	1.99744
cg1024334	ITGBL1	ER-alpha [	1892	1896	0	GGTCA	1.95312	1.99744
cg1024334	ITGBL1	RXR-alpha	1003	1009	0	TGAACC	0.24414	0.24342
cg1024334	ITGBL1	SRY [T00	30	38	0	CTTTGTT	0.03052	0.02847
cg1024334	ITGBL1	TCF-4E [T	1106	1112	0	CTTTGCT	0.12207	0.11933
cg1024334	ITGBL1	NFI/CTF [	1950	1957	0	GCGCTT	0.18311	0.191
cg1024334	ITGBL1	GR [T050	41	47	0	TTTTTTG	0.36621	0.33174
cg1024334	ITGBL1	GATA-1 [	1694	1699	0	CAGATA	0.97656	0.92541
cg1024334	ITGBL1	Pax-5 [T0	535	541	0	CCGGCC	1.09863	1.24633
cg1024334	ITGBL1	Pax-5 [T0	1185	1191	0	CCTGCC	1.09863	1.24633
cg1024334	ITGBL1	Pax-5 [T0	1860	1866	0	GGGCAG	1.09863	1.24633
cg1024334	ITGBL1	p53 [T006	1185	1191	0	CCTGCC	0.36621	0.40082
cg1024334	ITGBL1	p53 [T006	1860	1866	0	GGGCAG	0.36621	0.40082
cg1024334	ITGBL1	AP-2alpha	878	883	0	GCAGGC	0.97656	1.07867
cg1024334	ITGBL1	HNF-1A [	1424	1431	0	GTTAAA	0.24414	0.20853
cg0272748	KCNMA1	STAT5A [	346	358	9.952027	TTTCAA	0.01878	0.01918
cg0272748	KCNMA1	LEF-1 [T0	1117	1124	9.937995	CTTTGG	0.12207	0.12154
cg1997264	KCNMA1	PEA3 [T0	670	678	9.937959	TGGATG	0.18311	0.18304
cg1997264	KCNMA1	NF-AT2 [	1494	1503	9.905562	GGAAAA	0.08774	0.08903
cg0272748	KCNMA1	c-Ets-1 [T	194	200	9.841249	AGGGAA	0.24414	0.2459
cg0272748	KCNMA1	c-Ets-1 [T	1228	1234	9.841249	ATTCCCT	0.24414	0.2459
cg0272748	KCNMA1	STAT1bet	892	901	9.807397	ACATGG	0.14877	0.1495
cg1997264	KCNMA1	XBP-1 [T	647	652	9.789909	AGCCAT	1.95312	1.95208
cg1997264	KCNMA1	XBP-1 [T	1322	1327	9.789909	AGACAT	1.95312	1.95208
cg0272748	KCNMA1	XBP-1 [T	1042	1047	9.789909	ATGTCG	1.95312	1.95208
cg0272748	KCNMA1	NF-1 [T00	29	36	9.761671	TTGGAG	0.24414	0.24405
cg1997264	KCNMA1	PR B [T00	1561	1567	9.743489	AACACA	1.09863	1.10292
cg1997264	KCNMA1	PR B [T00	1950	1956	9.743489	AACACC	1.09863	1.10292
cg1997264	KCNMA1	PR A [T01	1561	1567	9.743489	AACACA	1.09863	1.10292
cg1997264	KCNMA1	PR A [T01	1950	1956	9.743489	AACACC	1.09863	1.10292
cg0272748	KCNMA1	PR B [T00	159	165	9.743489	AACACA	1.09863	1.10292
cg0272748	KCNMA1	PR B [T00	400	406	9.743489	GTGTGTT	1.09863	1.10292

cg0272748	KCNMA1	PR B [T00	434	440	9.743489	GTGTGT	1.09863	1.10292
cg0272748	KCNMA1	PR B [T00	971	977	9.743489	AACACA	1.09863	1.10292
cg0272748	KCNMA1	PR B [T00	1795	1801	9.743489	CCGTGT	1.09863	1.10292
cg0272748	KCNMA1	PR B [T00	1954	1960	9.743489	TTGTGT	1.09863	1.10292
cg0272748	KCNMA1	PR A [T01	159	165	9.743489	AACACA	1.09863	1.10292
cg0272748	KCNMA1	PR A [T01	400	406	9.743489	GTGTGT	1.09863	1.10292
cg0272748	KCNMA1	PR A [T01	434	440	9.743489	GTGTGT	1.09863	1.10292
cg0272748	KCNMA1	PR A [T01	971	977	9.743489	AACACA	1.09863	1.10292
cg0272748	KCNMA1	PR A [T01	1795	1801	9.743489	CCGTGT	1.09863	1.10292
cg0272748	KCNMA1	PR A [T01	1954	1960	9.743489	TTGTGT	1.09863	1.10292
cg0272748	KCNMA1	AhR:Arnt	309	318	9.738501	GCACGC	0.17929	0.17456
cg1997264	KCNMA1	NF-AT1 [	1471	1479	9.691726	GGAAAC	0.16785	0.1682
cg0272748	KCNMA1	NF-AT1 [	896	904	9.691726	GGAAAC	0.16785	0.1682
cg1997264	KCNMA1	HNF-1C [	1424	1432	9.639597	ACAATT	0.19836	0.20229
cg0272748	KCNMA1	Elk-1 [T00	1588	1596	9.62002	GGAGGG	0.07629	0.07577
cg0272748	KCNMA1	RAR-beta	1577	1586	9.567396	AGGGTT	0.21362	0.21243
cg1997264	KCNMA1	Pax-5 [T0	977	983	9.552105	GGGCAA	1.46484	1.43083
cg1997264	KCNMA1	TFIID [T0	281	287	9.552105	TCCCAA	1.46484	1.48472
cg1997264	KCNMA1	TFIID [T0	1533	1539	9.552105	TTTGGT	1.46484	1.48472
cg0272748	KCNMA1	Pax-5 [T0	233	239	9.552105	TTTGCC	1.46484	1.43083
cg0272748	KCNMA1	TFIID [T0	763	769	9.552105	TTTCAC	1.46484	1.48472
cg0272748	KCNMA1	TFIID [T0	886	892	9.552105	TTTCTCA	1.46484	1.48472
cg0272748	KCNMA1	TFIID [T0	1344	1350	9.552105	TTCCAA	1.46484	1.48472
cg1997264	KCNMA1	NF-1 [T00	697	704	9.535536	GTGGCC	0.73242	0.73053
cg0272748	KCNMA1	NF-1 [T00	1812	1819	9.535536	TTGGAC	0.73242	0.73053
cg0272748	KCNMA1	HNF-1B [	703	711	9.522068	TTTGTA	0.09155	0.09374
cg1997264	KCNMA1	TFII-I [T0	774	779	9.512894	AATTCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	803	808	9.512894	GGATAA	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	807	812	9.512894	AAGTCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	812	817	9.512894	CCTTCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	840	845	9.512894	CCATCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	889	894	9.512894	CCTTCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	955	960	9.512894	GGACTT	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1195	1200	9.512894	GGACAA	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1211	1216	9.512894	GGACTT	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1216	1221	9.512894	TTATCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1375	1380	9.512894	GGACAA	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1461	1466	9.512894	TTATCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1471	1476	9.512894	GGAAAC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1494	1499	9.512894	GGAAAA	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1603	1608	9.512894	GGATAA	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1724	1729	9.512894	TTATCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1735	1740	9.512894	TTTTCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1739	1744	9.512894	CCTTCC	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1753	1758	9.512894	GGAAAA	7.32422	7.29728
cg1997264	KCNMA1	TFII-I [T0	1954	1959	9.512894	CCATCC	7.32422	7.29728
cg1997264	KCNMA1	FOXP3 [T	101	106	9.512894	CGCAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	227	232	9.512894	GTTGGC	7.32422	7.35678

cg1997264	KCNMA1	FOXP3 [T	659	664	9.512894	GTTGGC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	716	721	9.512894	GAGAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	978	983	9.512894	GGCAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1095	1100	9.512894	CCCAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1397	1402	9.512894	ACCAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1459	1464	9.512894	GTTTAT	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1713	1718	9.512894	GATAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1723	1728	9.512894	GTTATC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1764	1769	9.512894	CAGAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1805	1810	9.512894	GTTTAT	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1973	1978	9.512894	AGCAAC	7.32422	7.35678
cg1997264	KCNMA1	FOXP3 [T	1982	1987	9.512894	GTTCTT	7.32422	7.35678
cg0272748	KCNMA1	TFII-I [T0	541	546	9.512894	GGAAGG	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	572	577	9.512894	GGATGG	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	583	588	9.512894	GGATAC	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	716	721	9.512894	GGATAA	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	896	901	9.512894	GGAAAC	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	902	907	9.512894	TTATCC	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	1096	1101	9.512894	CCATCC	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	1616	1621	9.512894	CCATCC	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	1814	1819	9.512894	GGACAA	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	1927	1932	9.512894	AATTCC	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	1937	1942	9.512894	GGATTT	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	1945	1950	9.512894	GGATAC	7.32422	7.29728
cg0272748	KCNMA1	TFII-I [T0	1975	1980	9.512894	AAGTCC	7.32422	7.29728
cg0272748	KCNMA1	FOXP3 [T	97	102	9.512894	GTTGGT	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	130	135	9.512894	GTTGGG	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	237	242	9.512894	CCCAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	607	612	9.512894	AATAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	624	629	9.512894	GATAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	653	658	9.512894	AATAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	676	681	9.512894	AATAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	876	881	9.512894	CTAAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	924	929	9.512894	GTTATT	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	968	973	9.512894	GAGAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	1051	1056	9.512894	GAGAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	1146	1151	9.512894	ACCAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	1422	1427	9.512894	GTTGCT	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	1580	1585	9.512894	GTTATG	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	1629	1634	9.512894	CTAAAC	7.32422	7.35678
cg0272748	KCNMA1	FOXP3 [T	1745	1750	9.512894	CCCAAC	7.32422	7.35678
cg0272748	KCNMA1	Ik-1 [T027	531	543	9.497194	CCAGAG	0.02941	0.02907
cg1997264	KCNMA1	TCF-4E [T	1018	1024	9.453578	CTCAAA	0.48828	0.49215
cg1997264	KCNMA1	TCF-4E [T	1301	1307	9.453578	CTTTGTA	0.48828	0.49215
cg0272748	KCNMA1	TCF-4E [T	710	716	9.453578	CTCAAA	0.48828	0.49215
cg0272748	KCNMA1	TCF-4E [T	1810	1816	9.453578	CTTTGGA	0.48828	0.49215
cg1997264	KCNMA1	c-Jun [T00	469	475	9.442241	TGACAG	0.73242	0.73031
cg0272748	KCNMA1	c-Jun [T00	1648	1654	9.442241	GCTGTCA	0.73242	0.73031

cg0272748	KCNMA1	c-Jun [T00	1711	1717	9.442241	GCTGTC	0.73242	0.73031
cg0272748	KCNMA1	NF-AT2 [T	896	905	9.386314	GGAAAC	0.04578	0.04604
cg1997264	KCNMA1	NFI/CTF [	797	804	9.352332	GACCTT	0.54932	0.54821
cg1997264	KCNMA1	NFI/CTF [	1718	1725	9.352332	CCAATG	0.54932	0.54821
cg0272748	KCNMA1	NFI/CTF [	1115	1122	9.352332	AGCTTT	0.54932	0.54821
cg0272748	KCNMA1	NFI/CTF [	1977	1984	9.352332	GTCCTT	0.54932	0.54821
cg1997264	KCNMA1	c-Myb [T0	1408	1415	9.29064	AAACTC	0.36621	0.37054
cg0272748	KCNMA1	c-Ets-1 [T0	1981	1987	9.19359	TTGGAA	0.85449	0.85523
cg1997264	KCNMA1	HNF-1C [T	1911	1919	9.116395	TTGAGT	0.12207	0.12495
cg0272748	KCNMA1	AP-1 [T00	18	26	9.116043	CATCAG	0.24414	0.24693
cg0272748	KCNMA1	LEF-1 [T0	427	434	9.099721	CTTTGTC	0.54932	0.55326
cg0272748	KCNMA1	c-Ets-1 [T0	1928	1934	9.065503	ATTCCA	0.85449	0.85523
cg1997264	KCNMA1	NFI/CTF [	575	582	9.042931	ACAGTT	0.48828	0.48804
cg1997264	KCNMA1	c-Jun [T00	1623	1629	9.013496	CATGTC	0.61035	0.61059
cg1997264	KCNMA1	NF-AT2 [T	1731	1740	8.984657	CTGTTTT	0.05341	0.05386
cg1997264	KCNMA1	LEF-1 [T0	281	288	8.973041	TCCCAA	0.54932	0.55326
cg1997264	KCNMA1	GR [T050	1948	1954	8.971049	CAAACA	0.61035	0.61632
cg0272748	KCNMA1	c-Myb [T0	920	927	8.947824	TGAAGT	0.39673	0.40028
cg0272748	KCNMA1	c-Ets-1 [T0	1057	1063	8.937416	GTGGAA	0.85449	0.85523
cg1997264	KCNMA1	IRF-1 [T0	1490	1498	8.916359	TTGTGG	0.09155	0.09147
cg0272748	KCNMA1	AP-1 [T00	1843	1851	8.915609	TGACTT	0.24414	0.24693
cg0272748	KCNMA1	AP-1 [T00	873	881	8.907204	TGACTA	0.24414	0.24693
cg0272748	KCNMA1	GATA-2 [	777	785	8.888889	CCTGTA	0.22888	0.22993
cg1997264	KCNMA1	c-Jun [T00	1366	1372	8.832178	AAGGTC	0.61035	0.61059
cg0272748	KCNMA1	PR B [T00	976	982	8.827054	AGCTGT	0.36621	0.36944
cg0272748	KCNMA1	PR B [T00	1369	1375	8.827054	ACCTGT	0.36621	0.36944
cg0272748	KCNMA1	PR A [T01	976	982	8.827054	AGCTGT	0.36621	0.36944
cg0272748	KCNMA1	PR A [T01	1369	1375	8.827054	ACCTGT	0.36621	0.36944
cg1997264	KCNMA1	NFI/CTF [	1220	1227	8.814757	CCAAAA	0.48828	0.48804
cg1997264	KCNMA1	NFI/CTF [	1845	1852	8.814757	CCAAGA	0.48828	0.48804
cg0272748	KCNMA1	NFI/CTF [	915	922	8.814757	CCAAGT	0.48828	0.48804
cg1997264	KCNMA1	c-Ets-1 [T0	775	781	8.809329	ATTCCA	0.85449	0.85523
cg0272748	KCNMA1	HNF-1B [T	822	830	8.799296	TATGTA	0.08392	0.0857
cg1997264	KCNMA1	NF-1 [T00	279	286	8.790071	CCTCCC	0.24414	0.24467
cg0272748	KCNMA1	NF-1 [T00	1119	1126	8.790071	TTGGCA	0.24414	0.24467
cg0272748	KCNMA1	MAZ [T00	1583	1595	8.779528	ATGCGG	0.01413	0.01385
cg1997264	KCNMA1	LEF-1 [T0	1301	1308	8.759086	CTTTGT	0.54932	0.55326
cg0272748	KCNMA1	LEF-1 [T0	321	328	8.759086	CTTTGC	0.54932	0.55326
cg0272748	KCNMA1	LEF-1 [T0	1012	1019	8.759086	TCACAA	0.54932	0.55326
cg1997264	KCNMA1	XBP-1 [T0	305	310	8.75604	ATGATC	2.92969	2.9674
cg1997264	KCNMA1	XBP-1 [T0	335	340	8.75604	TTTCAT	2.92969	2.9674
cg1997264	KCNMA1	XBP-1 [T0	390	395	8.75604	ATGAAC	2.92969	2.9674
cg1997264	KCNMA1	XBP-1 [T0	828	833	8.75604	TATCAT	2.92969	2.9674
cg1997264	KCNMA1	XBP-1 [T0	1328	1333	8.75604	GCTCAT	2.92969	2.9674
cg1997264	KCNMA1	XBP-1 [T0	1380	1385	8.75604	ATGAAA	2.92969	2.9674
cg1997264	KCNMA1	XBP-1 [T0	1886	1891	8.75604	GTTCAT	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T0	122	127	8.75604	TTTCAT	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T0	451	456	8.75604	TATCAT	2.92969	2.9674

cg0272748	KCNMA1	XBP-1 [T	791	796	8.75604	TCTCAT	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T	1388	1393	8.75604	ATGAAA	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T	1473	1478	8.75604	TCTCAT	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T	1531	1536	8.75604	ATGAGA	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T	1610	1615	8.75604	ATGAGC	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T	1673	1678	8.75604	ATGATC	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T	1772	1777	8.75604	ATGAGC	2.92969	2.9674
cg0272748	KCNMA1	XBP-1 [T	1883	1888	8.75604	ATGAAA	2.92969	2.9674
cg0272748	KCNMA1	c-Myb [T0	1089	1096	8.728118	AAACTT	0.30518	0.30924
cg0272748	KCNMA1	HNF-1B [	605	613	8.688037	TGAATA	0.11444	0.11669
cg1997264	KCNMA1	LEF-1 [T0	699	706	8.575454	GGCCAA	0.15259	0.15214
cg1997264	KCNMA1	c-Jun [T00	237	243	8.571705	CCAGTC	0.12207	0.12139
cg1997264	KCNMA1	c-Jun [T00	1344	1350	8.571705	CCAGTC	0.12207	0.12139
cg0272748	KCNMA1	c-Jun [T00	1735	1741	8.571705	CCAGTC	0.12207	0.12139
cg0272748	KCNMA1	RAR-beta	1728	1737	8.55975	CCCTAA	0.26703	0.26657
cg1997264	KCNMA1	USF2 [T0	538	547	8.532138	CAGGTG	0.103	0.10183
cg0272748	KCNMA1	c-Myb [T0	468	475	8.529773	CAACTT	0.30518	0.30924
cg0272748	KCNMA1	c-Ets-1 [T	1343	1349	8.501115	GTTCCA	0.24414	0.24529
cg1997264	KCNMA1	c-Myb [T0	574	581	8.443873	AACAGT	0.30518	0.30924
cg1997264	KCNMA1	c-Myb [T0	733	740	8.443873	CAACTG	0.30518	0.30924
cg0272748	KCNMA1	HNF-1B [	2	10	8.379818	AGTTAT	0.11444	0.11669
cg0272748	KCNMA1	c-Ets-1 [T	391	397	8.373028	GTTCCAT	0.24414	0.24529
cg1997264	KCNMA1	HNF-3alp	1331	1338	8.343064	CATTTT	0.27466	0.28528
cg0272748	KCNMA1	HNF-3alp	41	48	8.343064	AATTTA	0.27466	0.28528
cg0272748	KCNMA1	HNF-3alp	344	351	8.343064	TATTTC	0.27466	0.28528
cg0272748	KCNMA1	HNF-3alp	848	855	8.343064	AATTTA	0.27466	0.28528
cg0272748	KCNMA1	HNF-3alp	1818	1825	8.343064	AATTTT	0.27466	0.28528
cg1997264	KCNMA1	c-Ets-2 [T	891	899	8.339336	TTCCTA	0.13733	0.13681
cg1997264	KCNMA1	PR B [T00	1729	1735	8.338824	CTCTGTT	1.09863	1.10009
cg1997264	KCNMA1	PR B [T00	1943	1949	8.338824	AACAGC	1.09863	1.10009
cg1997264	KCNMA1	PR B [T00	1978	1984	8.338824	CCCTGTT	1.09863	1.10009
cg1997264	KCNMA1	PR A [T01	1729	1735	8.338824	CTCTGTT	1.09863	1.10009
cg1997264	KCNMA1	PR A [T01	1943	1949	8.338824	AACAGC	1.09863	1.10009
cg1997264	KCNMA1	PR A [T01	1978	1984	8.338824	CCCTGTT	1.09863	1.10009
cg0272748	KCNMA1	PR B [T00	1077	1083	8.338824	AACAGA	1.09863	1.10009
cg0272748	KCNMA1	PR B [T00	1149	1155	8.338824	AACAGA	1.09863	1.10009
cg0272748	KCNMA1	PR A [T01	1077	1083	8.338824	AACAGA	1.09863	1.10009
cg0272748	KCNMA1	PR A [T01	1149	1155	8.338824	AACAGA	1.09863	1.10009
cg1997264	KCNMA1	GR-alpha [	112	116	8.281568	CCTCC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	144	148	8.281568	CCTCC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	279	283	8.281568	CCTCC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	710	714	8.281568	CCTTC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	799	803	8.281568	CCTTG	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	812	816	8.281568	CCTTC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	860	864	8.281568	GGAGG	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	889	893	8.281568	CCTTC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	897	901	8.281568	CCTCC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	1046	1050	8.281568	GGAGG	7.8125	7.72956

cg1997264	KCNMA1	GR-alpha [	1371	1375	8.281568	CAAGG	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	1465	1469	8.281568	CCTTC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	1633	1637	8.281568	CCTCC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	1692	1696	8.281568	CCTTG	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	1739	1743	8.281568	CCTTC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	1743	1747	8.281568	CCTCC	7.8125	7.72956
cg1997264	KCNMA1	GR-alpha [	1836	1840	8.281568	GGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	27	31	8.281568	CCTTG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	148	152	8.281568	GGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	258	262	8.281568	CAAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	270	274	8.281568	CAAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	542	546	8.281568	GAAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	560	564	8.281568	GGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	565	569	8.281568	GGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	906	910	8.281568	CCTCG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1000	1004	8.281568	CGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1047	1051	8.281568	GAAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1232	1236	8.281568	CCTTC	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1492	1496	8.281568	CCTCC	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1555	1559	8.281568	GAAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1588	1592	8.281568	GGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1598	1602	8.281568	GGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1643	1647	8.281568	CGAGG	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1684	1688	8.281568	CCTCC	7.8125	7.72956
cg0272748	KCNMA1	GR-alpha [	1979	1983	8.281568	CCTTG	7.8125	7.72956
cg1997264	KCNMA1	c-Jun [T00	925	931	8.242207	TGACCT	0.48828	0.49076
cg1997264	KCNMA1	ENKTF-1	229	236	8.19852	TGGCCA	0.73242	0.71737
cg0272748	KCNMA1	NF-1 [T00	1143	1150	8.191058	CAGACC	0.24414	0.24409
cg1997264	KCNMA1	PXR-1:RX	1883	1890	8.180749	AATGTT	0.12207	0.12407
cg1997264	KCNMA1	NF-AT1 [	1494	1502	8.12076	GGAAAA	0.1297	0.12988
cg1997264	KCNMA1	LEF-1 [T0	1017	1024	8.117221	ACTCAA	0.12207	0.1241
cg0272748	KCNMA1	LEF-1 [T0	709	716	8.117221	ACTCAA	0.12207	0.1241
cg1997264	KCNMA1	c-Ets-1 [T	570	576	8.116854	CTGGAA	0.24414	0.2425
cg1997264	KCNMA1	VDR [T00	584	592	8.079962	GTTCAG	0.24414	0.24712
cg1997264	KCNMA1	VDR [T00	1635	1643	8.079962	TCCCTG	0.24414	0.24712
cg1997264	KCNMA1	IRF-1 [T0	1467	1475	8.078284	TTCTGG	0.25177	0.25263
cg1997264	KCNMA1	GR-alpha [	65	69	8.073878	CCTGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	116	120	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	134	138	8.073878	CCTGC	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	171	175	8.073878	CCTGC	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	232	236	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	323	327	8.073878	CCTAC	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	492	496	8.073878	GCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	509	513	8.073878	CCTGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	527	531	8.073878	GCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	537	541	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	607	611	8.073878	CCTGC	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	664	668	8.073878	CCTAC	7.8125	7.72238

cg1997264	KCNMA1	GR-alpha [	676	680	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	818	822	8.073878	CCTGC	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	893	897	8.073878	CCTAC	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	900	904	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	941	945	8.073878	CCTGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1087	1091	8.073878	CCTGC	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1192	1196	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1414	1418	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1442	1446	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1643	1647	8.073878	CTAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1747	1751	8.073878	CCAGG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1770	1774	8.073878	CCTAG	7.8125	7.72238
cg1997264	KCNMA1	GR-alpha [	1828	1832	8.073878	CTAGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	206	210	8.073878	CCTGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	220	224	8.073878	CCTGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	253	257	8.073878	GCAGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	331	335	8.073878	CCAGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	569	573	8.073878	GCAGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	614	618	8.073878	CCTAC	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	817	821	8.073878	CCTAC	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	1027	1031	8.073878	GCAGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	1362	1366	8.073878	CCTAG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	1397	1401	8.073878	CCAGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	1467	1471	8.073878	CCTGG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	1541	1545	8.073878	CCTAG	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	1662	1666	8.073878	CCTGC	7.8125	7.72238
cg0272748	KCNMA1	GR-alpha [	1699	1703	8.073878	GCAGG	7.8125	7.72238
cg1997264	KCNMA1	Pax-5 [T0	12	18	8.014558	TATGCC	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	314	320	8.014558	TGTGCC	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	362	368	8.014558	GGGCAC	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	531	537	8.014558	GGGCTT	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	679	685	8.014558	GGGCTC	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	1068	1074	8.014558	GGGCTC	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	1606	1612	8.014558	TAAGCC	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	1627	1633	8.014558	TCAGCC	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	1674	1680	8.014558	GGGCAG	2.19727	2.14502
cg1997264	KCNMA1	Pax-5 [T0	1686	1692	8.014558	TCTGCC	2.19727	2.14502
cg1997264	KCNMA1	TFIID [T0	35	41	8.014558	TTTGAG	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	241	247	8.014558	TCACAA	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	335	341	8.014558	TTTCATA	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	1159	1165	8.014558	TCTGAA	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	1181	1187	8.014558	TTTGAA	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	1302	1308	8.014558	TTTGTA	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	1482	1488	8.014558	TTTCTGA	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	1698	1704	8.014558	TTTCTTA	2.19727	2.24348
cg1997264	KCNMA1	TFIID [T0	1820	1826	8.014558	TCTCAA	2.19727	2.24348
cg0272748	KCNMA1	Pax-5 [T0	797	803	8.014558	GGGCTC	2.19727	2.14502
cg0272748	KCNMA1	Pax-5 [T0	1611	1617	8.014558	TGAGCC	2.19727	2.14502

cg0272748	KCNMA1	TFIID [T0	703	709	8.014558	TTTGTA	2.19727	2.24348
cg0272748	KCNMA1	TFIID [T0	781	787	8.014558	TATCAA	2.19727	2.24348
cg0272748	KCNMA1	TFIID [T0	1012	1018	8.014558	TCACAA	2.19727	2.24348
cg0272748	KCNMA1	TFIID [T0	1266	1272	8.014558	TTTCTG	2.19727	2.24348
cg0272748	KCNMA1	TFIID [T0	1276	1282	8.014558	TCTCAA	2.19727	2.24348
cg0272748	KCNMA1	TFIID [T0	1308	1314	8.014558	TTAGAA	2.19727	2.24348
cg0272748	KCNMA1	HNF-1C [	821	829	8.002145	CTATGT	0.19836	0.20224
cg0272748	KCNMA1	MEF-2A [	1870	1880	7.982343	ACATTA	0.04005	0.04149
cg1997264	KCNMA1	HNF-1B [	1912	1920	7.973785	TGAGTA	0.06866	0.07026
cg1997264	KCNMA1	c-Ets-2 [T	1412	1420	7.84116	TCCCAG	0.32043	0.32298
cg1997264	KCNMA1	p53 [T006	1068	1074	7.833758	GGGCTC	0.48828	0.47377
cg0272748	KCNMA1	p53 [T006	797	803	7.833758	GGGCTC	0.48828	0.47377
cg0272748	KCNMA1	RXR-alpha	1443	1449	7.815913	GGGTGG	0.24414	0.24104
cg0272748	KCNMA1	GATA-2 [	1830	1838	7.777778	ACGATA	0.30518	0.30758
cg1997264	KCNMA1	NF-AT1 [	555	563	7.744746	GGAAAG	0.19836	0.19941
cg0272748	KCNMA1	NF-AT1 [	1019	1027	7.744746	GGAAAG	0.19836	0.19941
cg1997264	KCNMA1	IRF-1 [T0	551	559	7.732782	CTCTGG	0.14496	0.14449
cg0272748	KCNMA1	NF-1 [T00	1342	1349	7.693985	AGTTCC	0.24414	0.24565
cg1997264	KCNMA1	c-Myb [T0	655	662	7.662426	TGAAGT	0.42725	0.43114
cg0272748	KCNMA1	LEF-1 [T0	1810	1817	7.6105	CTTTGG	0.21362	0.21302
cg0272748	KCNMA1	NFI/CTF [	91	98	7.587343	CCAATA	0.36621	0.36674
cg0272748	KCNMA1	NFI/CTF [	1165	1172	7.587343	CCAAAT	0.36621	0.36674
cg1997264	KCNMA1	c-Jun [T00	1139	1145	7.538568	GATGTC	0.48828	0.48775
cg0272748	KCNMA1	c-Jun [T00	265	271	7.538568	GATGTC	0.48828	0.48775
cg0272748	KCNMA1	c-Jun [T00	1517	1523	7.538568	TGACAT	0.48828	0.48775
cg1997264	KCNMA1	GR [T050	650	656	7.527031	CATTTC	1.83105	1.86007
cg1997264	KCNMA1	GR [T050	771	777	7.527031	CAAAAT	1.83105	1.86007
cg1997264	KCNMA1	GR [T050	1221	1227	7.527031	CAAAAG	1.83105	1.86007
cg1997264	KCNMA1	GR [T050	1299	1305	7.527031	AGCTTT	1.83105	1.86007
cg1997264	KCNMA1	GR [T050	1447	1453	7.527031	ATATTT	1.83105	1.86007
cg1997264	KCNMA1	GR [T050	1530	1536	7.527031	CTATTT	1.83105	1.86007
cg0272748	KCNMA1	GR [T050	485	491	7.527031	ATATTT	1.83105	1.86007
cg0272748	KCNMA1	GR [T050	700	706	7.527031	TTGTTT	1.83105	1.86007
cg0272748	KCNMA1	GR [T050	1115	1121	7.527031	AGCTTT	1.83105	1.86007
cg0272748	KCNMA1	GR [T050	1849	1855	7.527031	AATTTT	1.83105	1.86007
cg1997264	KCNMA1	RAR-beta	1763	1772	7.47824	TCAGAA	0.24414	0.24343
cg0272748	KCNMA1	C/EBPalph	768	774	7.465744	CATTGC	0.48828	0.49653
cg1997264	KCNMA1	PEA3 [T0	838	846	7.421728	GACCAT	0.34332	0.34161
cg1997264	KCNMA1	PEA3 [T0	1952	1960	7.421728	CACCAT	0.34332	0.34161
cg0272748	KCNMA1	PEA3 [T0	571	579	7.421728	AGGATG	0.34332	0.34161
cg0272748	KCNMA1	C/EBPalph	38	44	7.396431	TCCAAT	0.48828	0.49653
cg0272748	KCNMA1	C/EBPalph	661	667	7.396431	AATTGT	0.48828	0.49653
cg1997264	KCNMA1	PXR-1:RX	391	398	7.362674	TGAACA	0.24414	0.24395
cg0272748	KCNMA1	ELF-1 [T0	1620	1632	7.3253	CCACTT	0.00846	0.00852
cg0272748	KCNMA1	HOXD9 [	607	616	7.270719	AATAAC	0.06866	0.07152
cg0272748	KCNMA1	HOXD10 [	607	616	7.270719	AATAAC	0.06866	0.07152
cg0272748	KCNMA1	p53 [T006	1357	1363	7.266844	ACAGCC	0.73242	0.7186
cg0272748	KCNMA1	p53 [T006	1646	1652	7.266844	GGGCTG	0.73242	0.7186

cg0272748	KCNMA1	SRY [T00	427	435	7.175614	CTTTGTC	0.30518	0.30739
cg0272748	KCNMA1	SRY [T00	1011	1019	7.175614	CTCACA	0.30518	0.30739
cg1997264	KCNMA1	XBP-1 [T0	476	481	7.172312	ATGAGT	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	497	502	7.172312	ATGAAT	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	844	849	7.172312	CCTCAT	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	934	939	7.172312	AATCAT	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	951	956	7.172312	ATGAGG	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	967	972	7.172312	ATGATG	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	1552	1557	7.172312	ATGATT	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	1784	1789	7.172312	ATGAAT	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	1811	1816	7.172312	ATGAGT	2.92969	2.97018
cg1997264	KCNMA1	XBP-1 [T0	1872	1877	7.172312	ATTCAT	2.92969	2.97018
cg0272748	KCNMA1	XBP-1 [T0	604	609	7.172312	ATGAAT	2.92969	2.97018
cg0272748	KCNMA1	XBP-1 [T0	734	739	7.172312	ATGAAT	2.92969	2.97018
cg0272748	KCNMA1	XBP-1 [T0	751	756	7.172312	ATGATG	2.92969	2.97018
cg0272748	KCNMA1	XBP-1 [T0	1339	1344	7.172312	ATGAGT	2.92969	2.97018
cg0272748	KCNMA1	XBP-1 [T0	1520	1525	7.172312	CATCAT	2.92969	2.97018
cg0272748	KCNMA1	XBP-1 [T0	1904	1909	7.172312	CCTCAT	2.92969	2.97018
cg1997264	KCNMA1	c-Myb [T0	567	574	7.127234	GAACTG	0.18311	0.18399
cg0272748	KCNMA1	c-Myb [T0	692	699	7.127234	TAACTG	0.18311	0.18399
cg1997264	KCNMA1	NF-AT1 [	1753	1761	7.095752	GGAAAA	0.15259	0.1548
cg0272748	KCNMA1	c-Jun [T00	639	645	7.052189	TGACTA	0.73242	0.73173
cg0272748	KCNMA1	c-Jun [T00	644	650	7.052189	ATAGTC	0.73242	0.73173
cg0272748	KCNMA1	NFI/CTF [	1746	1753	7.014249	CCAACC	0.73242	0.73214
cg1997264	KCNMA1	C/EBPalph	1196	1202	7.00174	GACAAT	0.73242	0.74337
cg1997264	KCNMA1	C/EBPalph	1376	1382	7.00174	GACAAT	0.73242	0.74337
cg0272748	KCNMA1	C/EBPalph	1858	1864	7.00174	GCCAAT	0.73242	0.74337
cg1997264	KCNMA1	HNF-3alph	650	657	7.000129	CATTTC	0.82397	0.84946
cg1997264	KCNMA1	HNF-3alph	1103	1110	7.000129	CATTTT	0.82397	0.84946
cg1997264	KCNMA1	HNF-3alph	1284	1291	7.000129	TATAAA	0.82397	0.84946
cg1997264	KCNMA1	HNF-3alph	1288	1295	7.000129	AATTTT	0.82397	0.84946
cg1997264	KCNMA1	HNF-3alph	1381	1388	7.000129	TGAAAA	0.82397	0.84946
cg0272748	KCNMA1	HNF-3alph	5	12	7.000129	TATAAA	0.82397	0.84946
cg0272748	KCNMA1	HNF-3alph	1305	1312	7.000129	AATTTA	0.82397	0.84946
cg0272748	KCNMA1	HNF-3alph	1849	1856	7.000129	AATTTC	0.82397	0.84946
cg1997264	KCNMA1	RXR-alph	1031	1037	6.967687	GGGTGG	0.36621	0.36214
cg1997264	KCNMA1	NF-1 [T00	907	914	6.948522	TGCACC	0.48828	0.4856
cg1997264	KCNMA1	c-Ets-1 [T	1751	1757	6.943262	GGGGAA	0.73242	0.73099
cg1997264	KCNMA1	ENKTF-1	232	239	6.942764	CCAGGC	1.46484	1.44228
cg1997264	KCNMA1	ENKTF-1	481	488	6.942764	TGGCTG	1.46484	1.44228
cg1997264	KCNMA1	ENKTF-1	644	651	6.942764	CACAGC	1.46484	1.44228
cg1997264	KCNMA1	ENKTF-1	765	772	6.942764	CACTGC	1.46484	1.44228
cg1997264	KCNMA1	ENKTF-1	1513	1520	6.942764	CTCTGC	1.46484	1.44228
cg0272748	KCNMA1	ENKTF-1	551	558	6.942764	TGGCGG	1.46484	1.44228
cg0272748	KCNMA1	ENKTF-1	1120	1127	6.942764	TGGCAG	1.46484	1.44228
cg1997264	KCNMA1	VDR [T00	1886	1894	6.925682	GTTCAT	0.42725	0.43062
cg0272748	KCNMA1	VDR [T00	404	412	6.925682	GTTCAG	0.42725	0.43062
cg0272748	KCNMA1	VDR [T00	438	446	6.925682	GTTCAA	0.42725	0.43062

cg1997264	KCNMA1	NF-AT1 [T	554	563	6.890694	TGGAAA	0.01907	0.01922
cg1997264	KCNMA1	EBF [T05	897	907	6.872118	CCTCCA	0.03052	0.02964
cg0272748	KCNMA1	C/EBPalp	1511	1517	6.85549	TGCAAT	0.73242	0.74337
cg1997264	KCNMA1	HOXD9 [T	1921	1930	6.852796	CATTGA	0.07629	0.0789
cg1997264	KCNMA1	HOXD10 [	1921	1930	6.852796	CATTGA	0.07629	0.0789
cg1997264	KCNMA1	c-Jun [T00	53	59	6.787369	TCTGTC	0.73242	0.73173
cg1997264	KCNMA1	c-Jun [T00	1310	1316	6.787369	TGACAG	0.73242	0.73173
cg1997264	KCNMA1	c-Jun [T00	1649	1655	6.787369	TCTGTC	0.73242	0.73173
cg1997264	KCNMA1	NFI/CTF [	88	95	6.786076	CGGCTT	0.73242	0.73214
cg1997264	KCNMA1	NFI/CTF [	1034	1041	6.786076	TGGTTT	0.73242	0.73214
cg0272748	KCNMA1	NFI/CTF [	554	561	6.786076	CGGATT	0.73242	0.73214
cg1997264	KCNMA1	RXR-alph	407	413	6.785809	GGGTAA	0.36621	0.36214
cg1997264	KCNMA1	p53 [T006	679	685	6.778774	GGGCTC	1.09863	1.07125
cg0272748	KCNMA1	p53 [T006	1611	1617	6.778774	TGAGCC	1.09863	1.07125
cg0272748	KCNMA1	ATF3 [T0	264	271	6.744803	TGATGT	0.27466	0.27656
cg0272748	KCNMA1	ATF3 [T0	1517	1524	6.744803	TGACAT	0.27466	0.27656
cg0272748	KCNMA1	ATF3 [T0	1843	1850	6.744803	TGACTT	0.27466	0.27656
cg0272748	KCNMA1	POU2F2 (	703	713	6.735173	TTTGTA	0.04292	0.04408
cg1997264	KCNMA1	NF-1 [T00	228	235	6.722386	TTGGCC	0.24414	0.24147
cg0272748	KCNMA1	NF-1 [T00	234	241	6.722386	TTGCCC	0.24414	0.24147
cg1997264	KCNMA1	T3R-beta1	220	228	6.702681	TCACCA	0.21362	0.21147
cg1997264	KCNMA1	T3R-beta1	97	105	6.683388	TCACCG	0.21362	0.21147
cg0272748	KCNMA1	PXR-1:RX	401	408	6.668182	TGTGTT	0.24414	0.24672
cg0272748	KCNMA1	PXR-1:RX	435	442	6.668182	TGTGTT	0.24414	0.24672
cg1997264	KCNMA1	T3R-beta1	996	1004	6.664094	TCACCG	0.21362	0.21147
cg1997264	KCNMA1	T3R-beta1	997	1005	6.664094	CACCGG	0.21362	0.21147
cg1997264	KCNMA1	TFII-I [T0	603	608	6.581441	ATCTCC	0.97656	0.97366
cg1997264	KCNMA1	FOXP3 [T	456	461	6.581441	GTTTTA	0.97656	0.99397
cg1997264	KCNMA1	FOXP3 [T	731	736	6.581441	TTCAAC	0.97656	0.99397
cg0272748	KCNMA1	TFII-I [T0	327	332	6.581441	ATCTCC	0.97656	0.97366
cg0272748	KCNMA1	TFII-I [T0	547	552	6.581441	GGAGTG	0.97656	0.97366
cg0272748	KCNMA1	TFII-I [T0	730	735	6.581441	GGAGAT	0.97656	0.97366
cg0272748	KCNMA1	FOXP3 [T	186	191	6.581441	TAAAAC	0.97656	0.99397
cg0272748	KCNMA1	FOXP3 [T	444	449	6.581441	GTTTTA	0.97656	0.99397
cg0272748	KCNMA1	FOXP3 [T	466	471	6.581441	TTCAAC	0.97656	0.99397
cg0272748	KCNMA1	FOXP3 [T	839	844	6.581441	GTTTTA	0.97656	0.99397
cg0272748	KCNMA1	FOXP3 [T	1074	1079	6.581441	TAAAAC	0.97656	0.99397
cg1997264	KCNMA1	RXR-alph	863	869	6.563693	GGGTGT	0.24414	0.2434
cg0272748	KCNMA1	RXR-alph	1741	1747	6.563693	AATACC	0.24414	0.2434
cg1997264	KCNMA1	p53 [T006	531	537	6.563521	GGGCTT	0.48828	0.47541
cg1997264	KCNMA1	PXR-1:RX	1148	1155	6.5446	TGAACA	0.24414	0.24672
cg0272748	KCNMA1	CTF [T001	1856	1867	6.536593	TAGCCA	0.02003	0.02007
cg1997264	KCNMA1	PPAR-alp	154	164	6.51544	AGCTGG	0.03719	0.03639
cg0272748	KCNMA1	PPAR-alp	1239	1249	6.51544	CTCTGG	0.03719	0.03639
cg0272748	KCNMA1	PPAR-alp	1466	1476	6.51544	ACCTGG	0.03719	0.03639
cg1997264	KCNMA1	XBP-1 [T	13	18	6.478682	ATGCCC	0.97656	0.97062
cg1997264	KCNMA1	XBP-1 [T	328	333	6.478682	ATGCCC	0.97656	0.97062
cg1997264	KCNMA1	XBP-1 [T	673	678	6.478682	ATGCCA	0.97656	0.97062

cg0272748	KCNMA1	C/EBPalph	245	251	6.460799	GGCAAT	0.48828	0.49071
cg1997264	KCNMA1	RAR-beta	214	223	6.415195	GGGGTT	0.18311	0.183
cg0272748	KCNMA1	C/EBPalph	1815	1821	6.391486	GACAAT	0.48828	0.49071
cg0272748	KCNMA1	MEF-2A [	587	597	6.342474	ACAAAA	0.02384	0.02461
cg1997264	KCNMA1	TCF-4E [T	1150	1156	6.302385	AACAAA	0.61035	0.61344
cg0272748	KCNMA1	c-Ets-1 [T	894	900	6.295602	ATGGAA	0.48828	0.48798
cg0272748	KCNMA1	c-Ets-1 [T	1093	1099	6.295602	TTTCCAT	0.48828	0.48798
cg1997264	KCNMA1	c-Jun [T00	1389	1395	6.293948	TGACCC	0.61035	0.60769
cg1997264	KCNMA1	c-Jun [T00	1568	1574	6.293948	TGACCC	0.61035	0.60769
cg1997264	KCNMA1	GR-alpha [	250	254	6.263098	CCTCA	3.90625	3.91061
cg1997264	KCNMA1	GR-alpha [	255	259	6.263098	CCTCA	3.90625	3.91061
cg1997264	KCNMA1	GR-alpha [	844	848	6.263098	CCTCA	3.90625	3.91061
cg1997264	KCNMA1	GR-alpha [	928	932	6.263098	CCTCA	3.90625	3.91061
cg1997264	KCNMA1	GR-alpha [	952	956	6.263098	TGAGG	3.90625	3.91061
cg1997264	KCNMA1	GR-alpha [	1393	1397	6.263098	CCTTA	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	727	731	6.263098	TGAGG	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	1140	1144	6.263098	CCTCA	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	1315	1319	6.263098	CCTCA	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	1460	1464	6.263098	TGAGG	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	1688	1692	6.263098	CCTCA	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	1766	1770	6.263098	CCTCA	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	1788	1792	6.263098	TAAGG	3.90625	3.91061
cg0272748	KCNMA1	GR-alpha [	1904	1908	6.263098	CCTCA	3.90625	3.91061
cg0272748	KCNMA1	c-Myb [T0	1909	1916	6.259888	TGCAGT	0.30518	0.3056
cg1997264	KCNMA1	C/EBPalph	1866	1872	6.245236	TGCAAT	0.97656	0.99
cg0272748	KCNMA1	IRF-1 [T0	1597	1605	6.24301	AGGAGG	0.16785	0.16909
cg1997264	KCNMA1	c-Fos [T00	1011	1020	6.236188	TGGTTG	0.09155	0.09126
cg1997264	KCNMA1	NF-AT1 [	1470	1479	6.201624	TGGAAA	0.03815	0.03846
cg1997264	KCNMA1	c-Ets-1 [T	1492	1498	6.167515	GTGGAA	0.36621	0.36731
cg1997264	KCNMA1	HNF-1B [	1927	1935	6.086797	TATTTA	0.09918	0.10196
cg1997264	KCNMA1	GR-alpha [	257	261	6.055408	TCAGG	3.90625	3.9065
cg1997264	KCNMA1	GR-alpha [	792	796	6.055408	TCAGG	3.90625	3.9065
cg1997264	KCNMA1	GR-alpha [	1206	1210	6.055408	TCAGG	3.90625	3.9065
cg1997264	KCNMA1	GR-alpha [	1572	1576	6.055408	CCTGA	3.90625	3.9065
cg1997264	KCNMA1	GR-alpha [	1637	1641	6.055408	CCTGA	3.90625	3.9065
cg1997264	KCNMA1	GR-alpha [	1671	1675	6.055408	TTAGG	3.90625	3.9065
cg1997264	KCNMA1	GR-alpha [	1958	1962	6.055408	CCTGA	3.90625	3.9065
cg0272748	KCNMA1	GR-alpha [	1065	1069	6.055408	CCTAA	3.90625	3.9065
cg0272748	KCNMA1	GR-alpha [	1301	1305	6.055408	CCTGA	3.90625	3.9065
cg0272748	KCNMA1	GR-alpha [	1440	1444	6.055408	TTAGG	3.90625	3.9065
cg0272748	KCNMA1	GR-alpha [	1721	1725	6.055408	CCTGA	3.90625	3.9065
cg0272748	KCNMA1	GR-alpha [	1729	1733	6.055408	CCTAA	3.90625	3.9065
cg0272748	KCNMA1	GR-alpha [	1987	1991	6.055408	TCAGG	3.90625	3.9065
cg1997264	KCNMA1	c-Ets-1 [T	553	559	6.039428	CTGGAA	0.36621	0.36731
cg1997264	KCNMA1	c-Ets-1 [T	1469	1475	6.039428	CTGGAA	0.36621	0.36731
cg1997264	KCNMA1	C/EBPalph	1232	1238	5.996794	AACAAT	0.97656	0.99
cg1997264	KCNMA1	C/EBPalph	1717	1723	5.996794	ACCAAT	0.97656	0.99
cg1997264	KCNMA1	C/EBPalph	1880	1886	5.996794	AACAAT	0.97656	0.99

cg0272748	KCNMA1	C/EBPalph	105	111	5.996794	CATTGG	0.97656	0.99
cg0272748	KCNMA1	AR [T000	908	916	5.970632	TCGATG	0.24414	0.24229
cg1997264	KCNMA1	GATA-3 [	781	792	5.946993	GTCCCT	0.00668	0.00669
cg1997264	KCNMA1	RXR-alpha	56	62	5.937582	GTCACC	0.73242	0.72249
cg1997264	KCNMA1	RXR-alpha	1704	1710	5.937582	ATTACC	0.73242	0.72249
cg0272748	KCNMA1	RXR-alpha	636	642	5.937582	GGGTGA	0.73242	0.72249
cg1997264	KCNMA1	STAT4 [T	812	817	5.882353	CCTTCC	0.48828	0.48408
cg1997264	KCNMA1	STAT4 [T	889	894	5.882353	CCTTCC	0.48828	0.48408
cg1997264	KCNMA1	STAT4 [T	1739	1744	5.882353	CCTTCC	0.48828	0.48408
cg0272748	KCNMA1	STAT4 [T	541	546	5.882353	GGAAGG	0.48828	0.48408
cg0272748	KCNMA1	C/EBPalph	1514	1520	5.850545	AATTGA	0.97656	0.99
cg0272748	KCNMA1	c-Myb [T0	1949	1956	5.841835	ACCAGT	0.21362	0.21535
cg0272748	KCNMA1	c-Ets-1 [T	539	545	5.814485	TGGGAA	0.36621	0.36731
cg0272748	KCNMA1	STAT1beta	1597	1606	5.796867	AGGAGG	0.1545	0.1557
cg1997264	KCNMA1	VDR [T00	1144	1152	5.771401	CATTTG	0.42725	0.42999
cg0272748	KCNMA1	c-Jun [T00	1723	1729	5.703976	TGACCC	0.48828	0.48665
cg0272748	KCNMA1	c-Ets-1 [T	272	278	5.686398	AGGGAA	0.36621	0.3623
cg0272748	KCNMA1	c-Ets-1 [T	1590	1596	5.686398	AGGGAA	0.36621	0.3623
cg1997264	KCNMA1	c-Fos [T00	999	1008	5.679695	CCGGTG	0.04578	0.04537
cg0272748	KCNMA1	NF-1 [T00	98	105	5.626299	TTGGTC	0.24414	0.24258
cg1997264	KCNMA1	NF-AT1 [	1732	1740	5.604085	TGTTTT	0.03815	0.03856
cg1997264	KCNMA1	T3R-beta1	940	948	5.591999	GCCTGG	0.21362	0.21287
cg1997264	KCNMA1	c-Jun [T00	445	451	5.590308	TGACAC	0.48828	0.48665
cg0272748	KCNMA1	c-Jun [T00	1270	1276	5.590308	TGACAC	0.48828	0.48665
cg1997264	KCNMA1	AP-2alpha	339	344	5.568965	ATAGGC	0.48828	0.4878
cg1997264	KCNMA1	AP-2alpha	591	596	5.568965	ATAGGC	0.48828	0.4878
cg1997264	KCNMA1	AP-2alpha	1528	1533	5.568965	GCCTAT	0.48828	0.4878
cg0272748	KCNMA1	C/EBPalph	556	562	5.565669	GATTGG	0.73242	0.74391
cg0272748	KCNMA1	IRF-1 [T0	1093	1101	5.564062	TTTCCA	0.22888	0.23087
cg1997264	KCNMA1	c-Ets-1 [T	813	819	5.558311	CTTCCC	0.36621	0.3623
cg1997264	KCNMA1	c-Ets-1 [T	1453	1459	5.558311	GGGGAA	0.36621	0.3623
cg1997264	KCNMA1	TFIID [T0	458	464	5.544826	TTTATC	0.73242	0.75085
cg1997264	KCNMA1	TFIID [T0	737	743	5.544826	TGATAA	0.73242	0.75085
cg1997264	KCNMA1	TFIID [T0	1556	1562	5.544826	TTTAGA	0.73242	0.75085
cg1997264	KCNMA1	TFIID [T0	1929	1935	5.544826	TTTAAC	0.73242	0.75085
cg0272748	KCNMA1	Pax-5 [T0	244	250	5.544826	GGGCAA	0.73242	0.72046
cg0272748	KCNMA1	TFIID [T0	108	114	5.544826	TGGTAA	0.73242	0.75085
cg0272748	KCNMA1	TFIID [T0	446	452	5.544826	TTTAGT	0.73242	0.75085
cg0272748	KCNMA1	TFIID [T0	1307	1313	5.544826	TTTAGA	0.73242	0.75085
cg1997264	KCNMA1	p53 [T006	1606	1612	5.508538	TAAGCC	0.61035	0.59991
cg1997264	KCNMA1	p53 [T006	1627	1633	5.508538	TCAGCC	0.61035	0.59991
cg1997264	KCNMA1	C/EBPalph	1921	1927	5.455853	CATTGA	0.73242	0.74391
cg1997264	KCNMA1	HOXD9 [	24	33	5.453039	TTCTTT	0.04578	0.04743
cg1997264	KCNMA1	HOXD9 [	1253	1262	5.453039	TGCTTT	0.04578	0.04743
cg1997264	KCNMA1	HOXD10 [	24	33	5.453039	TTCTTT	0.04578	0.04743
cg1997264	KCNMA1	HOXD10 [	1253	1262	5.453039	TGCTTT	0.04578	0.04743
cg1997264	KCNMA1	C/EBPalph	910	916	5.38654	ACCAAT	0.73242	0.74391
cg1997264	KCNMA1	C/EBPalph	1801	1807	5.38654	AATTGT	0.73242	0.74391

cg1997264	KCNMA1	C/EBPalph	1990	1996	5.38654	AATTGT	0.73242	0.74391
cg0272748	KCNMA1	C/EBPalph	835	841	5.38654	AATTGT	0.73242	0.74391
cg1997264	KCNMA1	NF-1 [T00	660	667	5.377909	TTGGCC	0.24414	0.24258
cg1997264	KCNMA1	IRF-1 [T0	1736	1744	5.309227	TTTCCTT	0.22888	0.23087
cg0272748	KCNMA1	HOXD9 [T	1072	1081	5.275652	AATAAA	0.04578	0.04743
cg0272748	KCNMA1	HOXD10 [	1072	1081	5.275652	AATAAA	0.04578	0.04743
cg1997264	KCNMA1	RXR-alpha	854	860	5.271235	GGGTGG	0.61035	0.6044
cg1997264	KCNMA1	RXR-alpha	1974	1980	5.271235	GCAACC	0.61035	0.6044
cg0272748	KCNMA1	RXR-alpha	1420	1426	5.271235	GGGTTG	0.61035	0.6044
cg1997264	KCNMA1	c-Myb [T0	1455	1462	5.258734	GGAAGT	0.09155	0.09192
cg0272748	KCNMA1	C/EBPalph	647	653	5.240291	GTCAAT	0.97656	0.99332
cg0272748	KCNMA1	C/EBPalph	1738	1744	5.240291	GTCAAT	0.97656	0.99332
cg0272748	KCNMA1	POU2F2 (	355	365	5.23012	AGTGTA	0.02432	0.02504
cg0272748	KCNMA1	HNF-1C [	3	11	5.214027	GTTATA	0.04578	0.04693
cg1997264	KCNMA1	AP-2alpha	1021	1026	5.100982	AAAGGC	0.97656	0.97567
cg0272748	KCNMA1	AP-2alpha	319	324	5.100982	GCCTTT	0.97656	0.97567
cg0272748	KCNMA1	NF-Y [T0	557	564	5.094053	ATTGGA	0.36621	0.36847
cg1997264	KCNMA1	GR-beta [T	197	201	5.042296	GTATT	3.90625	3.95351
cg1997264	KCNMA1	GR-beta [T	294	298	5.042296	GGATT	3.90625	3.95351
cg1997264	KCNMA1	GR-beta [T	348	352	5.042296	AATAC	3.90625	3.95351
cg1997264	KCNMA1	GR-beta [T	989	993	5.042296	GGATT	3.90625	3.95351
cg1997264	KCNMA1	GR-beta [T	1280	1284	5.042296	GTATT	3.90625	3.95351
cg0272748	KCNMA1	GR-beta [T	555	559	5.042296	GGATT	3.90625	3.95351
cg0272748	KCNMA1	GR-beta [T	697	701	5.042296	GGATT	3.90625	3.95351
cg0272748	KCNMA1	GR-beta [T	1393	1397	5.042296	AATAC	3.90625	3.95351
cg0272748	KCNMA1	GR-beta [T	1741	1745	5.042296	AATAC	3.90625	3.95351
cg0272748	KCNMA1	GR-beta [T	1891	1895	5.042296	AATAC	3.90625	3.95351
cg0272748	KCNMA1	GR-beta [T	1937	1941	5.042296	GGATT	3.90625	3.95351
cg0272748	KCNMA1	E2F-1 [T0	1585	1592	5.042045	GCGGGA	0.18311	0.17901
cg0272748	KCNMA1	NFI/CTF [	103	110	5.021086	CCCATT	0.24414	0.24103
cg1997264	KCNMA1	c-Myb [T0	438	445	4.974489	CAACTG	0.30518	0.30568
cg1997264	KCNMA1	IRF-1 [T0	1749	1757	4.968836	AGGGGG	0.1297	0.1302
cg1997264	KCNMA1	XBP-1 [T0	938	943	4.894955	ATGCCT	0.97656	0.96979
cg0272748	KCNMA1	XBP-1 [T0	774	779	4.894955	ATGCCT	0.97656	0.96979
cg0272748	KCNMA1	XBP-1 [T0	1062	1067	4.894955	ATGCCT	0.97656	0.96979
cg0272748	KCNMA1	AP-2alpha	1064	1069	4.890408	GCCTAA	0.97656	0.97567
cg1997264	KCNMA1	NF-1 [T00	1092	1099	4.880836	AGTCCC	0.24414	0.24398
cg0272748	KCNMA1	RXR-alpha	1470	1476	4.86724	GGGTCT	0.48828	0.484
cg0272748	KCNMA1	NF-Y [T0	88	95	4.867193	GCCCCA	0.36621	0.36847
cg0272748	KCNMA1	HNF-3alph	841	848	4.842999	TTTAAA	0.09155	0.09582
cg0272748	KCNMA1	C/EBPalph	879	885	4.776286	AACAAT	0.97656	0.99332
cg0272748	KCNMA1	C/EBPalph	1888	1894	4.776286	AACAAT	0.97656	0.99332
cg1997264	KCNMA1	SRF [T007	841	853	4.760245	CATCCT	0.00125	0.00125
cg1997264	KCNMA1	TFII-I [T0	779	784	4.756447	CAGTCC	2.92969	2.93695
cg1997264	KCNMA1	TFII-I [T0	989	994	4.756447	GGATTG	2.92969	2.93695
cg1997264	KCNMA1	TFII-I [T0	1091	1096	4.756447	CAGTCC	2.92969	2.93695
cg1997264	KCNMA1	TFII-I [T0	1445	1450	4.756447	GGATAT	2.92969	2.93695
cg1997264	KCNMA1	FOXP3 [T	1013	1018	4.756447	GTTGAC	2.92969	2.96063

cg1997264	KCNMA1	FOXP3 [T	1184	1189	4.756447	GAAAAC	2.92969	2.96063
cg1997264	KCNMA1	FOXP3 [T	1347	1352	4.756447	GTCAAC	2.92969	2.96063
cg1997264	KCNMA1	FOXP3 [T	1733	1738	4.756447	GTTTTT	2.92969	2.96063
cg1997264	KCNMA1	FOXP3 [T	1823	1828	4.756447	CAAAAC	2.92969	2.96063
cg1997264	KCNMA1	FOXP3 [T	1937	1942	4.756447	CAAAAC	2.92969	2.96063
cg0272748	KCNMA1	TFII-I [T0	196	201	4.756447	GGAATG	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	555	560	4.756447	GGATTG	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	697	702	4.756447	GGATTG	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	911	916	4.756447	ATGTCC	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	1059	1064	4.756447	GGAATG	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	1456	1461	4.756447	GGACTG	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	1601	1606	4.756447	GGAAAT	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	1669	1674	4.756447	GGATAT	2.92969	2.93695
cg0272748	KCNMA1	TFII-I [T0	1762	1767	4.756447	CAGTCC	2.92969	2.93695
cg0272748	KCNMA1	FOXP3 [T	55	60	4.756447	GTTTTT	2.92969	2.96063
cg0272748	KCNMA1	FOXP3 [T	156	161	4.756447	AAAAAC	2.92969	2.96063
cg0272748	KCNMA1	FOXP3 [T	409	414	4.756447	GTTTTG	2.92969	2.96063
cg0272748	KCNMA1	FOXP3 [T	784	789	4.756447	CAAAAC	2.92969	2.96063
cg0272748	KCNMA1	FOXP3 [T	1087	1092	4.756447	GAAAAC	2.92969	2.96063
cg0272748	KCNMA1	FOXP3 [T	1257	1262	4.756447	GTTTTG	2.92969	2.96063
cg0272748	KCNMA1	FOXP3 [T	1280	1285	4.756447	AAAAAC	2.92969	2.96063
cg0272748	KCNMA1	FOXP3 [T	1885	1890	4.756447	GAAAAC	2.92969	2.96063
cg1997264	KCNMA1	Ik-1 [T027	149	161	4.748597	CGAGTA	0.00313	0.00308
cg1997264	KCNMA1	c-Ets-1 [T	534	540	4.654478	CTTCCA	0.85449	0.85764
cg1997264	KCNMA1	TCF-4 [T0	1016	1025	4.639022	GACTCA	0.04196	0.04202
cg0272748	KCNMA1	TCF-4 [T0	708	717	4.639022	AACTCA	0.04196	0.04202
cg1997264	KCNMA1	VDR [T00	387	395	4.617121	AGAATG	0.37384	0.37445
cg0272748	KCNMA1	VDR [T00	465	473	4.617121	GTTCAA	0.37384	0.37445
cg1997264	KCNMA1	NF-kappa	1836	1846	4.600708	GGAGGG	0.03242	0.03169
cg0272748	KCNMA1	RAR-alph	1717	1729	4.596281	ACTGCC	0.00376	0.0037
cg1997264	KCNMA1	c-Ets-2 [T	1737	1745	4.589988	TTCCTTC	0.06866	0.06881
cg1997264	KCNMA1	c-Fos [T00	1813	1822	4.563121	GAGTCA	0.04578	0.04591
cg1997264	KCNMA1	USF2 [T0	258	267	4.528187	CAGGTG	0.06866	0.06782
cg0272748	KCNMA1	USF2 [T0	1656	1665	4.528187	GGATCA	0.06866	0.06782
cg1997264	KCNMA1	GATA-2 [	1213	1221	4.444445	ACTTTA	0.24414	0.24541
cg0272748	KCNMA1	T3R-beta1	24	32	4.442729	TCACCT	0.27466	0.27551
cg0272748	KCNMA1	c-Jun [T00	20	26	4.441904	TCAGTC	0.12207	0.12266
cg1997264	KCNMA1	AP-2alpha	1643	1648	4.438035	CTAGGC	0.97656	0.96979
cg0272748	KCNMA1	HNF-1B [	11	19	4.435774	TTATTA	0.05341	0.0549
cg1997264	KCNMA1	RXR-alph	1042	1048	4.423008	GGGTGG	0.24414	0.24292
cg1997264	KCNMA1	RXR-alph	1072	1078	4.423008	TCCACC	0.24414	0.24292
cg0272748	KCNMA1	RXR-alph	940	946	4.423008	GGGTTG	0.24414	0.24292
cg1997264	KCNMA1	STAT4 [T	533	538	4.411765	GCTTCC	1.95312	1.94235
cg1997264	KCNMA1	STAT4 [T	1417	1422	4.411765	GGAAGC	1.95312	1.94235
cg0272748	KCNMA1	STAT4 [T	196	201	4.411765	GGAATG	1.95312	1.94235
cg0272748	KCNMA1	STAT4 [T	274	279	4.411765	GGAAGA	1.95312	1.94235
cg0272748	KCNMA1	STAT4 [T	1059	1064	4.411765	GGAATG	1.95312	1.94235
cg0272748	KCNMA1	STAT4 [T	1592	1597	4.411765	GGAAGA	1.95312	1.94235

cg1997264	KCNMA1	RXR-alpha	1388	1394	4.24113	GTGACC	0.97656	0.9671
cg1997264	KCNMA1	RXR-alpha	1839	1845	4.24113	GGGTCC	0.97656	0.9671
cg0272748	KCNMA1	C/EBPalph	1429	1435	4.235345	TATTGC	0.48828	0.49358
cg1997264	KCNMA1	AP-2alpha	322	327	4.211849	GCCTAC	0.97656	0.96469
cg1997264	KCNMA1	AP-2alpha	663	668	4.211849	GCCTAC	0.97656	0.96469
cg1997264	KCNMA1	GR-beta [	5	9	4.201913	CTATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	29	33	4.201913	TTATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	127	131	4.201913	CGATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	205	209	4.201913	AATAG	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	413	417	4.201913	CTATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	429	433	4.201913	AATCA	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	590	594	4.201913	AATAG	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	934	938	4.201913	AATCA	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	946	950	4.201913	TGATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	1249	1253	4.201913	CGATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	1258	1262	4.201913	TTATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	1486	1490	4.201913	TGATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	1530	1534	4.201913	CTATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	1553	1557	4.201913	TGATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	1702	1706	4.201913	TTATT	7.8125	7.94607
cg1997264	KCNMA1	GR-beta [	1902	1906	4.201913	CTATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	11	15	4.201913	TTATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	93	97	4.201913	AATAG	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	343	347	4.201913	TTATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	377	381	4.201913	TGATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	504	508	4.201913	AATCA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	594	598	4.201913	AATAG	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	607	611	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	632	636	4.201913	AATAG	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	650	654	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	653	657	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	676	680	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	760	764	4.201913	TTATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	845	849	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	867	871	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	925	929	4.201913	TTATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	935	939	4.201913	AATAG	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1072	1076	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1210	1214	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1213	1217	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1428	1432	4.201913	TTATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1436	1440	4.201913	TTATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1604	1608	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1802	1806	4.201913	CGATT	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1877	1881	4.201913	AATAA	7.8125	7.94607
cg0272748	KCNMA1	GR-beta [	1985	1989	4.201913	AATCA	7.8125	7.94607
cg0272748	KCNMA1	NF-Y [T0	36	43	4.186615	TCTCCA	0.18311	0.1853
cg0272748	KCNMA1	HNF-1C [	604	612	4.175118	ATGAAT	0.04578	0.04699

cg1997264	KCNMA1	NF-1 [T00	92	99	4.135372	TTGGCT	0.24414	0.24154
cg0272748	KCNMA1	NF-1 [T00	87	94	4.135372	TGCCC	0.24414	0.24154
cg0272748	KCNMA1	NF-AT1 [	895	904	4.134416	TGGAAA	0.08392	0.08485
cg0272748	KCNMA1	POU2F2 (	838	848	4.120113	TGTTTTA	0.01717	0.0178
cg1997264	KCNMA1	SRY [T00	1301	1309	4.087393	CTTTGTA	0.12207	0.12407
cg1997264	KCNMA1	RXR-alph	179	185	4.019014	CACACC	0.97656	0.9671
cg1997264	KCNMA1	RXR-alph	215	221	4.019014	GGGTTT	0.97656	0.9671
cg0272748	KCNMA1	RXR-alph	398	404	4.019014	GGGTGT	0.97656	0.9671
cg0272748	KCNMA1	c-Ets-2 [T	1014	1022	4.017001	ACAAAG	0.16022	0.16243
cg1997264	KCNMA1	TFIID [T0	202	208	4.007279	TTTAAT	1.09863	1.13456
cg1997264	KCNMA1	TFIID [T0	1257	1263	4.007279	TTTATTA	1.09863	1.13456
cg1997264	KCNMA1	TFIID [T0	1283	1289	4.007279	TTATAA	1.09863	1.13456
cg1997264	KCNMA1	TFIID [T0	1293	1299	4.007279	TTTAAG	1.09863	1.13456
cg0272748	KCNMA1	Pax-5 [T0	85	91	4.007279	ACTGCC	1.09863	1.07975
cg0272748	KCNMA1	Pax-5 [T0	1357	1363	4.007279	ACAGCC	1.09863	1.07975
cg0272748	KCNMA1	Pax-5 [T0	1646	1652	4.007279	GGGCTG	1.09863	1.07975
cg0272748	KCNMA1	TFIID [T0	4	10	4.007279	TTATAA	1.09863	1.13456
cg0272748	KCNMA1	TFIID [T0	58	64	4.007279	TTTTAA	1.09863	1.13456
cg0272748	KCNMA1	TFIID [T0	670	676	4.007279	TTTTAA	1.09863	1.13456
cg0272748	KCNMA1	TFIID [T0	840	846	4.007279	TTTTAA	1.09863	1.13456
cg0272748	KCNMA1	TFIID [T0	861	867	4.007279	TTTTAA	1.09863	1.13456
cg0272748	KCNMA1	TFIID [T0	1071	1077	4.007279	TAATAA	1.09863	1.13456
cg0272748	KCNMA1	AP-2alpha	258	263	3.970052	CAAGGC	0.97656	0.96469
cg0272748	KCNMA1	HOXD9 [	1922	1931	3.903508	AATATA	0.03052	0.03168
cg0272748	KCNMA1	HOXD10 [	1922	1931	3.903508	AATATA	0.03052	0.03168
cg0272748	KCNMA1	c-Myb [T0	239	246	3.85204	CAACTG	0.09155	0.09154
cg0272748	KCNMA1	c-Jun [T00	873	879	3.807346	TGACTA	0.24414	0.24526
cg1997264	KCNMA1	GR [T050	702	708	3.763516	CAAAGA	0.73242	0.74251
cg1997264	KCNMA1	GR [T050	1152	1158	3.763516	CAAAGA	0.73242	0.74251
cg1997264	KCNMA1	GR [T050	1169	1175	3.763516	CAAAGA	0.73242	0.74251
cg1997264	KCNMA1	GR [T050	1823	1829	3.763516	CAAAAC	0.73242	0.74251
cg1997264	KCNMA1	GR [T050	1937	1943	3.763516	CAAAAC	0.73242	0.74251
cg0272748	KCNMA1	GR [T050	408	414	3.763516	AGTTTT	0.73242	0.74251
cg0272748	KCNMA1	GR [T050	784	790	3.763516	CAAAAC	0.73242	0.74251
cg0272748	KCNMA1	GR [T050	1256	1262	3.763516	TGTTTT	0.73242	0.74251
cg0272748	KCNMA1	GR [T050	1808	1814	3.763516	TTCTTTG	0.73242	0.74251
cg1997264	KCNMA1	AP-2alpha	888	893	3.743866	GCCTTC	0.48828	0.48238
cg0272748	KCNMA1	AP-2alpha	1555	1560	3.743866	GAAGGC	0.48828	0.48238
cg0272748	KCNMA1	p53 [T006	244	250	3.728319	GGGCAA	0.73242	0.7189
cg1997264	KCNMA1	PEA3 [T0	494	502	3.710864	AGGATG	0.09155	0.09258
cg0272748	KCNMA1	PEA3 [T0	382	390	3.710864	TGGATG	0.09155	0.09258
cg1997264	KCNMA1	c-Ets-1 [T	564	570	3.590463	GAGGAA	0.61035	0.60765
cg0272748	KCNMA1	NF-AT2 [	1601	1610	3.571424	GGAAAT	0.03433	0.03499
cg0272748	KCNMA1	C/EBPalp	698	704	3.555778	GATTGT	0.24414	0.24752
cg0272748	KCNMA1	p53 [T006	85	91	3.516613	ACTGCC	0.73242	0.7189
cg1997264	KCNMA1	HNF-3alp	6	13	3.500065	TATTTAT	0.27466	0.28532
cg1997264	KCNMA1	HNF-3alp	30	37	3.500065	TATTTTT	0.27466	0.28532
cg0272748	KCNMA1	HNF-3alp	590	597	3.500065	AAAAAA	0.27466	0.28532

cg1997264	KCNMA1	RXR-alpha	1567	1573	3.392904	ATGACC	1.09863	1.08572
cg1997264	KCNMA1	RXR-alpha	1915	1921	3.392904	GTAACC	1.09863	1.08572
cg0272748	KCNMA1	RXR-alpha	825	831	3.392904	GTAACC	1.09863	1.08572
cg0272748	KCNMA1	AR [T000	1814	1822	3.382886	GGACAA	0.06866	0.06905
cg1997264	KCNMA1	GR-beta [T	500	504	3.361531	AATCT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	602	606	3.361531	AATCT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	627	631	3.361531	AATCT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1155	1159	3.361531	AGATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1447	1451	3.361531	ATATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1508	1512	3.361531	ATATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1869	1873	3.361531	AATAT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1870	1874	3.361531	ATATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1926	1930	3.361531	ATATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	65	69	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	113	117	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	415	419	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	455	459	3.361531	ATATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	484	488	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	485	489	3.361531	ATATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	667	671	3.361531	ATATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	737	741	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	738	742	3.361531	ATATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	807	811	3.361531	AATCT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	882	886	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	883	887	3.361531	ATATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1225	1229	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1226	1230	3.361531	ATATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1607	1611	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1922	1926	3.361531	AATAT	3.90625	3.99611
cg0272748	KCNMA1	IRF-1 [T0	1015	1023	3.347186	CAAAGG	0.06866	0.06927
cg1997264	KCNMA1	PR B [T00	1801	1807	3.29756	AATTGT	0.24414	0.25122
cg1997264	KCNMA1	PR B [T00	1990	1996	3.29756	AATTGT	0.24414	0.25122
cg1997264	KCNMA1	PR A [T01	1801	1807	3.29756	AATTGT	0.24414	0.25122
cg1997264	KCNMA1	PR A [T01	1990	1996	3.29756	AATTGT	0.24414	0.25122
cg0272748	KCNMA1	PR B [T00	835	841	3.29756	AATTGT	0.24414	0.25122
cg0272748	KCNMA1	PR B [T00	1253	1259	3.29756	AAATGT	0.24414	0.25122
cg0272748	KCNMA1	PR A [T01	835	841	3.29756	AATTGT	0.24414	0.25122
cg0272748	KCNMA1	PR A [T01	1253	1259	3.29756	AAATGT	0.24414	0.25122
cg0272748	KCNMA1	AP-2alpha	533	538	3.229049	AGAGGC	0.48828	0.48238
cg0272748	KCNMA1	RAR-beta	132	141	3.226064	TGGGTT	0.12207	0.12169
cg1997264	KCNMA1	RXR-alpha	513	519	3.170788	GGGTGT	0.24414	0.24522
cg1997264	KCNMA1	TCF-4E [T	1167	1173	3.151193	ATCAAA	0.24414	0.24672
cg0272748	KCNMA1	TCF-4E [T	321	327	3.151193	CTTTGC	0.24414	0.24672
cg0272748	KCNMA1	IRF-1 [T0	892	900	3.145547	ACATGG	0.07629	0.07756
cg1997264	KCNMA1	EBF [T05	1744	1754	3.135622	CTCCCA	0.00763	0.00736
cg1997264	KCNMA1	SRY [T00	1165	1173	3.088221	AGATCA	0.06104	0.06203
cg0272748	KCNMA1	TFIID [T0	949	955	3.075094	TGCAAA	0.12207	0.12409
cg1997264	KCNMA1	p53 [T006	314	320	3.028543	TGTGCC	0.48828	0.47786

cg1997264	KCNMA1	p53 [T006	362	368	3.028543	GGGCAC	0.48828	0.47786
cg1997264	KCNMA1	p53 [T006	977	983	3.024997	GGGCAA	0.48828	0.47786
cg1997264	KCNMA1	C/EBPalph	990	996	3.014837	GATTGC	0.48828	0.4911
cg1997264	KCNMA1	C/EBPalph	1250	1256	3.014837	GATTGC	0.48828	0.4911
cg1997264	KCNMA1	C/EBPalph	1563	1569	2.981957	CACAAT	0.48828	0.4911
cg0272748	KCNMA1	C/EBPalph	1527	1533	2.981957	CACAAT	0.48828	0.4911
cg1997264	KCNMA1	STAT4 [T	555	560	2.941176	GGAAAG	2.92969	2.929
cg1997264	KCNMA1	STAT4 [T	572	577	2.941176	GGAACA	2.92969	2.929
cg1997264	KCNMA1	STAT4 [T	1455	1460	2.941176	GGAAGT	2.92969	2.929
cg0272748	KCNMA1	STAT4 [T	1019	1024	2.941176	GGAAAG	2.92969	2.929
cg0272748	KCNMA1	STAT4 [T	1092	1097	2.941176	CTTTCC	2.92969	2.929
cg0272748	KCNMA1	STAT4 [T	1227	1232	2.941176	TATTCC	2.92969	2.929
cg0272748	KCNMA1	STAT4 [T	1622	1627	2.941176	ACTTCC	2.92969	2.929
cg0272748	KCNMA1	STAT4 [T	1983	1988	2.941176	GGAATC	2.92969	2.929
cg1997264	KCNMA1	TCF-4 [T0	1165	1174	2.859093	AGATCA	0.03433	0.0351
cg1997264	KCNMA1	p53 [T006	1674	1680	2.813291	GGGCAG	0.48828	0.47786
cg1997264	KCNMA1	PR B [T00	1232	1238	2.80933	AACAAT	0.73242	0.74818
cg1997264	KCNMA1	PR B [T00	1336	1342	2.80933	TAATGT	0.73242	0.74818
cg1997264	KCNMA1	PR B [T00	1719	1725	2.80933	CAATGT	0.73242	0.74818
cg1997264	KCNMA1	PR B [T00	1880	1886	2.80933	AACAAT	0.73242	0.74818
cg1997264	KCNMA1	PR B [T00	1882	1888	2.80933	CAATGT	0.73242	0.74818
cg1997264	KCNMA1	PR A [T01	1232	1238	2.80933	AACAAT	0.73242	0.74818
cg1997264	KCNMA1	PR A [T01	1336	1342	2.80933	TAATGT	0.73242	0.74818
cg1997264	KCNMA1	PR A [T01	1719	1725	2.80933	CAATGT	0.73242	0.74818
cg1997264	KCNMA1	PR A [T01	1880	1886	2.80933	AACAAT	0.73242	0.74818
cg1997264	KCNMA1	PR A [T01	1882	1888	2.80933	CAATGT	0.73242	0.74818
cg0272748	KCNMA1	PR B [T00	698	704	2.80933	GATTGT	0.73242	0.74818
cg0272748	KCNMA1	PR B [T00	879	885	2.80933	AACAAT	0.73242	0.74818
cg0272748	KCNMA1	PR B [T00	1888	1894	2.80933	AACAAT	0.73242	0.74818
cg0272748	KCNMA1	PR A [T01	698	704	2.80933	GATTGT	0.73242	0.74818
cg0272748	KCNMA1	PR A [T01	879	885	2.80933	AACAAT	0.73242	0.74818
cg0272748	KCNMA1	PR A [T01	1888	1894	2.80933	AACAAT	0.73242	0.74818
cg1997264	KCNMA1	TBP [T007	1280	1289	2.807313	GTATTA	0.12207	0.12635
cg1997264	KCNMA1	TBP [T007	1806	1815	2.807313	TTTATA	0.12207	0.12635
cg0272748	KCNMA1	TBP [T007	985	994	2.807313	CACCTA	0.12207	0.12635
cg0272748	KCNMA1	NF-AT1 [	1089	1098	2.756277	AAACTT	0.05913	0.05995
cg0272748	KCNMA1	RXR-alpha	1639	1645	2.726556	GGGTCG	0.85449	0.84796
cg0272748	KCNMA1	NF-AT1 [	1089	1097	2.619709	AAACTT	0.09155	0.0926
cg1997264	KCNMA1	POU2F2 (	1785	1795	2.61506	TGAATT	0.01001	0.0104
cg1997264	KCNMA1	PXR-1:RX	581	588	2.577808	GGAGTT	0.12207	0.12266
cg0272748	KCNMA1	AP-2alpha	1139	1144	2.550491	GCCTCA	0.48828	0.48266
cg1997264	KCNMA1	RXR-alpha	904	910	2.544678	GGGTGC	0.85449	0.84796
cg1997264	KCNMA1	RXR-alpha	1765	1771	2.544678	AGAACC	0.85449	0.84796
cg0272748	KCNMA1	RXR-alpha	1578	1584	2.544678	GGGTTA	0.85449	0.84796
cg0272748	KCNMA1	c-Jun [T00	1843	1849	2.538231	TGACTT	0.48828	0.48929
cg1997264	KCNMA1	RAR-beta:	309	320	2.492665	TCCACT	0.00215	0.00209
cg1997264	KCNMA1	C/EBPalph	1909	1915	2.441016	CATTGA	0.48828	0.49114
cg0272748	KCNMA1	NF-AT2 [	1088	1097	2.430885	AAAACT	0.01144	0.01167

cg1997264	KCNMA1	Ik-1 [T027	284	296	2.374299	CAAAGT	0.00063	0.00061
cg1997264	KCNMA1	C/EBPalph	1423	1429	2.371703	CACAAT	0.48828	0.49114
cg1997264	KCNMA1	Elk-1 [T00	1413	1421	2.299314	CCCAGG	0.09155	0.09114
cg0272748	KCNMA1	Elk-1 [T00	1623	1631	2.299314	CTTCCTC	0.09155	0.09114
cg0272748	KCNMA1	T3R-beta1	1659	1667	2.240658	TCACCTC	0.15259	0.15262
cg0272748	KCNMA1	GATA-2 [	1475	1483	2.222222	TCATTAT	0.22888	0.23091
cg1997264	KCNMA1	T3R-beta1	256	264	2.221365	CTCAGG	0.15259	0.15262
cg1997264	KCNMA1	T3R-beta1	463	471	2.221365	CACTGG	0.15259	0.15262
cg1997264	KCNMA1	NF-Y [T0	908	915	2.194008	GCACCA	0.21362	0.21508
cg1997264	KCNMA1	GATA-1 [	802	807	2.176375	TGGATA	3.90625	3.92756
cg1997264	KCNMA1	GATA-1 [	1217	1222	2.176375	TATCCA	3.90625	3.92756
cg1997264	KCNMA1	GATA-1 [	1444	1449	2.176375	AGGATA	3.90625	3.92756
cg1997264	KCNMA1	GATA-1 [	1462	1467	2.176375	TATCCT	3.90625	3.92756
cg1997264	KCNMA1	GATA-1 [	1602	1607	2.176375	TGGATA	3.90625	3.92756
cg1997264	KCNMA1	GATA-1 [	1725	1730	2.176375	TATCCT	3.90625	3.92756
cg0272748	KCNMA1	GATA-1 [	582	587	2.176375	TGGATA	3.90625	3.92756
cg0272748	KCNMA1	GATA-1 [	715	720	2.176375	AGGATA	3.90625	3.92756
cg0272748	KCNMA1	GATA-1 [	903	908	2.176375	TATCCT	3.90625	3.92756
cg0272748	KCNMA1	GATA-1 [	1830	1835	2.176375	ACGATA	3.90625	3.92756
cg0272748	KCNMA1	GATA-1 [	1944	1949	2.176375	TGGATA	3.90625	3.92756
cg0272748	KCNMA1	p53 [T006	233	239	1.970013	TTTGCCC	0.36621	0.36261
cg0272748	KCNMA1	NF-AT1 [	1601	1609	1.94698	GGAAAT	0.06866	0.07012
cg1997264	KCNMA1	HNF-1C [	1926	1934	1.940349	ATATTTA	0.02289	0.02363
cg0272748	KCNMA1	GATA-1 [	1668	1673	1.896347	CGGATA	3.90625	3.92756
cg1997264	KCNMA1	AP-2alpha	111	116	1.871933	GCCTCC	0.97656	0.95407
cg1997264	KCNMA1	AP-2alpha	143	148	1.871933	GCCTCC	0.97656	0.95407
cg1997264	KCNMA1	AP-2alpha	278	283	1.871933	GCCTCC	0.97656	0.95407
cg1997264	KCNMA1	AP-2alpha	1046	1051	1.871933	GGAGGC	0.97656	0.95407
cg0272748	KCNMA1	AP-2alpha	565	570	1.871933	GGAGGC	0.97656	0.95407
cg0272748	KCNMA1	AP-2alpha	1683	1688	1.871933	GCCTCC	0.97656	0.95407
cg0272748	KCNMA1	TBP [T007	1	10	1.871542	TAGTTAT	0.18311	0.18942
cg1997264	KCNMA1	TFII-I [T0	871	876	1.824994	CTCTCC	0.48828	0.48408
cg1997264	KCNMA1	TFII-I [T0	1082	1087	1.824994	CTCTCC	0.48828	0.48408
cg0272748	KCNMA1	TFII-I [T0	35	40	1.824994	CTCTCC	0.48828	0.48408
cg0272748	KCNMA1	TFII-I [T0	224	229	1.824994	GGAGAG	0.48828	0.48408
cg0272748	KCNMA1	TFII-I [T0	745	750	1.824994	CTCTCC	0.48828	0.48408
cg0272748	KCNMA1	FOXP3 [T	1970	1975	1.824994	GTTGTA	0.48828	0.49451
cg0272748	KCNMA1	C/EBPalph	90	96	1.761449	CCCAAT	0.48828	0.49438
cg0272748	KCNMA1	C/EBPalph	926	932	1.761449	TATTGTC	0.48828	0.49438
cg1997264	KCNMA1	p53 [T006	12	18	1.758307	TATGCCC	0.36621	0.36261
cg1997264	KCNMA1	p53 [T006	1686	1692	1.758307	TCTGCCC	0.36621	0.36261
cg0272748	KCNMA1	RXR-alph	1722	1728	1.696452	CTGACC	0.48828	0.48222
cg1997264	KCNMA1	GR-beta [	434	438	1.680765	AATGC	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [	688	692	1.680765	AATTC	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [	729	733	1.680765	AATTC	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [	774	778	1.680765	AATTC	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [	913	917	1.680765	AATTC	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [	1199	1203	1.680765	AATGC	3.90625	3.94936

cg1997264	KCNMA1	GR-beta [T	1479	1483	1.680765	GAATT	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [T	1498	1502	1.680765	AATTC	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [T	1759	1763	1.680765	GAATT	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [T	1760	1764	1.680765	AATTC	3.90625	3.94936
cg1997264	KCNMA1	GR-beta [T	1786	1790	1.680765	GAATT	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	198	202	1.680765	AATGC	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	294	298	1.680765	AATGC	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	721	725	1.680765	AATGC	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	955	959	1.680765	AATTC	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	1061	1065	1.680765	AATGC	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	1168	1172	1.680765	AATGC	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	1304	1308	1.680765	GAATT	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	1349	1353	1.680765	AATTC	3.90625	3.94936
cg0272748	KCNMA1	GR-beta [T	1927	1931	1.680765	AATTC	3.90625	3.94936
cg1997264	KCNMA1	Elk-1 [T00	890	898	1.645354	CTTCCTA	0.00763	0.00763
cg1997264	KCNMA1	c-Ets-2 [T	1741	1749	1.64415	TTCCTCC	0.04578	0.04579
cg0272748	KCNMA1	c-Ets-2 [T	1596	1604	1.64415	GAGGAG	0.04578	0.04579
cg1997264	KCNMA1	c-Ets-1 [T	1736	1742	1.641124	TTTCCTT	0.36621	0.36952
cg0272748	KCNMA1	c-Ets-1 [T	1017	1023	1.641124	AAGGAA	0.36621	0.36952
cg1997264	KCNMA1	C/EBPbeta	92	95	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	228	231	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	283	286	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	579	582	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	660	663	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	669	672	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	701	704	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	770	773	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	801	804	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	911	914	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1038	1041	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1096	1099	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1124	1127	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1135	1138	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1220	1223	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1398	1401	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1451	1454	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1534	1537	1.639871	TTGG	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1718	1721	1.639871	CCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1845	1848	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	29	32	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	39	42	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	91	94	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	98	101	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	107	110	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	131	134	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	173	176	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	238	241	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	381	384	1.639871	TTGG	15.625	15.72563

cg0272748	KCNMA1	C/EBPbeta	558	561	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	915	918	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1119	1122	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1147	1150	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1165	1168	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1181	1184	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1346	1349	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1746	1749	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1812	1815	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1859	1862	1.639871	CCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1981	1984	1.639871	TTGG	15.625	15.72563
cg0272748	KCNMA1	PXR-1:RX	462	469	1.63615	ATAGTT	0.06104	0.06239
cg1997264	KCNMA1	XBP-1 [T	924	929	1.583727	ATGACC	0.97656	0.98146
cg1997264	KCNMA1	XBP-1 [T	1141	1146	1.583727	TGTCAT	0.97656	0.98146
cg1997264	KCNMA1	XBP-1 [T	1567	1572	1.583727	ATGACC	0.97656	0.98146
cg0272748	KCNMA1	XBP-1 [T	1650	1655	1.583727	TGTCAT	0.97656	0.98146
cg1997264	KCNMA1	TFIID [T0	193	199	1.537547	TTTTGTA	0.73242	0.75096
cg1997264	KCNMA1	TFIID [T0	652	658	1.537547	TTTTGA	0.73242	0.75096
cg1997264	KCNMA1	TFIID [T0	1219	1225	1.537547	TCCAAA	0.73242	0.75096
cg1997264	KCNMA1	TFIID [T0	1493	1499	1.537547	TGGAAA	0.73242	0.75096
cg0272748	KCNMA1	TFIID [T0	410	416	1.537547	TTTTGA	0.73242	0.75096
cg0272748	KCNMA1	TFIID [T0	586	592	1.537547	TACAAA	0.73242	0.75096
cg0272748	KCNMA1	TFIID [T0	1258	1264	1.537547	TTTTGA	0.73242	0.75096
cg0272748	KCNMA1	TFIID [T0	1851	1857	1.537547	TTTTGTA	0.73242	0.75096
cg0272748	KCNMA1	NF-Y [T0	106	113	1.51343	ATTGGT	0.18311	0.18459
cg1997264	KCNMA1	AR [T000	1375	1383	1.513096	GGACAA	0.09155	0.09119
cg0272748	KCNMA1	c-Ets-1 [T	1599	1605	1.513038	GAGGAA	0.36621	0.36952
cg1997264	KCNMA1	POU2F2 (	1553	1563	1.505053	TGATTT	0.00858	0.0089
cg0272748	KCNMA1	PU.1 [T02	1620	1632	1.489595	CCACTT	0.00083	0.00084
cg0272748	KCNMA1	RXR-alph	133	139	1.474336	GGGTTT	0.48828	0.48222
cg1997264	KCNMA1	STAT4 [T	566	571	1.470588	GGAACT	1.95312	1.96333
cg1997264	KCNMA1	STAT4 [T	774	779	1.470588	AATTCC	1.95312	1.96333
cg1997264	KCNMA1	STAT4 [T	1471	1476	1.470588	GGAAAC	1.95312	1.96333
cg1997264	KCNMA1	STAT4 [T	1494	1499	1.470588	GGAAAA	1.95312	1.96333
cg1997264	KCNMA1	STAT4 [T	1735	1740	1.470588	TTTTCC	1.95312	1.96333
cg1997264	KCNMA1	STAT4 [T	1753	1758	1.470588	GGAAAA	1.95312	1.96333
cg0272748	KCNMA1	STAT4 [T	390	395	1.470588	AGTTCC	1.95312	1.96333
cg0272748	KCNMA1	STAT4 [T	896	901	1.470588	GGAAAC	1.95312	1.96333
cg0272748	KCNMA1	STAT4 [T	1342	1347	1.470588	AGTTCC	1.95312	1.96333
cg0272748	KCNMA1	STAT4 [T	1927	1932	1.470588	AATTCC	1.95312	1.96333
cg0272748	KCNMA1	NF-Y [T0	1856	1863	1.447632	TAGCCA	0.18311	0.18459
cg0272748	KCNMA1	GR [T050	1279	1285	1.444018	CAAAAA	0.12207	0.1245
cg0272748	KCNMA1	PR B [T00	1632	1638	1.404665	AACACT	0.36621	0.37023
cg0272748	KCNMA1	PR A [T01	1632	1638	1.404665	AACACT	0.36621	0.37023
cg1997264	KCNMA1	C/EBPbeta	36	39	1.366559	TTGA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	122	125	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	431	434	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	504	507	1.366559	TTGA	15.625	15.72563

cg1997264	KCNMA1	C/EBPbeta	654	657	1.366559	TTGA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	683	686	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	732	735	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1014	1017	1.366559	TTGA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1019	1022	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1147	1150	1.366559	TTGA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1168	1171	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1182	1185	1.366559	TTGA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1348	1351	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1370	1373	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1433	1436	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1822	1825	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1911	1914	1.366559	TTGA	15.625	15.72563
cg1997264	KCNMA1	C/EBPbeta	1923	1926	1.366559	TTGA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	142	145	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	269	272	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	348	351	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	376	379	1.366559	TTGA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	412	415	1.366559	TTGA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	440	443	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	467	470	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	472	475	1.366559	TTGA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	506	509	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	648	651	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	711	714	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	726	729	1.366559	TTGA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	783	786	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1251	1254	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1260	1263	1.366559	TTGA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1278	1281	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1516	1519	1.366559	TTGA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1739	1742	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1753	1756	1.366559	TCAA	15.625	15.72563
cg0272748	KCNMA1	C/EBPbeta	1768	1771	1.366559	TCAA	15.625	15.72563
cg1997264	KCNMA1	AP-2alpha	164	169	1.357116	ACAGGC	0.48828	0.48203
cg1997264	KCNMA1	AP-2alpha	378	383	1.357116	ACAGGC	0.48828	0.48203
cg0272748	KCNMA1	AP-2alpha	776	781	1.357116	GCCTGT	0.48828	0.48203
cg0272748	KCNMA1	HNF-3alpl	668	675	1.342935	TATTTTA	0.03052	0.03194
cg0272748	KCNMA1	HNF-3alpl	672	679	1.342935	TTAAAA	0.03052	0.03194
cg0272748	KCNMA1	HNF-3alpl	863	870	1.342935	TTAAAA	0.03052	0.03194
cg0272748	KCNMA1	HNF-3alpl	1873	1880	1.342935	TTAAAA	0.03052	0.03194
cg1997264	KCNMA1	GATA-2 [	782	790	1.111111	TCCCTA	0.09155	0.09208
cg1997264	KCNMA1	T3R-beta1	252	260	1.110682	TCACCT	0.07629	0.07585
cg1997264	KCNMA1	c-Ets-2 [T	561	569	1.071163	CAAGAG	0.06104	0.06166
cg0272748	KCNMA1	c-Ets-2 [T	1624	1632	1.071163	TTCCTCT	0.06104	0.06166
cg0272748	KCNMA1	HNF-1A [	577	584	1.069403	GTTAAT	0.48828	0.49664
cg1997264	KCNMA1	GATA-1 [	828	833	1.038567	TATCAT	1.95312	1.98662
cg1997264	KCNMA1	GATA-1 [	1923	1928	1.038567	TTGATA	1.95312	1.98662

cg0272748	KCNMA1	GATA-1 [	451	456	1.038567	TATCAT	1.95312	1.98662
cg0272748	KCNMA1	GATA-1 [	781	786	1.038567	TATCAA	1.95312	1.98662
cg1997264	KCNMA1	SRY [T00	1148	1156	0.999172	TGAACA	0.06104	0.06205
cg1997264	KCNMA1	TBP [T00	8	17	0.935771	TTTATAT	0.12207	0.12628
cg1997264	KCNMA1	HNF-1A [	1425	1432	0.925521	CAATTA	0.48828	0.49664
cg0272748	KCNMA1	HNF-1C [	10	18	0.90144	ATTATTA	0.00763	0.00794
cg1997264	KCNMA1	GATA-1 [	460	465	0.863549	TATCAC	1.95312	1.98662
cg1997264	KCNMA1	GATA-1 [	1266	1271	0.863549	GTGATA	1.95312	1.98662
cg0272748	KCNMA1	RXR-alph	1730	1736	0.848226	CTAACC	0.48828	0.48333
cg1997264	KCNMA1	GR-beta [	17	21	0.840383	CCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	189	193	0.840383	TAATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	332	336	0.840383	CCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	389	393	0.840383	AATGA	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	649	653	0.840383	CCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	912	916	0.840383	CAATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1102	1106	0.840383	CCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1143	1147	0.840383	TCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1330	1334	0.840383	TCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1379	1383	0.840383	AATGA	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1425	1429	0.840383	CAATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1426	1430	0.840383	AATTA	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1566	1570	0.840383	AATGA	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1611	1615	0.840383	CCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1787	1791	0.840383	AATTA	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1801	1805	0.840383	AATTG	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1816	1820	0.840383	TCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1908	1912	0.840383	CCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1920	1924	0.840383	CCATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1989	1993	0.840383	TAATT	7.8125	7.94706
cg1997264	KCNMA1	GR-beta [	1990	1994	0.840383	AATTG	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	9	13	0.840383	AATTA	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	40	44	0.840383	CAATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	104	108	0.840383	CCATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	145	149	0.840383	AATGG	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	509	513	0.840383	AATTA	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	580	584	0.840383	AATGG	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	603	607	0.840383	AATGA	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	660	664	0.840383	TAATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	661	665	0.840383	AATTG	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	835	839	0.840383	AATTG	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	847	851	0.840383	TAATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	871	875	0.840383	AATGA	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	1387	1391	0.840383	AATGA	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	1475	1479	0.840383	TCATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	1513	1517	0.840383	CAATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	1514	1518	0.840383	AATTG	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	1530	1534	0.840383	AATGA	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [	1771	1775	0.840383	AATGA	7.8125	7.94706

cg0272748	KCNMA1	GR-beta [T	1817	1821	0.840383	CAATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [T	1848	1852	0.840383	TAATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [T	1917	1921	0.840383	TAATT	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [T	1918	1922	0.840383	AATTA	7.8125	7.94706
cg0272748	KCNMA1	GR-beta [T	1926	1930	0.840383	TAATT	7.8125	7.94706
cg1997264	KCNMA1	PXR-1:RX	1639	1646	0.818075	TGAACT	0.12207	0.12266
cg1997264	KCNMA1	MAZ [T00	855	867	0.783759	GGTGGG	0.0006	0.00059
cg1997264	KCNMA1	GATA-1 [	736	741	0.758539	CTGATA	1.95312	1.98662
cg1997264	KCNMA1	GATA-1 [	790	795	0.758539	TATCAG	1.95312	1.98662
cg1997264	KCNMA1	GATA-1 [	1573	1578	0.758539	CTGATA	1.95312	1.98662
cg1997264	KCNMA1	GATA-1 [	1959	1964	0.758539	CTGATA	1.95312	1.98662
cg0272748	KCNMA1	GATA-1 [	622	627	0.758539	CTGATA	1.95312	1.98662
cg0272748	KCNMA1	GATA-1 [	1483	1488	0.758539	TATCAG	1.95312	1.98662
cg0272748	KCNMA1	AP-2alpha	1300	1305	0.678558	GCCTGA	0.48828	0.48199
cg0272748	KCNMA1	AP-2alpha	1720	1725	0.678558	GCCTGA	0.48828	0.48199
cg0272748	KCNMA1	AP-2alpha	1987	1992	0.678558	TCAGGC	0.48828	0.48199
cg1997264	KCNMA1	AR [T0004	1195	1203	0.649362	GGACAA	0.01526	0.01505
cg1997264	KCNMA1	LEF-1 [T0	1149	1156	0.641865	GAACAA	0.06104	0.06131
cg1997264	KCNMA1	C/EBPalph	931	937	0.540941	CACAAT	0.24414	0.24507
cg1997264	KCNMA1	AP-1 [T00	1015	1023	0.489074	TGACTC	0.09155	0.09215
cg1997264	KCNMA1	PR B [T00	574	580	0.48823	AACAGT	0.12207	0.12407
cg1997264	KCNMA1	PR A [T01	574	580	0.48823	AACAGT	0.12207	0.12407
cg0272748	KCNMA1	PR B [T00	51	57	0.48823	AACAGT	0.12207	0.12407
cg0272748	KCNMA1	PR A [T01	51	57	0.48823	AACAGT	0.12207	0.12407
cg1997264	KCNMA1	AP-1 [T00	1810	1818	0.436196	TATGAG	0.09155	0.09215
cg1997264	KCNMA1	c-Ets-1 [T	890	896	0.384261	CTTCCTA	0.24414	0.24569
cg1997264	KCNMA1	NF-Y [T0	1715	1722	0.378358	TAACCA	0.09155	0.09259
cg1997264	KCNMA1	AP-1 [T00	1003	1011	0.348957	TGACTC	0.09155	0.09215
cg1997264	KCNMA1	GATA-1 [	786	791	0.280028	TATCTA	0.97656	0.99875
cg1997264	KCNMA1	GATA-1 [	1505	1510	0.280028	TAGATA	0.97656	0.99875
cg0272748	KCNMA1	GATA-1 [	1479	1484	0.280028	TATCTA	0.97656	0.99875
cg0272748	KCNMA1	GATA-1 [	1834	1839	0.280028	TATCTA	0.97656	0.99875
cg1997264	KCNMA1	AP-2alpha	64	69	0.226186	GCCTGG	0.97656	0.95305
cg1997264	KCNMA1	AP-2alpha	116	121	0.226186	CCAGGC	0.97656	0.95305
cg1997264	KCNMA1	AP-2alpha	232	237	0.226186	CCAGGC	0.97656	0.95305
cg1997264	KCNMA1	AP-2alpha	508	513	0.226186	GCCTGG	0.97656	0.95305
cg1997264	KCNMA1	AP-2alpha	940	945	0.226186	GCCTGG	0.97656	0.95305
cg0272748	KCNMA1	AP-2alpha	205	210	0.226186	GCCTGG	0.97656	0.95305
cg0272748	KCNMA1	AP-2alpha	1397	1402	0.226186	CCAGGC	0.97656	0.95305
cg1997264	KCNMA1	GR-alpha [	106	110	0.207689	CCTCT	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	404	408	0.207689	AGAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	550	554	0.207689	CCTCT	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	563	567	0.207689	AGAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	877	881	0.207689	CCTCT	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	1021	1025	0.207689	AAAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	1028	1032	0.207689	AGAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	1052	1056	0.207689	AGAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	1077	1081	0.207689	CCTTT	7.8125	7.81264

cg1997264	KCNMA1	GR-alpha [	1365	1369	0.207689	AAAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	1728	1732	0.207689	CCTCT	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	214	218	0.207689	CCTCT	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	320	324	0.207689	CCTTT	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	533	537	0.207689	AGAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	713	717	0.207689	AAAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	1016	1020	0.207689	AAAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	1238	1242	0.207689	CCTCT	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	1379	1383	0.207689	AGAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	1575	1579	0.207689	AGAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	1595	1599	0.207689	AGAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	1626	1630	0.207689	CCTCT	7.8125	7.81264
cg1997264	KCNMA1	HNF-1A [	1927	1934	0.143882	TATTTA	0.24414	0.25261
cg1997264	KCNMA1	c-Ets-1 [T	1740	1746	0.128087	CTTCCTC	0.24414	0.2429
cg0272748	KCNMA1	c-Ets-1 [T	1623	1629	0.128087	CTTCCTC	0.24414	0.2429
cg1997264	KCNMA1	GATA-1 [	1243	1248	0.105011	GAGATA	0.97656	0.98738
cg1997264	KCNMA1	GR-alpha [	164	168	0	ACAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	339	343	0	ATAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	359	363	0	ATAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	378	382	0	ACAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	591	595	0	ATAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	784	788	0	CCTAT	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	985	989	0	ACAGG	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	1529	1533	0	CCTAT	7.8125	7.81264
cg1997264	KCNMA1	GR-alpha [	1979	1983	0	CCTGT	7.8125	7.81264
cg1997264	KCNMA1	AP-2alpha	170	175	0	GCCTGC	0.97656	0.95305
cg1997264	KCNMA1	XBP-1 [T	1814	1819	0	AGTCAT	0.97656	0.98127
cg1997264	KCNMA1	Pax-5 [T0	327	333	0	CATGCC	1.09863	1.06846
cg1997264	KCNMA1	p53 [T006	327	333	0	CATGCC	0.36621	0.35912
cg1997264	KCNMA1	TFII-I [T0	555	560	0	GGAAAG	1.46484	1.45997
cg1997264	KCNMA1	c-Ets-1 [T	1415	1421	0	CAGGAA	0.24414	0.2429
cg1997264	KCNMA1	YY1 [T00	17	20	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	212	215	0	ATGG	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	223	226	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	332	335	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	649	652	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	840	843	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	850	853	0	ATGG	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	1102	1105	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	1611	1614	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	1908	1911	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	1920	1923	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	YY1 [T00	1954	1957	0	CCAT	7.8125	7.81711
cg1997264	KCNMA1	Elk-1 [T00	1740	1748	0	CTTCCTC	0.06104	0.06047
cg1997264	KCNMA1	ER-alpha [	925	929	0	TGACC	1.95312	1.9404
cg1997264	KCNMA1	ER-alpha [	1368	1372	0	GGTCA	1.95312	1.9404
cg1997264	KCNMA1	ER-alpha [	1389	1393	0	TGACC	1.95312	1.9404
cg1997264	KCNMA1	ER-alpha [	1568	1572	0	TGACC	1.95312	1.9404

cg1997264	KCNMA1	GATA-1 [	1109	1114	0	TATCTG	0.97656	0.98738
cg1997264	KCNMA1	GATA-1 [	1711	1716	0	CAGATA	0.97656	0.98738
cg1997264	KCNMA1	C/EBPbeta	102	105	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	195	198	0	TTGT	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	243	246	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	343	346	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	384	387	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	394	397	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	420	423	0	TTGT	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	424	427	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	437	440	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	560	563	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	726	729	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	745	748	0	TTGT	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	932	935	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	979	982	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	992	995	0	TTGC	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1151	1154	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1197	1200	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1230	1233	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1233	1236	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1252	1255	0	TTGC	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1303	1306	0	TTGT	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1377	1380	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1424	1427	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1490	1493	0	TTGT	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1564	1567	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1694	1697	0	TTGC	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1798	1801	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1803	1806	0	TTGT	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1856	1859	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1865	1868	0	TTGC	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1867	1870	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1881	1884	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1933	1936	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1936	1939	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1941	1944	0	ACAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1947	1950	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1974	1977	0	GCAA	15.625	15.71349
cg1997264	KCNMA1	C/EBPbeta	1992	1995	0	TTGT	15.625	15.71349
cg1997264	KCNMA1	c-Jun [T00	1003	1009	0	TGACTC	0.12207	0.12266
cg1997264	KCNMA1	c-Jun [T00	1015	1021	0	TGACTC	0.12207	0.12266
cg1997264	KCNMA1	c-Jun [T00	1812	1818	0	TGAGTC	0.12207	0.12266
cg1997264	KCNMA1	TFIID [T0	33	39	0	TTTTTGA	1.09863	1.13474
cg1997264	KCNMA1	TFIID [T0	200	206	0	TTTTTAA	1.09863	1.13474
cg1997264	KCNMA1	TFIID [T0	597	603	0	TAAAAA	1.09863	1.13474
cg1997264	KCNMA1	TFIID [T0	683	689	0	TCAAAA	1.09863	1.13474
cg1997264	KCNMA1	TFIID [T0	756	762	0	TAGAAA	1.09863	1.13474

cg1997264	KCNMA1	TFIID [T0	1182	1188	0	TTGAAA	1.09863	1.13474
cg1997264	KCNMA1	TFIID [T0	1290	1296	0	TTTTTTA	1.09863	1.13474
cg1997264	KCNMA1	TFIID [T0	1291	1297	0	TTTTTAA	1.09863	1.13474
cg1997264	KCNMA1	TFIID [T0	1967	1973	0	TTTAAA	1.09863	1.13474
cg1997264	KCNMA1	FOXP3 [T	1932	1937	0	AACAAC	1.46484	1.47315
cg1997264	KCNMA1	FOXP3 [T	1940	1945	0	AACAAC	1.46484	1.47315
cg1997264	KCNMA1	GR-beta [T	190	194	0	AATTT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	687	691	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	694	698	0	AATGT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	728	732	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	741	745	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	742	746	0	AATTT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	773	777	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1235	1239	0	AATGT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1287	1291	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1288	1292	0	AATTT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1337	1341	0	AATGT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1385	1389	0	AATGT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1480	1484	0	AATTT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1497	1501	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1720	1724	0	AATGT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1800	1804	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1858	1862	0	AAATT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1859	1863	0	AATTT	3.90625	3.99611
cg1997264	KCNMA1	GR-beta [T	1883	1887	0	AATGT	3.90625	3.99611
cg1997264	KCNMA1	NF-AT1 [T	1493	1502	0	TGGAAA	0.00191	0.00195
cg1997264	KCNMA1	GR [T0507	32	38	0	TTTTTTG	0.36621	0.37562
cg1997264	KCNMA1	GR [T0507	191	197	0	ATTTTTC	0.36621	0.37562
cg1997264	KCNMA1	GR [T0507	684	690	0	CAAAAA	0.36621	0.37562
cg1997264	KCNMA1	HNF-3alph	198	205	0	TATTTTT	0.09155	0.09511
cg1997264	KCNMA1	LEF-1 [T0	1166	1173	0	GATCAA	0.03052	0.03083
cg1997264	KCNMA1	IRF-2 [T01	1307	1312	0	AAGTGA	0.48828	0.49387
cg1997264	KCNMA1	IRF-2 [T01	1316	1321	0	AAGTGA	0.48828	0.49387
cg0272748	KCNMA1	GR-alpha [	192	196	0	ATAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	633	637	0	ATAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	777	781	0	CCTGT	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	936	940	0	ATAGG	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	987	991	0	CCTAT	7.8125	7.81264
cg0272748	KCNMA1	GR-alpha [	1370	1374	0	CCTGT	7.8125	7.81264
cg0272748	KCNMA1	AP-2alpha	253	258	0	GCAGGC	0.97656	0.95305
cg0272748	KCNMA1	AP-2alpha	1699	1704	0	GCAGGC	0.97656	0.95305
cg0272748	KCNMA1	XBP-1 [T0	872	877	0	ATGACT	0.97656	0.98127
cg0272748	KCNMA1	XBP-1 [T0	1842	1847	0	ATGACT	0.97656	0.98127
cg0272748	KCNMA1	TFII-I [T0	1019	1024	0	GGAAAG	1.46484	1.45997
cg0272748	KCNMA1	TFII-I [T0	1092	1097	0	CTTTCC	1.46484	1.45997
cg0272748	KCNMA1	STAT4 [T	1601	1606	0	GGAAAT	0.48828	0.49387
cg0272748	KCNMA1	YY1 [T009	104	107	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T009	146	149	0	ATGG	7.8125	7.81711

cg0272748	KCNMA1	YY1 [T00	394	397	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	396	399	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	574	577	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	581	584	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	749	752	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	795	798	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	802	805	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	894	897	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1096	1099	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1322	1325	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1616	1619	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1654	1657	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1750	1753	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1840	1843	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1931	1934	0	CCAT	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1935	1938	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	YY1 [T00	1943	1946	0	ATGG	7.8125	7.81711
cg0272748	KCNMA1	ER-alpha [	1723	1727	0	TGACC	1.95312	1.9404
cg0272748	KCNMA1	GATA-1 [	619	624	0	TATCTG	0.97656	0.98738
cg0272748	KCNMA1	GATA-1 [	1823	1828	0	TATCTG	0.97656	0.98738
cg0272748	KCNMA1	C/EBPbeta	137	140	0	TTGC	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	201	204	0	GCAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	234	237	0	TTGC	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	246	249	0	GCAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	257	260	0	GCAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	313	316	0	GCAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	323	326	0	TTGC	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	429	432	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	489	492	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	587	590	0	ACAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	663	666	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	700	703	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	704	707	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	770	773	0	TTGC	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	832	835	0	ACAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	837	840	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	880	883	0	ACAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	928	931	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	943	946	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	950	953	0	GCAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1014	1017	0	ACAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1129	1132	0	TTGC	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1191	1194	0	GCAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1416	1419	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1423	1426	0	TTGC	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1431	1434	0	TTGC	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1512	1515	0	GCAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1528	1531	0	ACAA	15.625	15.71349

cg0272748	KCNMA1	C/EBPbeta	1816	1819	0	ACAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1853	1856	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1889	1892	0	ACAA	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1954	1957	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	C/EBPbeta	1971	1974	0	TTGT	15.625	15.71349
cg0272748	KCNMA1	TFIID [T0	56	62	0	TTTTTTA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	57	63	0	TTTTTAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	59	65	0	TTTAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	60	66	0	TTAAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	153	159	0	TATAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	472	478	0	TTGAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	497	503	0	TCTAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	499	505	0	TAAAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	671	677	0	TTTAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	850	856	0	TTTAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	859	865	0	TTTTTTA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	860	866	0	TTTTTAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	862	868	0	TTTAAA	1.09863	1.13474
cg0272748	KCNMA1	TFIID [T0	1278	1284	0	TCAAAA	1.09863	1.13474
cg0272748	KCNMA1	FOXP3 [T	942	947	0	GTTGTG	1.46484	1.47315
cg0272748	KCNMA1	FOXP3 [T	1953	1958	0	GTTGTG	1.46484	1.47315
cg0272748	KCNMA1	GR-beta [T	8	12	0	AAATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	41	45	0	AATTT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	230	234	0	AAATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	231	235	0	AATTT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	248	252	0	AATGT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	508	512	0	AAATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	688	692	0	AATGT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	767	771	0	ACATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	834	838	0	AAATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	848	852	0	AATTT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	954	958	0	AAATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1186	1190	0	AATGT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1254	1258	0	AATGT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1305	1309	0	AATTT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1348	1352	0	AAATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1503	1507	0	ACATT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1818	1822	0	AATTT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1849	1853	0	AATTT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1861	1865	0	AATGT	3.90625	3.99611
cg0272748	KCNMA1	GR-beta [T	1870	1874	0	ACATT	3.90625	3.99611
cg0272748	KCNMA1	PR B [T00	1966	1972	0	CACTGT	0.36621	0.36944
cg0272748	KCNMA1	PR A [T01	1966	1972	0	CACTGT	0.36621	0.36944
cg0272748	KCNMA1	GR [T050	588	594	0	CAAAAA	0.36621	0.37562
cg0272748	KCNMA1	GR [T050	951	957	0	CAAAAA	0.36621	0.37562
cg0272748	KCNMA1	HNF-3alp	61	68	0	TAAAAA	0.09155	0.09511
cg0272748	KCNMA1	HNF-3alp	480	487	0	TAAAAA	0.09155	0.09511
cg0272748	KCNMA1	HNF-3alp	1389	1396	0	TGAAAA	0.09155	0.09511

cg0272748	KCNMA1	HNF-1A [	11	18	0	TTATTA	0.24414	0.25261
cg0272748	KCNMA1	IRF-2 [T01	917	922	0	AAGTGA	0.48828	0.49387
cg0272748	KCNMA1	IRF-2 [T01	1778	1783	0	TCACTT	0.48828	0.49387
cg0272748	KCNMA1	TBP [T00	149	158	0	GAGGTA	0.03052	0.03159
cg0708381	KIAA1683	RAR-beta:	327	338	9.97066	TCCCTA	0.06974	0.06822
cg0708381	KIAA1683	c-Ets-1 [T	1966	1972	9.969337	TGGGAA	0.24414	0.2459
cg0708381	KIAA1683	COUP-TF	708	720	9.965635	CCAAAG	0.02503	0.0249
cg0708381	KIAA1683	LEF-1 [T0	104	111	9.937995	TGCCAA	0.12207	0.12154
cg0708381	KIAA1683	LEF-1 [T0	1208	1215	9.937995	AGCCAA	0.12207	0.12154
cg0708381	KIAA1683	STAT1bet	61	70	9.807397	ATTTCC	0.14877	0.1495
cg0708381	KIAA1683	XBP-1 [T	79	84	9.789909	AGACAT	1.95312	1.95208
cg0708381	KIAA1683	XBP-1 [T	225	230	9.789909	ATGTCT	1.95312	1.95208
cg0708381	KIAA1683	XBP-1 [T	259	264	9.789909	AGACAT	1.95312	1.95208
cg0708381	KIAA1683	XBP-1 [T	872	877	9.789909	ATGTCT	1.95312	1.95208
cg0708381	KIAA1683	XBP-1 [T	915	920	9.789909	ATGGCT	1.95312	1.95208
cg0708381	KIAA1683	XBP-1 [T	974	979	9.789909	ATGTCT	1.95312	1.95208
cg0708381	KIAA1683	RBP-Jkap	1962	1973	9.774182	ATATTG	0.02193	0.02195
cg0708381	KIAA1683	NF-1 [T00	581	588	9.761671	TTGGAG	0.24414	0.24405
cg0708381	KIAA1683	PR B [T00	1756	1762	9.743489	AACACA	1.09863	1.10292
cg0708381	KIAA1683	PR A [T01	1756	1762	9.743489	AACACA	1.09863	1.10292
cg0708381	KIAA1683	LEF-1 [T0	1405	1412	9.72404	CTTTGT	0.21362	0.2139
cg0708381	KIAA1683	GATA-3 [	63	74	9.652214	TTCCCT	0.01597	0.01612
cg0708381	KIAA1683	Pax-5 [T0	131	137	9.552105	GGGCGC	1.46484	1.43083
cg0708381	KIAA1683	Pax-5 [T0	218	224	9.552105	GGGCAA	1.46484	1.43083
cg0708381	KIAA1683	Pax-5 [T0	349	355	9.552105	GGGCCA	1.46484	1.43083
cg0708381	KIAA1683	Pax-5 [T0	705	711	9.552105	GGGCCA	1.46484	1.43083
cg0708381	KIAA1683	Pax-5 [T0	864	870	9.552105	TTTGCC	1.46484	1.43083
cg0708381	KIAA1683	Pax-5 [T0	1164	1170	9.552105	GGGCCA	1.46484	1.43083
cg0708381	KIAA1683	Pax-5 [T0	1438	1444	9.552105	GTTGCC	1.46484	1.43083
cg0708381	KIAA1683	Pax-5 [T0	1557	1563	9.552105	GACGCC	1.46484	1.43083
cg0708381	KIAA1683	TFIID [T0	1659	1665	9.552105	TCCCAA	1.46484	1.48472
cg0708381	KIAA1683	NF-1 [T00	1355	1362	9.535536	TTGGAC	0.73242	0.73053
cg0708381	KIAA1683	NF-1 [T00	1008	1015	9.513281	TTGGGG	0.73242	0.73053
cg0708381	KIAA1683	TFII-I [T0	4	9	9.512894	GGACAC	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	92	97	9.512894	CCATCC	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	184	189	9.512894	GGATCG	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	302	307	9.512894	AAATCC	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	459	464	9.512894	AAGTCC	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	860	865	9.512894	GGAATT	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	880	885	9.512894	GGATAC	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	926	931	9.512894	GGAAGG	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	1021	1026	9.512894	GGACTT	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	1273	1278	9.512894	GGACAA	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	1330	1335	9.512894	CCTTCC	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	1357	1362	9.512894	GGACAA	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	1593	1598	9.512894	GGATTT	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	1952	1957	9.512894	GGAAGG	7.32422	7.29728
cg0708381	KIAA1683	TFII-I [T0	1968	1973	9.512894	GGAATT	7.32422	7.29728

cg0708381	KIAA1683	FOXP3 [T	41	46	9.512894	GTAAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	102	107	9.512894	GTTGCC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	219	224	9.512894	GGCAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	262	267	9.512894	CATAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	424	429	9.512894	GAGAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	553	558	9.512894	CTAAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	623	628	9.512894	GTTCTG	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	682	687	9.512894	GTTGGG	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	723	728	9.512894	GTTGCT	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	759	764	9.512894	GTTCTC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	964	969	9.512894	GTTCTC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1266	1271	9.512894	GTTGCC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1277	1282	9.512894	AAGAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1386	1391	9.512894	GTTGGG	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1396	1401	9.512894	GTTTAT	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1438	1443	9.512894	GTTGCC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1605	1610	9.512894	GTTGGC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1722	1727	9.512894	CAGAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1753	1758	9.512894	CTAAAC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1770	1775	9.512894	GTTCTC	7.32422	7.35678
cg0708381	KIAA1683	FOXP3 [T	1913	1918	9.512894	CAGAAC	7.32422	7.35678
cg0708381	KIAA1683	c-Jun [T00	1630	1636	9.511322	TGACCA	0.73242	0.73031
cg0708381	KIAA1683	Ik-1 [T027	1527	1539	9.497194	TGAGTA	0.02941	0.02907
cg0708381	KIAA1683	TCF-4E [T	612	618	9.453578	CTCAAA	0.48828	0.49215
cg0708381	KIAA1683	TCF-4E [T	751	757	9.453578	TACAAA	0.48828	0.49215
cg0708381	KIAA1683	TCF-4E [T	892	898	9.453578	CTCAAA	0.48828	0.49215
cg0708381	KIAA1683	TCF-4E [T	1353	1359	9.453578	CTTTGG	0.48828	0.49215
cg0708381	KIAA1683	TCF-4E [T	1707	1713	9.453578	CTTTGG	0.48828	0.49215
cg0708381	KIAA1683	c-Jun [T00	1741	1747	9.442241	GCTGTC	0.73242	0.73031
cg0708381	KIAA1683	PPAR-alpl	386	396	9.39865	AAGGCC	0.00286	0.0028
cg0708381	KIAA1683	NFI/CTF [	518	525	9.352332	CCAAAG	0.54932	0.54821
cg0708381	KIAA1683	NFI/CTF [	1167	1174	9.352332	CCAAGG	0.54932	0.54821
cg0708381	KIAA1683	NFI/CTF [	1210	1217	9.352332	CCAAAG	0.54932	0.54821
cg0708381	KIAA1683	NFI/CTF [	1351	1358	9.352332	GACTTT	0.54932	0.54821
cg0708381	KIAA1683	PEA3 [T0	820	828	9.340643	TTTCAT	0.03052	0.03072
cg0708381	KIAA1683	LEF-1 [T0	163	170	9.313676	CTTTGG	0.21362	0.2139
cg0708381	KIAA1683	LEF-1 [T0	516	523	9.313676	CCCCAA	0.21362	0.2139
cg0708381	KIAA1683	c-Ets-1 [T	772	778	9.148774	AGGGAA	0.85449	0.85523
cg0708381	KIAA1683	PXR-1:RX	568	575	9.122407	TGAACG	0.24414	0.2439
cg0708381	KIAA1683	USF2 [T0	1543	1552	9.056375	CAGGTG	0.1545	0.15287
cg0708381	KIAA1683	NFI/CTF [	1383	1390	9.042931	GCAGTT	0.48828	0.48804
cg0708381	KIAA1683	c-Ets-1 [T	685	691	9.020687	GGGGAA	0.85449	0.85523
cg0708381	KIAA1683	LEF-1 [T0	1659	1666	8.973041	TCCCAA	0.54932	0.55326
cg0708381	KIAA1683	LEF-1 [T0	1707	1714	8.973041	CTTTGG	0.54932	0.55326
cg0708381	KIAA1683	GR [T050	519	525	8.971049	CAAAGC	0.61035	0.61632
cg0708381	KIAA1683	GR [T050	614	620	8.971049	CAAAGC	0.61035	0.61632
cg0708381	KIAA1683	GR [T050	1211	1217	8.971049	CAAAGC	0.61035	0.61632
cg0708381	KIAA1683	GR [T050	1360	1366	8.971049	CAAAAT	0.61035	0.61632

cg0708381	KIAA168	Elk-1 [T00	1893	1901	8.931691	TGGGGG	0.24414	0.24034
cg0708381	KIAA168	c-Ets-2 [T	1947	1955	8.912323	GGCCAG	0.27466	0.27495
cg0708381	KIAA168	T3R-beta1	378	386	8.904753	TCACCC	0.2594	0.25766
cg0708381	KIAA168	c-Jun [T00	711	717	8.832178	AAGGTC	0.61035	0.61059
cg0708381	KIAA168	PR B [T00	1725	1731	8.827054	AACAGG	0.36621	0.36944
cg0708381	KIAA168	PR A [T01	1725	1731	8.827054	AACAGG	0.36621	0.36944
cg0708381	KIAA168	NFI/CTF [	1029	1036	8.814757	TCTCTT	0.48828	0.48804
cg0708381	KIAA168	c-Ets-1 [T	858	864	8.809329	CTGGAA	0.85449	0.85523
cg0708381	KIAA168	NF-1 [T00	1657	1664	8.790071	CCTCCC	0.24414	0.24467
cg0708381	KIAA168	LEF-1 [T0	604	611	8.759086	CTTTGT	0.54932	0.55326
cg0708381	KIAA168	XBP-1 [T	739	744	8.75604	GCTCAT	2.92969	2.9674
cg0708381	KIAA168	XBP-1 [T	820	825	8.75604	TTTCAT	2.92969	2.9674
cg0708381	KIAA168	XBP-1 [T	1683	1688	8.75604	ATGAGC	2.92969	2.9674
cg0708381	KIAA168	XBP-1 [T	1700	1705	8.75604	GCTCAT	2.92969	2.9674
cg0708381	KIAA168	XBP-1 [T	1716	1721	8.75604	TTTCAT	2.92969	2.9674
cg0708381	KIAA168	LEF-1 [T0	706	713	8.575454	GGCCAA	0.15259	0.15214
cg0708381	KIAA168	c-Jun [T00	955	961	8.571705	CCAGTC	0.12207	0.12139
cg0708381	KIAA168	c-Jun [T00	1889	1895	8.571705	TGACTG	0.12207	0.12139
cg0708381	KIAA168	RAR-beta	772	781	8.55975	AGGGAA	0.26703	0.26657
cg0708381	KIAA168	p53 [T006	332	338	8.537081	AGAGCC	0.12207	0.11986
cg0708381	KIAA168	p53 [T006	397	403	8.537081	GGGCTC	0.12207	0.11986
cg0708381	KIAA168	PR B [T00	118	124	8.338824	AACAGG	1.09863	1.10009
cg0708381	KIAA168	PR B [T00	210	216	8.338824	AACAGC	1.09863	1.10009
cg0708381	KIAA168	PR B [T00	265	271	8.338824	AACAGG	1.09863	1.10009
cg0708381	KIAA168	PR B [T00	689	695	8.338824	AACAGG	1.09863	1.10009
cg0708381	KIAA168	PR B [T00	1409	1415	8.338824	GTCTGT	1.09863	1.10009
cg0708381	KIAA168	PR B [T00	1434	1440	8.338824	CTCTGT	1.09863	1.10009
cg0708381	KIAA168	PR A [T01	118	124	8.338824	AACAGG	1.09863	1.10009
cg0708381	KIAA168	PR A [T01	210	216	8.338824	AACAGC	1.09863	1.10009
cg0708381	KIAA168	PR A [T01	265	271	8.338824	AACAGG	1.09863	1.10009
cg0708381	KIAA168	PR A [T01	689	695	8.338824	AACAGG	1.09863	1.10009
cg0708381	KIAA168	PR A [T01	1409	1415	8.338824	GTCTGT	1.09863	1.10009
cg0708381	KIAA168	PR A [T01	1434	1440	8.338824	CTCTGT	1.09863	1.10009
cg0708381	KIAA168	E2F-1 [T0	479	486	8.336446	TCACCC	0.15259	0.14963
cg0708381	KIAA168	E2F-1 [T0	508	515	8.336446	TCACCC	0.15259	0.14963
cg0708381	KIAA168	GR-alpha [	174	178	8.281568	CAAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	181	185	8.281568	GGAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	313	317	8.281568	CAAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	353	357	8.281568	CAAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	385	389	8.281568	GAAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	394	398	8.281568	GAAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	449	453	8.281568	CCTCG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	463	467	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	666	670	8.281568	GAAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	791	795	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	927	931	8.281568	GAAGG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	1006	1010	8.281568	CCTTG	7.8125	7.72956
cg0708381	KIAA168	GR-alpha [	1120	1124	8.281568	CCTCC	7.8125	7.72956

cg0708381	KIAA1683	GR-alpha [	1168	1172	8.281568	CAAGG	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1183	1187	8.281568	CCTTG	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1247	1251	8.281568	CCTTG	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1299	1303	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1321	1325	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1330	1334	8.281568	CCTTC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1483	1487	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1489	1493	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1522	1526	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1657	1661	8.281568	CCTCC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1733	1737	8.281568	CCTTC	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1846	1850	8.281568	CGAGG	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1869	1873	8.281568	GGAGG	7.8125	7.72956
cg0708381	KIAA1683	GR-alpha [	1953	1957	8.281568	GAAGG	7.8125	7.72956
cg0708381	KIAA1683	c-Jun [T00	1296	1302	8.242207	TGACCTC	0.48828	0.49076
cg0708381	KIAA1683	p53 [T006	1137	1143	8.208781	GGGGCC	0.48828	0.47377
cg0708381	KIAA1683	ENKTF-1	1159	1166	8.19852	TGGCTGC	0.73242	0.71737
cg0708381	KIAA1683	ENKTF-1	1607	1614	8.19852	TGGCCAC	0.73242	0.71737
cg0708381	KIAA1683	SRY [T00	1405	1413	8.174786	CTTTGTC	0.15259	0.15383
cg0708381	KIAA1683	EBF [T05	1939	1949	8.152312	GACCCTC	0.04196	0.04106
cg0708381	KIAA1683	LEF-1 [T0	611	618	8.117221	ACTCAA	0.12207	0.1241
cg0708381	KIAA1683	LEF-1 [T0	891	898	8.117221	ACTCAA	0.12207	0.1241
cg0708381	KIAA1683	GR-alpha [	1	5	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	144	148	8.073878	CCTGC	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	215	219	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	329	333	8.073878	CCTAG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	338	342	8.073878	CCTGC	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	540	544	8.073878	CCTGC	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	558	562	8.073878	CCTAG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	588	592	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	636	640	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	697	701	8.073878	GCAGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	702	706	8.073878	GCAGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	730	734	8.073878	CCTAC	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	801	805	8.073878	CCTAG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	847	851	8.073878	CCTAC	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1111	1115	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1123	1127	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1220	1224	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1239	1243	8.073878	CCTGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1285	1289	8.073878	GCAGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1443	1447	8.073878	CCAGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1610	1614	8.073878	CCAGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1647	1651	8.073878	CCTGC	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1792	1796	8.073878	GTAGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1815	1819	8.073878	CCTAG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1831	1835	8.073878	CTAGG	7.8125	7.72238
cg0708381	KIAA1683	GR-alpha [	1949	1953	8.073878	CCAGG	7.8125	7.72238

cg0708381	KIAA1683	GR-alpha [	1957	1961	8.073878	GCAGG	7.8125	7.72238
cg0708381	KIAA1683	Pax-5 [T0	192	198	8.014558	GCAGCC	2.19727	2.14502
cg0708381	KIAA1683	Pax-5 [T0	583	589	8.014558	GGAGCC	2.19727	2.14502
cg0708381	KIAA1683	Pax-5 [T0	1001	1007	8.014558	GGGCTC	2.19727	2.14502
cg0708381	KIAA1683	Pax-5 [T0	1046	1052	8.014558	TGGGCC	2.19727	2.14502
cg0708381	KIAA1683	Pax-5 [T0	1137	1143	8.014558	GGGGCC	2.19727	2.14502
cg0708381	KIAA1683	Pax-5 [T0	1138	1144	8.014558	GGGCCC	2.19727	2.14502
cg0708381	KIAA1683	Pax-5 [T0	1795	1801	8.014558	GGAGCC	2.19727	2.14502
cg0708381	KIAA1683	TFIID [T0	204	210	8.014558	TTTGAA	2.19727	2.24348
cg0708381	KIAA1683	TFIID [T0	451	457	8.014558	TCGCAA	2.19727	2.24348
cg0708381	KIAA1683	TFIID [T0	605	611	8.014558	TTTGTG	2.19727	2.24348
cg0708381	KIAA1683	TFIID [T0	837	843	8.014558	TTTCTG	2.19727	2.24348
cg0708381	KIAA1683	TFIID [T0	1417	1423	8.014558	TTTGAG	2.19727	2.24348
cg0708381	KIAA1683	TFIID [T0	1619	1625	8.014558	TCTCAA	2.19727	2.24348
cg0708381	KIAA1683	c-Myb [T0	1766	1773	8.005241	GGGAGT	0.21362	0.21454
cg0708381	KIAA1683	ETF [T002	408	418	7.870358	GCACTG	0.07153	0.06862
cg0708381	KIAA1683	NF-kappa	1251	1261	7.856943	GGGGAG	0.0329	0.03218
cg0708381	KIAA1683	AR [T000	277	285	7.840422	ATGATG	0.19836	0.19634
cg0708381	KIAA1683	p53 [T006	583	589	7.833758	GGAGCC	0.48828	0.47377
cg0708381	KIAA1683	p53 [T006	1001	1007	7.833758	GGGCTC	0.48828	0.47377
cg0708381	KIAA1683	p53 [T006	1795	1801	7.833758	GGAGCC	0.48828	0.47377
cg0708381	KIAA1683	c-Myb [T0	619	626	7.825375	CCAAGT	0.21362	0.21454
cg0708381	KIAA1683	T3R-beta1	479	487	7.813363	TCACCC	0.27466	0.27236
cg0708381	KIAA1683	T3R-beta1	508	516	7.813363	TCACCC	0.27466	0.27236
cg0708381	KIAA1683	Egr-3 [T0	1339	1351	7.69229	TACTGT	0.01192	0.0119
cg0708381	KIAA1683	p53 [T006	386	392	7.641867	AAGGCC	0.73242	0.7186
cg0708381	KIAA1683	AR [T000	1357	1365	7.623968	GGACAA	0.25177	0.25079
cg0708381	KIAA1683	LEF-1 [T0	1353	1360	7.6105	CTTTGG	0.21362	0.21302
cg0708381	KIAA1683	NFI/CTF [	197	204	7.587343	CCAAGA	0.36621	0.36674
cg0708381	KIAA1683	NFI/CTF [	1779	1786	7.587343	GCAATT	0.36621	0.36674
cg0708381	KIAA1683	GR [T050	33	39	7.527031	AATTTT	1.83105	1.86007
cg0708381	KIAA1683	GR [T050	454	460	7.527031	CAAACA	1.83105	1.86007
cg0708381	KIAA1683	GR [T050	602	608	7.527031	AGCTTT	1.83105	1.86007
cg0708381	KIAA1683	GR [T050	885	891	7.527031	CAAACA	1.83105	1.86007
cg0708381	KIAA1683	GR [T050	1055	1061	7.527031	CAAAAG	1.83105	1.86007
cg0708381	KIAA1683	RAR-beta	756	765	7.47824	AGGGTT	0.24414	0.24343
cg0708381	KIAA1683	RAR-beta	961	970	7.47824	AGGGTT	0.24414	0.24343
cg0708381	KIAA1683	AR [T000	1273	1281	7.467081	GGACAA	0.25177	0.25079
cg0708381	KIAA1683	AR [T000	1835	1843	7.429939	GGACAG	0.25177	0.25079
cg0708381	KIAA1683	PEA3 [T0	90	98	7.421728	CACCAT	0.34332	0.34161
cg0708381	KIAA1683	AR [T000	1104	1112	7.406474	CTGCTG	0.25177	0.25079
cg0708381	KIAA1683	LEF-1 [T0	750	757	7.396545	GTACAA	0.21362	0.21302
cg0708381	KIAA1683	LEF-1 [T0	1932	1939	7.396545	GTGCAA	0.21362	0.21302
cg0708381	KIAA1683	C/EBPalph	1781	1787	7.396431	AATTGG	0.48828	0.49653
cg0708381	KIAA1683	PPAR-alph	1122	1132	7.370536	TCCTGG	0.04482	0.04393
cg0708381	KIAA1683	GCF [T00	133	141	7.186486	GCGCAG	0.45776	0.44706
cg0708381	KIAA1683	XBP-1 [T	277	282	7.172312	ATGATG	2.92969	2.97018
cg0708381	KIAA1683	XBP-1 [T	366	371	7.172312	CATCAT	2.92969	2.97018

cg0708381	KIAA1683	XBP-1 [T0	1147	1152	7.172312	ATGAGT	2.92969	2.97018
cg0708381	KIAA1683	p53 [T006	1046	1052	7.153797	TGGGCC	1.09863	1.07125
cg0708381	KIAA1683	p53 [T006	1138	1144	7.153797	GGGCCC	1.09863	1.07125
cg0708381	KIAA1683	c-Jun [T00	374	380	7.096776	GCAGTC	0.73242	0.73173
cg0708381	KIAA1683	c-Ets-1 [T0	62	68	7.071349	TTTCCCT	0.73242	0.73099
cg0708381	KIAA1683	NFI/CTF [	679	686	7.014249	GAGGTT	0.73242	0.73214
cg0708381	KIAA1683	HNF-3alph	232	239	7.000129	TATTTAT	0.82397	0.84946
cg0708381	KIAA1683	ENKTF-1	24	31	6.942764	TGGCTC	1.46484	1.44228
cg0708381	KIAA1683	ENKTF-1	671	678	6.942764	CACAGC	1.46484	1.44228
cg0708381	KIAA1683	E2F-1 [T0	591	598	6.839754	GGTGCC	0.30518	0.29782
cg0708381	KIAA1683	PEA3 [T0	692	700	6.824411	AGGATG	0.22888	0.22933
cg0708381	KIAA1683	c-Jun [T00	70	76	6.787369	TCTGTCA	0.73242	0.73173
cg0708381	KIAA1683	EBF [T05	1771	1781	6.76967	TTCTCAC	0.03052	0.02964
cg0708381	KIAA1683	TCF-4 [T0	890	899	6.735684	AACTCA	0.04959	0.05016
cg0708381	KIAA1683	NF-1 [T00	626	633	6.722386	CTGGCC	0.24414	0.24147
cg0708381	KIAA1683	NF-1 [T00	1606	1613	6.722386	TTGGCC	0.24414	0.24147
cg0708381	KIAA1683	T3R-beta1	1315	1323	6.702681	TCACCC	0.21362	0.21147
cg0708381	KIAA1683	T3R-beta1	1598	1606	6.702681	TCACCAT	0.21362	0.21147
cg0708381	KIAA1683	TFII-I [T0	784	789	6.581441	ATCTCC	0.97656	0.97366
cg0708381	KIAA1683	TFII-I [T0	1450	1455	6.581441	GGAGTG	0.97656	0.97366
cg0708381	KIAA1683	FOXP3 [T	1578	1583	6.581441	GTTTTA	0.97656	0.99397
cg0708381	KIAA1683	p53 [T006	192	198	6.563521	GCAGCC	0.48828	0.47541
cg0708381	KIAA1683	PXR-1:RX	297	304	6.5446	TGAACA	0.24414	0.24672
cg0708381	KIAA1683	PPAR-alph	1532	1542	6.51544	AGCTGG	0.03719	0.03639
cg0708381	KIAA1683	XBP-1 [T0	831	836	6.478682	GGGCAT	0.97656	0.97062
cg0708381	KIAA1683	c-Jun [T00	1174	1180	6.475265	TGACAC	0.61035	0.60769
cg0708381	KIAA1683	RAR-beta	1393	1402	6.452127	GGGGTT	0.18311	0.183
cg0708381	KIAA1683	c-Myb [T0	1761	1768	6.422836	AAACTG	0.30518	0.3056
cg0708381	KIAA1683	p53 [T006	131	137	6.403751	GGGCGC	0.48828	0.47541
cg0708381	KIAA1683	PPAR-alph	1043	1053	6.299891	CACTGG	0.03719	0.03639
cg0708381	KIAA1683	c-Jun [T00	1068	1074	6.293948	TGACCCT	0.61035	0.60769
cg0708381	KIAA1683	GR-alpha [	56	60	6.263098	CCTCA	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	96	100	6.263098	CCTCA	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	345	349	6.263098	TGAGG	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	903	907	6.263098	TGAGG	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	1089	1093	6.263098	TAAGG	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	1516	1520	6.263098	CCTCA	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	1804	1808	6.263098	TAAGG	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	1822	1826	6.263098	TGAGG	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	1861	1865	6.263098	TGAGG	3.90625	3.91061
cg0708381	KIAA1683	GR-alpha [	1944	1948	6.263098	TGAGG	3.90625	3.91061
cg0708381	KIAA1683	c-Fos [T00	1149	1158	6.236188	GAGTCA	0.09155	0.09126
cg0708381	KIAA1683	p53 [T006	1557	1563	6.188498	GACGCC	0.61035	0.594
cg0708381	KIAA1683	SRY [T00	604	612	6.176442	CTTTGTC	0.15259	0.15366
cg0708381	KIAA1683	p53 [T006	349	355	6.095267	GGGCCA	0.61035	0.594
cg0708381	KIAA1683	p53 [T006	705	711	6.095267	GGGCCA	0.61035	0.594
cg0708381	KIAA1683	p53 [T006	1164	1170	6.095267	GGGCCA	0.61035	0.594
cg0708381	KIAA1683	GR-alpha [	98	102	6.055408	TCAGG	3.90625	3.9065

cg0708381	KIAA168	GR-alpha [	488	492	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	546	550	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	647	651	6.055408	TTAGG	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	745	749	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	959	963	6.055408	TCAGG	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1072	1076	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1099	1103	6.055408	TCAGG	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1294	1298	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1365	1369	6.055408	TCAGG	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1525	1529	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1628	1632	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1774	1778	6.055408	TCAGG	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1820	1824	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1942	1946	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	GR-alpha [	1988	1992	6.055408	CCTGA	3.90625	3.9065
cg0708381	KIAA168	RXR-alph	377	383	5.937582	GTCACC	0.73242	0.72249
cg0708381	KIAA168	RXR-alph	1062	1068	5.937582	GGGTAC	0.73242	0.72249
cg0708381	KIAA168	RXR-alph	1289	1295	5.937582	GGGTGC	0.73242	0.72249
cg0708381	KIAA168	GCF [T00	1078	1086	5.917256	CCGCAG	0.64087	0.6219
cg0708381	KIAA168	HOXD9 [	246	255	5.898575	AATAAT	0.05722	0.0598
cg0708381	KIAA168	HOXD10 [	246	255	5.898575	AATAAT	0.05722	0.0598
cg0708381	KIAA168	STAT4 [T	926	931	5.882353	GGAAGG	0.48828	0.48408
cg0708381	KIAA168	STAT4 [T	1330	1335	5.882353	CCTTCC	0.48828	0.48408
cg0708381	KIAA168	STAT4 [T	1952	1957	5.882353	GGAAGG	0.48828	0.48408
cg0708381	KIAA168	C/EBPalp	1778	1784	5.850545	GGCAAT	0.97656	0.99
cg0708381	KIAA168	c-Ets-1 [T	924	930	5.814485	TGGGAA	0.36621	0.36731
cg0708381	KIAA168	AR [T000	1369	1377	5.813745	GGACAT	0.24414	0.24229
cg0708381	KIAA168	c-Jun [T00	1350	1356	5.783074	TGACTT	0.36621	0.37082
cg0708381	KIAA168	VDR [T00	564	572	5.771401	AGTCTG	0.42725	0.42999
cg0708381	KIAA168	AR [T000	4	12	5.754178	GGACAC	0.24414	0.24229
cg0708381	KIAA168	PPAR-alp	1160	1170	5.741676	GGCTGG	0.03529	0.03451
cg0708381	KIAA168	PPAR-alp	1221	1231	5.741676	CTGGCC	0.03529	0.03451
cg0708381	KIAA168	ENKTF-1	519	526	5.687009	CAAAGC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	614	621	5.687009	CAAAGC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	703	710	5.687009	CAGGGC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	986	993	5.687009	TGGCTC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	1162	1169	5.687009	CTGGGC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	1211	1218	5.687009	CAAAGC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	1222	1229	5.687009	TGGCCC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	1812	1819	5.687009	TGGCCT	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	1874	1881	5.687009	TGGCGC	0.73242	0.7249
cg0708381	KIAA168	ENKTF-1	1908	1915	5.687009	TGGCAC	0.73242	0.7249
cg0708381	KIAA168	c-Ets-1 [T	1331	1337	5.686398	CTTCCC	0.36621	0.3623
cg0708381	KIAA168	NF-1 [T00	169	176	5.626299	GGGACC	0.24414	0.24258
cg0708381	KIAA168	NF-1 [T00	930	937	5.626299	GGGACC	0.24414	0.24258
cg0708381	KIAA168	NFI/CTF [	156	163	5.558661	CCAAGC	0.54932	0.55038
cg0708381	KIAA168	NFI/CTF [	630	637	5.558661	CCAATC	0.54932	0.55038
cg0708381	KIAA168	c-Ets-1 [T	1092	1098	5.558311	GGGGAA	0.36621	0.3623

cg0708381	KIAA1683	c-Ets-1 [T	1895	1901	5.558311	GGGGAA	0.36621	0.3623
cg0708381	KIAA1683	T3R-beta1	1152	1160	5.553412	TCACCG	0.21362	0.21287
cg0708381	KIAA1683	Pax-5 [T0	1777	1783	5.544826	GGGCAA	0.73242	0.72046
cg0708381	KIAA1683	TFIID [T0	1580	1586	5.544826	TTTAGT	0.73242	0.75085
cg0708381	KIAA1683	p53 [T006	1047	1053	5.39549	GGGCCC	0.61035	0.59991
cg0708381	KIAA1683	NF-1 [T00	193	200	5.377909	CAGCCC	0.24414	0.24258
cg0708381	KIAA1683	TCF-4 [T0	610	619	5.337909	GACTCA	0.04959	0.04964
cg0708381	KIAA1683	RXR-alph	652	658	5.271235	GGGTGG	0.61035	0.6044
cg0708381	KIAA1683	RXR-alph	1011	1017	5.271235	GGGTGG	0.61035	0.6044
cg0708381	KIAA1683	RXR-alph	1264	1270	5.271235	GGGTTG	0.61035	0.6044
cg0708381	KIAA1683	RXR-alph	1389	1395	5.271235	GGGTGG	0.61035	0.6044
cg0708381	KIAA1683	GR [T050	1325	1331	5.207533	CAAAAC	0.24414	0.24606
cg0708381	KIAA1683	GR [T050	1935	1941	5.207533	CAAAGA	0.24414	0.24606
cg0708381	KIAA1683	c-Jun [T00	1095	1101	5.193102	GAAGTC	0.61035	0.61057
cg0708381	KIAA1683	c-Ets-2 [T	1245	1253	5.162974	TTCCTT	0.13733	0.13828
cg0708381	KIAA1683	AP-2alpha	404	409	5.100982	AAAGGC	0.97656	0.97567
cg0708381	KIAA1683	RXR-alph	1314	1320	5.089356	ATCACC	0.48828	0.484
cg0708381	KIAA1683	USF2 [T0	534	543	5.052423	CACTCA	0.103	0.10178
cg0708381	KIAA1683	GR-beta [	153	157	5.042296	AATCC	3.90625	3.95351
cg0708381	KIAA1683	GR-beta [	303	307	5.042296	AATCC	3.90625	3.95351
cg0708381	KIAA1683	GR-beta [	632	636	5.042296	AATCC	3.90625	3.95351
cg0708381	KIAA1683	GR-beta [	658	662	5.042296	GGATT	3.90625	3.95351
cg0708381	KIAA1683	GR-beta [	1593	1597	5.042296	GGATT	3.90625	3.95351
cg0708381	KIAA1683	GR-beta [	1672	1676	5.042296	GGATT	3.90625	3.95351
cg0708381	KIAA1683	NFI/CTF [	1705	1712	5.021086	TCCTTT	0.24414	0.24103
cg0708381	KIAA1683	c-Jun [T00	1556	1562	5.000337	TGACGC	0.61035	0.61057
cg0708381	KIAA1683	XBP-1 [T	1679	1684	4.894955	AGGCAT	0.97656	0.96979
cg0708381	KIAA1683	HNF-3alp	236	243	4.842999	TATTTA	0.09155	0.09582
cg0708381	KIAA1683	TFII-I [T0	61	66	4.756447	ATTTCC	2.92969	2.93695
cg0708381	KIAA1683	TFII-I [T0	280	285	4.756447	ATGTCC	2.92969	2.93695
cg0708381	KIAA1683	TFII-I [T0	631	636	4.756447	CAATCC	2.92969	2.93695
cg0708381	KIAA1683	TFII-I [T0	1369	1374	4.756447	GGACAT	2.92969	2.93695
cg0708381	KIAA1683	TFII-I [T0	1400	1405	4.756447	ATATCC	2.92969	2.93695
cg0708381	KIAA1683	TFII-I [T0	1849	1854	4.756447	GGACTG	2.92969	2.93695
cg0708381	KIAA1683	TFII-I [T0	1960	1965	4.756447	GGATAT	2.92969	2.93695
cg0708381	KIAA1683	FOXP3 [T	207	212	4.756447	GAAAAC	2.92969	2.96063
cg0708381	KIAA1683	FOXP3 [T	1325	1330	4.756447	CAAAAC	2.92969	2.96063
cg0708381	KIAA1683	FOXP3 [T	1413	1418	4.756447	GTTTTT	2.92969	2.96063
cg0708381	KIAA1683	FOXP3 [T	1744	1749	4.756447	GTCAAC	2.92969	2.96063
cg0708381	KIAA1683	C/EBPalp	629	635	4.560723	GCCAAT	0.24414	0.24411
cg0708381	KIAA1683	USF2 [T0	293	302	4.528187	CAGGTG	0.06866	0.06782
cg0708381	KIAA1683	T3R-beta1	89	97	4.481316	TCACCA	0.27466	0.27551
cg0708381	KIAA1683	AP-2alpha	1814	1819	4.438035	GCCTAG	0.97656	0.96979
cg0708381	KIAA1683	RXR-alph	1975	1981	4.423008	GGGTGG	0.24414	0.24292
cg0708381	KIAA1683	STAT4 [T	1243	1248	4.411765	GCTTCC	1.95312	1.94235
cg0708381	KIAA1683	STAT4 [T	1841	1846	4.411765	GCTTCC	1.95312	1.94235
cg0708381	KIAA1683	STAT4 [T	1897	1902	4.411765	GGAAGA	1.95312	1.94235
cg0708381	KIAA1683	p53 [T006	415	421	4.33696	GGGCCA	0.24414	0.23584

cg0708381	KIAA168	p53 [T006	952	958	4.33696	GGGCCA	0.24414	0.23584
cg0708381	KIAA168	p53 [T006	1221	1227	4.33696	CTGGCC	0.24414	0.23584
cg0708381	KIAA168	RAR-beta	1495	1504	4.326039	CGGGTT	0.14496	0.1447
cg0708381	KIAA168	PEA3 [T0	739	747	4.30818	GCTCAT	0.13733	0.13791
cg0708381	KIAA168	PEA3 [T0	1700	1708	4.30818	GCTCAT	0.13733	0.13791
cg0708381	KIAA168	PEA3 [T0	1710	1718	4.30818	TGGATG	0.13733	0.13791
cg0708381	KIAA168	RAR-beta	40	49	4.307573	AGTAAA	0.14496	0.1447
cg0708381	KIAA168	RAR-beta	442	451	4.289108	CACGAA	0.14496	0.1447
cg0708381	KIAA168	RXR-alpha	434	440	4.24113	GGGTCC	0.97656	0.9671
cg0708381	KIAA168	PXR-1:RX	1495	1502	4.213958	CGGGTT	0.12207	0.12119
cg0708381	KIAA168	GR-beta [	231	235	4.201913	CTATT	7.8125	7.94607
cg0708381	KIAA168	GR-beta [	235	239	4.201913	TTATT	7.8125	7.94607
cg0708381	KIAA168	GR-beta [	246	250	4.201913	AATAA	7.8125	7.94607
cg0708381	KIAA168	GR-beta [	249	253	4.201913	AATAA	7.8125	7.94607
cg0708381	KIAA168	GR-beta [	252	256	4.201913	AATAA	7.8125	7.94607
cg0708381	KIAA168	GR-beta [	1363	1367	4.201913	AATCA	7.8125	7.94607
cg0708381	KIAA168	GR-beta [	1505	1509	4.201913	CGATT	7.8125	7.94607
cg0708381	KIAA168	GR-beta [	1567	1571	4.201913	TGATT	7.8125	7.94607
cg0708381	KIAA168	NF-Y [T0	1782	1789	4.186615	ATTGGA	0.18311	0.1853
cg0708381	KIAA168	NF-Y [T0	1964	1971	4.186615	ATTGGG	0.18311	0.1853
cg0708381	KIAA168	p53 [T006	1016	1022	4.125254	GGGCCG	0.73242	0.71379
cg0708381	KIAA168	RXR-alpha	981	987	4.019014	GGGTGT	0.97656	0.9671
cg0708381	KIAA168	RXR-alpha	1345	1351	4.019014	GGGTGT	0.97656	0.9671
cg0708381	KIAA168	RXR-alpha	1937	1943	4.019014	AAGACC	0.97656	0.9671
cg0708381	KIAA168	Pax-5 [T0	332	338	4.007279	AGAGCC	1.09863	1.07975
cg0708381	KIAA168	Pax-5 [T0	386	392	4.007279	AAGGCC	1.09863	1.07975
cg0708381	KIAA168	Pax-5 [T0	397	403	4.007279	GGGCTC	1.09863	1.07975
cg0708381	KIAA168	Pax-5 [T0	831	837	4.007279	GGGCAT	1.09863	1.07975
cg0708381	KIAA168	TFIID [T0	251	257	4.007279	TAATAA	1.09863	1.13456
cg0708381	KIAA168	AP-2alpha	313	318	3.970052	CAAGGC	0.97656	0.96469
cg0708381	KIAA168	AP-2alpha	1168	1173	3.970052	CAAGGC	0.97656	0.96469
cg0708381	KIAA168	c-Fos [T00	605	614	3.849714	TTTGTGA	0.03815	0.03825
cg0708381	KIAA168	NFI/CTF [	708	715	3.793671	CCAAAG	0.18311	0.18109
cg0708381	KIAA168	GR [T050	107	113	3.763516	CAAAGA	0.73242	0.74251
cg0708381	KIAA168	GR [T050	894	900	3.763516	CAAAGA	0.73242	0.74251
cg0708381	KIAA168	p53 [T006	469	475	3.750231	CCAGCC	0.73242	0.71379
cg0708381	KIAA168	p53 [T006	498	504	3.750231	CCAGCC	0.73242	0.71379
cg0708381	KIAA168	p53 [T006	527	533	3.750231	CCAGCC	0.73242	0.71379
cg0708381	KIAA168	p53 [T006	1127	1133	3.750231	GGGCTG	0.73242	0.71379
cg0708381	KIAA168	p53 [T006	1132	1138	3.750231	GGGCTG	0.73242	0.71379
cg0708381	KIAA168	AP-2alpha	385	390	3.743866	GAAGGC	0.48828	0.48238
cg0708381	KIAA168	AP-2alpha	666	671	3.743866	GAAGGC	0.48828	0.48238
cg0708381	KIAA168	AP-2alpha	1953	1958	3.743866	GAAGGC	0.48828	0.48238
cg0708381	KIAA168	p53 [T006	1777	1783	3.728319	GGGCAA	0.73242	0.7189
cg0708381	KIAA168	p53 [T006	831	837	3.516613	GGGCAT	0.73242	0.7189
cg0708381	KIAA168	HNF-3alph	33	40	3.500065	AATTTC	0.27466	0.28532
cg0708381	KIAA168	HNF-3alph	242	249	3.500065	AAAAAA	0.27466	0.28532
cg0708381	KIAA168	c-Ets-1 [T	1842	1848	3.487246	CTTCCGA	0.61035	0.60765

cg0708381	KIAA1683	VDR [T00	1498	1506	3.462841	GTTCAA	0.21362	0.21341
cg0708381	KIAA1683	RXR-alph	478	484	3.392904	CTCACC	1.09863	1.08572
cg0708381	KIAA1683	RXR-alph	507	513	3.392904	CTCACC	1.09863	1.08572
cg0708381	KIAA1683	RXR-alph	774	780	3.392904	GGAACC	1.09863	1.08572
cg0708381	KIAA1683	RXR-alph	1825	1831	3.392904	GGGTTA	1.09863	1.08572
cg0708381	KIAA1683	p53 [T006	482	488	3.375208	CCCGCC	0.73242	0.7189
cg0708381	KIAA1683	p53 [T006	511	517	3.375208	CCCGCC	0.73242	0.7189
cg0708381	KIAA1683	T3R-beta1	537	545	3.370634	TCACCT	0.27466	0.2755
cg0708381	KIAA1683	GR-beta [	783	787	3.361531	AATCT	3.90625	3.99611
cg0708381	KIAA1683	GR-beta [	1421	1425	3.361531	AGATT	3.90625	3.99611
cg0708381	KIAA1683	GR-beta [	1962	1966	3.361531	ATATT	3.90625	3.99611
cg0708381	KIAA1683	AP-2alpha	804	809	3.229049	AGAGGC	0.48828	0.48238
cg0708381	KIAA1683	AP-2alpha	1232	1237	3.229049	GCCTCT	0.48828	0.48238
cg0708381	KIAA1683	AP-2alpha	1981	1986	3.229049	AGAGGC	0.48828	0.48238
cg0708381	KIAA1683	TCF-4E [	1933	1939	3.151193	TGCAAA	0.24414	0.24672
cg0708381	KIAA1683	Elk-1 [T00	1244	1252	3.121991	CTTCCTT	0.07629	0.07656
cg0708381	KIAA1683	SRY [T00	749	757	3.088221	AGTACA	0.06104	0.06203
cg0708381	KIAA1683	c-Jun [T00	361	367	3.049104	TGACCC	0.24414	0.24403
cg0708381	KIAA1683	p53 [T006	218	224	3.024997	GGGCAA	0.48828	0.47786
cg0708381	KIAA1683	p53 [T006	1438	1444	3.024997	GTTGCC	0.48828	0.47786
cg0708381	KIAA1683	STAT4 [T	687	692	2.941176	GGAACA	2.92969	2.929
cg0708381	KIAA1683	STAT4 [T	774	779	2.941176	GGAACC	2.92969	2.929
cg0708381	KIAA1683	STAT4 [T	1094	1099	2.941176	GGAAGT	2.92969	2.929
cg0708381	KIAA1683	NF-1 [T00	348	355	2.813149	GGGGCC	0.24414	0.24101
cg0708381	KIAA1683	NF-1 [T00	704	711	2.813149	AGGGCC	0.24414	0.24101
cg0708381	KIAA1683	c-Myb [T0	807	814	2.570796	GGCAGT	0.06104	0.06117
cg0708381	KIAA1683	AP-2alpha	55	60	2.550491	GCCTCA	0.48828	0.48266
cg0708381	KIAA1683	AP-2alpha	903	908	2.550491	TGAGGC	0.48828	0.48266
cg0708381	KIAA1683	AP-2alpha	1515	1520	2.550491	GCCTCA	0.48828	0.48266
cg0708381	KIAA1683	AP-2alpha	1861	1866	2.550491	TGAGGC	0.48828	0.48266
cg0708381	KIAA1683	AP-2alpha	1944	1949	2.550491	TGAGGC	0.48828	0.48266
cg0708381	KIAA1683	RXR-alph	757	763	2.544678	GGGTTC	0.85449	0.84796
cg0708381	KIAA1683	RXR-alph	943	949	2.544678	GGGTGC	0.85449	0.84796
cg0708381	KIAA1683	RXR-alph	962	968	2.544678	GGGTTC	0.85449	0.84796
cg0708381	KIAA1683	RXR-alph	1692	1698	2.544678	TGCACC	0.85449	0.84796
cg0708381	KIAA1683	Ik-1 [T027	1662	1674	2.374299	CAAAGT	0.00063	0.00061
cg0708381	KIAA1683	VDR [T00	293	301	2.308561	CAGGTG	0.10681	0.10609
cg0708381	KIAA1683	T3R-beta1	1117	1125	2.259951	TCACCT	0.03052	0.03041
cg0708381	KIAA1683	T3R-beta1	291	299	2.221365	CACAGG	0.15259	0.15262
cg0708381	KIAA1683	GATA-1 [	1401	1406	2.176375	TATCCT	3.90625	3.92756
cg0708381	KIAA1683	GATA-1 [	1959	1964	2.176375	AGGATA	3.90625	3.92756
cg0708381	KIAA1683	Elk-1 [T00	1948	1956	2.164966	GCCAGG	0.05341	0.05317
cg0708381	KIAA1683	GATA-1 [	879	884	2.001358	GGGATA	3.90625	3.92756
cg0708381	KIAA1683	p53 [T006	864	870	1.970013	TTTGCC	0.36621	0.36261
cg0708381	KIAA1683	AP-2alpha	1521	1526	1.871933	GCCTCC	0.97656	0.95407
cg0708381	KIAA1683	AP-2alpha	1656	1661	1.871933	GCCTCC	0.97656	0.95407
cg0708381	KIAA1683	C/EBPalp	57	63	1.830762	CTCAAT	0.48828	0.49438
cg0708381	KIAA1683	TFII-I [T0	271	276	1.824994	CTCTCC	0.48828	0.48408

cg0708381	KIAA168	TFII-I [T0	1979	1984	1.824994	GGAGAG	0.48828	0.48408
cg0708381	KIAA168	C/EBPalph	1963	1969	1.761449	TATTGG	0.48828	0.49438
cg0708381	KIAA168	RXR-alpha	360	366	1.696452	CTGACC	0.48828	0.48222
cg0708381	KIAA168	RXR-alpha	1067	1073	1.696452	CTGACC	0.48828	0.48222
cg0708381	KIAA168	GR-beta [	833	837	1.680765	GCATT	3.90625	3.94936
cg0708381	KIAA168	GR-beta [	861	865	1.680765	GAATT	3.90625	3.94936
cg0708381	KIAA168	GR-beta [	898	902	1.680765	GAATT	3.90625	3.94936
cg0708381	KIAA168	GR-beta [	1969	1973	1.680765	GAATT	3.90625	3.94936
cg0708381	KIAA168	C/EBPbeta	15	18	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	106	109	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	156	159	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	165	168	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	173	176	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	197	200	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	352	355	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	518	521	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	581	584	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	619	622	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	630	633	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	683	686	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	708	711	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	780	783	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	934	937	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	979	982	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1008	1011	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1033	1036	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1167	1170	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1185	1188	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1210	1213	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1249	1252	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1324	1327	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1355	1358	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1387	1390	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1606	1609	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1661	1664	1.639871	CCAA	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1709	1712	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1783	1786	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1965	1968	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	C/EBPbeta	1973	1976	1.639871	TTGG	15.625	15.72563
cg0708381	KIAA168	IRF-1 [T0	62	70	1.616539	TTTCCCT	0.04578	0.04655
cg0708381	KIAA168	XBP-1 [T	713	718	1.583727	GGTCAT	0.97656	0.98146
cg0708381	KIAA168	Sp1 [T007	480	489	1.566059	CACCCG	0.03242	0.03129
cg0708381	KIAA168	Sp1 [T007	509	518	1.566059	CACCCG	0.03242	0.03129
cg0708381	KIAA168	Pax-5 [T0	415	421	1.537547	GGGCCA	0.73242	0.71311
cg0708381	KIAA168	Pax-5 [T0	482	488	1.537547	CCCGCC	0.73242	0.71311
cg0708381	KIAA168	Pax-5 [T0	511	517	1.537547	CCCGCC	0.73242	0.71311
cg0708381	KIAA168	Pax-5 [T0	952	958	1.537547	GGGCCA	0.73242	0.71311
cg0708381	KIAA168	Pax-5 [T0	1221	1227	1.537547	CTGGCC	0.73242	0.71311

cg0708381	KIAA1683	TFIID [T0	909	915	1.537547	TGTAAA	0.73242	0.75096
cg0708381	KIAA1683	TFIID [T0	1323	1329	1.537547	TCCAAA	0.73242	0.75096
cg0708381	KIAA1683	STAT4 [T	860	865	1.470588	GGAATT	1.95312	1.96333
cg0708381	KIAA1683	STAT4 [T	1968	1973	1.470588	GGAATT	1.95312	1.96333
cg0708381	KIAA1683	C/EBPbeta	37	40	1.366559	TTGA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	58	61	1.366559	TCAA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	205	208	1.366559	TTGA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	312	315	1.366559	TCAA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	613	616	1.366559	TCAA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	893	896	1.366559	TCAA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	902	905	1.366559	TTGA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	1025	1028	1.366559	TTGA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	1418	1421	1.366559	TTGA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	1424	1427	1.366559	TTGA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	1500	1503	1.366559	TCAA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	1621	1624	1.366559	TCAA	15.625	15.72563
cg0708381	KIAA1683	C/EBPbeta	1745	1748	1.366559	TCAA	15.625	15.72563
cg0708381	KIAA1683	AP-2alpha	119	124	1.357116	ACAGGC	0.48828	0.48203
cg0708381	KIAA1683	AP-2alpha	266	271	1.357116	ACAGGC	0.48828	0.48203
cg0708381	KIAA1683	AP-2alpha	1677	1682	1.357116	ACAGGC	0.48828	0.48203
cg0708381	KIAA1683	AP-2alpha	1837	1842	1.357116	ACAGGC	0.48828	0.48203
cg0708381	KIAA1683	NFI/CTF [	15	22	1.227415	CCAAGC	0.18311	0.18127
cg0708381	KIAA1683	GATA-2 [	64	72	1.111111	TCCCTAT	0.09155	0.09208
cg0708381	KIAA1683	NF-Y [T0	627	634	1.069274	TGGCCA	0.12207	0.12315
cg0708381	KIAA1683	RXR-alpha	444	450	0.848226	CGAACC	0.48828	0.48333
cg0708381	KIAA1683	GR-beta [T	32	36	0.840383	TAATT	7.8125	7.94706
cg0708381	KIAA1683	GR-beta [T	59	63	0.840383	CAATT	7.8125	7.94706
cg0708381	KIAA1683	GR-beta [T	368	372	0.840383	TCATT	7.8125	7.94706
cg0708381	KIAA1683	GR-beta [T	914	918	0.840383	AATGG	7.8125	7.94706
cg0708381	KIAA1683	GR-beta [T	1780	1784	0.840383	CAATT	7.8125	7.94706
cg0708381	KIAA1683	GR-beta [T	1781	1785	0.840383	AATTG	7.8125	7.94706
cg0708381	KIAA1683	AP-2alpha	1099	1104	0.678558	TCAGGC	0.48828	0.48199
cg0708381	KIAA1683	AP-2alpha	1293	1298	0.678558	GCCTGA	0.48828	0.48199
cg0708381	KIAA1683	AP-2alpha	1819	1824	0.678558	GCCTGA	0.48828	0.48199
cg0708381	KIAA1683	RXR-alpha	42	48	0.62611	TAAACC	0.12207	0.12313
cg0708381	KIAA1683	RXR-alpha	1394	1400	0.62611	GGGTTT	0.12207	0.12313
cg0708381	KIAA1683	AP-1 [T00	609	617	0.489074	TGACTC	0.09155	0.09215
cg0708381	KIAA1683	AP-1 [T00	1146	1154	0.261718	CATGAG	0.09155	0.09215
cg0708381	KIAA1683	c-Ets-1 [T	1244	1250	0.256174	CTTCCTT	0.24414	0.24569
cg0708381	KIAA1683	AP-2alpha	214	219	0.226186	GCCTGG	0.97656	0.95305
cg0708381	KIAA1683	AP-2alpha	1219	1224	0.226186	GCCTGG	0.97656	0.95305
cg0708381	KIAA1683	AP-2alpha	1238	1243	0.226186	GCCTGG	0.97656	0.95305
cg0708381	KIAA1683	AP-2alpha	1443	1448	0.226186	CCAGGC	0.97656	0.95305
cg0708381	KIAA1683	AP-2alpha	1610	1615	0.226186	CCAGGC	0.97656	0.95305
cg0708381	KIAA1683	GR-alpha [	48	52	0.207689	CCTCT	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	322	326	0.207689	AGAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	404	408	0.207689	AAAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	420	424	0.207689	AGAGG	7.8125	7.81264

cg0708381	KIAA1683	GR-alpha [	678	682	0.207689	AGAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	710	714	0.207689	AAAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	754	758	0.207689	AAAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	770	774	0.207689	AGAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	804	808	0.207689	AGAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	938	942	0.207689	AAAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1233	1237	0.207689	CCTCT	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1303	1307	0.207689	CCTCT	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1404	1408	0.207689	CCTTT	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1706	1710	0.207689	CCTTT	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1981	1985	0.207689	AGAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1992	1996	0.207689	AAAGG	7.8125	7.81264
cg0708381	KIAA1683	GATA-1 [	1587	1592	0.105011	GAGATA	0.97656	0.98738
cg0708381	KIAA1683	GR-alpha [	66	70	0	CCTAT	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	119	123	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	266	270	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	292	296	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	431	435	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	690	694	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1335	1339	0	CCTAT	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1542	1546	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1590	1594	0	ATAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1677	1681	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1726	1730	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	GR-alpha [	1837	1841	0	ACAGG	7.8125	7.81264
cg0708381	KIAA1683	AP-2alpha	1646	1651	0	GCCTGC	0.97656	0.95305
cg0708381	KIAA1683	XBP-1 [T0	1555	1560	0	ATGACG	0.97656	0.98127
cg0708381	KIAA1683	XBP-1 [T0	1888	1893	0	ATGACT	0.97656	0.98127
cg0708381	KIAA1683	RXR-alpha	1496	1502	0	GGGTTC	0.24414	0.2444
cg0708381	KIAA1683	Pax-5 [T0	144	150	0	CCTGCC	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	469	475	0	CCAGCC	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	498	504	0	CCAGCC	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	527	533	0	CCAGCC	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	540	546	0	CCTGCC	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	700	706	0	GGGCAG	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	1016	1022	0	GGGCCG	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	1047	1053	0	GGGCCC	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	1127	1133	0	GGGCTG	1.09863	1.06846
cg0708381	KIAA1683	Pax-5 [T0	1132	1138	0	GGGCTG	1.09863	1.06846
cg0708381	KIAA1683	p53 [T006	144	150	0	CCTGCC	0.36621	0.35912
cg0708381	KIAA1683	p53 [T006	540	546	0	CCTGCC	0.36621	0.35912
cg0708381	KIAA1683	p53 [T006	700	706	0	GGGCAG	0.36621	0.35912
cg0708381	KIAA1683	TFII-I [T0	1107	1112	0	CTGTCC	1.46484	1.45997
cg0708381	KIAA1683	TFII-I [T0	1835	1840	0	GGACAG	1.46484	1.45997
cg0708381	KIAA1683	STAT4 [T	61	66	0	ATTTCC	0.48828	0.49387
cg0708381	KIAA1683	c-Ets-1 [T	1950	1956	0	CAGGAA	0.24414	0.2429
cg0708381	KIAA1683	YY1 [T00	92	95	0	CCAT	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T00	275	278	0	CCAT	7.8125	7.81711

cg0708381	KIAA1683	YY1 [T009	287	290	0	CCAT	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	309	312	0	CCAT	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	365	368	0	CCAT	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	717	720	0	ATGG	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	794	797	0	CCAT	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	870	873	0	CCAT	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	915	918	0	ATGG	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	923	926	0	ATGG	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	1373	1376	0	ATGG	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	1380	1383	0	ATGG	7.8125	7.81711
cg0708381	KIAA1683	YY1 [T009	1601	1604	0	CCAT	7.8125	7.81711
cg0708381	KIAA1683	ER-alpha [	361	365	0	TGACC	1.95312	1.9404
cg0708381	KIAA1683	ER-alpha [	713	717	0	GGTCA	1.95312	1.9404
cg0708381	KIAA1683	ER-alpha [	1068	1072	0	TGACC	1.95312	1.9404
cg0708381	KIAA1683	ER-alpha [	1296	1300	0	TGACC	1.95312	1.9404
cg0708381	KIAA1683	ER-alpha [	1630	1634	0	TGACC	1.95312	1.9404
cg0708381	KIAA1683	GATA-1 [	68	73	0	TATCTG	0.97656	0.98738
cg0708381	KIAA1683	C/EBPbeta	76	79	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	103	106	0	TTGC	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	116	119	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	220	223	0	GCAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	300	303	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	372	375	0	TTGC	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	453	456	0	GCAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	457	460	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	606	609	0	TTGT	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	724	727	0	TTGC	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	752	755	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	865	868	0	TTGC	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	884	887	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	888	891	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	947	950	0	GCAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1054	1057	0	GCAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1267	1270	0	TTGC	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1275	1278	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1359	1362	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1407	1410	0	TTGT	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1439	1442	0	TTGC	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1479	1482	0	GCAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1635	1638	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1759	1762	0	ACAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1779	1782	0	GCAA	15.625	15.71349
cg0708381	KIAA1683	C/EBPbeta	1934	1937	0	GCAA	15.625	15.71349
cg0708381	KIAA1683	NF-1 [T00	1163	1170	0	TGGGCC	0.12207	0.11983
cg0708381	KIAA1683	c-Jun [T00	609	615	0	TGACTC	0.12207	0.12266
cg0708381	KIAA1683	c-Jun [T00	1148	1154	0	TGAGTC	0.12207	0.12266
cg0708381	KIAA1683	TFIID [T0	205	211	0	TTGAAA	1.09863	1.13474
cg0708381	KIAA1683	TFIID [T0	238	244	0	TTTAAA	1.09863	1.13474

cg0708381	KIAA1683	TFIID [T0	239	245	0	TTAAAA	1.09863	1.13474
cg0708381	KIAA1683	TFIID [T0	240	246	0	TAAAAA	1.09863	1.13474
cg0708381	KIAA1683	TFIID [T0	1415	1421	0	TTTTTGA	1.09863	1.13474
cg0708381	KIAA1683	FOXP3 [T	115	120	0	CACAAC	1.46484	1.47315
cg0708381	KIAA1683	FOXP3 [T	887	892	0	AACAAC	1.46484	1.47315
cg0708381	KIAA1683	c-Myb [T0	1382	1389	0	GGCAGT	0.03052	0.03022
cg0708381	KIAA1683	GR-beta [T	33	37	0	AATTT	3.90625	3.99611
cg0708381	KIAA1683	GR-beta [T	60	64	0	AATTT	3.90625	3.99611
cg0708381	KIAA1683	GR-beta [T	862	866	0	AATTT	3.90625	3.99611
cg0708381	KIAA1683	GR-beta [T	899	903	0	AATTT	3.90625	3.99611
cg0708381	KIAA1683	GR-beta [T	1970	1974	0	AATTT	3.90625	3.99611
cg0708381	KIAA1683	C/EBPalph	1422	1428	0	GATTGA	0.24414	0.2444
cg0708381	KIAA1683	GR [T050	935	941	0	CAAAAA	0.36621	0.37562
cg0708381	KIAA1683	GR [T050	1414	1420	0	TTTTTTG	0.36621	0.37562
cg0708381	KIAA1683	IRF-2 [T0	1637	1642	0	AAGTGA	0.48828	0.49387
cg0708381	KIAA1683	TBP [T00	1397	1406	0	TTTATAT	0.03052	0.03159
cg1002882	MAD1L1	Elk-1 [T00	891	899	9.979803	TTCCGG	0.10681	0.11027
cg1151970	MAD1L1	RAR-beta:	81	92	9.97066	GGGCCC	0.06974	0.07677
cg1151970	MAD1L1	RAR-beta:	1261	1272	9.97066	GGGCTC	0.06974	0.07677
cg0611220	MAD1L1	STAT5A [	1659	1671	9.952027	TTGACA	0.01878	0.01703
cg1578384	MAD1L1	LEF-1 [T0	1114	1121	9.937995	CTTTGG	0.12207	0.1238
cg0231133	MAD1L1	PEA3 [T0	86	94	9.937959	GGGATG	0.18311	0.18382
cg1151970	MAD1L1	PEA3 [T0	1478	1486	9.937959	GTCCAT	0.18311	0.18382
cg1002882	MAD1L1	PEA3 [T0	708	716	9.937959	TCTCAT	0.18311	0.18382
cg1002882	MAD1L1	NF-AT2 [T	1026	1035	9.873347	ATTAAT	0.08774	0.08205
cg1578384	MAD1L1	HNF-1C [	1708	1716	9.870625	GTGTCT	0.10681	0.09927
cg0231133	MAD1L1	c-Ets-1 [T	1059	1065	9.841249	AGGGAA	0.24414	0.23698
cg0372348	MAD1L1	c-Ets-1 [T	877	883	9.841249	AGGGAA	0.24414	0.23698
cg1151970	MAD1L1	MAZ [T00	1365	1377	9.840436	GCACGG	0.00435	0.00501
cg0611220	MAD1L1	MAZ [T00	1966	1978	9.826821	GACCCT	0.00435	0.00501
cg1151970	MAD1L1	c-Myb [T0	594	601	9.815171	TCAAGT	0.36621	0.34605
cg0231133	MAD1L1	STAT1bet	927	936	9.807397	TTTTCC	0.14877	0.14533
cg1578384	MAD1L1	STAT1bet	845	854	9.807397	ACAGGG	0.14877	0.14533
cg1151970	MAD1L1	STAT1bet	811	820	9.807397	TGAAGG	0.14877	0.14533
cg1151970	MAD1L1	STAT1bet	1321	1330	9.807397	CTTTCC	0.14877	0.14533
cg0231133	MAD1L1	XBP-1 [T	1731	1736	9.789909	ATGGCG	1.95312	1.94901
cg1578384	MAD1L1	XBP-1 [T	405	410	9.789909	ATGTCG	1.95312	1.94901
cg1578384	MAD1L1	XBP-1 [T	621	626	9.789909	ATGTCG	1.95312	1.94901
cg1578384	MAD1L1	XBP-1 [T	743	748	9.789909	ATGTCG	1.95312	1.94901
cg1578384	MAD1L1	XBP-1 [T	793	798	9.789909	ATGTCG	1.95312	1.94901
cg1578384	MAD1L1	XBP-1 [T	1571	1576	9.789909	AGCCAT	1.95312	1.94901
cg1151970	MAD1L1	XBP-1 [T	1974	1979	9.789909	AGCCAT	1.95312	1.94901
cg1002882	MAD1L1	XBP-1 [T	225	230	9.789909	ATGGCG	1.95312	1.94901
cg1002882	MAD1L1	XBP-1 [T	1900	1905	9.789909	CGCCAT	1.95312	1.94901
cg0611220	MAD1L1	XBP-1 [T	714	719	9.789909	AGCCAT	1.95312	1.94901
cg0372348	MAD1L1	XBP-1 [T	575	580	9.789909	AGCCAT	1.95312	1.94901
cg0372348	MAD1L1	XBP-1 [T	707	712	9.789909	ATGGCT	1.95312	1.94901
cg0611220	MAD1L1	NF-1 [T00	505	512	9.761671	TTGGAG	0.24414	0.24488

cg0611220	MAD1L1	NF-1 [T00	1633	1640	9.761671	TTGGTT	0.24414	0.24488
cg1151970	MAD1L1	Elk-1 [T00	1235	1243	9.754368	CGAGGG	0.10681	0.11027
cg1002882	MAD1L1	Elk-1 [T00	1087	1095	9.754368	AGAGGG	0.10681	0.11027
cg1002882	MAD1L1	Elk-1 [T00	1799	1807	9.754368	AGAGGG	0.10681	0.11027
cg0231133	MAD1L1	PR B [T00	119	125	9.743489	CTGTGT	1.09863	1.0981
cg0231133	MAD1L1	PR B [T00	358	364	9.743489	AACACC	1.09863	1.0981
cg0231133	MAD1L1	PR B [T00	725	731	9.743489	CGGTGT	1.09863	1.0981
cg0231133	MAD1L1	PR B [T00	1175	1181	9.743489	AACACA	1.09863	1.0981
cg0231133	MAD1L1	PR B [T00	1349	1355	9.743489	AACACC	1.09863	1.0981
cg0231133	MAD1L1	PR B [T00	1650	1656	9.743489	AACACA	1.09863	1.0981
cg0231133	MAD1L1	PR A [T01	119	125	9.743489	CTGTGT	1.09863	1.0981
cg0231133	MAD1L1	PR A [T01	358	364	9.743489	AACACC	1.09863	1.0981
cg0231133	MAD1L1	PR A [T01	725	731	9.743489	CGGTGT	1.09863	1.0981
cg0231133	MAD1L1	PR A [T01	1175	1181	9.743489	AACACA	1.09863	1.0981
cg0231133	MAD1L1	PR A [T01	1349	1355	9.743489	AACACC	1.09863	1.0981
cg0231133	MAD1L1	PR A [T01	1650	1656	9.743489	AACACA	1.09863	1.0981
cg1578384	MAD1L1	PR B [T00	52	58	9.743489	AACACC	1.09863	1.0981
cg1578384	MAD1L1	PR B [T00	918	924	9.743489	AACACA	1.09863	1.0981
cg1578384	MAD1L1	PR A [T01	52	58	9.743489	AACACC	1.09863	1.0981
cg1578384	MAD1L1	PR A [T01	918	924	9.743489	AACACA	1.09863	1.0981
cg1151970	MAD1L1	PR B [T00	111	117	9.743489	AACACG	1.09863	1.0981
cg1151970	MAD1L1	PR B [T00	406	412	9.743489	AACACC	1.09863	1.0981
cg1151970	MAD1L1	PR B [T00	864	870	9.743489	AACACC	1.09863	1.0981
cg1151970	MAD1L1	PR B [T00	1984	1990	9.743489	AACACA	1.09863	1.0981
cg1151970	MAD1L1	PR A [T01	111	117	9.743489	AACACG	1.09863	1.0981
cg1151970	MAD1L1	PR A [T01	406	412	9.743489	AACACC	1.09863	1.0981
cg1151970	MAD1L1	PR A [T01	864	870	9.743489	AACACC	1.09863	1.0981
cg1151970	MAD1L1	PR A [T01	1984	1990	9.743489	AACACA	1.09863	1.0981
cg1002882	MAD1L1	PR B [T00	871	877	9.743489	AACACG	1.09863	1.0981
cg1002882	MAD1L1	PR A [T01	871	877	9.743489	AACACG	1.09863	1.0981
cg0611220	MAD1L1	PR B [T00	7	13	9.743489	AACACC	1.09863	1.0981
cg0611220	MAD1L1	PR B [T00	1595	1601	9.743489	AACACA	1.09863	1.0981
cg0611220	MAD1L1	PR B [T00	1867	1873	9.743489	AACACA	1.09863	1.0981
cg0611220	MAD1L1	PR A [T01	7	13	9.743489	AACACC	1.09863	1.0981
cg0611220	MAD1L1	PR A [T01	1595	1601	9.743489	AACACA	1.09863	1.0981
cg0611220	MAD1L1	PR A [T01	1867	1873	9.743489	AACACA	1.09863	1.0981
cg0372348	MAD1L1	PR B [T00	63	69	9.743489	AACACC	1.09863	1.0981
cg0372348	MAD1L1	PR B [T00	436	442	9.743489	TTGTGT	1.09863	1.0981
cg0372348	MAD1L1	PR B [T00	1113	1119	9.743489	GTGTGT	1.09863	1.0981
cg0372348	MAD1L1	PR A [T01	63	69	9.743489	AACACC	1.09863	1.0981
cg0372348	MAD1L1	PR A [T01	436	442	9.743489	TTGTGT	1.09863	1.0981
cg0372348	MAD1L1	PR A [T01	1113	1119	9.743489	GTGTGT	1.09863	1.0981
cg0231133	MAD1L1	AhR:Arnt	1620	1629	9.738501	GCACGC	0.17929	0.20119
cg0231133	MAD1L1	AhR:Arnt	1679	1688	9.738501	GCACGC	0.17929	0.20119
cg0231133	MAD1L1	AhR:Arnt	1712	1721	9.738501	ACACGC	0.17929	0.20119
cg1578384	MAD1L1	AhR:Arnt	1470	1479	9.738501	CTGGGC	0.17929	0.20119
cg1578384	MAD1L1	AhR:Arnt	1480	1489	9.738501	TGGCGC	0.17929	0.20119
cg1002882	MAD1L1	AhR:Arnt	238	247	9.738501	CCCTGC	0.17929	0.20119

cg0611220	MAD1L1	c-Myb [T0	68	75	9.729271	TACAGT	0.36621	0.34746
cg0372348	MAD1L1	c-Myb [T0	902	909	9.729271	TACAGT	0.36621	0.34746
cg1578384	MAD1L1	LEF-1 [T0	1121	1128	9.72404	AGGCAA	0.21362	0.21229
cg0611220	MAD1L1	LEF-1 [T0	1420	1427	9.72404	CTTTGTC	0.21362	0.21229
cg0231133	MAD1L1	c-Ets-1 [T	1455	1461	9.713162	ATTCCC	0.36621	0.37402
cg0372348	MAD1L1	c-Ets-1 [T	457	463	9.713162	ATTCCC	0.36621	0.37402
cg1151970	MAD1L1	NF-kappaI	517	527	9.693435	GGGGAC	0.02193	0.02416
cg1151970	MAD1L1	NF-AT1 [	815	823	9.691726	GGAAAC	0.16785	0.16528
cg1002882	MAD1L1	EBF [T05	1614	1624	9.678925	GGCCCT	0.06866	0.07687
cg1002882	MAD1L1	EBF [T05	236	246	9.652631	GGCCCT	0.06866	0.07687
cg1002882	MAD1L1	RAR-beta	1629	1638	9.641259	GGGGTT	0.21362	0.22369
cg0372348	MAD1L1	RAR-beta	831	840	9.622793	CGGGTT	0.21362	0.22369
cg1002882	MAD1L1	Elk-1 [T00	900	908	9.62002	CTTCCCT	0.07629	0.0786
cg1151970	MAD1L1	c-Ets-1 [T	1641	1647	9.585075	ATTCCC	0.36621	0.37402
cg0231133	MAD1L1	TFIID [T0	74	80	9.552105	TCCCAA	1.46484	1.37777
cg0231133	MAD1L1	TFIID [T0	147	153	9.552105	TTTGTCA	1.46484	1.37777
cg0231133	MAD1L1	TFIID [T0	543	549	9.552105	TCCGAA	1.46484	1.37777
cg0231133	MAD1L1	TFIID [T0	1160	1166	9.552105	TGAGAA	1.46484	1.37777
cg0231133	MAD1L1	Pax-5 [T0	234	240	9.552105	GGGCCA	1.46484	1.61918
cg0231133	MAD1L1	Pax-5 [T0	347	353	9.552105	GGGCGC	1.46484	1.61918
cg0231133	MAD1L1	Pax-5 [T0	940	946	9.552105	GGGCCA	1.46484	1.61918
cg0231133	MAD1L1	Pax-5 [T0	1793	1799	9.552105	TTAGCC	1.46484	1.61918
cg1578384	MAD1L1	TFIID [T0	1036	1042	9.552105	TTTCACA	1.46484	1.37777
cg1578384	MAD1L1	TFIID [T0	1270	1276	9.552105	TTTCACA	1.46484	1.37777
cg1578384	MAD1L1	TFIID [T0	1372	1378	9.552105	TTTGGA	1.46484	1.37777
cg1578384	MAD1L1	Pax-5 [T0	962	968	9.552105	GGGCCA	1.46484	1.61918
cg1578384	MAD1L1	Pax-5 [T0	1590	1596	9.552105	GGGCAA	1.46484	1.61918
cg1151970	MAD1L1	TFIID [T0	145	151	9.552105	TCCCAA	1.46484	1.37777
cg1151970	MAD1L1	Pax-5 [T0	552	558	9.552105	TGCGCC	1.46484	1.61918
cg1151970	MAD1L1	Pax-5 [T0	1071	1077	9.552105	GTGGCC	1.46484	1.61918
cg1151970	MAD1L1	Pax-5 [T0	1613	1619	9.552105	GGGCCA	1.46484	1.61918
cg1002882	MAD1L1	TFIID [T0	413	419	9.552105	TGAGAA	1.46484	1.37777
cg1002882	MAD1L1	TFIID [T0	1031	1037	9.552105	TTTCCCA	1.46484	1.37777
cg0611220	MAD1L1	TFIID [T0	1197	1203	9.552105	TTTGACA	1.46484	1.37777
cg0611220	MAD1L1	TFIID [T0	1305	1311	9.552105	TTTGGTA	1.46484	1.37777
cg0611220	MAD1L1	TFIID [T0	1391	1397	9.552105	TTTCTCA	1.46484	1.37777
cg0611220	MAD1L1	TFIID [T0	1421	1427	9.552105	TTTGTCA	1.46484	1.37777
cg0611220	MAD1L1	TFIID [T0	1846	1852	9.552105	TACCAA	1.46484	1.37777
cg0611220	MAD1L1	Pax-5 [T0	411	417	9.552105	TCCGCC	1.46484	1.61918
cg0611220	MAD1L1	Pax-5 [T0	1499	1505	9.552105	GGGCAA	1.46484	1.61918
cg0611220	MAD1L1	Pax-5 [T0	1678	1684	9.552105	GGGCCA	1.46484	1.61918
cg0372348	MAD1L1	TFIID [T0	403	409	9.552105	TTTCACA	1.46484	1.37777
cg0372348	MAD1L1	TFIID [T0	418	424	9.552105	TGACAA	1.46484	1.37777
cg0372348	MAD1L1	TFIID [T0	732	738	9.552105	TTTGACA	1.46484	1.37777
cg0372348	MAD1L1	TFIID [T0	768	774	9.552105	TGGGAA	1.46484	1.37777
cg0372348	MAD1L1	TFIID [T0	1298	1304	9.552105	TGGGAA	1.46484	1.37777
cg0372348	MAD1L1	Pax-5 [T0	760	766	9.552105	GGGCAA	1.46484	1.61918
cg0372348	MAD1L1	Pax-5 [T0	803	809	9.552105	GGGCCA	1.46484	1.61918

cg0372348	MAD1L1	Pax-5 [T0	1057	1063	9.552105	GACGCC	1.46484	1.61918
cg0372348	MAD1L1	Pax-5 [T0	1846	1852	9.552105	GGCGCC	1.46484	1.61918
cg0231133	MAD1L1	MAZ [T00	1351	1363	9.549672	CACCGG	0.01425	0.01587
cg1002882	MAD1L1	NF-1 [T00	16	23	9.535536	CTGTCC	0.73242	0.74634
cg1002882	MAD1L1	NF-1 [T00	122	129	9.535536	ATGGCC	0.73242	0.74634
cg0611220	MAD1L1	NF-1 [T00	950	957	9.535536	TTGGCC	0.73242	0.74634
cg0372348	MAD1L1	NF-1 [T00	1274	1281	9.535536	TTGGCC	0.73242	0.74634
cg0611220	MAD1L1	NF-AT1 [	1237	1245	9.521781	TGCATT	0.16785	0.16528
cg1578384	MAD1L1	NF-1 [T00	606	613	9.513281	TACGCC	0.73242	0.74634
cg1578384	MAD1L1	NF-1 [T00	1855	1862	9.513281	CACCCC	0.73242	0.74634
cg1002882	MAD1L1	NF-1 [T00	1633	1640	9.513281	TTGGCG	0.73242	0.74634
cg0372348	MAD1L1	NF-1 [T00	1928	1935	9.513281	TTGGGG	0.73242	0.74634
cg0231133	MAD1L1	FOXP3 [T	83	88	9.512894	GTTGGG	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	158	163	9.512894	AGCAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	270	275	9.512894	AGCAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	419	424	9.512894	GTTGCT	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	450	455	9.512894	ATAAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	494	499	9.512894	GAGAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	901	906	9.512894	AGCAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	1004	1009	9.512894	CAGAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	1172	1177	9.512894	GAGAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	1346	1351	9.512894	ACCAAC	7.32422	7.22156
cg0231133	MAD1L1	FOXP3 [T	1921	1926	9.512894	GTTGCC	7.32422	7.22156
cg0231133	MAD1L1	TFII-I [T0	208	213	9.512894	TTTTCC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	375	380	9.512894	GGACAC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	435	440	9.512894	GGAAAC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	512	517	9.512894	GGACGG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	540	545	9.512894	CGGTCC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	574	579	9.512894	GGAAGG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	600	605	9.512894	GGAAAA	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	644	649	9.512894	GGACGG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	668	673	9.512894	GGACGG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	687	692	9.512894	GGAACG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	783	788	9.512894	GGAAGG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	787	792	9.512894	GGACCG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	927	932	9.512894	TTTTCC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1015	1020	9.512894	GGATAA	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1061	1066	9.512894	GGAATT	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1071	1076	9.512894	GGACAA	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1101	1106	9.512894	GGAAAA	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1200	1205	9.512894	GGATTT	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1414	1419	9.512894	GGAAAC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1454	1459	9.512894	AATTCC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1473	1478	9.512894	GGAACG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1485	1490	9.512894	GTATCC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1747	1752	9.512894	GGACAC	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1779	1784	9.512894	GGAAGG	7.32422	7.44385
cg0231133	MAD1L1	TFII-I [T0	1892	1897	9.512894	GTGTCC	7.32422	7.44385

cg0231133	MAD1L1	TFII-I [T0	1971	1976	9.512894	CGATCC	7.32422	7.44385
cg1578384	MAD1L1	FOXP3 [T	716	721	9.512894	GATAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	733	738	9.512894	GATAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	783	788	9.512894	GATAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	868	873	9.512894	GGCAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	891	896	9.512894	GTAAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1041	1046	9.512894	CAGAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1053	1058	9.512894	AGCAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1068	1073	9.512894	GTAAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1082	1087	9.512894	GTTTAG	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1242	1247	9.512894	GATAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1286	1291	9.512894	AAGAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1303	1308	9.512894	AAGAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1425	1430	9.512894	ACCAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1591	1596	9.512894	GGCAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1769	1774	9.512894	AAGAAC	7.32422	7.22156
cg1578384	MAD1L1	FOXP3 [T	1858	1863	9.512894	CCCAAC	7.32422	7.22156
cg1578384	MAD1L1	TFII-I [T0	146	151	9.512894	AAGTCC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	231	236	9.512894	AAATCC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	563	568	9.512894	CGATCC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	579	584	9.512894	CGATCC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	841	846	9.512894	GGACAC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	849	854	9.512894	GGAAAC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	858	863	9.512894	GGAAGG	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	941	946	9.512894	GGACGG	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	1203	1208	9.512894	AATTCC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	1335	1340	9.512894	GGACGG	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	1339	1344	9.512894	GGATAC	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	1375	1380	9.512894	GGAAGG	7.32422	7.44385
cg1578384	MAD1L1	TFII-I [T0	1848	1853	9.512894	CCATCC	7.32422	7.44385
cg1151970	MAD1L1	FOXP3 [T	130	135	9.512894	GATAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	197	202	9.512894	GTTCTT	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	252	257	9.512894	AAGAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	619	624	9.512894	GGCAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	854	859	9.512894	GTTCTT	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	890	895	9.512894	CCCAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	1179	1184	9.512894	GAGAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	1197	1202	9.512894	CATAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	1213	1218	9.512894	GAGAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	1276	1281	9.512894	GGCAAC	7.32422	7.22156
cg1151970	MAD1L1	FOXP3 [T	1615	1620	9.512894	GCCAAC	7.32422	7.22156
cg1151970	MAD1L1	TFII-I [T0	18	23	9.512894	CCGTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	108	113	9.512894	GGAAAC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	142	147	9.512894	GTGTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	454	459	9.512894	CCATCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	519	524	9.512894	GGACTT	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	631	636	9.512894	CGTTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	644	649	9.512894	GGAACG	7.32422	7.44385

cg1151970	MAD1L1	TFII-I [T0	724	729	9.512894	GTTTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	755	760	9.512894	GGAAAC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	777	782	9.512894	GGATTT	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	815	820	9.512894	GGAAAC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	958	963	9.512894	GTGTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	986	991	9.512894	TTGTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1318	1323	9.512894	GGACTT	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1448	1453	9.512894	CGTTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1456	1461	9.512894	CCATCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1460	1465	9.512894	CCTTCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1480	1485	9.512894	CCATCC	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1713	1718	9.512894	GGACCG	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1909	1914	9.512894	GGATGG	7.32422	7.44385
cg1151970	MAD1L1	TFII-I [T0	1917	1922	9.512894	GGACGG	7.32422	7.44385
cg1002882	MAD1L1	FOXP3 [T	260	265	9.512894	CAGAAC	7.32422	7.22156
cg1002882	MAD1L1	FOXP3 [T	438	443	9.512894	GTTGGG	7.32422	7.22156
cg1002882	MAD1L1	FOXP3 [T	868	873	9.512894	CAGAAC	7.32422	7.22156
cg1002882	MAD1L1	FOXP3 [T	1048	1053	9.512894	CAGAAC	7.32422	7.22156
cg1002882	MAD1L1	FOXP3 [T	1365	1370	9.512894	GTTCTG	7.32422	7.22156
cg1002882	MAD1L1	FOXP3 [T	1632	1637	9.512894	GTTGGC	7.32422	7.22156
cg1002882	MAD1L1	FOXP3 [T	1646	1651	9.512894	AGCAAC	7.32422	7.22156
cg1002882	MAD1L1	TFII-I [T0	169	174	9.512894	GTTTCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	185	190	9.512894	AAATCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	200	205	9.512894	GGAAAC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	292	297	9.512894	GGAAAC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	327	332	9.512894	GGATGG	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	378	383	9.512894	GGAAAA	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	581	586	9.512894	CCATCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	619	624	9.512894	CGGTCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	665	670	9.512894	CCATCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	684	689	9.512894	GGAACG	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	688	693	9.512894	CGGTCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	889	894	9.512894	GTTTCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1186	1191	9.512894	TTTTCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1294	1299	9.512894	GGACAC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1341	1346	9.512894	GGAAGG	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1719	1724	9.512894	GGATTT	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1782	1787	9.512894	GGACAA	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1819	1824	9.512894	GGACAC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1853	1858	9.512894	CCGTCC	7.32422	7.44385
cg1002882	MAD1L1	TFII-I [T0	1938	1943	9.512894	GGAAAC	7.32422	7.44385
cg0611220	MAD1L1	FOXP3 [T	4	9	9.512894	CTAAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	564	569	9.512894	AGCAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	749	754	9.512894	AATAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	812	817	9.512894	CTAAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	841	846	9.512894	GTTTAT	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1301	1306	9.512894	GTTATT	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1407	1412	9.512894	GATAAC	7.32422	7.22156

cg0611220	MAD1L1	FOXP3 [T	1592	1597	9.512894	AAGAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1632	1637	9.512894	GTTGGT	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1636	1641	9.512894	GTTCTG	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1649	1654	9.512894	AGCAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1680	1685	9.512894	GCCAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1720	1725	9.512894	GTTGGG	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1803	1808	9.512894	AATAAC	7.32422	7.22156
cg0611220	MAD1L1	FOXP3 [T	1892	1897	9.512894	CAGAAC	7.32422	7.22156
cg0611220	MAD1L1	TFII-I [T0	88	93	9.512894	CGATCC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	113	118	9.512894	GGACAA	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	378	383	9.512894	GGATGG	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	664	669	9.512894	TTGTCC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	716	721	9.512894	CCATCC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	843	848	9.512894	TTATCC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	855	860	9.512894	AATTCC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	995	1000	9.512894	TTGTCC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	1181	1186	9.512894	GTGTCC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	1551	1556	9.512894	GGAACG	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	1689	1694	9.512894	GGAAAC	7.32422	7.44385
cg0611220	MAD1L1	TFII-I [T0	1747	1752	9.512894	CCTTCC	7.32422	7.44385
cg0372348	MAD1L1	FOXP3 [T	280	285	9.512894	GTTCTG	7.32422	7.22156
cg0372348	MAD1L1	FOXP3 [T	727	732	9.512894	GTTTAT	7.32422	7.22156
cg0372348	MAD1L1	FOXP3 [T	761	766	9.512894	GGCAAC	7.32422	7.22156
cg0372348	MAD1L1	FOXP3 [T	1092	1097	9.512894	CAGAAC	7.32422	7.22156
cg0372348	MAD1L1	FOXP3 [T	1707	1712	9.512894	CAGAAC	7.32422	7.22156
cg0372348	MAD1L1	FOXP3 [T	1747	1752	9.512894	AAGAAC	7.32422	7.22156
cg0372348	MAD1L1	FOXP3 [T	1987	1992	9.512894	ATAAAC	7.32422	7.22156
cg0372348	MAD1L1	TFII-I [T0	153	158	9.512894	CCTTCC	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	268	273	9.512894	GGAAAA	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	356	361	9.512894	GGAAGG	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	423	428	9.512894	AATTCC	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	561	566	9.512894	CCATCC	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	770	775	9.512894	GGAAAC	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	859	864	9.512894	CGTTCC	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	879	884	9.512894	GGAATT	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	889	894	9.512894	GGACTT	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	1018	1023	9.512894	GTTTCC	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	1208	1213	9.512894	GGACAA	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	1223	1228	9.512894	GGAAGG	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	1439	1444	9.512894	CCTTCC	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	1792	1797	9.512894	GGAAGG	7.32422	7.44385
cg0372348	MAD1L1	TFII-I [T0	1952	1957	9.512894	GGACAC	7.32422	7.44385
cg0231133	MAD1L1	c-Jun [T00	1325	1331	9.511322	GTGGTC	0.73242	0.7366
cg1151970	MAD1L1	c-Jun [T00	1767	1773	9.511322	TGACCA	0.73242	0.7366
cg1002882	MAD1L1	c-Jun [T00	862	868	9.511322	TGACCA	0.73242	0.7366
cg1002882	MAD1L1	E2F [T002	1632	1641	9.503023	GTTGGC	0.01907	0.02086
cg0231133	MAD1L1	Ik-1 [T027	564	576	9.497194	CACCTG	0.02941	0.03137
cg1578384	MAD1L1	Ik-1 [T027	1496	1508	9.497194	TCCCAG	0.02941	0.03137

cg1578384	MAD1L1	TCF-4E [T	1371	1377	9.453578	CTTTGG	0.48828	0.46934
cg0611220	MAD1L1	TCF-4E [T	428	434	9.453578	CTCAAA	0.48828	0.46934
cg0611220	MAD1L1	TCF-4E [T	1196	1202	9.453578	CTTTGA	0.48828	0.46934
cg0231133	MAD1L1	c-Jun [T00	1539	1545	9.442241	TGACAG	0.73242	0.7366
cg0372348	MAD1L1	c-Jun [T00	213	219	9.442241	GCCGTC	0.73242	0.7366
cg1578384	MAD1L1	PPAR-alph	1327	1337	9.39865	AAGGCC	0.00286	0.00313
cg0231133	MAD1L1	NFI/CTF [	953	960	9.352332	CCAATG	0.54932	0.55369
cg1578384	MAD1L1	NFI/CTF [	610	617	9.352332	CCAATG	0.54932	0.55369
cg1578384	MAD1L1	NFI/CTF [	1112	1119	9.352332	AACTTT	0.54932	0.55369
cg1151970	MAD1L1	NFI/CTF [	1050	1057	9.352332	CCAAGG	0.54932	0.55369
cg0611220	MAD1L1	c-Myb [T0	814	821	9.29064	AAACTC	0.36621	0.34746
cg0231133	MAD1L1	NF-kappa	598	609	9.263487	GGGGAA	0.01776	0.01845
cg1151970	MAD1L1	NF-AT1 [	1318	1326	9.248801	GGACTT	0.22888	0.22581
cg0611220	MAD1L1	VDR [T00	1188	1196	9.234242	TTTCTG	0.12207	0.11552
cg1578384	MAD1L1	MEF-2A [	1449	1459	9.220261	TACTAA	0.07343	0.06466
cg0611220	MAD1L1	MEF-2A [	341	351	9.220261	TATTTTT	0.07343	0.06466
cg0231133	MAD1L1	AP-1 [T00	131	139	9.203282	ACTCAG	0.24414	0.23028
cg1002882	MAD1L1	AP-1 [T00	1951	1959	9.203282	ACTCAG	0.24414	0.23028
cg0231133	MAD1L1	RAR-alph	1050	1062	9.192562	GGGGTC	0.02065	0.02209
cg0372348	MAD1L1	PPAR-alph	798	808	9.158357	CTCTGG	0.0515	0.05878
cg0372348	MAD1L1	PPAR-alph	1232	1242	9.158357	GCGCCC	0.0515	0.05878
cg0231133	MAD1L1	NF-AT1 [	435	443	9.158155	GGAAAC	0.22888	0.22581
cg1002882	MAD1L1	NF-AT1 [	886	894	9.158155	TCTGTTT	0.22888	0.22581
cg0372348	MAD1L1	NF-AT1 [	770	778	9.158155	GGAAAC	0.22888	0.22581
cg1578384	MAD1L1	E2F [T002	605	614	9.15812	ATACGC	0.09537	0.09726
cg1002882	MAD1L1	c-Ets-1 [T	1518	1524	9.148774	AGGGAA	0.85449	0.84987
cg1578384	MAD1L1	c-Myb [T0	1111	1118	9.142015	CAACTT	0.39673	0.37851
cg0372348	MAD1L1	PXR-1:RX	61	68	9.122407	TGAACA	0.24414	0.24356
cg0231133	MAD1L1	HNF-1C [	124	132	9.116395	TTGAGT	0.12207	0.10938
cg0611220	MAD1L1	AP-1 [T00	1250	1258	9.116043	TGACTA	0.24414	0.23028
cg0231133	MAD1L1	NF-kappa	1931	1941	9.110464	TGCAGC	0.03576	0.03905
cg0372348	MAD1L1	LEF-1 [T0	925	932	9.099721	CTGCAA	0.54932	0.53171
cg0611220	MAD1L1	LEF-1 [T0	1196	1203	9.082175	CTTTGA	0.54932	0.53171
cg1578384	MAD1L1	c-Ets-1 [T	883	889	9.065503	ATGGAA	0.85449	0.84987
cg1151970	MAD1L1	c-Ets-1 [T	1803	1809	9.065503	ATTCCA	0.85449	0.84987
cg0611220	MAD1L1	c-Ets-1 [T	442	448	9.065503	ATTCCA	0.85449	0.84987
cg0231133	MAD1L1	USF2 [T0	560	569	9.056375	GCAGCA	0.1545	0.16206
cg1578384	MAD1L1	USF2 [T0	1924	1933	9.056375	GCCACA	0.1545	0.16206
cg1151970	MAD1L1	USF2 [T0	434	443	9.056375	CAGGTG	0.1545	0.16206
cg1151970	MAD1L1	USF2 [T0	1080	1089	9.056375	CTTCCA	0.1545	0.16206
cg1151970	MAD1L1	USF2 [T0	1840	1849	9.056375	CAGGTG	0.1545	0.16206
cg1002882	MAD1L1	USF2 [T0	487	496	9.056375	CAGGTG	0.1545	0.16206
cg0372348	MAD1L1	USF2 [T0	466	475	9.056375	CATCCA	0.1545	0.16206
cg0372348	MAD1L1	USF2 [T0	505	514	9.056375	CTCACA	0.1545	0.16206
cg0372348	MAD1L1	USF2 [T0	1294	1303	9.056375	CAGGTG	0.1545	0.16206
cg1151970	MAD1L1	NFI/CTF [	891	898	9.042931	CCAACA	0.48828	0.48845
cg1002882	MAD1L1	NFI/CTF [	435	442	9.042931	GCAGTT	0.48828	0.48845
cg0611220	MAD1L1	NFI/CTF [	1717	1724	9.042931	GCAGTT	0.48828	0.48845

cg1002882	MAD1L1	NF-AT1 [	1027	1035	9.042733	TTAATT	0.22888	0.22581
cg1002882	MAD1L1	NF-kappa	1769	1779	9.041011	GGCCTC	0.03576	0.03905
cg0231133	MAD1L1	MAZ [T00	503	515	9.029448	AGCCGG	0.01413	0.01595
cg0231133	MAD1L1	E2F-1 [T0	1670	1677	9.028527	GCGGGG	0.27466	0.30178
cg0231133	MAD1L1	E2F-1 [T0	1743	1750	9.028527	GCGGGG	0.27466	0.30178
cg0231133	MAD1L1	E2F-1 [T0	1876	1883	9.028527	GCGGGG	0.27466	0.30178
cg1002882	MAD1L1	E2F-1 [T0	1686	1693	9.028527	GCGGGG	0.27466	0.30178
cg1151970	MAD1L1	c-Myb [T0	844	851	9.024874	AAACTG	0.39673	0.37851
cg1151970	MAD1L1	c-Ets-1 [T	598	604	9.020687	GTTCCC	0.85449	0.84987
cg1002882	MAD1L1	c-Ets-1 [T	400	406	9.020687	GGGGAA	0.85449	0.84987
cg1002882	MAD1L1	c-Ets-1 [T	682	688	9.020687	GGGGAA	0.85449	0.84987
cg0611220	MAD1L1	NF-AT2 [	1266	1275	9.016873	ACATCT	0.05341	0.05145
cg0231133	MAD1L1	c-Jun [T00	1654	1660	9.013496	CACGTC	0.61035	0.60549
cg1578384	MAD1L1	c-Jun [T00	45	51	9.013496	CACGTC	0.61035	0.60549
cg1578384	MAD1L1	c-Jun [T00	209	215	9.013496	TGACAT	0.61035	0.60549
cg1151970	MAD1L1	c-Jun [T00	1509	1515	9.013496	TGACAT	0.61035	0.60549
cg1578384	MAD1L1	PXR-1:RX	1187	1194	8.998824	TGAACA	0.24414	0.24356
cg0611220	MAD1L1	PXR-1:RX	1263	1270	8.998824	TGAACA	0.24414	0.24356
cg0231133	MAD1L1	LEF-1 [T0	74	81	8.973041	TCCCAA	0.54932	0.53171
cg1578384	MAD1L1	LEF-1 [T0	1371	1378	8.973041	CTTTGG	0.54932	0.53171
cg1578384	MAD1L1	GR [T050	50	56	8.971049	CAAACA	0.61035	0.5928
cg1578384	MAD1L1	GR [T050	184	190	8.971049	CAAATA	0.61035	0.5928
cg1578384	MAD1L1	GR [T050	1046	1052	8.971049	CAAAAG	0.61035	0.5928
cg1578384	MAD1L1	GR [T050	1146	1152	8.971049	CAAAAG	0.61035	0.5928
cg1151970	MAD1L1	GR [T050	789	795	8.971049	CAAAAG	0.61035	0.5928
cg1151970	MAD1L1	GR [T050	948	954	8.971049	CAAAGC	0.61035	0.5928
cg1151970	MAD1L1	GR [T050	1982	1988	8.971049	CAAACA	0.61035	0.5928
cg1002882	MAD1L1	GR [T050	183	189	8.971049	CAAAAT	0.61035	0.5928
cg0611220	MAD1L1	GR [T050	962	968	8.971049	CAAAAG	0.61035	0.5928
cg0611220	MAD1L1	GR [T050	1839	1845	8.971049	CAAAAG	0.61035	0.5928
cg0372348	MAD1L1	EBF [T05	977	987	8.948874	TGCCCA	0.01526	0.01642
cg1151970	MAD1L1	c-Myb [T0	850	857	8.947824	AGAAGT	0.39673	0.37851
cg0372348	MAD1L1	c-Ets-1 [T	363	369	8.937416	GTGGAA	0.85449	0.84987
cg0372348	MAD1L1	c-Ets-1 [T	424	430	8.937416	ATTCCA	0.85449	0.84987
cg1151970	MAD1L1	Elk-1 [T00	1080	1088	8.931691	CTTCCA	0.24414	0.26271
cg1151970	MAD1L1	Elk-1 [T00	1844	1852	8.931691	TGCTGG	0.24414	0.26271
cg0611220	MAD1L1	Elk-1 [T00	42	50	8.931691	TGCTGG	0.24414	0.26271
cg0231133	MAD1L1	T3R-beta1	1396	1404	8.924046	AACGGG	0.2594	0.2685
cg1151970	MAD1L1	T3R-beta1	324	332	8.924046	TCACCC	0.2594	0.2685
cg1151970	MAD1L1	T3R-beta1	353	361	8.924046	TCACCC	0.2594	0.2685
cg1151970	MAD1L1	T3R-beta1	877	885	8.924046	TCACCC	0.2594	0.2685
cg0231133	MAD1L1	IRF-1 [T0	928	936	8.916359	TTTCCG	0.09155	0.09193
cg1578384	MAD1L1	c-Ets-2 [T	119	127	8.912323	GGCCAG	0.27466	0.27171
cg1578384	MAD1L1	c-Ets-2 [T	1757	1765	8.912323	CCTCAG	0.27466	0.27171
cg1151970	MAD1L1	c-Ets-2 [T	750	758	8.912323	GTCCAG	0.27466	0.27171
cg1002882	MAD1L1	c-Ets-2 [T	905	913	8.912323	CTCCAG	0.27466	0.27171
cg0611220	MAD1L1	c-Ets-2 [T	1031	1039	8.912323	ACCCAG	0.27466	0.27171
cg0372348	MAD1L1	c-Ets-2 [T	1102	1110	8.912323	GCTCAG	0.27466	0.27171

cg1002882	MAD1L1	p53 [T006	235	241	8.912104	GGGCCC	0.12207	0.13824
cg1002882	MAD1L1	p53 [T006	756	762	8.912104	AGGGCC	0.12207	0.13824
cg1002882	MAD1L1	p53 [T006	1981	1987	8.912104	GGGCCC	0.12207	0.13824
cg1578384	MAD1L1	c-Ets-1 [T	1908	1914	8.8926	CGGGAA	0.85449	0.84987
cg1151970	MAD1L1	c-Ets-1 [T	1065	1071	8.8926	GTTCCC	0.85449	0.84987
cg1002882	MAD1L1	c-Ets-1 [T	114	120	8.8926	CGGGAA	0.85449	0.84987
cg0231133	MAD1L1	GATA-2 [	1482	1490	8.888889	ACTGTA	0.22888	0.22339
cg1578384	MAD1L1	GATA-2 [	756	764	8.888889	CCAATA	0.22888	0.22339
cg1578384	MAD1L1	GATA-2 [	1339	1347	8.888889	GGATAC	0.22888	0.22339
cg0372348	MAD1L1	GATA-2 [	668	676	8.888889	GGATAT	0.22888	0.22339
cg1151970	MAD1L1	ETF [T002	220	230	8.876947	GAAGGC	0.02384	0.02809
cg0611220	MAD1L1	ATF-1 [T0	751	761	8.876947	TAACGT	0.02384	0.02296
cg0372348	MAD1L1	ETF [T002	1316	1326	8.876947	GCCCTG	0.02384	0.02809
cg0231133	MAD1L1	NF-kappa	1745	1755	8.843866	GGGGAC	0.03576	0.03905
cg0611220	MAD1L1	c-Jun [T00	1744	1750	8.832178	TGACCT	0.61035	0.60549
cg0231133	MAD1L1	PR B [T00	438	444	8.827054	AACAGA	0.36621	0.35051
cg0231133	MAD1L1	PR A [T01	438	444	8.827054	AACAGA	0.36621	0.35051
cg1578384	MAD1L1	PR B [T00	1775	1781	8.827054	AACAGC	0.36621	0.35051
cg1578384	MAD1L1	PR A [T01	1775	1781	8.827054	AACAGC	0.36621	0.35051
cg1002882	MAD1L1	PR B [T00	885	891	8.827054	ATCTGT	0.36621	0.35051
cg1002882	MAD1L1	PR A [T01	885	891	8.827054	ATCTGT	0.36621	0.35051
cg0611220	MAD1L1	PR B [T00	1782	1788	8.827054	AACAGC	0.36621	0.35051
cg0611220	MAD1L1	PR A [T01	1782	1788	8.827054	AACAGC	0.36621	0.35051
cg0372348	MAD1L1	PR B [T00	1095	1101	8.827054	AACAGG	0.36621	0.35051
cg0372348	MAD1L1	PR B [T00	1419	1425	8.827054	AACAGC	0.36621	0.35051
cg0372348	MAD1L1	PR A [T01	1095	1101	8.827054	AACAGG	0.36621	0.35051
cg0372348	MAD1L1	PR A [T01	1419	1425	8.827054	AACAGC	0.36621	0.35051
cg1151970	MAD1L1	NFI/CTF [	1966	1973	8.814757	CCAAGA	0.48828	0.48845
cg1002882	MAD1L1	NFI/CTF [	394	401	8.814757	CCTTTT	0.48828	0.48845
cg1002882	MAD1L1	NFI/CTF [	1192	1199	8.814757	CCTTTT	0.48828	0.48845
cg0611220	MAD1L1	NFI/CTF [	501	508	8.814757	TCACTT	0.48828	0.48845
cg1151970	MAD1L1	c-Ets-1 [T	1282	1288	8.809329	ATTCCA	0.85449	0.84987
cg0611220	MAD1L1	c-Ets-1 [T	1020	1026	8.809329	CTGGAA	0.85449	0.84987
cg0611220	MAD1L1	c-Ets-1 [T	1987	1993	8.809329	CTGGAA	0.85449	0.84987
cg1578384	MAD1L1	c-Jun [T00	72	78	8.807683	GTTGTC	0.61035	0.60549
cg0372348	MAD1L1	c-Jun [T00	520	526	8.807683	TGACGA	0.61035	0.60549
cg1151970	MAD1L1	Elk-1 [T00	1750	1758	8.797343	CTTCCA	0.24414	0.26271
cg0231133	MAD1L1	NF-1 [T00	72	79	8.790071	CCTCCC	0.24414	0.24339
cg1578384	MAD1L1	NF-1 [T00	1116	1123	8.790071	TTGGCA	0.24414	0.24339
cg0611220	MAD1L1	NF-1 [T00	286	293	8.790071	CCTCCC	0.24414	0.24339
cg0611220	MAD1L1	NF-1 [T00	555	562	8.790071	CCTCCC	0.24414	0.24339
cg0231133	MAD1L1	MAZ [T00	520	532	8.765913	AGATGG	0.01413	0.01595
cg0231133	MAD1L1	MAZ [T00	1457	1469	8.765913	TCCCCT	0.01413	0.01595
cg0231133	MAD1L1	Elk-1 [T00	478	486	8.762973	GAGCGG	0.24414	0.26271
cg0231133	MAD1L1	LEF-1 [T0	1491	1498	8.759086	ACACAA	0.54932	0.53171
cg1002882	MAD1L1	LEF-1 [T0	1006	1013	8.759086	CTTTGC	0.54932	0.53171
cg0231133	MAD1L1	XBP-1 [T	396	401	8.75604	ATGAAC	2.92969	2.75329
cg0231133	MAD1L1	XBP-1 [T	1170	1175	8.75604	ATGAGA	2.92969	2.75329

cg0231133	MAD1L1	XBP-1 [T0	1866	1871	8.75604	ATGATC	2.92969	2.75329
cg1578384	MAD1L1	XBP-1 [T0	163	168	8.75604	ATGAAA	2.92969	2.75329
cg1578384	MAD1L1	XBP-1 [T0	1186	1191	8.75604	ATGAAC	2.92969	2.75329
cg1002882	MAD1L1	XBP-1 [T0	407	412	8.75604	ATGAGC	2.92969	2.75329
cg1002882	MAD1L1	XBP-1 [T0	708	713	8.75604	TCTCAT	2.92969	2.75329
cg1002882	MAD1L1	XBP-1 [T0	1019	1024	8.75604	GTTCAT	2.92969	2.75329
cg1002882	MAD1L1	XBP-1 [T0	1106	1111	8.75604	GCTCAT	2.92969	2.75329
cg1002882	MAD1L1	XBP-1 [T0	1214	1219	8.75604	ATGAAA	2.92969	2.75329
cg1002882	MAD1L1	XBP-1 [T0	1260	1265	8.75604	ATGAAC	2.92969	2.75329
cg1002882	MAD1L1	XBP-1 [T0	1722	1727	8.75604	TTTCAT	2.92969	2.75329
cg0611220	MAD1L1	XBP-1 [T0	614	619	8.75604	ATGATA	2.92969	2.75329
cg0611220	MAD1L1	XBP-1 [T0	638	643	8.75604	TTTCAT	2.92969	2.75329
cg0611220	MAD1L1	XBP-1 [T0	768	773	8.75604	GATCAT	2.92969	2.75329
cg0611220	MAD1L1	XBP-1 [T0	1393	1398	8.75604	TCTCAT	2.92969	2.75329
cg0611220	MAD1L1	XBP-1 [T0	1472	1477	8.75604	TTTCAT	2.92969	2.75329
cg0611220	MAD1L1	XBP-1 [T0	1818	1823	8.75604	ATGAAC	2.92969	2.75329
cg0372348	MAD1L1	XBP-1 [T0	18	23	8.75604	ATGAAC	2.92969	2.75329
cg0372348	MAD1L1	XBP-1 [T0	1130	1135	8.75604	ATGAAC	2.92969	2.75329
cg0372348	MAD1L1	XBP-1 [T0	1455	1460	8.75604	GCTCAT	2.92969	2.75329
cg0372348	MAD1L1	XBP-1 [T0	1984	1989	8.75604	ATGATA	2.92969	2.75329
cg0611220	MAD1L1	HNF-1B [	71	79	8.696557	AGTTAC	0.11444	0.10456
cg0231133	MAD1L1	STAT1bet	1447	1456	8.695301	ATGTGG	0.22316	0.2175
cg1002882	MAD1L1	STAT1bet	196	205	8.695301	TGGGGG	0.22316	0.2175
cg1002882	MAD1L1	STAT1bet	1030	1039	8.695301	ATTTCC	0.22316	0.2175
cg1002882	MAD1L1	STAT1bet	1934	1943	8.695301	TGCAGG	0.22316	0.2175
cg0611220	MAD1L1	STAT1bet	1270	1279	8.695301	CTTTCC	0.22316	0.2175
cg1002882	MAD1L1	EBF [T05	1659	1669	8.642083	CTCGCA	0.03052	0.03497
cg0231133	MAD1L1	NF-AT1 [	600	608	8.599808	GGAAAA	0.10681	0.10494
cg1002882	MAD1L1	LEF-1 [T0	1545	1552	8.575454	GGCCAA	0.15259	0.154
cg1002882	MAD1L1	c-Jun [T00	1119	1125	8.571705	TGACTG	0.12207	0.1249
cg0611220	MAD1L1	c-Jun [T00	1165	1171	8.571705	TGACTG	0.12207	0.1249
cg0372348	MAD1L1	c-Jun [T00	1975	1981	8.571705	TGACTG	0.12207	0.1249
cg0611220	MAD1L1	IRF-1 [T0	1271	1279	8.570857	TTTCCA	0.20599	0.20245
cg0611220	MAD1L1	RAR-beta	989	998	8.55975	CGGGTT	0.26703	0.27434
cg0372348	MAD1L1	NF-AT2 [	374	383	8.550786	TATGAT	0.04959	0.04758
cg1578384	MAD1L1	p53 [T006	907	913	8.537081	AGAGCC	0.12207	0.13169
cg1151970	MAD1L1	p53 [T006	1261	1267	8.537081	GGGCTC	0.12207	0.13169
cg1151970	MAD1L1	p53 [T006	1349	1355	8.537081	AGAGCC	0.12207	0.13169
cg1002882	MAD1L1	p53 [T006	1334	1340	8.537081	GGGCTC	0.12207	0.13169
cg1002882	MAD1L1	p53 [T006	1471	1477	8.537081	GGGCTC	0.12207	0.13169
cg1002882	MAD1L1	p53 [T006	1666	1672	8.537081	GGGCTC	0.12207	0.13169
cg0611220	MAD1L1	p53 [T006	797	803	8.537081	GGGCTC	0.12207	0.13169
cg0372348	MAD1L1	p53 [T006	1268	1274	8.537081	GGGCTC	0.12207	0.13169
cg0372348	MAD1L1	p53 [T006	1321	1327	8.537081	GGGCTC	0.12207	0.13169
cg0372348	MAD1L1	NF-AT1 [	268	276	8.532897	GGAAAA	0.10681	0.10494
cg1151970	MAD1L1	USF2 [T0	1489	1498	8.532138	CGCACA	0.103	0.10815
cg0611220	MAD1L1	USF2 [T0	1202	1211	8.532138	CAGGTG	0.103	0.10815
cg0372348	MAD1L1	USF2 [T0	1097	1106	8.532138	CAGGTG	0.103	0.10815

cg0611220	MAD1L1	LEF-1 [T0	98	105	8.457856	CTTCAA	0.15259	0.154
cg0231133	MAD1L1	EBF [T05	1368	1378	8.453294	GCCCCT	0.03052	0.03497
cg0611220	MAD1L1	c-Myb [T0	1531	1538	8.443873	TTCAGT	0.30518	0.28602
cg0372348	MAD1L1	c-Myb [T0	1446	1453	8.443873	CAACTG	0.30518	0.28602
cg0231133	MAD1L1	AhR:Arnt	751	760	8.431005	GCACGC	0.07439	0.08553
cg1002882	MAD1L1	AhR:Arnt	1632	1641	8.431005	GTTGGC	0.07439	0.08553
cg0372348	MAD1L1	AhR:Arnt	145	154	8.431005	GCACGC	0.07439	0.08553
cg0611220	MAD1L1	c-Myb [T0	942	949	8.412632	TCCAGT	0.30518	0.28602
cg1002882	MAD1L1	PPAR-alp	3	13	8.384593	GGCTGG	0.02003	0.02186
cg1578384	MAD1L1	c-Ets-1 [T	914	920	8.373028	ATGGAA	0.24414	0.23702
cg0231133	MAD1L1	LEF-1 [T0	1071	1078	8.361499	GGACAA	0.15259	0.154
cg1002882	MAD1L1	LEF-1 [T0	1782	1789	8.361499	GGACAA	0.15259	0.154
cg0372348	MAD1L1	EBF [T05	1215	1225	8.349314	GCTCCA	0.03052	0.03497
cg1578384	MAD1L1	HNF-3alp	182	189	8.343064	TTCAAA	0.27466	0.23078
cg1578384	MAD1L1	HNF-3alp	1626	1633	8.343064	ATAAAA	0.27466	0.23078
cg1578384	MAD1L1	c-Ets-2 [T	1667	1675	8.339336	GGGTAG	0.13733	0.13927
cg1151970	MAD1L1	c-Ets-2 [T	639	647	8.339336	GGGCAG	0.13733	0.13927
cg1002882	MAD1L1	c-Ets-2 [T	1933	1941	8.339336	CTGCAG	0.13733	0.13927
cg0372348	MAD1L1	c-Ets-2 [T	208	216	8.339336	TTCCTG	0.13733	0.13927
cg0231133	MAD1L1	PR B [T00	161	167	8.338824	AACAGG	1.09863	1.09384
cg0231133	MAD1L1	PR B [T00	1002	1008	8.338824	AACAGA	1.09863	1.09384
cg0231133	MAD1L1	PR A [T01	161	167	8.338824	AACAGG	1.09863	1.09384
cg0231133	MAD1L1	PR A [T01	1002	1008	8.338824	AACAGA	1.09863	1.09384
cg1578384	MAD1L1	PR B [T00	1027	1033	8.338824	AACAGC	1.09863	1.09384
cg1578384	MAD1L1	PR B [T00	1195	1201	8.338824	AACAGA	1.09863	1.09384
cg1578384	MAD1L1	PR B [T00	1594	1600	8.338824	AACAGA	1.09863	1.09384
cg1578384	MAD1L1	PR B [T00	1674	1680	8.338824	AACAGA	1.09863	1.09384
cg1578384	MAD1L1	PR B [T00	1861	1867	8.338824	AACAGG	1.09863	1.09384
cg1578384	MAD1L1	PR A [T01	1027	1033	8.338824	AACAGC	1.09863	1.09384
cg1578384	MAD1L1	PR A [T01	1195	1201	8.338824	AACAGA	1.09863	1.09384
cg1578384	MAD1L1	PR A [T01	1594	1600	8.338824	AACAGA	1.09863	1.09384
cg1578384	MAD1L1	PR A [T01	1674	1680	8.338824	AACAGA	1.09863	1.09384
cg1578384	MAD1L1	PR A [T01	1861	1867	8.338824	AACAGG	1.09863	1.09384
cg1151970	MAD1L1	PR B [T00	829	835	8.338824	AACAGA	1.09863	1.09384
cg1151970	MAD1L1	PR B [T00	1939	1945	8.338824	AACAGC	1.09863	1.09384
cg1151970	MAD1L1	PR A [T01	829	835	8.338824	AACAGA	1.09863	1.09384
cg1151970	MAD1L1	PR A [T01	1939	1945	8.338824	AACAGC	1.09863	1.09384
cg1002882	MAD1L1	PR B [T00	459	465	8.338824	TCCTGT	1.09863	1.09384
cg1002882	MAD1L1	PR A [T01	459	465	8.338824	TCCTGT	1.09863	1.09384
cg0611220	MAD1L1	PR B [T00	32	38	8.338824	AACAGC	1.09863	1.09384
cg0611220	MAD1L1	PR B [T00	124	130	8.338824	TGCTGT	1.09863	1.09384
cg0611220	MAD1L1	PR B [T00	1355	1361	8.338824	GTCTGT	1.09863	1.09384
cg0611220	MAD1L1	PR B [T00	1652	1658	8.338824	AACAGA	1.09863	1.09384
cg0611220	MAD1L1	PR B [T00	1895	1901	8.338824	AACAGC	1.09863	1.09384
cg0611220	MAD1L1	PR A [T01	32	38	8.338824	AACAGC	1.09863	1.09384
cg0611220	MAD1L1	PR A [T01	124	130	8.338824	TGCTGT	1.09863	1.09384
cg0611220	MAD1L1	PR A [T01	1355	1361	8.338824	GTCTGT	1.09863	1.09384
cg0611220	MAD1L1	PR A [T01	1652	1658	8.338824	AACAGA	1.09863	1.09384

cg0611220	MAD1L1	PR A [T01	1895	1901	8.338824	AACAGC	1.09863	1.09384
cg0372348	MAD1L1	PR B [T00	276	282	8.338824	GGCTGT	1.09863	1.09384
cg0372348	MAD1L1	PR B [T00	773	779	8.338824	AACAGA	1.09863	1.09384
cg0372348	MAD1L1	PR B [T00	874	880	8.338824	AACAGG	1.09863	1.09384
cg0372348	MAD1L1	PR B [T00	960	966	8.338824	AACAGG	1.09863	1.09384
cg0372348	MAD1L1	PR B [T00	1090	1096	8.338824	AACAGA	1.09863	1.09384
cg0372348	MAD1L1	PR B [T00	1750	1756	8.338824	AACAGG	1.09863	1.09384
cg0372348	MAD1L1	PR B [T00	1990	1996	8.338824	AACAGA	1.09863	1.09384
cg0372348	MAD1L1	PR A [T01	276	282	8.338824	GGCTGT	1.09863	1.09384
cg0372348	MAD1L1	PR A [T01	773	779	8.338824	AACAGA	1.09863	1.09384
cg0372348	MAD1L1	PR A [T01	874	880	8.338824	AACAGG	1.09863	1.09384
cg0372348	MAD1L1	PR A [T01	960	966	8.338824	AACAGG	1.09863	1.09384
cg0372348	MAD1L1	PR A [T01	1090	1096	8.338824	AACAGA	1.09863	1.09384
cg0372348	MAD1L1	PR A [T01	1750	1756	8.338824	AACAGG	1.09863	1.09384
cg0372348	MAD1L1	PR A [T01	1990	1996	8.338824	AACAGA	1.09863	1.09384
cg1151970	MAD1L1	E2F-1 [T0	132	139	8.336446	TAACCC	0.15259	0.16676
cg1151970	MAD1L1	ATF3 [T0	589	596	8.313799	GGACGT	0.27466	0.27379
cg0231133	MAD1L1	GR-alpha [	72	76	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	224	228	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	473	477	8.281568	CCTTG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	508	512	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	525	529	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	531	535	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	575	579	8.281568	GAAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	684	688	8.281568	CGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	698	702	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	744	748	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	763	767	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	780	784	8.281568	CAAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	784	788	8.281568	GAAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	985	989	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1356	1360	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1410	1414	8.281568	CCTCG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1437	1441	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1460	1464	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1470	1474	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1666	1670	8.281568	CGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1739	1743	8.281568	GGAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1776	1780	8.281568	CAAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1780	1784	8.281568	GAAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1799	1803	8.281568	CCTCG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1816	1820	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1829	1833	8.281568	CAAGG	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1925	1929	8.281568	CCTCC	7.8125	8.20394
cg0231133	MAD1L1	GR-alpha [	1940	1944	8.281568	CCTCC	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha [	68	72	8.281568	CAAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha [	268	272	8.281568	CAAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha [	337	341	8.281568	CGAGG	7.8125	8.20394

cg1578384	MAD1L1	GR-alpha |	859	863	8.281568	GAAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	862	866	8.281568	GGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	865	869	8.281568	GGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	950	954	8.281568	CGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	995	999	8.281568	GAAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1003	1007	8.281568	CCTTG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1308	1312	8.281568	CAAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1376	1380	8.281568	GAAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1398	1402	8.281568	CGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1541	1545	8.281568	GGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1547	1551	8.281568	GGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1821	1825	8.281568	GGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1835	1839	8.281568	GGAGG	7.8125	8.20394
cg1578384	MAD1L1	GR-alpha |	1947	1951	8.281568	CAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	69	73	8.281568	CAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	178	182	8.281568	CCTTC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	220	224	8.281568	GAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	282	286	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	308	312	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	311	315	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	328	332	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	337	341	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	357	361	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	383	387	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	392	396	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	417	421	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	423	427	8.281568	GAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	430	434	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	440	444	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	443	447	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	474	478	8.281568	CAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	479	483	8.281568	CCTCG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	498	502	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	528	532	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	812	816	8.281568	GAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	932	936	8.281568	GAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	990	994	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1051	1055	8.281568	CAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1095	1099	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1222	1226	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1229	1233	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1235	1239	8.281568	CGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1246	1250	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1343	1347	8.281568	GAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1370	1374	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1436	1440	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1460	1464	8.281568	CCTTC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1607	1611	8.281568	CCTCC	7.8125	8.20394

cg1151970	MAD1L1	GR-alpha |	1632	1636	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1651	1655	8.281568	CCTCC	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1657	1661	8.281568	GAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1660	1664	8.281568	GGAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1724	1728	8.281568	CAAGG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1811	1815	8.281568	CCTCG	7.8125	8.20394
cg1151970	MAD1L1	GR-alpha |	1914	1918	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	29	33	8.281568	CCTCC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	173	177	8.281568	CCTTC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	300	304	8.281568	CAAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	324	328	8.281568	GAAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	457	461	8.281568	CCTCC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	571	575	8.281568	CAAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	597	601	8.281568	CCTCC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	794	798	8.281568	CCTCC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	904	908	8.281568	CCTCC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	960	964	8.281568	CGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1039	1043	8.281568	CGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1238	1242	8.281568	CGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1243	1247	8.281568	CCTCG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1342	1346	8.281568	GAAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1354	1358	8.281568	CAAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1387	1391	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1421	1425	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1484	1488	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1516	1520	8.281568	GAAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1532	1536	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1559	1563	8.281568	CCTTC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1589	1593	8.281568	CCTTG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1658	1662	8.281568	CCTCG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1690	1694	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1701	1705	8.281568	CCTCG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1748	1752	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1875	1879	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1880	1884	8.281568	GGAGG	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1896	1900	8.281568	CCTCC	7.8125	8.20394
cg1002882	MAD1L1	GR-alpha |	1975	1979	8.281568	CCTCC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	37	41	8.281568	CCTTC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	97	101	8.281568	CCTTC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	248	252	8.281568	CCTCC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	254	258	8.281568	CCTTC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	286	290	8.281568	CCTCC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	419	423	8.281568	CCTCG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	555	559	8.281568	CCTCC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	657	661	8.281568	CCTCG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	686	690	8.281568	CCTCC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	785	789	8.281568	CCTTC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha |	859	863	8.281568	CCTTC	7.8125	8.20394

cg0611220	MAD1L1	GR-alpha [	891	895	8.281568	GGAGG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	923	927	8.281568	GAAGG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1004	1008	8.281568	CCTCG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1086	1090	8.281568	CCTCG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1133	1137	8.281568	CAAGG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1464	1468	8.281568	CCTTG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1548	1552	8.281568	GAAGG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1686	1690	8.281568	CAAGG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1747	1751	8.281568	CCTTC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1809	1813	8.281568	GGAGG	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1960	1964	8.281568	CCTCC	7.8125	8.20394
cg0611220	MAD1L1	GR-alpha [	1969	1973	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	45	49	8.281568	GAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	55	59	8.281568	GGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	153	157	8.281568	CCTTC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	197	201	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	223	227	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	235	239	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	262	266	8.281568	GGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	357	361	8.281568	GAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	384	388	8.281568	CGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	488	492	8.281568	CCTTG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	547	551	8.281568	GGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	618	622	8.281568	GGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	621	625	8.281568	GGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	633	637	8.281568	CCTCG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	638	642	8.281568	CAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	852	856	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1004	1008	8.281568	CCTTG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1012	1016	8.281568	CAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1160	1164	8.281568	CCTCG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1171	1175	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1192	1196	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1211	1215	8.281568	CAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1224	1228	8.281568	GAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1249	1253	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1439	1443	8.281568	CCTTC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1480	1484	8.281568	CCTTG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1485	1489	8.281568	CCTTC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1494	1498	8.281568	CCTTC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1577	1581	8.281568	CCTCC	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1591	1595	8.281568	CGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1726	1730	8.281568	GGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1756	1760	8.281568	CGAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1793	1797	8.281568	GAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1843	1847	8.281568	CAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1858	1862	8.281568	GAAGG	7.8125	8.20394
cg0372348	MAD1L1	GR-alpha [	1923	1927	8.281568	CCTTC	7.8125	8.20394

cg0611220	MAD1L1	AR [T000	926	934	8.272289	GGACAT	0.10681	0.10838
cg0231133	MAD1L1	c-Ets-1 [T	729	735	8.244941	GTTCCA	0.24414	0.2494
cg0231133	MAD1L1	c-Ets-1 [T	1552	1558	8.244941	GTGGAA	0.24414	0.2494
cg1578384	MAD1L1	c-Ets-1 [T	279	285	8.244941	GTGGAA	0.24414	0.2494
cg1151970	MAD1L1	c-Ets-1 [T	632	638	8.244941	GTTCCA	0.24414	0.2494
cg1002882	MAD1L1	c-Ets-1 [T	71	77	8.244941	GTTCCA	0.24414	0.2494
cg1578384	MAD1L1	c-Jun [T00	1399	1405	8.242207	GAGGTC	0.48828	0.47447
cg1151970	MAD1L1	c-Jun [T00	1433	1439	8.242207	TGACCT	0.48828	0.47447
cg0611220	MAD1L1	c-Jun [T00	398	404	8.242207	TGACCT	0.48828	0.47447
cg1002882	MAD1L1	NFI/CTF [	20	27	8.241664	CCAACC	0.18311	0.1922
cg0611220	MAD1L1	NFI/CTF [	1681	1688	8.241664	CCAACC	0.18311	0.1922
cg0231133	MAD1L1	p53 [T006	1365	1371	8.208781	GGGGCC	0.48828	0.55336
cg0231133	MAD1L1	p53 [T006	1366	1372	8.208781	GGGCCC	0.48828	0.55336
cg1151970	MAD1L1	p53 [T006	81	87	8.208781	GGGCCC	0.48828	0.55336
cg1151970	MAD1L1	p53 [T006	1682	1688	8.208781	GGGGCC	0.48828	0.55336
cg1002882	MAD1L1	p53 [T006	234	240	8.208781	GGGGCC	0.48828	0.55336
cg1002882	MAD1L1	p53 [T006	757	763	8.208781	GGGCCC	0.48828	0.55336
cg1151970	MAD1L1	NF-AT1 [	108	116	8.200059	GGAAAC	0.1297	0.12846
cg0231133	MAD1L1	ENKTF-1	568	575	8.19852	TGGCTG	0.73242	0.80254
cg0231133	MAD1L1	ENKTF-1	1194	1201	8.19852	TGGCAG	0.73242	0.80254
cg1578384	MAD1L1	ENKTF-1	974	981	8.19852	TGGCAG	0.73242	0.80254
cg1151970	MAD1L1	ENKTF-1	618	625	8.19852	TGGCAA	0.73242	0.80254
cg1151970	MAD1L1	ENKTF-1	680	687	8.19852	CCCAGC	0.73242	0.80254
cg1151970	MAD1L1	ENKTF-1	1729	1736	8.19852	TGGCTG	0.73242	0.80254
cg1002882	MAD1L1	ENKTF-1	211	218	8.19852	TGGCAG	0.73242	0.80254
cg1002882	MAD1L1	ENKTF-1	226	233	8.19852	TGGCGG	0.73242	0.80254
cg0611220	MAD1L1	ENKTF-1	372	379	8.19852	TGGCCA	0.73242	0.80254
cg0372348	MAD1L1	ENKTF-1	643	650	8.19852	TCTCGC	0.73242	0.80254
cg0372348	MAD1L1	ENKTF-1	1395	1402	8.19852	TGGCCA	0.73242	0.80254
cg0372348	MAD1L1	ENKTF-1	1966	1973	8.19852	CGCTGC	0.73242	0.80254
cg1578384	MAD1L1	NF-1 [T00	1657	1664	8.191058	AAGCCC	0.24414	0.24485
cg1151970	MAD1L1	NF-1 [T00	792	799	8.191058	AAGCCC	0.24414	0.24485
cg1151970	MAD1L1	NF-1 [T00	1046	1053	8.191058	GAGGCC	0.24414	0.24485
cg1002882	MAD1L1	NF-1 [T00	1543	1550	8.191058	GAGGCC	0.24414	0.24485
cg1578384	MAD1L1	AhR [T01	1350	1360	8.184723	CTCACG	0.04864	0.05013
cg0231133	MAD1L1	PXR-1:RX	863	870	8.180749	AATGTT	0.12207	0.11255
cg1578384	MAD1L1	PXR-1:RX	178	185	8.180749	AATGTT	0.12207	0.11255
cg1151970	MAD1L1	PXR-1:RX	622	629	8.180749	AACGTT	0.12207	0.11255
cg0231133	MAD1L1	SRY [T00	1490	1498	8.174786	CACACA	0.15259	0.14791
cg0611220	MAD1L1	SRY [T00	97	105	8.174786	CCTTCA	0.15259	0.14791
cg1151970	MAD1L1	p53 [T006	901	907	8.162057	AGCGCC	0.48828	0.55336
cg0231133	MAD1L1	IRF-1 [T0	1410	1418	8.151819	CCTCGG	0.25177	0.2462
cg1578384	MAD1L1	c-Jun [T00	1970	1976	8.128539	AACGTC	0.48828	0.47447
cg0611220	MAD1L1	c-Jun [T00	752	758	8.128539	AACGTC	0.48828	0.47447
cg0231133	MAD1L1	NF-AT1 [	924	932	8.12076	GTCTTTT	0.1297	0.12846
cg0611220	MAD1L1	LEF-1 [T0	427	434	8.117221	TCTCAA	0.12207	0.11275
cg0611220	MAD1L1	c-Ets-1 [T	1096	1102	8.116854	GTTCCA	0.24414	0.2494
cg0372348	MAD1L1	c-Ets-1 [T	1086	1092	8.116854	CTGGAA	0.24414	0.2494

cg1002882	MAD1L1	AR [T000	13	21	8.11332	CACCTG	0.19836	0.20641
cg1578384	MAD1L1	VDR [T00	181	189	8.079962	GTTCAA	0.24414	0.22992
cg1002882	MAD1L1	VDR [T00	1019	1027	8.079962	GTTCATC	0.24414	0.22992
cg1002882	MAD1L1	VDR [T00	1257	1265	8.079962	GTAATG	0.24414	0.22992
cg0611220	MAD1L1	VDR [T00	1815	1823	8.079962	GAAATG	0.24414	0.22992
cg0372348	MAD1L1	VDR [T00	15	23	8.079962	TCCATG	0.24414	0.22992
cg0372348	MAD1L1	VDR [T00	906	914	8.079962	GTTCAA	0.24414	0.22992
cg0611220	MAD1L1	AR [T000	113	121	8.079301	GGACAA	0.19836	0.20641
cg1151970	MAD1L1	IRF-1 [T0	1517	1525	8.078284	TTTCCAC	0.25177	0.2462
cg1002882	MAD1L1	IRF-1 [T0	890	898	8.078284	TTTCCGC	0.25177	0.2462
cg0231133	MAD1L1	GR-alpha [	26	30	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	66	70	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	115	119	8.073878	CCTGC	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	228	232	8.073878	CCTGC	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	247	251	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	276	280	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	283	287	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	324	328	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	352	356	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	364	368	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	404	408	8.073878	CCTGC	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	431	435	8.073878	CTAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	556	560	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	566	570	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	583	587	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	633	637	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	639	643	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	651	655	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	759	763	8.073878	CCTGC	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	854	858	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1057	1061	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1196	1200	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1208	1212	8.073878	GTAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1230	1234	8.073878	CCTAG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1231	1235	8.073878	CTAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1286	1290	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1371	1375	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1441	1445	8.073878	CCTAG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1613	1617	8.073878	CTAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1819	1823	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1825	1829	8.073878	CCTGC	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1848	1852	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1853	1857	8.073878	CCAGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1858	1862	8.073878	CCTGG	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1929	1933	8.073878	CCTGC	7.8125	8.20289
cg0231133	MAD1L1	GR-alpha [	1988	1992	8.073878	CCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha [	82	86	8.073878	GCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha [	95	99	8.073878	GCAGG	7.8125	8.20289

cg1578384	MAD1L1	GR-alpha |	121	125	8.073878	CCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	191	195	8.073878	GCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	838	842	8.073878	CCTGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1119	1123	8.073878	GCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1332	1336	8.073878	CCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1386	1390	8.073878	GCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1519	1523	8.073878	GCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1587	1591	8.073878	CCTGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1669	1673	8.073878	GTAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1688	1692	8.073878	CCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1698	1702	8.073878	CCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1800	1804	8.073878	CCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1818	1822	8.073878	GCAGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1874	1878	8.073878	CCTGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1930	1934	8.073878	CCTGG	7.8125	8.20289
cg1578384	MAD1L1	GR-alpha |	1956	1960	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	11	15	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	59	63	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	246	250	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	257	261	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	317	321	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	346	350	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	372	376	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	397	401	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	433	437	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	458	462	8.073878	CCTAG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	484	488	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	501	505	8.073878	CCTAC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	525	529	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	616	620	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	641	645	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	685	689	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	713	717	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	752	756	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	906	910	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	980	984	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1016	1020	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1022	1026	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1061	1065	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1086	1090	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1092	1096	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1101	1105	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1130	1134	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1152	1156	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1171	1175	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1188	1192	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1226	1230	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1258	1262	8.073878	CTAGG	7.8125	8.20289

cg1151970	MAD1L1	GR-alpha |	1285	1289	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1292	1296	8.073878	CCTAG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1326	1330	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1337	1341	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1355	1359	8.073878	CCTAG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1424	1428	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1452	1456	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1520	1524	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1526	1530	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1610	1614	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1678	1682	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1687	1691	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1701	1705	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1757	1761	8.073878	CCTGC	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1776	1780	8.073878	CCTGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1839	1843	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1854	1858	8.073878	GCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1890	1894	8.073878	CCAGG	7.8125	8.20289
cg1151970	MAD1L1	GR-alpha |	1951	1955	8.073878	CCTGC	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	42	46	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	142	146	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	213	217	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	231	235	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	239	243	8.073878	CCTGC	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	479	483	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	486	490	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	499	503	8.073878	CCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	536	540	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	542	546	8.073878	CCTGC	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	600	604	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	610	614	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	624	628	8.073878	CCTGC	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	670	674	8.073878	CCTGC	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	724	728	8.073878	CCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	754	758	8.073878	CCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	767	771	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	771	775	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	907	911	8.073878	CCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	944	948	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	966	970	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1066	1070	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1221	1225	8.073878	CCTGC	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1230	1234	8.073878	GTAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1276	1280	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1360	1364	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1383	1387	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1432	1436	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1510	1514	8.073878	CCTGG	7.8125	8.20289

cg1002882	MAD1L1	GR-alpha |	1582	1586	8.073878	CCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1599	1603	8.073878	CCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1605	1609	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1617	1621	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1625	1629	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1651	1655	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1662	1666	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1779	1783	8.073878	CCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1848	1852	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1888	1892	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1932	1936	8.073878	CCTGC	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1935	1939	8.073878	GCAGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1978	1982	8.073878	CCTGG	7.8125	8.20289
cg1002882	MAD1L1	GR-alpha |	1985	1989	8.073878	CCTGC	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	58	62	8.073878	CTAGG	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	93	97	8.073878	CCTGC	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	208	212	8.073878	CCAGG	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	276	280	8.073878	CCTGC	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	375	379	8.073878	CCAGG	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	393	397	8.073878	CCTGC	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	820	824	8.073878	CCTGG	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	971	975	8.073878	CTAGG	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	1033	1037	8.073878	CCAGG	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	1099	1103	8.073878	CCAGG	7.8125	8.20289
cg0611220	MAD1L1	GR-alpha |	1931	1935	8.073878	CCTGC	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	28	32	8.073878	CCTAC	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	52	56	8.073878	GCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	67	71	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	120	124	8.073878	CCTGC	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	132	136	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	158	162	8.073878	CCTGC	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	210	214	8.073878	CCTGC	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	303	307	8.073878	CCTGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	353	357	8.073878	GTAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	511	515	8.073878	CCTGC	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	614	618	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	757	761	8.073878	GCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	847	851	8.073878	CTAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	934	938	8.073878	CTAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	965	969	8.073878	GCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	980	984	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	988	992	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	1085	1089	8.073878	CCTGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	1180	1184	8.073878	GCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	1218	1222	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	1237	1241	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	1265	1269	8.073878	CCTGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha |	1293	1297	8.073878	GCAGG	7.8125	8.20289

cg0372348	MAD1L1	GR-alpha [	1318	1322	8.073878	CCTGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1398	1402	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1404	1408	8.073878	GCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1584	1588	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1631	1635	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1650	1654	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1667	1671	8.073878	CCTAG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1697	1701	8.073878	CCTGC	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1717	1721	8.073878	CCTGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1765	1769	8.073878	GCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1789	1793	8.073878	CCAGG	7.8125	8.20289
cg0372348	MAD1L1	GR-alpha [	1834	1838	8.073878	GCAGG	7.8125	8.20289
cg0231133	MAD1L1	Ik-1 [T027	77	89	8.033887	CAAAGC	0.00355	0.00395
cg0231133	MAD1L1	TFIID [T0	883	889	8.014558	TTTCAA	2.19727	1.99811
cg0231133	MAD1L1	TFIID [T0	1144	1150	8.014558	TATCAA	2.19727	1.99811
cg0231133	MAD1L1	TFIID [T0	1329	1335	8.014558	TCAGAA	2.19727	1.99811
cg0231133	MAD1L1	TFIID [T0	1412	1418	8.014558	TCGGAA	2.19727	1.99811
cg0231133	MAD1L1	Pax-5 [T0	21	27	8.014558	GCTGCC	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	69	75	8.014558	GGGCCT	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	198	204	8.014558	GGGCCT	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	534	540	8.014558	GGGCTG	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	587	593	8.014558	GGGCAG	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	678	684	8.014558	GGGCAG	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	1022	1028	8.014558	GGGCTT	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	1256	1262	8.014558	GGTGCC	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	1365	1371	8.014558	GGGGCC	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	1366	1372	8.014558	GGGCCC	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	1768	1774	8.014558	TGAGCC	2.19727	2.42766
cg0231133	MAD1L1	Pax-5 [T0	1843	1849	8.014558	GCTGCC	2.19727	2.42766
cg1578384	MAD1L1	TFIID [T0	1611	1617	8.014558	TCTCAA	2.19727	1.99811
cg1578384	MAD1L1	Pax-5 [T0	194	200	8.014558	GGGCAG	2.19727	2.42766
cg1578384	MAD1L1	Pax-5 [T0	1691	1697	8.014558	GGTGCC	2.19727	2.42766
cg1578384	MAD1L1	Pax-5 [T0	1901	1907	8.014558	GCAGCC	2.19727	2.42766
cg1578384	MAD1L1	Pax-5 [T0	1950	1956	8.014558	GGGCAC	2.19727	2.42766
cg1151970	MAD1L1	TFIID [T0	125	131	8.014558	TTTCAG	2.19727	1.99811
cg1151970	MAD1L1	TFIID [T0	1979	1985	8.014558	TTTCAA	2.19727	1.99811
cg1151970	MAD1L1	Pax-5 [T0	62	68	8.014558	GGGCAC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	80	86	8.014558	TGGGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	81	87	8.014558	GGGCCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	210	216	8.014558	GGGCTG	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	277	283	8.014558	TCAGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	465	471	8.014558	GCTGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	689	695	8.014558	GGTGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1096	1102	8.014558	GAGGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1125	1131	8.014558	GGGCAC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1174	1180	8.014558	GGGCTG	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1191	1197	8.014558	GGGCTC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1374	1380	8.014558	GGGCAG	2.19727	2.42766

cg1151970	MAD1L1	Pax-5 [T0	1383	1389	8.014558	GGGCAC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1530	1536	8.014558	GATGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1672	1678	8.014558	TGAGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1682	1688	8.014558	GGGGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1683	1689	8.014558	GGGCCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1779	1785	8.014558	GGGCAG	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1815	1821	8.014558	GGAGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1866	1872	8.014558	GGAGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1879	1885	8.014558	GAGGCC	2.19727	2.42766
cg1151970	MAD1L1	Pax-5 [T0	1893	1899	8.014558	GGGCAG	2.19727	2.42766
cg1002882	MAD1L1	TFIID [T0	1213	1219	8.014558	TATGAA	2.19727	1.99811
cg1002882	MAD1L1	Pax-5 [T0	7	13	8.014558	GGGCCT	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	45	51	8.014558	GGGCAG	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	107	113	8.014558	GGGCTG	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	234	240	8.014558	GGGGCC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	494	500	8.014558	GGGCAC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	576	582	8.014558	GGTGCC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	613	619	8.014558	GGGCTG	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	757	763	8.014558	GGGCCC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	775	781	8.014558	GGAGCC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	994	1000	8.014558	GGGCTC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	1463	1469	8.014558	GGGCAG	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	1696	1702	8.014558	GGAGCC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	1757	1763	8.014558	GCAGCC	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	1838	1844	8.014558	GGGCTG	2.19727	2.42766
cg1002882	MAD1L1	Pax-5 [T0	1980	1986	8.014558	TGGGCC	2.19727	2.42766
cg0611220	MAD1L1	TFIID [T0	106	112	8.014558	TTTCAG	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	178	184	8.014558	TTTGAG	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	427	433	8.014558	TCTCAA	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	1078	1084	8.014558	TAAGAA	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	1188	1194	8.014558	TTTCTGA	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	1339	1345	8.014558	TTTGCTA	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	1382	1388	8.014558	TTTGAG	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	1409	1415	8.014558	TAACAA	2.19727	1.99811
cg0611220	MAD1L1	TFIID [T0	1438	1444	8.014558	TTGCAA	2.19727	1.99811
cg0611220	MAD1L1	Pax-5 [T0	1278	1284	8.014558	GGGCTT	2.19727	2.42766
cg0372348	MAD1L1	TFIID [T0	1198	1204	8.014558	TTTCAG	2.19727	1.99811
cg0372348	MAD1L1	Pax-5 [T0	285	291	8.014558	GGGCTC	2.19727	2.42766
cg0372348	MAD1L1	Pax-5 [T0	1348	1354	8.014558	GGGCAG	2.19727	2.42766
cg0372348	MAD1L1	Pax-5 [T0	1510	1516	8.014558	GGGCTG	2.19727	2.42766
cg0372348	MAD1L1	Pax-5 [T0	1641	1647	8.014558	GGGCTC	2.19727	2.42766
cg0372348	MAD1L1	Pax-5 [T0	1778	1784	8.014558	GGAGCC	2.19727	2.42766
cg0372348	MAD1L1	Pax-5 [T0	1872	1878	8.014558	GGGCAC	2.19727	2.42766
cg0372348	MAD1L1	Pax-5 [T0	1888	1894	8.014558	GATGCC	2.19727	2.42766
cg0372348	MAD1L1	Pax-5 [T0	1945	1951	8.014558	GGGCTG	2.19727	2.42766
cg1151970	MAD1L1	AhR:Arnt	1665	1674	8.006459	CCACGC	0.01717	0.01925
cg0611220	MAD1L1	HNF-1C [	72	80	8.002145	GTTACA	0.19836	0.18126
cg1578384	MAD1L1	MEF-2A [	1645	1655	7.982343	AAATAA	0.04005	0.03447

cg1002882	MAD1L1	RAR-alpha	172	184	7.963622	TCCTTCT	0.01627	0.01726
cg0231133	MAD1L1	ETF [T002	222	232	7.870358	GCCCTC	0.07153	0.08737
cg1151970	MAD1L1	ETF [T002	1533	1543	7.870358	GCCCTC	0.07153	0.08737
cg1002882	MAD1L1	ETF [T002	237	247	7.870358	GCCCTG	0.07153	0.08737
cg0372348	MAD1L1	ATF-1 [T0	624	634	7.870358	GGACGT	0.07153	0.07126
cg0372348	MAD1L1	ETF [T002	1627	1637	7.870358	GCGCCC	0.07153	0.08737
cg0611220	MAD1L1	HNF-1B [	747	755	7.862525	TTAATA	0.06866	0.0616
cg0611220	MAD1L1	HNF-1B [	1801	1809	7.862525	TTAATA	0.06866	0.0616
cg1151970	MAD1L1	AR [T000	1249	1257	7.861806	GGACAG	0.19836	0.20641
cg1151970	MAD1L1	EBF [T05	1887	1897	7.856915	TCTCCA	0.04196	0.04563
cg1002882	MAD1L1	p53 [T006	1612	1618	7.853573	ATGGCC	0.48828	0.55336
cg0372348	MAD1L1	p53 [T006	675	681	7.853573	GGGCCA	0.48828	0.55336
cg0611220	MAD1L1	c-Ets-2 [T	969	977	7.84116	TGCTAG	0.32043	0.30792
cg0372348	MAD1L1	c-Ets-2 [T	1787	1795	7.84116	CACCAG	0.32043	0.30792
cg1151970	MAD1L1	p53 [T006	1191	1197	7.833758	GGGCTC	0.48828	0.55336
cg1151970	MAD1L1	p53 [T006	1815	1821	7.833758	GGAGCC	0.48828	0.55336
cg1151970	MAD1L1	p53 [T006	1866	1872	7.833758	GGAGCC	0.48828	0.55336
cg1002882	MAD1L1	p53 [T006	775	781	7.833758	GGAGCC	0.48828	0.55336
cg1002882	MAD1L1	p53 [T006	994	1000	7.833758	GGGCTC	0.48828	0.55336
cg1002882	MAD1L1	p53 [T006	1696	1702	7.833758	GGAGCC	0.48828	0.55336
cg0372348	MAD1L1	p53 [T006	285	291	7.833758	GGGCTC	0.48828	0.55336
cg0372348	MAD1L1	p53 [T006	1641	1647	7.833758	GGGCTC	0.48828	0.55336
cg0372348	MAD1L1	p53 [T006	1778	1784	7.833758	GGAGCC	0.48828	0.55336
cg0231133	MAD1L1	RelA [T00	597	607	7.829093	AGGGGA	0.02003	0.02093
cg1578384	MAD1L1	c-Myb [T0	488	495	7.825375	CCAAGT	0.21362	0.20997
cg1151970	MAD1L1	IRF-1 [T0	751	759	7.82345	TCCAGG	0.25177	0.2462
cg1002882	MAD1L1	IRF-1 [T0	1934	1942	7.82345	TGCAGG	0.25177	0.2462
cg1578384	MAD1L1	RXR-alpha	1896	1902	7.815913	GGGTGG	0.24414	0.26389
cg1002882	MAD1L1	RXR-alpha	208	214	7.815913	GGGTGG	0.24414	0.26389
cg1002882	MAD1L1	RXR-alpha	516	522	7.815913	GGGTGG	0.24414	0.26389
cg1002882	MAD1L1	RXR-alpha	948	954	7.815913	GGGTGG	0.24414	0.26389
cg1002882	MAD1L1	RXR-alpha	1436	1442	7.815913	GGGTGG	0.24414	0.26389
cg0611220	MAD1L1	RXR-alpha	1102	1108	7.815913	GGGTGG	0.24414	0.26389
cg0372348	MAD1L1	RXR-alpha	1685	1691	7.815913	GGGTGG	0.24414	0.26389
cg0372348	MAD1L1	T3R-beta1	109	117	7.813363	TCACCC	0.27466	0.28753
cg0231133	MAD1L1	AR [T000	1747	1755	7.804321	GGACAC	0.19836	0.20641
cg1151970	MAD1L1	AR [T000	139	147	7.804321	CGTGTG	0.19836	0.20641
cg1002882	MAD1L1	T3R-beta1	464	472	7.79407	TTTGGG	0.27466	0.28753
cg1151970	MAD1L1	NF-AT2 [	1512	1521	7.779688	CATGAT	0.08965	0.08482
cg1002882	MAD1L1	NF-AT2 [	1093	1102	7.779688	AAGCCT	0.08965	0.08482
cg1002882	MAD1L1	GATA-2 [	837	845	7.777778	GCGATA	0.30518	0.29346
cg0611220	MAD1L1	GATA-2 [	588	596	7.777778	ACAGTA	0.30518	0.29346
cg0611220	MAD1L1	GATA-2 [	615	623	7.777778	TGATAC	0.30518	0.29346
cg0611220	MAD1L1	T3R-beta1	204	212	7.774776	TCACCC	0.27466	0.28753
cg0231133	MAD1L1	c-Ets-2 [T	1096	1104	7.76635	CCACAG	0.32043	0.30792
cg1002882	MAD1L1	c-Ets-2 [T	1250	1258	7.76635	TTCCTAT	0.32043	0.30792
cg1578384	MAD1L1	NF-AT1 [	1762	1770	7.744746	GGAAAG	0.19836	0.19379
cg0372348	MAD1L1	NF-AT1 [	835	843	7.744746	TTCCTTT	0.19836	0.19379

cg1002882	MAD1L1	c-Myb [T0	1968	1975	7.739476	CACAGT	0.42725	0.40917
cg0372348	MAD1L1	c-Myb [T0	1108	1115	7.739476	GAACTG	0.42725	0.40917
cg0231133	MAD1L1	IRF-1 [T0	209	217	7.732782	TTTCCAC	0.14496	0.14723
cg1002882	MAD1L1	IRF-1 [T0	1098	1106	7.732782	TTTCCAC	0.14496	0.14723
cg0611220	MAD1L1	NF-AT1 [	1689	1697	7.72101	GGAAAC	0.19836	0.19379
cg0231133	MAD1L1	NF-kappa	598	608	7.716553	GGGGAA	0.04435	0.04858
cg0231133	MAD1L1	MAZ [T00	1937	1949	7.713557	TCCCCTC	0.00641	0.00703
cg0231133	MAD1L1	c-Jun [T00	775	781	7.686747	ACAGTC	0.48828	0.48672
cg0611220	MAD1L1	c-Jun [T00	619	625	7.686747	ACAGTC	0.48828	0.48672
cg0231133	MAD1L1	MAZ [T00	221	233	7.686328	AGCCCTC	0.00641	0.00703
cg0611220	MAD1L1	c-Myb [T0	1527	1534	7.662426	CAACTTC	0.42725	0.40917
cg1578384	MAD1L1	c-Ets-1 [T	1204	1210	7.642098	ATTCCG	0.48828	0.48642
cg1578384	MAD1L1	p53 [T006	1327	1333	7.641867	AAGGCC	0.73242	0.79826
cg1151970	MAD1L1	p53 [T006	1919	1925	7.641867	ACGGCC	0.73242	0.79826
cg0372348	MAD1L1	p53 [T006	603	609	7.641867	ACGGCC	0.73242	0.79826
cg0372348	MAD1L1	p53 [T006	1001	1007	7.641867	GGGCCT	0.73242	0.79826
cg0611220	MAD1L1	AR [T000	1178	1186	7.623968	ATGGTG	0.25177	0.2544
cg1578384	MAD1L1	LEF-1 [T0	1659	1666	7.6105	GCCCAA	0.21362	0.21504
cg1151970	MAD1L1	NFI/CTF [	788	795	7.587343	CCAAAA	0.36621	0.36269
cg0611220	MAD1L1	NFI/CTF [	559	566	7.587343	CCAATA	0.36621	0.36269
cg0372348	MAD1L1	NFI/CTF [	1270	1277	7.587343	GCTCTTC	0.36621	0.36269
cg0231133	MAD1L1	NF-AT1 [	205	213	7.574801	TGGTTTT	0.19836	0.19379
cg0231133	MAD1L1	c-Myb [T0	1136	1143	7.545286	AAACTG	0.42725	0.40917
cg0611220	MAD1L1	c-Myb [T0	1069	1076	7.545286	TGCAGT	0.42725	0.40917
cg0372348	MAD1L1	c-Myb [T0	723	730	7.545286	TGCAGT	0.42725	0.40917
cg1578384	MAD1L1	c-Jun [T00	660	666	7.538568	GATGTC	0.48828	0.48672
cg1151970	MAD1L1	c-Jun [T00	590	596	7.538568	GACGTC	0.48828	0.48672
cg0372348	MAD1L1	c-Jun [T00	1427	1433	7.538568	TGACATC	0.48828	0.48672
cg0231133	MAD1L1	NF-kappa	1862	1872	7.534163	GGGGAT	0.04435	0.04858
cg0231133	MAD1L1	PPAR-alp	65	75	7.529496	ACCTGG	0.04482	0.04884
cg0231133	MAD1L1	GR [T050	77	83	7.527031	CAAAGC	1.83105	1.71535
cg0231133	MAD1L1	GR [T050	1074	1080	7.527031	CAAAGC	1.83105	1.71535
cg0231133	MAD1L1	GR [T050	1147	1153	7.527031	CAAAAG	1.83105	1.71535
cg0231133	MAD1L1	GR [T050	1213	1219	7.527031	TATTTTC	1.83105	1.71535
cg1578384	MAD1L1	GR [T050	896	902	7.527031	CAAATA	1.83105	1.71535
cg1578384	MAD1L1	GR [T050	1262	1268	7.527031	CAAAAG	1.83105	1.71535
cg1578384	MAD1L1	GR [T050	1313	1319	7.527031	CAAACA	1.83105	1.71535
cg1151970	MAD1L1	GR [T050	148	154	7.527031	CAAAAT	1.83105	1.71535
cg1151970	MAD1L1	GR [T050	159	165	7.527031	TCTTTTG	1.83105	1.71535
cg1151970	MAD1L1	GR [T050	1937	1943	7.527031	CAAACA	1.83105	1.71535
cg1002882	MAD1L1	GR [T050	373	379	7.527031	CAAAAG	1.83105	1.71535
cg1002882	MAD1L1	GR [T050	394	400	7.527031	CCTTTTC	1.83105	1.71535
cg1002882	MAD1L1	GR [T050	461	467	7.527031	CTGTTTC	1.83105	1.71535
cg1002882	MAD1L1	GR [T050	1004	1010	7.527031	CGCTTTC	1.83105	1.71535
cg1002882	MAD1L1	GR [T050	1192	1198	7.527031	CCTTTTC	1.83105	1.71535
cg1002882	MAD1L1	GR [T050	1785	1791	7.527031	CAAAGC	1.83105	1.71535
cg0611220	MAD1L1	GR [T050	480	486	7.527031	TATTTTC	1.83105	1.71535
cg0611220	MAD1L1	GR [T050	1302	1308	7.527031	TTATTTC	1.83105	1.71535

cg0611220	MAD1L1	GR [T050	1328	1334	7.527031	TCTTTTG	1.83105	1.71535
cg0611220	MAD1L1	GR [T050	1336	1342	7.527031	TTGTTT	1.83105	1.71535
cg0611220	MAD1L1	GR [T050	1441	1447	7.527031	CAAATA	1.83105	1.71535
cg0372348	MAD1L1	GR [T050	714	720	7.527031	TATTTT	1.83105	1.71535
cg0372348	MAD1L1	GR [T050	729	735	7.527031	TTATTT	1.83105	1.71535
cg0372348	MAD1L1	GR [T050	1417	1423	7.527031	CAAACA	1.83105	1.71535
cg0372348	MAD1L1	GR [T050	1615	1621	7.527031	CATTTT	1.83105	1.71535
cg1002882	MAD1L1	c-Ets-1 [T	1861	1867	7.514011	ATTCCG	0.48828	0.48642
cg0611220	MAD1L1	HNF-1C [	904	912	7.498386	TTGTTTA	0.08392	0.07663
cg0611220	MAD1L1	c-Jun [T00	1617	1623	7.491008	TCGGTC	0.48828	0.48672
cg1002882	MAD1L1	PXR-1:RX	1016	1023	7.486257	CGCGTT	0.24414	0.24326
cg1002882	MAD1L1	RAR-beta	1362	1371	7.47824	AGGGTT	0.24414	0.25121
cg1151970	MAD1L1	RAR-beta:	236	247	7.477995	TCAGCT	0.02861	0.03163
cg1578384	MAD1L1	IRF-1 [T0	1758	1766	7.477948	CTCAGG	0.14496	0.14723
cg0231133	MAD1L1	AR [T000	1889	1897	7.467081	TTCGTG	0.25177	0.2544
cg1578384	MAD1L1	C/EBPalp	1574	1580	7.465744	CATTGC	0.48828	0.45033
cg1002882	MAD1L1	C/EBPalp	1842	1848	7.465744	TGCAAT	0.48828	0.45033
cg0611220	MAD1L1	RAR-beta	1079	1088	7.459774	AAGAAA	0.24414	0.25121
cg0231133	MAD1L1	p53 [T006	347	353	7.458735	GGGCGC	0.73242	0.79826
cg0372348	MAD1L1	p53 [T006	1846	1852	7.458735	GGCGCC	0.73242	0.79826
cg0231133	MAD1L1	NF-1 [T00	84	91	7.445595	TTGGGA	0.24414	0.23756
cg1578384	MAD1L1	NF-1 [T00	752	759	7.445595	TATGCC	0.24414	0.23756
cg1151970	MAD1L1	c-Myb [T0	1307	1314	7.442719	GTAAGT	0.42725	0.40917
cg0611220	MAD1L1	c-Myb [T0	1488	1495	7.442719	GAACTT	0.42725	0.40917
cg0231133	MAD1L1	AR [T000	1387	1395	7.432021	GGACAT	0.25177	0.2544
cg1578384	MAD1L1	AR [T000	1681	1689	7.429939	AGCCTG	0.25177	0.2544
cg0231133	MAD1L1	PEA3 [T0	1585	1593	7.421728	TGGATG	0.34332	0.35389
cg1151970	MAD1L1	PEA3 [T0	452	460	7.421728	GACCAT	0.34332	0.35389
cg1151970	MAD1L1	PEA3 [T0	492	500	7.421728	CAGCAT	0.34332	0.35389
cg1002882	MAD1L1	PEA3 [T0	74	82	7.421728	CCACAT	0.34332	0.35389
cg1002882	MAD1L1	PEA3 [T0	326	334	7.421728	AGGATG	0.34332	0.35389
cg1002882	MAD1L1	PEA3 [T0	579	587	7.421728	GCCCAT	0.34332	0.35389
cg0611220	MAD1L1	PEA3 [T0	377	385	7.421728	AGGATG	0.34332	0.35389
cg0372348	MAD1L1	PEA3 [T0	559	567	7.421728	GACCAT	0.34332	0.35389
cg1151970	MAD1L1	LEF-1 [T0	945	952	7.396545	GTGCAA	0.21362	0.21504
cg1002882	MAD1L1	C/EBPalp	1314	1320	7.396431	AATTGG	0.48828	0.45033
cg0611220	MAD1L1	C/EBPalp	488	494	7.396431	TCCAAT	0.48828	0.45033
cg0372348	MAD1L1	C/EBPalp	312	318	7.396431	TACAAT	0.48828	0.45033
cg1151970	MAD1L1	IRF-1 [T0	725	733	7.387351	TTTCCC	0.14496	0.14723
cg1002882	MAD1L1	IRF-1 [T0	196	204	7.387351	TGGGGG	0.14496	0.14723
cg1151970	MAD1L1	PPAR-alp	662	672	7.370536	CAGCCC	0.04482	0.04884
cg1151970	MAD1L1	PPAR-alp	1135	1145	7.370536	GGCTGG	0.04482	0.04884
cg1002882	MAD1L1	PPAR-alp	729	739	7.370536	CAGACC	0.04482	0.04884
cg0372348	MAD1L1	PXR-1:RX	1131	1138	7.362674	TGAACG	0.24414	0.24326
cg0231133	MAD1L1	E2F-1 [T0	480	487	7.336545	GCGGAA	0.45776	0.49661
cg1002882	MAD1L1	E2F-1 [T0	228	235	7.336545	GCGGCA	0.45776	0.49661
cg1002882	MAD1L1	E2F-1 [T0	483	490	7.336545	GCGGCA	0.45776	0.49661
cg1002882	MAD1L1	E2F-1 [T0	624	631	7.336545	CCTGCC	0.45776	0.49661

cg1002882	MAD1L1	E2F-1 [T0	1011	1018	7.336545	CATGCC	0.45776	0.49661
cg1002882	MAD1L1	E2F-1 [T0	1575	1582	7.336545	GCGGCA	0.45776	0.49661
cg1151970	MAD1L1	AR [T000	955	963	7.324759	ACCGTG	0.25177	0.2544
cg0611220	MAD1L1	HNF-4alp	1188	1200	7.282735	TTTCTGA	0.0051	0.00479
cg0611220	MAD1L1	HOXD9 [	1297	1306	7.270719	ATATGTT	0.06866	0.05771
cg0611220	MAD1L1	HOXD10 [	1297	1306	7.270719	ATATGTT	0.06866	0.05771
cg0231133	MAD1L1	c-Ets-2 [T	245	253	7.268173	CAGCAG	0.09155	0.08977
cg1151970	MAD1L1	c-Ets-2 [T	1450	1458	7.268173	TTCCTGC	0.09155	0.08977
cg0372348	MAD1L1	c-Ets-2 [T	351	359	7.268173	TTGTAGC	0.09155	0.08977
cg0231133	MAD1L1	p53 [T006	1320	1326	7.266844	GGGCTG	0.73242	0.79826
cg1578384	MAD1L1	p53 [T006	928	934	7.266844	AAAGCC	0.73242	0.79826
cg1578384	MAD1L1	p53 [T006	1656	1662	7.266844	AAAGCC	0.73242	0.79826
cg1151970	MAD1L1	p53 [T006	227	233	7.266844	GGGCTG	0.73242	0.79826
cg1151970	MAD1L1	p53 [T006	661	667	7.266844	ACAGCC	0.73242	0.79826
cg1151970	MAD1L1	p53 [T006	791	797	7.266844	AAAGCC	0.73242	0.79826
cg1002882	MAD1L1	p53 [T006	985	991	7.266844	GGGCTG	0.73242	0.79826
cg0611220	MAD1L1	p53 [T006	61	67	7.266844	GGGCTTT	0.73242	0.79826
cg0372348	MAD1L1	p53 [T006	275	281	7.266844	GGGCTG	0.73242	0.79826
cg0372348	MAD1L1	p53 [T006	1339	1345	7.266844	AAAGCC	0.73242	0.79826
cg0372348	MAD1L1	p53 [T006	1634	1640	7.266844	GGGCTG	0.73242	0.79826
cg1151970	MAD1L1	AR [T000	1924	1932	7.266233	CCTATGT	0.25177	0.2544
cg1002882	MAD1L1	c-Ets-1 [T	1031	1037	7.199436	TTTCCCA	0.73242	0.73732
cg0372348	MAD1L1	c-Ets-1 [T	768	774	7.199436	TGGGAA	0.73242	0.73732
cg0372348	MAD1L1	c-Ets-1 [T	1298	1304	7.199436	TGGGAA	0.73242	0.73732
cg1151970	MAD1L1	GCF [T00	1784	1792	7.186486	GCGCAG	0.45776	0.50397
cg1578384	MAD1L1	SRY [T00	1809	1817	7.175614	AAACCA	0.30518	0.29547
cg0611220	MAD1L1	SRY [T00	1420	1428	7.175614	CTTTGTC	0.30518	0.29547
cg0611220	MAD1L1	SRY [T00	1896	1904	7.175614	ACAGCA	0.30518	0.29547
cg0231133	MAD1L1	XBP-1 [T	98	103	7.172312	ATGAGT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	169	174	7.172312	CCTCAT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	311	316	7.172312	ATTCAT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1121	1126	7.172312	CTTCAT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1167	1172	7.172312	ATGATG	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1262	1267	7.172312	CATCAT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1534	1539	7.172312	ACTCAT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1588	1593	7.172312	ATGAGT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1724	1729	7.172312	ATGAGG	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1884	1889	7.172312	ATGAAT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1944	1949	7.172312	CCTCAT	2.92969	2.7512
cg0231133	MAD1L1	XBP-1 [T	1948	1953	7.172312	ATGAGT	2.92969	2.7512
cg1578384	MAD1L1	XBP-1 [T	36	41	7.172312	ATGAGT	2.92969	2.7512
cg1578384	MAD1L1	XBP-1 [T	293	298	7.172312	ATTCAT	2.92969	2.7512
cg1578384	MAD1L1	XBP-1 [T	1136	1141	7.172312	AATCAT	2.92969	2.7512
cg1578384	MAD1L1	XBP-1 [T	1318	1323	7.172312	AATCAT	2.92969	2.7512
cg1578384	MAD1L1	XBP-1 [T	1504	1509	7.172312	ACTCAT	2.92969	2.7512
cg1578384	MAD1L1	XBP-1 [T	1508	1513	7.172312	ATGAGG	2.92969	2.7512
cg1151970	MAD1L1	XBP-1 [T	707	712	7.172312	CATCAT	2.92969	2.7512
cg1151970	MAD1L1	XBP-1 [T	719	724	7.172312	ATGAGG	2.92969	2.7512

cg1151970	MAD1L1	XBP-1 [T	810	815	7.172312	ATGAAG	2.92969	2.7512
cg1151970	MAD1L1	XBP-1 [T	1513	1518	7.172312	ATGATT	2.92969	2.7512
cg1151970	MAD1L1	XBP-1 [T	1571	1576	7.172312	ACTCAT	2.92969	2.7512
cg1002882	MAD1L1	XBP-1 [T	322	327	7.172312	ATGAAG	2.92969	2.7512
cg1002882	MAD1L1	XBP-1 [T	881	886	7.172312	CCTCAT	2.92969	2.7512
cg1002882	MAD1L1	XBP-1 [T	1023	1028	7.172312	ATGATT	2.92969	2.7512
cg1002882	MAD1L1	XBP-1 [T	1480	1485	7.172312	ATGAGG	2.92969	2.7512
cg1002882	MAD1L1	XBP-1 [T	1715	1720	7.172312	ATGAGG	2.92969	2.7512
cg1002882	MAD1L1	XBP-1 [T	1726	1731	7.172312	ATGATT	2.92969	2.7512
cg0611220	MAD1L1	XBP-1 [T	139	144	7.172312	ATGAAG	2.92969	2.7512
cg0611220	MAD1L1	XBP-1 [T	194	199	7.172312	ACTCAT	2.92969	2.7512
cg0611220	MAD1L1	XBP-1 [T	543	548	7.172312	ATTCAT	2.92969	2.7512
cg0611220	MAD1L1	XBP-1 [T	1245	1250	7.172312	CCTCAT	2.92969	2.7512
cg0611220	MAD1L1	XBP-1 [T	1256	1261	7.172312	ATGATG	2.92969	2.7512
cg0611220	MAD1L1	XBP-1 [T	1431	1436	7.172312	ATGAAG	2.92969	2.7512
cg0372348	MAD1L1	XBP-1 [T	375	380	7.172312	ATGATT	2.92969	2.7512
cg0372348	MAD1L1	XBP-1 [T	430	435	7.172312	CTTCAT	2.92969	2.7512
cg0372348	MAD1L1	XBP-1 [T	1043	1048	7.172312	CCTCAT	2.92969	2.7512
cg0372348	MAD1L1	XBP-1 [T	1047	1052	7.172312	ATTCAT	2.92969	2.7512
cg0372348	MAD1L1	XBP-1 [T	1204	1209	7.172312	ATGAGG	2.92969	2.7512
cg0372348	MAD1L1	XBP-1 [T	1279	1284	7.172312	CATCAT	2.92969	2.7512
cg0372348	MAD1L1	XBP-1 [T	1535	1540	7.172312	ATGAGG	2.92969	2.7512
cg1151970	MAD1L1	p53 [T006	80	86	7.153797	TGGGCC	1.09863	1.22478
cg1151970	MAD1L1	p53 [T006	1683	1689	7.153797	GGGCCC	1.09863	1.22478
cg1002882	MAD1L1	p53 [T006	1980	1986	7.153797	TGGGCC	1.09863	1.22478
cg0231133	MAD1L1	p53 [T006	234	240	7.150251	GGGCCA	1.09863	1.22478
cg1578384	MAD1L1	p53 [T006	962	968	7.150251	GGGCCA	1.09863	1.22478
cg1151970	MAD1L1	p53 [T006	1071	1077	7.150251	GTGGCC	1.09863	1.22478
cg0372348	MAD1L1	p53 [T006	803	809	7.150251	GGGCCA	1.09863	1.22478
cg1151970	MAD1L1	c-Myb [T0	1199	1206	7.127234	TAACTG	0.18311	0.17765
cg0611220	MAD1L1	c-Myb [T0	548	555	7.127234	TCCAGT	0.18311	0.17765
cg1151970	MAD1L1	c-Jun [T00	3	9	7.096776	GCAGTC	0.73242	0.73062
cg0372348	MAD1L1	c-Jun [T00	822	828	7.096776	GCAGTC	0.73242	0.73062
cg1002882	MAD1L1	NF-AT1 [	1183	1191	7.095752	CTCTTTT	0.15259	0.14325
cg0231133	MAD1L1	c-Ets-1 [T	433	439	7.071349	AGGGAA	0.73242	0.73732
cg1578384	MAD1L1	c-Ets-1 [T	847	853	7.071349	AGGGAA	0.73242	0.73732
cg1151970	MAD1L1	c-Ets-1 [T	1322	1328	7.071349	TTTCCC	0.73242	0.73732
cg0611220	MAD1L1	c-Ets-1 [T	1241	1247	7.071349	TTTCCC	0.73242	0.73732
cg1578384	MAD1L1	AR [T000	841	849	7.049779	GGACAC	0.23651	0.23986
cg0231133	MAD1L1	HNF-1B [	125	133	7.045535	TGAGTA	0.07629	0.07044
cg0372348	MAD1L1	IRF-1 [T0	839	847	7.044985	TTTCCT	0.1297	0.12685
cg0611220	MAD1L1	HNF-1C [	746	754	7.028835	TTTAAT	0.08392	0.07499
cg1002882	MAD1L1	NFI/CTF [	1629	1636	7.014249	GGGGTT	0.73242	0.74795
cg1578384	MAD1L1	C/EBPalp	609	615	7.00174	GCCAAT	0.73242	0.68282
cg0611220	MAD1L1	C/EBPalp	610	616	7.00174	GACAAT	0.73242	0.68282
cg0231133	MAD1L1	HNF-3alp	1213	1220	7.000129	TATTTC	0.82397	0.71909
cg1578384	MAD1L1	HNF-3alp	1246	1253	7.000129	ACTAAA	0.82397	0.71909
cg1151970	MAD1L1	HNF-3alp	147	154	7.000129	CCAAAA	0.82397	0.71909

cg0611220	MAD1L1	HNF-3alp	332	339	7.000129	AATTTT	0.82397	0.71909
cg0611220	MAD1L1	HNF-3alp	1439	1446	7.000129	TGCAAA	0.82397	0.71909
cg0611220	MAD1L1	HNF-3alp	1561	1568	7.000129	AATAAA	0.82397	0.71909
cg0611220	MAD1L1	HNF-3alp	1575	1582	7.000129	CAAAAA	0.82397	0.71909
cg0372348	MAD1L1	HNF-3alp	1615	1622	7.000129	CATTTC	0.82397	0.71909
cg1002882	MAD1L1	GCF [T00	1489	1497	6.987525	AATCCG	0.45776	0.50397
cg1151970	MAD1L1	EBF [T05	56	66	6.983657	GCCGCA	0.03052	0.03432
cg1002882	MAD1L1	IRF-1 [T0	1031	1039	6.968314	TTTCCC	0.1297	0.12685
cg0372348	MAD1L1	IRF-1 [T0	1296	1304	6.968314	GGTGGG	0.1297	0.12685
cg0231133	MAD1L1	RXR-alph	1557	1563	6.967687	ACCACC	0.36621	0.38841
cg1151970	MAD1L1	RXR-alph	1387	1393	6.967687	ACCACC	0.36621	0.38841
cg0372348	MAD1L1	RXR-alph	240	246	6.967687	ACCACC	0.36621	0.38841
cg0231133	MAD1L1	E2F-1 [T0	1734	1741	6.967231	GCGGGG	0.30518	0.33862
cg1002882	MAD1L1	IRF-1 [T0	288	296	6.954318	CAGTGG	0.1297	0.12685
cg0372348	MAD1L1	c-Ets-1 [T	1162	1168	6.949623	TCGGAA	0.73242	0.73732
cg0231133	MAD1L1	NF-1 [T00	475	482	6.948522	TTGGAG	0.48828	0.50205
cg1578384	MAD1L1	NF-1 [T00	98	105	6.948522	GGACCC	0.48828	0.50205
cg1002882	MAD1L1	NF-1 [T00	1316	1323	6.948522	TTGGAG	0.48828	0.50205
cg0611220	MAD1L1	NF-1 [T00	485	492	6.948522	TGATCC	0.48828	0.50205
cg0372348	MAD1L1	NF-1 [T00	1381	1388	6.948522	TTGGTG	0.48828	0.50205
cg0231133	MAD1L1	c-Ets-1 [T	598	604	6.943262	GGGGAA	0.73242	0.73732
cg0231133	MAD1L1	c-Ets-1 [T	912	918	6.943262	GGGGAA	0.73242	0.73732
cg1151970	MAD1L1	c-Ets-1 [T	725	731	6.943262	TTTCCC	0.73242	0.73732
cg1002882	MAD1L1	c-Ets-1 [T	198	204	6.943262	GGGGAA	0.73242	0.73732
cg1002882	MAD1L1	c-Ets-1 [T	1187	1193	6.943262	TTTCCC	0.73242	0.73732
cg0372348	MAD1L1	c-Ets-1 [T	266	272	6.943262	GGGGAA	0.73242	0.73732
cg0231133	MAD1L1	ENKTF-1	929	936	6.942764	TTCCGC	1.46484	1.56616
cg0231133	MAD1L1	ENKTF-1	938	945	6.942764	CGGGGC	1.46484	1.56616
cg0231133	MAD1L1	ENKTF-1	992	999	6.942764	TCACGC	1.46484	1.56616
cg0231133	MAD1L1	ENKTF-1	1712	1719	6.942764	ACACGC	1.46484	1.56616
cg0231133	MAD1L1	ENKTF-1	1848	1855	6.942764	CCAGGC	1.46484	1.56616
cg1578384	MAD1L1	ENKTF-1	12	19	6.942764	CATGGC	1.46484	1.56616
cg1578384	MAD1L1	ENKTF-1	387	394	6.942764	CGAAGC	1.46484	1.56616
cg1578384	MAD1L1	ENKTF-1	467	474	6.942764	CGATGC	1.46484	1.56616
cg1578384	MAD1L1	ENKTF-1	960	967	6.942764	CCGGGC	1.46484	1.56616
cg1578384	MAD1L1	ENKTF-1	966	973	6.942764	CACGGC	1.46484	1.56616
cg1578384	MAD1L1	ENKTF-1	1480	1487	6.942764	TGGCGC	1.46484	1.56616
cg1578384	MAD1L1	ENKTF-1	1552	1559	6.942764	TGGCAG	1.46484	1.56616
cg1151970	MAD1L1	ENKTF-1	796	803	6.942764	CCAAGC	1.46484	1.56616
cg1151970	MAD1L1	ENKTF-1	916	923	6.942764	TGGCCC	1.46484	1.56616
cg1151970	MAD1L1	ENKTF-1	1032	1039	6.942764	CGGAGC	1.46484	1.56616
cg1151970	MAD1L1	ENKTF-1	1072	1079	6.942764	TGGCCC	1.46484	1.56616
cg1151970	MAD1L1	ENKTF-1	1159	1166	6.942764	TGGCAC	1.46484	1.56616
cg1151970	MAD1L1	ENKTF-1	1822	1829	6.942764	GCGCGC	1.46484	1.56616
cg1002882	MAD1L1	ENKTF-1	121	128	6.942764	CATGGC	1.46484	1.56616
cg1002882	MAD1L1	ENKTF-1	749	756	6.942764	CACAGC	1.46484	1.56616
cg1002882	MAD1L1	ENKTF-1	873	880	6.942764	CACGGC	1.46484	1.56616
cg1002882	MAD1L1	ENKTF-1	1619	1626	6.942764	TGGCGT	1.46484	1.56616

cg0611220	MAD1L1	ENKTF-1	673	680	6.942764	CACAGC	1.46484	1.56616
cg0372348	MAD1L1	ENKTF-1	186	193	6.942764	CTCAGC	1.46484	1.56616
cg0372348	MAD1L1	ENKTF-1	583	590	6.942764	CCAAGC	1.46484	1.56616
cg0372348	MAD1L1	ENKTF-1	1273	1280	6.942764	CTTGGC	1.46484	1.56616
cg0372348	MAD1L1	ENKTF-1	1393	1400	6.942764	CATGGC	1.46484	1.56616
cg0372348	MAD1L1	ENKTF-1	1979	1986	6.942764	TGGCCA	1.46484	1.56616
cg0231133	MAD1L1	p53 [T006	69	75	6.938545	GGGCCT	1.09863	1.22478
cg0231133	MAD1L1	p53 [T006	198	204	6.938545	GGGCCT	1.09863	1.22478
cg1151970	MAD1L1	p53 [T006	1096	1102	6.938545	GAGGCC	1.09863	1.22478
cg1151970	MAD1L1	p53 [T006	1879	1885	6.938545	GAGGCC	1.09863	1.22478
cg1002882	MAD1L1	p53 [T006	7	13	6.938545	GGGCCT	1.09863	1.22478
cg1002882	MAD1L1	AhR:Arnt	1492	1501	6.928166	CCGCGC	0.0515	0.0599
cg0231133	MAD1L1	VDR [T00	393	401	6.925682	GAGATG	0.42725	0.41
cg1578384	MAD1L1	VDR [T00	1183	1191	6.925682	TGCATG	0.42725	0.41
cg0372348	MAD1L1	VDR [T00	470	478	6.925682	CACCTG	0.42725	0.41
cg0372348	MAD1L1	VDR [T00	1117	1125	6.925682	GTTCAA	0.42725	0.41
cg0372348	MAD1L1	VDR [T00	1127	1135	6.925682	AAAATG	0.42725	0.41
cg0372348	MAD1L1	RAR-alph	1032	1044	6.894422	GCTCCC	0.00751	0.00805
cg0231133	MAD1L1	p53 [T006	1686	1692	6.891821	GGGCGG	1.09863	1.22478
cg0372348	MAD1L1	C/EBPalph	1118	1124	6.85549	TTCAAT	0.73242	0.68282
cg0231133	MAD1L1	E2F-1 [T0	101	108	6.839754	AGTGCC	0.30518	0.33862
cg1151970	MAD1L1	PEA3 [T0	1454	1462	6.824411	TGCCAT	0.22888	0.22744
cg1002882	MAD1L1	PEA3 [T0	319	327	6.824411	TGGATG	0.22888	0.22744
cg0611220	MAD1L1	PEA3 [T0	543	551	6.824411	ATTCAT	0.22888	0.22744
cg1002882	MAD1L1	c-Ets-1 [T	1298	1304	6.821536	ACGGAA	0.73242	0.73732
cg0372348	MAD1L1	c-Ets-1 [T	379	385	6.815175	TTTCCC	0.73242	0.73732
cg1002882	MAD1L1	EBF [T05	1392	1402	6.79542	ACCCCT	0.03052	0.03432
cg1151970	MAD1L1	c-Jun [T00	90	96	6.787369	TGACGG	0.73242	0.73062
cg0611220	MAD1L1	c-Jun [T00	200	206	6.787369	TCTGTC	0.73242	0.73062
cg0611220	MAD1L1	c-Jun [T00	887	893	6.787369	TGACGG	0.73242	0.73062
cg0611220	MAD1L1	c-Jun [T00	1660	1666	6.787369	TGACAG	0.73242	0.73062
cg0372348	MAD1L1	C/EBPalph	349	355	6.786177	TATTGT	0.73242	0.68282
cg1151970	MAD1L1	NFI/CTF [	796	803	6.786076	CCAAGC	0.73242	0.74795
cg1002882	MAD1L1	NFI/CTF [	461	468	6.786076	CTGTTT	0.73242	0.74795
cg1002882	MAD1L1	NFI/CTF [	1986	1993	6.786076	CTGCTT	0.73242	0.74795
cg0611220	MAD1L1	NFI/CTF [	1541	1548	6.786076	CCAAGC	0.73242	0.74795
cg0372348	MAD1L1	NFI/CTF [	583	590	6.786076	CCAAGC	0.73242	0.74795
cg0372348	MAD1L1	NFI/CTF [	1151	1158	6.786076	CCAATC	0.73242	0.74795
cg0372348	MAD1L1	NFI/CTF [	1416	1423	6.786076	CCAAAC	0.73242	0.74795
cg0372348	MAD1L1	RXR-alph	180	186	6.785809	GTTACC	0.36621	0.38841
cg0372348	MAD1L1	RXR-alph	956	962	6.785809	GGGTAA	0.36621	0.38841
cg0231133	MAD1L1	p53 [T006	1768	1774	6.778774	TGAGCC	1.09863	1.22478
cg1151970	MAD1L1	p53 [T006	1672	1678	6.778774	TGAGCC	1.09863	1.22478
cg0611220	MAD1L1	ATF3 [T0	751	758	6.744803	TAACGT	0.27466	0.26471
cg0372348	MAD1L1	ATF3 [T0	1427	1434	6.744803	TGACAT	0.27466	0.26471
cg1151970	MAD1L1	AR [T000	609	617	6.725174	TGGATG	0.19836	0.20813
cg0611220	MAD1L1	HNF-1B [	905	913	6.706829	TGTTTA	0.04578	0.04078
cg1578384	MAD1L1	T3R-beta1	1429	1437	6.702681	ACATGG	0.21362	0.2251

cg0611220	MAD1L1	T3R-beta1	363	371	6.702681	TCACCA	0.21362	0.2251
cg0611220	MAD1L1	c-Ets-2 [T	1482	1490	6.695187	TCACAG	0.09155	0.08559
cg0372348	MAD1L1	c-Ets-2 [T	567	575	6.695187	TGACAG	0.09155	0.08559
cg0372348	MAD1L1	c-Ets-2 [T	861	869	6.695187	TTCCTAT	0.09155	0.08559
cg1002882	MAD1L1	T3R-beta1	1913	1921	6.683388	TCACCC	0.21362	0.2251
cg0611220	MAD1L1	PXR-1:RX	667	674	6.668182	TCCGTTC	0.24414	0.23169
cg0372348	MAD1L1	PXR-1:RX	1114	1121	6.668182	TGTGTTC	0.24414	0.23169
cg0231133	MAD1L1	c-Jun [T00	1706	1712	6.668031	CAAGTC	0.61035	0.6179
cg0611220	MAD1L1	GATA-2 [	1322	1330	6.666667	TCTATAT	0.24414	0.2357
cg0372348	MAD1L1	IRF-1 [T0	766	774	6.622811	CGTGGG	0.19073	0.1875
cg0231133	MAD1L1	AR [T000	375	383	6.617912	GGACAC	0.19836	0.20813
cg0231133	MAD1L1	FOXP3 [T	426	431	6.581441	TTCAAC	0.97656	0.904
cg0231133	MAD1L1	FOXP3 [T	1041	1046	6.581441	TTCAAC	0.97656	0.904
cg0231133	MAD1L1	FOXP3 [T	1134	1139	6.581441	TAAAAC	0.97656	0.904
cg0231133	MAD1L1	TFII-I [T0	518	523	6.581441	GGAGAT	0.97656	0.9991
cg0231133	MAD1L1	TFII-I [T0	1301	1306	6.581441	CACTCC	0.97656	0.9991
cg0231133	MAD1L1	TFII-I [T0	1880	1885	6.581441	GGAGAT	0.97656	0.9991
cg1578384	MAD1L1	FOXP3 [T	1257	1262	6.581441	TTCAAC	0.97656	0.904
cg1578384	MAD1L1	FOXP3 [T	1986	1991	6.581441	TAAAAC	0.97656	0.904
cg1578384	MAD1L1	TFII-I [T0	1579	1584	6.581441	CACTCC	0.97656	0.9991
cg1578384	MAD1L1	TFII-I [T0	1865	1870	6.581441	GGAGTG	0.97656	0.9991
cg1151970	MAD1L1	FOXP3 [T	172	177	6.581441	TTCAAC	0.97656	0.904
cg1151970	MAD1L1	FOXP3 [T	403	408	6.581441	TTCAAC	0.97656	0.904
cg1151970	MAD1L1	FOXP3 [T	626	631	6.581441	TTCAAC	0.97656	0.904
cg1151970	MAD1L1	FOXP3 [T	842	847	6.581441	TAAAAC	0.97656	0.904
cg1151970	MAD1L1	TFII-I [T0	1947	1952	6.581441	CACTCC	0.97656	0.9991
cg1002882	MAD1L1	FOXP3 [T	1167	1172	6.581441	GTTTTA	0.97656	0.904
cg1002882	MAD1L1	TFII-I [T0	59	64	6.581441	GGAGTG	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	549	554	6.581441	GGAGAT	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	700	705	6.581441	CACTCC	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	811	816	6.581441	CACTCC	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	1174	1179	6.581441	ATCTCC	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	1198	1203	6.581441	GGAGAT	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	1411	1416	6.581441	CACTCC	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	1608	1613	6.581441	GGAGAT	0.97656	0.9991
cg1002882	MAD1L1	TFII-I [T0	1870	1875	6.581441	GGAGTG	0.97656	0.9991
cg0611220	MAD1L1	FOXP3 [T	29	34	6.581441	TAAAAC	0.97656	0.904
cg0611220	MAD1L1	FOXP3 [T	1009	1014	6.581441	GTTTTA	0.97656	0.904
cg0611220	MAD1L1	FOXP3 [T	1228	1233	6.581441	GTTTTA	0.97656	0.904
cg0611220	MAD1L1	FOXP3 [T	1261	1266	6.581441	GTTGAA	0.97656	0.904
cg0611220	MAD1L1	TFII-I [T0	132	137	6.581441	GGAGAT	0.97656	0.9991
cg0611220	MAD1L1	TFII-I [T0	823	828	6.581441	GGAGAT	0.97656	0.9991
cg0611220	MAD1L1	TFII-I [T0	1724	1729	6.581441	GGAGTG	0.97656	0.9991
cg0372348	MAD1L1	FOXP3 [T	318	323	6.581441	TTCAAC	0.97656	0.904
cg0372348	MAD1L1	TFII-I [T0	360	365	6.581441	GGAGTG	0.97656	0.9991
cg0372348	MAD1L1	TFII-I [T0	995	1000	6.581441	CACTCC	0.97656	0.9991
cg0372348	MAD1L1	AR [T000	1759	1767	6.566205	GGACAG	0.19836	0.20813
cg0231133	MAD1L1	RXR-alpha	1912	1918	6.563693	GGGTGT	0.24414	0.25119

cg0611220	MAD1L1	RXR-alpha	1028	1034	6.563693	GACACC	0.24414	0.25119
cg0372348	MAD1L1	RXR-alpha	1953	1959	6.563693	GACACC	0.24414	0.25119
cg0231133	MAD1L1	p53 [T006	534	540	6.563521	GGGCTG	0.48828	0.54643
cg1578384	MAD1L1	p53 [T006	1901	1907	6.563521	GCAGCC	0.48828	0.54643
cg1151970	MAD1L1	p53 [T006	210	216	6.563521	GGGCTG	0.48828	0.54643
cg1002882	MAD1L1	p53 [T006	613	619	6.563521	GGGCTG	0.48828	0.54643
cg1002882	MAD1L1	p53 [T006	1757	1763	6.563521	GCAGCC	0.48828	0.54643
cg1002882	MAD1L1	p53 [T006	1838	1844	6.563521	GGGCTG	0.48828	0.54643
cg1151970	MAD1L1	RAR-alpha	1103	1115	6.547251	TGGGTC	0.00256	0.00272
cg0611220	MAD1L1	PXR-1:RX	1819	1826	6.5446	TGAACA	0.24414	0.23169
cg1002882	MAD1L1	NF-AT2 [	378	387	6.521557	GGAAAA	0.01907	0.01803
cg1578384	MAD1L1	PPAR-alph	1493	1503	6.51544	TAGTCC	0.03719	0.04058
cg0372348	MAD1L1	AR [T000	1952	1960	6.50872	GGACAC	0.19836	0.20813
cg0231133	MAD1L1	IRF-1 [T0	1447	1455	6.497844	ATGTGG	0.19073	0.1875
cg0231133	MAD1L1	XBP-1 [T	179	184	6.478682	TGGCAT	0.97656	0.99906
cg0231133	MAD1L1	XBP-1 [T	1341	1346	6.478682	ATGCCA	0.97656	0.99906
cg0231133	MAD1L1	XBP-1 [T	1898	1903	6.478682	ATGCCC	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	289	294	6.478682	TGGCAT	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	357	362	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	421	426	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	469	474	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	485	490	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	613	618	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	637	642	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	753	758	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	809	814	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	1922	1927	6.478682	ATGCCA	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	1933	1938	6.478682	GGGCAT	0.97656	0.99906
cg1578384	MAD1L1	XBP-1 [T	1937	1942	6.478682	ATGCCC	0.97656	0.99906
cg1151970	MAD1L1	XBP-1 [T	1531	1536	6.478682	ATGCCC	0.97656	0.99906
cg1151970	MAD1L1	XBP-1 [T	1589	1594	6.478682	TGGCAT	0.97656	0.99906
cg1002882	MAD1L1	XBP-1 [T	359	364	6.478682	GGGCAT	0.97656	0.99906
cg1002882	MAD1L1	XBP-1 [T	553	558	6.478682	ATGCCA	0.97656	0.99906
cg1002882	MAD1L1	XBP-1 [T	915	920	6.478682	ATGCCC	0.97656	0.99906
cg1002882	MAD1L1	XBP-1 [T	1959	1964	6.478682	ATGCCC	0.97656	0.99906
cg0611220	MAD1L1	XBP-1 [T	1169	1174	6.478682	TGGCAT	0.97656	0.99906
cg0372348	MAD1L1	XBP-1 [T	1612	1617	6.478682	TGGCAT	0.97656	0.99906
cg0372348	MAD1L1	XBP-1 [T	1889	1894	6.478682	ATGCCC	0.97656	0.99906
cg1151970	MAD1L1	c-Jun [T00	232	238	6.462218	GTAGTC	0.61035	0.6179
cg1002882	MAD1L1	AR [T000	1294	1302	6.461025	GGACAC	0.19836	0.20813
cg1578384	MAD1L1	C/EBPalph	87	93	6.460799	GTCAAT	0.48828	0.47407
cg1002882	MAD1L1	c-Myb [T0	202	209	6.422836	AAACTG	0.30518	0.30272
cg1151970	MAD1L1	RAR-beta	171	180	6.415195	CTTCAA	0.18311	0.1857
cg1002882	MAD1L1	RAR-beta	18	27	6.415195	GTCCAA	0.18311	0.1857
cg1578384	MAD1L1	HOXD9 [T	1652	1661	6.40726	AATAAA	0.01144	0.01024
cg1578384	MAD1L1	HOXD10 [	1652	1661	6.40726	AATAAA	0.01144	0.01024
cg1151970	MAD1L1	p53 [T006	552	558	6.403751	TGCGCC	0.48828	0.54643
cg1151970	MAD1L1	p53 [T006	1736	1742	6.400205	GGGCGA	0.48828	0.54643

cg1151970	MAD1L1	RAR-beta	1212	1221	6.39673	GGAGAA	0.18311	0.1857
cg1151970	MAD1L1	AR [T000	983	991	6.351833	GGCTTG	0.19836	0.20813
cg1002882	MAD1L1	AP-1 [T00	1132	1140	6.308058	TTCGAG	0.03052	0.03035
cg1578384	MAD1L1	TCF-4E [T	1122	1128	6.302385	GGCAAA	0.61035	0.59686
cg1578384	MAD1L1	TCF-4E [T	1811	1817	6.302385	ACCAAA	0.61035	0.59686
cg0611220	MAD1L1	TCF-4E [T	99	105	6.302385	TTCAAA	0.61035	0.59686
cg0372348	MAD1L1	c-Ets-1 [T	1019	1025	6.295602	TTTCCA	0.48828	0.48842
cg1578384	MAD1L1	c-Jun [T00	84	90	6.293948	AGGGTC	0.61035	0.6179
cg1578384	MAD1L1	c-Jun [T00	1915	1921	6.293948	TGACCC	0.61035	0.6179
cg0372348	MAD1L1	c-Jun [T00	629	635	6.293948	TGACCC	0.61035	0.6179
cg0372348	MAD1L1	c-Jun [T00	1652	1658	6.293948	AGGGTC	0.61035	0.6179
cg0231133	MAD1L1	GR-alpha [	169	173	6.263098	CCTCA	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	186	190	6.263098	TAAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	290	294	6.263098	CCTCA	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	372	376	6.263098	TGAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	665	669	6.263098	TGAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	990	994	6.263098	CCTCA	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1018	1022	6.263098	TAAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1032	1036	6.263098	TAAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1268	1272	6.263098	CCTCA	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1277	1281	6.263098	TGAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1378	1382	6.263098	CCTCA	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1422	1426	6.263098	TAAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1571	1575	6.263098	CCTCA	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1578	1582	6.263098	TGAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1725	1729	6.263098	TGAGG	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1773	1777	6.263098	CCTCA	3.90625	3.89624
cg0231133	MAD1L1	GR-alpha [	1944	1948	6.263098	CCTCA	3.90625	3.89624
cg1578384	MAD1L1	GR-alpha [	1382	1386	6.263098	TGAGG	3.90625	3.89624
cg1578384	MAD1L1	GR-alpha [	1509	1513	6.263098	TGAGG	3.90625	3.89624
cg1578384	MAD1L1	GR-alpha [	1515	1519	6.263098	TGAGG	3.90625	3.89624
cg1578384	MAD1L1	GR-alpha [	1757	1761	6.263098	CCTCA	3.90625	3.89624
cg1578384	MAD1L1	GR-alpha [	1826	1830	6.263098	TGAGG	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	206	210	6.263098	TGAGG	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	322	326	6.263098	CCTCA	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	351	355	6.263098	CCTCA	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	377	381	6.263098	CCTCA	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	586	590	6.263098	TGAGG	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	720	724	6.263098	TGAGG	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	746	750	6.263098	TGAGG	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	782	786	6.263098	TAAGG	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	993	997	6.263098	CCTCA	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	1045	1049	6.263098	TGAGG	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	1473	1477	6.263098	CCTTA	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	1535	1539	6.263098	CCTCA	3.90625	3.89624
cg1151970	MAD1L1	GR-alpha [	1878	1882	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	10	14	6.263098	CCTCA	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	82	86	6.263098	CCTCA	3.90625	3.89624

cg1002882	MAD1L1	GR-alpha [	470	474	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	475	479	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	692	696	6.263098	CCTCA	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	738	742	6.263098	CCTCA	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	881	885	6.263098	CCTCA	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	1053	1057	6.263098	CCTCA	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	1404	1408	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	1481	1485	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	1542	1546	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	1716	1720	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	1791	1795	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	GR-alpha [	1965	1969	6.263098	CCTCA	3.90625	3.89624
cg0611220	MAD1L1	GR-alpha [	280	284	6.263098	CCTCA	3.90625	3.89624
cg0611220	MAD1L1	GR-alpha [	325	329	6.263098	CCTCA	3.90625	3.89624
cg0611220	MAD1L1	GR-alpha [	401	405	6.263098	CCTCA	3.90625	3.89624
cg0611220	MAD1L1	GR-alpha [	1218	1222	6.263098	CCTCA	3.90625	3.89624
cg0611220	MAD1L1	GR-alpha [	1245	1249	6.263098	CCTCA	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	185	189	6.263098	CCTCA	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	609	613	6.263098	CCTCA	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	1043	1047	6.263098	CCTCA	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	1176	1180	6.263098	TGAGG	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	1205	1209	6.263098	TGAGG	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	1443	1447	6.263098	CCTCA	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	1536	1540	6.263098	TGAGG	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	1679	1683	6.263098	TGAGG	3.90625	3.89624
cg0372348	MAD1L1	GR-alpha [	1949	1953	6.263098	TGAGG	3.90625	3.89624
cg1002882	MAD1L1	c-Myb [T0	1301	1308	6.259888	GAACTG	0.30518	0.30272
cg0372348	MAD1L1	c-Myb [T0	20	27	6.259888	GAACTG	0.30518	0.30272
cg1578384	MAD1L1	C/EBPalph	1006	1012	6.245236	TGCAAT	0.97656	0.91422
cg1002882	MAD1L1	c-Fos [T00	448	457	6.236188	GAGGTG	0.09155	0.09198
cg0372348	MAD1L1	c-Fos [T00	789	798	6.236188	GAGTCA	0.09155	0.09198
cg0372348	MAD1L1	IRF-1 [T0	379	387	6.203774	TTTCCC	0.16785	0.16217
cg1002882	MAD1L1	NF-AT1 [	1094	1103	6.201624	AGCCTT	0.03815	0.03661
cg0372348	MAD1L1	p53 [T006	1057	1063	6.188498	GACGCC	0.61035	0.68483
cg0231133	MAD1L1	SRY [T00	1070	1078	6.176442	GGGACA	0.15259	0.14742
cg1002882	MAD1L1	SRY [T00	1781	1789	6.176442	AGGACA	0.15259	0.14742
cg0231133	MAD1L1	c-Ets-1 [T	1449	1455	6.167515	GTGGAA	0.36621	0.36174
cg1002882	MAD1L1	c-Ets-1 [T	290	296	6.167515	GTGGAA	0.36621	0.36174
cg0611220	MAD1L1	c-Ets-1 [T	1271	1277	6.167515	TTTCCA	0.36621	0.36174
cg0231133	MAD1L1	c-Jun [T00	147	153	6.152811	TTTGTC	0.36621	0.34478
cg0611220	MAD1L1	c-Jun [T00	1421	1427	6.152811	TTTGTC	0.36621	0.34478
cg0372348	MAD1L1	c-Jun [T00	418	424	6.152811	TGACAA	0.36621	0.34478
cg1578384	MAD1L1	NF-kappa	1959	1969	6.141804	GGGGAT	0.04053	0.04443
cg0372348	MAD1L1	PPAR-alpl	1063	1073	6.14093	CGGCCC	0.02003	0.02202
cg1578384	MAD1L1	c-Myb [T0	240	247	6.12608	AAACTT	0.21362	0.2053
cg1151970	MAD1L1	RelA [T00	1638	1648	6.124867	GACATT	0.01097	0.01155
cg1578384	MAD1L1	RXR-alph	1667	1673	6.119461	GGGTAG	0.73242	0.78318
cg0231133	MAD1L1	AR [T000	621	629	6.110872	GGACAG	0.24414	0.25115

cg1002882	MAD1L1	c-Fos [T00	1135	1144	6.103724	GAGTCA	0.09155	0.09198
cg0231133	MAD1L1	p53 [T006	940	946	6.095267	GGGCCA	0.61035	0.68483
cg1151970	MAD1L1	p53 [T006	1613	1619	6.095267	GGGCCA	0.61035	0.68483
cg0611220	MAD1L1	p53 [T006	1678	1684	6.095267	GGGCCA	0.61035	0.68483
cg0231133	MAD1L1	GR-alpha [	370	374	6.055408	CCTGA	3.90625	3.89835
cg0231133	MAD1L1	GR-alpha [	409	413	6.055408	CCTAA	3.90625	3.89835
cg0231133	MAD1L1	GR-alpha [	595	599	6.055408	TTAGG	3.90625	3.89835
cg0231133	MAD1L1	GR-alpha [	674	678	6.055408	TCAGG	3.90625	3.89835
cg1578384	MAD1L1	GR-alpha [	227	231	6.055408	CCTAA	3.90625	3.89835
cg1578384	MAD1L1	GR-alpha [	933	937	6.055408	CCTGA	3.90625	3.89835
cg1578384	MAD1L1	GR-alpha [	1403	1407	6.055408	TCAGG	3.90625	3.89835
cg1578384	MAD1L1	GR-alpha [	1421	1425	6.055408	CCTAA	3.90625	3.89835
cg1578384	MAD1L1	GR-alpha [	1759	1763	6.055408	TCAGG	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	22	26	6.055408	CCTAA	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	420	424	6.055408	CCTGA	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	584	588	6.055408	CCTGA	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	732	736	6.055408	CCTGA	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	1313	1317	6.055408	TCAGG	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	1330	1334	6.055408	CCTAA	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	1670	1674	6.055408	CCTGA	3.90625	3.89835
cg1151970	MAD1L1	GR-alpha [	1792	1796	6.055408	TCAGG	3.90625	3.89835
cg1002882	MAD1L1	GR-alpha [	189	193	6.055408	CCTGA	3.90625	3.89835
cg1002882	MAD1L1	GR-alpha [	1395	1399	6.055408	CCTGA	3.90625	3.89835
cg1002882	MAD1L1	GR-alpha [	1460	1464	6.055408	TCAGG	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	129	133	6.055408	TTAGG	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	464	468	6.055408	CCTGA	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	788	792	6.055408	TCAGG	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	869	873	6.055408	CCTGA	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	1347	1351	6.055408	TTAGG	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	1626	1630	6.055408	CCTAA	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	1829	1833	6.055408	CCTGA	3.90625	3.89835
cg0611220	MAD1L1	GR-alpha [	1878	1882	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	42	46	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	472	476	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	565	569	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	656	660	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	685	689	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	817	821	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1036	1040	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1104	1108	6.055408	TCAGG	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1174	1178	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1336	1340	6.055408	CCTAA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1370	1374	6.055408	CCTGA	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1432	1436	6.055408	TCAGG	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1656	1660	6.055408	TCAGG	3.90625	3.89835
cg0372348	MAD1L1	GR-alpha [	1774	1778	6.055408	TCAGG	3.90625	3.89835
cg0231133	MAD1L1	ATF-2 [T0	1652	1661	6.05134	CACACG	0.11826	0.11557
cg1578384	MAD1L1	ATF-2 [T0	43	52	6.05134	TGCACG	0.11826	0.11557

cg0611220	MAD1L1	c-Myb [T0	1851	1858	6.04018	AAACTG.	0.21362	0.2053
cg0231133	MAD1L1	c-Ets-1 [T(	209	215	6.039428	TTTCCAC	0.36621	0.36174
cg1151970	MAD1L1	c-Ets-1 [T(	1517	1523	6.039428	TTTCCAC	0.36621	0.36174
cg1002882	MAD1L1	c-Ets-1 [T(	1098	1104	6.039428	TTTCCAC	0.36621	0.36174
cg0611220	MAD1L1	c-Ets-1 [T(	940	946	6.039428	TTTCCAC	0.36621	0.36174
cg0231133	MAD1L1	NF-AT1 [T	1414	1422	6.003834	GGAAAC	0.06866	0.06621
cg1578384	MAD1L1	RXR-alpha	1951	1957	5.937582	GGCACC(	0.73242	0.78318
cg1151970	MAD1L1	RXR-alpha	6	12	5.937582	GTCACC(	0.73242	0.78318
cg1151970	MAD1L1	RXR-alpha	688	694	5.937582	GGGTGC(	0.73242	0.78318
cg1151970	MAD1L1	RXR-alpha	876	882	5.937582	GTCACC(	0.73242	0.78318
cg1151970	MAD1L1	RXR-alpha	1858	1864	5.937582	GGGTAA'	0.73242	0.78318
cg1002882	MAD1L1	RXR-alpha	575	581	5.937582	GGGTGC(	0.73242	0.78318
cg0611220	MAD1L1	RXR-alpha	203	209	5.937582	GTCACC(	0.73242	0.78318
cg0372348	MAD1L1	RXR-alpha	529	535	5.937582	GGGTGC(	0.73242	0.78318
cg0372348	MAD1L1	RXR-alpha	983	989	5.937582	GGGTGC(	0.73242	0.78318
cg0372348	MAD1L1	RXR-alpha	1411	1417	5.937582	ATTACC(	0.73242	0.78318
cg1151970	MAD1L1	NF-kappaE	1635	1645	5.921388	GGGGAC	0.04053	0.04443
cg0231133	MAD1L1	GCF [T00	102	110	5.917256	GTGCCG(	0.64087	0.72542
cg0231133	MAD1L1	GCF [T00	298	306	5.917256	GCGCTG(	0.64087	0.72542
cg1151970	MAD1L1	GCF [T00	34	42	5.917256	GCGCTG(	0.64087	0.72542
cg1151970	MAD1L1	GCF [T00	897	905	5.917256	GTGCAG(	0.64087	0.72542
cg1002882	MAD1L1	GCF [T00	780	788	5.917256	CCACCG(	0.64087	0.72542
cg1578384	MAD1L1	HOXD9 [T	1619	1628	5.898575	AATAAT.	0.05722	0.04686
cg1578384	MAD1L1	HOXD10 [	1619	1628	5.898575	AATAAT.	0.05722	0.04686
cg0611220	MAD1L1	HNF-1A [T	1279	1286	5.898157	GGCTTA.	0.24414	0.24293
cg0611220	MAD1L1	AR [T0004	992	1000	5.8965	GTTTTGT	0.24414	0.25115
cg0231133	MAD1L1	STAT4 [T(	574	579	5.882353	GGAAGG	0.48828	0.51201
cg0231133	MAD1L1	STAT4 [T(	783	788	5.882353	GGAAGG	0.48828	0.51201
cg0231133	MAD1L1	STAT4 [T(	1779	1784	5.882353	GGAAGG	0.48828	0.51201
cg1578384	MAD1L1	STAT4 [T(	858	863	5.882353	GGAAGG	0.48828	0.51201
cg1578384	MAD1L1	STAT4 [T(	1375	1380	5.882353	GGAAGG	0.48828	0.51201
cg1151970	MAD1L1	STAT4 [T(	1460	1465	5.882353	CCTTCC	0.48828	0.51201
cg1002882	MAD1L1	STAT4 [T(	1341	1346	5.882353	GGAAGG	0.48828	0.51201
cg0611220	MAD1L1	STAT4 [T(	1747	1752	5.882353	CCTTCC	0.48828	0.51201
cg0372348	MAD1L1	STAT4 [T(	153	158	5.882353	CCTTCC	0.48828	0.51201
cg0372348	MAD1L1	STAT4 [T(	356	361	5.882353	GGAAGG	0.48828	0.51201
cg0372348	MAD1L1	STAT4 [T(	1223	1228	5.882353	GGAAGG	0.48828	0.51201
cg0372348	MAD1L1	STAT4 [T(	1439	1444	5.882353	CCTTCC	0.48828	0.51201
cg0372348	MAD1L1	STAT4 [T(	1792	1797	5.882353	GGAAGG	0.48828	0.51201
cg0372348	MAD1L1	AP-1 [T00	1557	1565	5.871862	TGACTC(	0.09155	0.09438
cg0231133	MAD1L1	IRF-1 [T0(	1097	1105	5.861409	CACAGG.	0.16785	0.16217
cg1151970	MAD1L1	AR [T0004	1497	1505	5.859358	TGTCTGT	0.24414	0.25115
cg0611220	MAD1L1	C/EBPalph	1657	1663	5.850545	AATTGA(	0.97656	0.91422
cg0372348	MAD1L1	C/EBPalph	387	393	5.850545	GGCAAT'	0.97656	0.91422
cg0231133	MAD1L1	PXR-1:RX	397	404	5.850108	TGAACC(	0.06104	0.06404
cg0611220	MAD1L1	c-Myb [T0	1984	1991	5.841835	CAACTG(	0.21362	0.2053
cg1002882	MAD1L1	AP-1 [T00	848	856	5.818984	GCCGAG'	0.09155	0.09438
cg0231133	MAD1L1	c-Ets-1 [T(	572	578	5.814485	TGGGAA(	0.36621	0.36174

cg1002882	MAD1L1	c-Ets-1 [T	1922	1928	5.814485	TGGGAA	0.36621	0.36174
cg0372348	MAD1L1	c-Ets-1 [T	1568	1574	5.814485	TGGGAA	0.36621	0.36174
cg0372348	MAD1L1	AR [T000	739	747	5.811663	GGACAG	0.24414	0.25115
cg0372348	MAD1L1	AR [T000	1072	1080	5.811663	TCCCTGT	0.24414	0.25115
cg1151970	MAD1L1	NF-kappa	1316	1326	5.809124	GGGGAC	0.04053	0.04443
cg0231133	MAD1L1	STAT1bet	910	919	5.796867	ACGGGG	0.1545	0.14881
cg1151970	MAD1L1	STAT1bet	751	760	5.796867	TCCAGG	0.1545	0.14881
cg1151970	MAD1L1	STAT1bet	1516	1525	5.796867	ATTTCC	0.1545	0.14881
cg0611220	MAD1L1	c-Jun [T00	149	155	5.783074	TGACTT	0.36621	0.34478
cg1578384	MAD1L1	C/EBPalp	755	761	5.781231	GCCAAT	0.97656	0.91422
cg0231133	MAD1L1	NF-AT1 [	914	922	5.77403	GGAAAG	0.06866	0.06621
cg0611220	MAD1L1	NF-AT1 [	1267	1275	5.77403	CATCTTT	0.06866	0.06621
cg1578384	MAD1L1	VDR [T00	1529	1537	5.771401	TGCTTG	0.42725	0.41266
cg1151970	MAD1L1	VDR [T00	1311	1319	5.771401	GTTCAG	0.42725	0.41266
cg0611220	MAD1L1	VDR [T00	262	270	5.771401	GTTCAA	0.42725	0.41266
cg0611220	MAD1L1	VDR [T00	670	678	5.771401	GTTCAC	0.42725	0.41266
cg0231133	MAD1L1	IRF-1 [T0	596	604	5.770812	TAGGGG	0.16785	0.16217
cg1578384	MAD1L1	ATF-2 [T	1968	1977	5.75773	CAAACG	0.11826	0.11557
cg0231133	MAD1L1	PPAR-alp	230	240	5.741676	TGCTGG	0.03529	0.03856
cg1151970	MAD1L1	PPAR-alp	1417	1427	5.741676	TTCTGG	0.03529	0.03856
cg1151970	MAD1L1	PPAR-alp	1609	1619	5.741676	TCCTGG	0.03529	0.03856
cg0231133	MAD1L1	p53 [T006	1793	1799	5.720243	TTAGCC	0.61035	0.65765
cg0231133	MAD1L1	RXR-alph	358	364	5.715466	AACACC	0.61035	0.65415
cg0231133	MAD1L1	c-Jun [T00	1050	1056	5.703976	GGGGTC	0.48828	0.49294
cg1151970	MAD1L1	c-Jun [T00	241	247	5.703976	TGACCC	0.48828	0.49294
cg1151970	MAD1L1	c-Jun [T00	538	544	5.703976	GGGGTC	0.48828	0.49294
cg1002882	MAD1L1	c-Jun [T00	441	447	5.703976	GGGGTC	0.48828	0.49294
cg1002882	MAD1L1	c-Jun [T00	1640	1646	5.703976	GGGGTC	0.48828	0.49294
cg0372348	MAD1L1	c-Jun [T00	1038	1044	5.703976	TGACCC	0.48828	0.49294
cg0372348	MAD1L1	c-Jun [T00	1357	1363	5.703976	TGACCC	0.48828	0.49294
cg0231133	MAD1L1	ENKTF-1	232	239	5.687009	CTGGGC	0.73242	0.76357
cg0231133	MAD1L1	ENKTF-1	634	641	5.687009	CAGGGC	0.73242	0.76357
cg0231133	MAD1L1	ENKTF-1	688	695	5.687009	GAACGC	0.73242	0.76357
cg1578384	MAD1L1	ENKTF-1	605	612	5.687009	ATACGC	0.73242	0.76357
cg1578384	MAD1L1	ENKTF-1	611	618	5.687009	CAATGC	0.73242	0.76357
cg1578384	MAD1L1	ENKTF-1	1876	1883	5.687009	TGGCAC	0.73242	0.76357
cg1578384	MAD1L1	ENKTF-1	1920	1927	5.687009	CTATGC	0.73242	0.76357
cg1151970	MAD1L1	ENKTF-1	69	76	5.687009	CAAGGC	0.73242	0.76357
cg1151970	MAD1L1	ENKTF-1	948	955	5.687009	CAAAGC	0.73242	0.76357
cg1151970	MAD1L1	ENKTF-1	1419	1426	5.687009	CTGGGC	0.73242	0.76357
cg1151970	MAD1L1	ENKTF-1	1611	1618	5.687009	CTGGGC	0.73242	0.76357
cg1002882	MAD1L1	ENKTF-1	300	307	5.687009	CAAGGC	0.73242	0.76357
cg1002882	MAD1L1	ENKTF-1	602	609	5.687009	TGGCAC	0.73242	0.76357
cg1002882	MAD1L1	ENKTF-1	640	647	5.687009	CAGAGC	0.73242	0.76357
cg1002882	MAD1L1	ENKTF-1	799	806	5.687009	CAGAGC	0.73242	0.76357
cg1002882	MAD1L1	ENKTF-1	1613	1620	5.687009	TGGCCC	0.73242	0.76357
cg1002882	MAD1L1	ENKTF-1	1827	1834	5.687009	CAGAGC	0.73242	0.76357
cg1002882	MAD1L1	ENKTF-1	1940	1947	5.687009	AAACGC	0.73242	0.76357

cg0611220	MAD1L1	ENKTF-1	1676	1683	5.687009	CTGGGC	0.73242	0.76357
cg0372348	MAD1L1	ENKTF-1	1477	1484	5.687009	TGGCCT	0.73242	0.76357
cg1151970	MAD1L1	c-Ets-1 [T	1237	1243	5.686398	AGGGAA	0.36621	0.38732
cg1151970	MAD1L1	c-Ets-1 [T	1469	1475	5.686398	CTTCCCT	0.36621	0.38732
cg1002882	MAD1L1	c-Ets-1 [T	900	906	5.686398	CTTCCCT	0.36621	0.38732
cg1002882	MAD1L1	c-Ets-1 [T	1089	1095	5.686398	AGGGAA	0.36621	0.38732
cg1002882	MAD1L1	c-Ets-1 [T	1801	1807	5.686398	AGGGAA	0.36621	0.38732
cg0372348	MAD1L1	c-Ets-1 [T	154	160	5.686398	CTTCCCT	0.36621	0.38732
cg0611220	MAD1L1	AR [T000	661	669	5.644986	GGGTTG	0.05341	0.05856
cg1151970	MAD1L1	NF-1 [T00	569	576	5.626299	TTGGAC	0.24414	0.25051
cg1151970	MAD1L1	NF-1 [T00	784	791	5.626299	AGGACC	0.24414	0.25051
cg1151970	MAD1L1	EBF [T05	1098	1108	5.623365	GGCCCT	0.01907	0.0226
cg1151970	MAD1L1	AhR:Arnt	1204	1213	5.620669	GGTGGC	0.0515	0.05997
cg1002882	MAD1L1	AhR:Arnt	1437	1446	5.620669	GGTGGC	0.0515	0.05997
cg0372348	MAD1L1	AR [T000	1208	1216	5.597291	GGACAA	0.05341	0.05856
cg1578384	MAD1L1	T3R-beta1	1749	1757	5.591999	TCACCA	0.21362	0.21789
cg0372348	MAD1L1	c-Jun [T00	1963	1969	5.590308	TGACGC	0.48828	0.49294
cg0231133	MAD1L1	c-Jun [T00	1227	1233	5.587335	TGACCT	0.48828	0.49294
cg1151970	MAD1L1	IRF-1 [T0	104	112	5.564062	GCACGG	0.22888	0.21959
cg0372348	MAD1L1	IRF-1 [T0	1019	1027	5.564062	TTTCCAT	0.22888	0.21959
cg1578384	MAD1L1	NFI/CTF [	1752	1759	5.558661	CCAAGC	0.54932	0.55504
cg1151970	MAD1L1	NFI/CTF [	868	875	5.558661	CCAATC	0.54932	0.55504
cg1151970	MAD1L1	NFI/CTF [	934	941	5.558661	AGGCTT	0.54932	0.55504
cg1151970	MAD1L1	NFI/CTF [	1745	1752	5.558661	CCAAAC	0.54932	0.55504
cg1002882	MAD1L1	NFI/CTF [	126	133	5.558661	CCAAAC	0.54932	0.55504
cg1578384	MAD1L1	c-Ets-1 [T	5	11	5.558311	GGGGAA	0.36621	0.38732
cg0372348	MAD1L1	c-Ets-1 [T	1221	1227	5.558311	GGGGAA	0.36621	0.38732
cg0611220	MAD1L1	GATA-2 [	626	634	5.555555	AGATAC	0.18311	0.18081
cg1578384	MAD1L1	c-Myb [T0	167	174	5.55549	AAACTG	0.09155	0.08971
cg1578384	MAD1L1	T3R-beta1	1168	1176	5.553412	CGTCGG	0.21362	0.21789
cg0231133	MAD1L1	Pax-5 [T0	1686	1692	5.544826	GGGCGG	0.73242	0.79
cg1578384	MAD1L1	TFIID [T0	1083	1089	5.544826	TTTAGA	0.73242	0.65314
cg1578384	MAD1L1	TFIID [T0	1449	1455	5.544826	TACTAA	0.73242	0.65314
cg1578384	MAD1L1	TFIID [T0	1983	1989	5.544826	TGTTAA	0.73242	0.65314
cg1151970	MAD1L1	Pax-5 [T0	901	907	5.544826	AGCGCC	0.73242	0.79
cg1002882	MAD1L1	TFIID [T0	423	429	5.544826	TGGTAA	0.73242	0.65314
cg1002882	MAD1L1	Pax-5 [T0	1612	1618	5.544826	ATGGCC	0.73242	0.79
cg0611220	MAD1L1	TFIID [T0	345	351	5.544826	TTTAGT	0.73242	0.65314
cg0611220	MAD1L1	TFIID [T0	1307	1313	5.544826	TGGTAA	0.73242	0.65314
cg0372348	MAD1L1	TFIID [T0	327	333	5.544826	TGATAA	0.73242	0.65314
cg0372348	MAD1L1	TFIID [T0	1985	1991	5.544826	TGATAA	0.73242	0.65314
cg0372348	MAD1L1	Pax-5 [T0	675	681	5.544826	GGGCCA	0.73242	0.79
cg1151970	MAD1L1	NF-AT1 [	1513	1522	5.512555	ATGATT	0.05913	0.05666
cg0611220	MAD1L1	NF-AT1 [	936	945	5.512555	ATTCTTT	0.05913	0.05666
cg0231133	MAD1L1	p53 [T006	1022	1028	5.508538	GGGCTT	0.61035	0.65765
cg1151970	MAD1L1	p53 [T006	277	283	5.508538	TCAGCC	0.61035	0.65765
cg1151970	MAD1L1	p53 [T006	1174	1180	5.508538	GGGCTG	0.61035	0.65765
cg1002882	MAD1L1	p53 [T006	107	113	5.508538	GGGCTG	0.61035	0.65765

cg0611220	MAD1L1	p53 [T006	1278	1284	5.508538	GGGCTT	0.61035	0.65765
cg0372348	MAD1L1	p53 [T006	1510	1516	5.508538	GGGCTG	0.61035	0.65765
cg0372348	MAD1L1	p53 [T006	1945	1951	5.508538	GGGCTG	0.61035	0.65765
cg0231133	MAD1L1	ATF [T00	1653	1664	5.46568	ACACGT	0.02575	0.02525
cg0611220	MAD1L1	ATF [T00	751	762	5.46568	TAACGT	0.02575	0.02525
cg1002882	MAD1L1	HOXD9 [T	1110	1119	5.453039	ATCTTTT	0.04578	0.03952
cg1002882	MAD1L1	HOXD10 [	1110	1119	5.453039	ATCTTTT	0.04578	0.03952
cg0611220	MAD1L1	HOXD9 [T	1606	1615	5.453039	AATAAA	0.04578	0.03952
cg0611220	MAD1L1	HOXD10 [	1606	1615	5.453039	AATAAA	0.04578	0.03952
cg0231133	MAD1L1	c-Ets-1 [T	614	620	5.430224	CTTCCC	0.36621	0.38732
cg1002882	MAD1L1	c-Ets-1 [T	1286	1292	5.430224	CGGGAA	0.36621	0.38732
cg0372348	MAD1L1	USF1 [T00	246	255	5.418177	CACGTG	0.04578	0.04717
cg1151970	MAD1L1	C/EBPalph	758	764	5.38654	AACAAT	0.73242	0.68229
cg1151970	MAD1L1	p53 [T006	928	934	5.345221	GGGCGA	0.61035	0.65765
cg1002882	MAD1L1	RAR-beta	68	77	5.333686	TGGGTT	0.15259	0.15813
cg1151970	MAD1L1	IRF-1 [T0	811	819	5.309227	TGAAGG	0.22888	0.21959
cg1151970	MAD1L1	RelA [T00	1319	1329	5.301165	GACTTT	0.0124	0.01273
cg0231133	MAD1L1	NF-kappa	51	61	5.289941	TGGCAA	0.02384	0.02626
cg0372348	MAD1L1	PPAR-alph	553	563	5.285833	CACTGG	0.03529	0.03856
cg0611220	MAD1L1	HOXD9 [T	474	483	5.275652	GCTTTTT	0.04578	0.03952
cg0611220	MAD1L1	HOXD9 [T	1007	1016	5.275652	CGGTTTT	0.04578	0.03952
cg0611220	MAD1L1	HOXD10 [	474	483	5.275652	GCTTTTT	0.04578	0.03952
cg0611220	MAD1L1	HOXD10 [	1007	1016	5.275652	CGGTTTT	0.04578	0.03952
cg0611220	MAD1L1	TCF-4 [T0	426	435	5.274366	CTCTCA	0.04959	0.04908
cg0611220	MAD1L1	TCF-4 [T0	1195	1204	5.274366	ACTTTG	0.04959	0.04908
cg0231133	MAD1L1	RXR-alph	271	277	5.271235	GCAACC	0.61035	0.65415
cg0231133	MAD1L1	RXR-alph	948	954	5.271235	ACGACC	0.61035	0.65415
cg1578384	MAD1L1	RXR-alph	222	228	5.271235	TCTACC	0.61035	0.65415
cg1151970	MAD1L1	RXR-alph	1391	1397	5.271235	CCCACC	0.61035	0.65415
cg1151970	MAD1L1	RXR-alph	1957	1963	5.271235	CCCACC	0.61035	0.65415
cg1002882	MAD1L1	RXR-alph	1375	1381	5.271235	GGGTGG	0.61035	0.65415
cg1002882	MAD1L1	RXR-alph	1446	1452	5.271235	GGGTGG	0.61035	0.65415
cg1151970	MAD1L1	c-Myb [T0	1747	1754	5.258734	AAACTT	0.09155	0.08971
cg0231133	MAD1L1	AR [T000	1674	1682	5.247138	GGACAG	0.11444	0.12256
cg1151970	MAD1L1	ETF [T002	670	680	5.246906	GCCCCC	0.02861	0.03569
cg1002882	MAD1L1	ETF [T002	778	788	5.246906	GCCCAC	0.02861	0.03569
cg1002882	MAD1L1	ETF [T002	978	988	5.246906	GGGGGC	0.02861	0.03569
cg0372348	MAD1L1	ETF [T002	1891	1901	5.246906	GCCCCC	0.02861	0.03569
cg1002882	MAD1L1	C/EBPalph	1116	1122	5.240291	TATTGA	0.97656	0.90302
cg1002882	MAD1L1	NF-AT2 [T	165	174	5.231211	GATAGT	0.03815	0.03519
cg0231133	MAD1L1	GR [T050	1494	1500	5.207533	CAAAGA	0.24414	0.24013
cg1578384	MAD1L1	GR [T050	1124	1130	5.207533	CAAAGA	0.24414	0.24013
cg0611220	MAD1L1	GR [T050	991	997	5.207533	GGTTTC	0.24414	0.24013
cg0611220	MAD1L1	GR [T050	1418	1424	5.207533	GTCTTTC	0.24414	0.24013
cg0611220	MAD1L1	GR [T050	1900	1906	5.207533	CAAAGA	0.24414	0.24013
cg0231133	MAD1L1	c-Ets-2 [T	778	786	5.162974	GTCAAG	0.13733	0.13279
cg0231133	MAD1L1	c-Ets-2 [T	1774	1782	5.162974	CTCAAG	0.13733	0.13279
cg0611220	MAD1L1	c-Ets-2 [T	1684	1692	5.162974	ACCAAG	0.13733	0.13279

cg0231133	MAD1L1	Sp1 [T007	1685	1694	5.161467	TGGGCG	0.06485	0.07101
cg0231133	MAD1L1	c-Myb [T0	251	258	5.137438	GAACTG	0.30518	0.30087
cg0611220	MAD1L1	p53 [T006	411	417	5.133514	TCCGCC	0.48828	0.53921
cg0231133	MAD1L1	AP-2alpha	548	553	5.100982	AAAGGC	0.97656	0.97517
cg1578384	MAD1L1	AP-2alpha	259	264	5.100982	AAAGGC	0.97656	0.97517
cg1578384	MAD1L1	AP-2alpha	1326	1331	5.100982	AAAGGC	0.97656	0.97517
cg1578384	MAD1L1	AP-2alpha	1814	1819	5.100982	AAAGGC	0.97656	0.97517
cg1002882	MAD1L1	AP-2alpha	1095	1100	5.100982	GCCTTT	0.97656	0.97517
cg1002882	MAD1L1	AP-2alpha	1549	1554	5.100982	AAAGGC	0.97656	0.97517
cg0611220	MAD1L1	AP-2alpha	742	747	5.100982	GCCTTT	0.97656	0.97517
cg0611220	MAD1L1	AP-2alpha	1759	1764	5.100982	AAAGGC	0.97656	0.97517
cg0611220	MAD1L1	NF-Y [T0	556	563	5.094053	CTCCCA	0.36621	0.35921
cg1151970	MAD1L1	AP-1 [T00	1786	1794	5.059986	GCAGAG	0.12207	0.12309
cg0231133	MAD1L1	USF2 [T0	1267	1276	5.052423	TCCTCAC	0.103	0.10797
cg1578384	MAD1L1	USF2 [T0	832	841	5.052423	GCTTCAC	0.103	0.10797
cg1578384	MAD1L1	USF2 [T0	1868	1877	5.052423	GTGCCAC	0.103	0.10797
cg1151970	MAD1L1	USF2 [T0	1702	1711	5.052423	CAGGTG	0.103	0.10797
cg1002882	MAD1L1	USF2 [T0	9	18	5.052423	GCCTCAC	0.103	0.10797
cg0231133	MAD1L1	GR-beta [	55	59	5.042296	AATCC	3.90625	3.7093
cg0231133	MAD1L1	GR-beta [	1180	1184	5.042296	AATCC	3.90625	3.7093
cg0231133	MAD1L1	GR-beta [	1200	1204	5.042296	GGATT	3.90625	3.7093
cg0231133	MAD1L1	GR-beta [	1212	1216	5.042296	GTATT	3.90625	3.7093
cg1578384	MAD1L1	GR-beta [	186	190	5.042296	AATAC	3.90625	3.7093
cg1578384	MAD1L1	GR-beta [	232	236	5.042296	AATCC	3.90625	3.7093
cg1578384	MAD1L1	GR-beta [	1250	1254	5.042296	AATAC	3.90625	3.7093
cg1578384	MAD1L1	GR-beta [	1456	1460	5.042296	AATAC	3.90625	3.7093
cg1151970	MAD1L1	GR-beta [	777	781	5.042296	GGATT	3.90625	3.7093
cg1151970	MAD1L1	GR-beta [	870	874	5.042296	AATCC	3.90625	3.7093
cg1151970	MAD1L1	GR-beta [	1551	1555	5.042296	AATAC	3.90625	3.7093
cg1002882	MAD1L1	GR-beta [	186	190	5.042296	AATCC	3.90625	3.7093
cg1002882	MAD1L1	GR-beta [	1247	1251	5.042296	GGATT	3.90625	3.7093
cg1002882	MAD1L1	GR-beta [	1489	1493	5.042296	AATCC	3.90625	3.7093
cg1002882	MAD1L1	GR-beta [	1719	1723	5.042296	GGATT	3.90625	3.7093
cg1002882	MAD1L1	GR-beta [	1859	1863	5.042296	GGATT	3.90625	3.7093
cg1002882	MAD1L1	GR-beta [	1929	1933	5.042296	AATCC	3.90625	3.7093
cg0611220	MAD1L1	GR-beta [	301	305	5.042296	GGATT	3.90625	3.7093
cg0611220	MAD1L1	GR-beta [	340	344	5.042296	GTATT	3.90625	3.7093
cg0611220	MAD1L1	GR-beta [	440	444	5.042296	GGATT	3.90625	3.7093
cg0611220	MAD1L1	GR-beta [	522	526	5.042296	AATAC	3.90625	3.7093
cg0611220	MAD1L1	GR-beta [	874	878	5.042296	GTATT	3.90625	3.7093
cg0611220	MAD1L1	GR-beta [	1773	1777	5.042296	AATAC	3.90625	3.7093
cg0611220	MAD1L1	GR-beta [	1910	1914	5.042296	GGATT	3.90625	3.7093
cg1578384	MAD1L1	c-Ets-1 [T	1373	1379	5.038739	TTGGAA	0.48828	0.48026
cg0372348	MAD1L1	EBF [T05	1315	1325	5.026987	AGCCCT	0.02289	0.02569
cg1578384	MAD1L1	NFI/CTF [	1661	1668	5.021086	CCAAAG	0.24414	0.25666
cg0231133	MAD1L1	p53 [T006	219	225	5.020467	CGAGCC	0.48828	0.53921
cg1002882	MAD1L1	p53 [T006	1071	1077	5.020467	CGAGCC	0.48828	0.53921
cg1002882	MAD1L1	c-Jun [T00	1708	1714	5.000337	TGACAC	0.61035	0.60573

cg0611220	MAD1L1	c-Jun [T00	1213	1219	5.000337	TGACAC(	0.61035	0.60573
cg1151970	MAD1L1	c-Myb [T0	40	47	4.974489	CAACTG(	0.30518	0.30087
cg1002882	MAD1L1	c-Myb [T0	434	441	4.974489	AGCAGT	0.30518	0.30087
cg0611220	MAD1L1	c-Myb [T0	1716	1723	4.974489	TGCAGT	0.30518	0.30087
cg0231133	MAD1L1	IRF-1 [T0(	910	918	4.968836	ACGGGG	0.1297	0.12724
cg0372348	MAD1L1	IRF-1 [T0(	264	272	4.968836	AGGGGG	0.1297	0.12724
cg0611220	MAD1L1	IRF-1 [T0(	1685	1693	4.963725	CCAAGG.	0.1297	0.12724
cg0231133	MAD1L1	AP-1 [T00	1831	1839	4.955822	AGGGAG	0.12207	0.12309
cg1578384	MAD1L1	PXR-1:RX	297	304	4.90845	ATGGTT(	0.12207	0.11843
cg0231133	MAD1L1	XBP-1 [T(	94	99	4.894955	AGGCAT	0.97656	0.99839
cg0231133	MAD1L1	XBP-1 [T(	1288	1293	4.894955	AGGCAT	0.97656	0.99839
cg0231133	MAD1L1	XBP-1 [T(	1727	1732	4.894955	AGGCAT	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	317	322	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	333	338	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	373	378	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	397	402	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	453	458	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	501	506	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	517	522	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	533	538	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	549	554	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	653	658	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	726	731	4.894955	ATGCCG	0.97656	0.99839
cg1578384	MAD1L1	XBP-1 [T(	770	775	4.894955	ATGCCG	0.97656	0.99839
cg1151970	MAD1L1	XBP-1 [T(	1808	1813	4.894955	ATGCCT	0.97656	0.99839
cg1002882	MAD1L1	XBP-1 [T(	1012	1017	4.894955	ATGCCG	0.97656	0.99839
cg0611220	MAD1L1	XBP-1 [T(	51	56	4.894955	ATGCCG	0.97656	0.99839
cg0611220	MAD1L1	XBP-1 [T(	605	610	4.894955	ATGCCG	0.97656	0.99839
cg0611220	MAD1L1	XBP-1 [T(	1791	1796	4.894955	ATGCCG	0.97656	0.99839
cg0372348	MAD1L1	XBP-1 [T(	653	658	4.894955	ATGCCT	0.97656	0.99839
cg1578384	MAD1L1	USF1 [T0(	1979	1988	4.89185	CACGTG	0.04578	0.04763
cg0372348	MAD1L1	USF1 [T0(	1910	1919	4.89185	CACGTG	0.04578	0.04763
cg0231133	MAD1L1	AR [T0004	1071	1079	4.890444	GGACAA	0.11444	0.12256
cg1002882	MAD1L1	AR [T0004	1782	1790	4.890444	GGACAA	0.11444	0.12256
cg1002882	MAD1L1	AR [T0004	1819	1827	4.890444	GGACAC.	0.11444	0.12256
cg1578384	MAD1L1	AP-2alpha	1420	1425	4.890408	GCCTAA	0.97656	0.97517
cg1151970	MAD1L1	AP-2alpha	1329	1334	4.890408	GCCTAA	0.97656	0.97517
cg0611220	MAD1L1	AP-2alpha	1625	1630	4.890408	GCCTAA	0.97656	0.97517
cg0611220	MAD1L1	PPAR-alpl	1674	1684	4.88658	AGCTGG(	0.01717	0.01861
cg0231133	MAD1L1	c-Ets-1 [T(	1412	1418	4.872197	TCGGAA.	0.48828	0.48026
cg0231133	MAD1L1	RXR-alpha	257	263	4.86724	GGGTCT(	0.48828	0.51407
cg0231133	MAD1L1	RXR-alpha	1811	1817	4.86724	CATACC(	0.48828	0.51407
cg1578384	MAD1L1	RXR-alpha	1436	1442	4.86724	GAGACC	0.48828	0.51407
cg1151970	MAD1L1	RXR-alpha	303	309	4.86724	GAGACC	0.48828	0.51407
cg0372348	MAD1L1	RXR-alpha	578	584	4.86724	CATACC(	0.48828	0.51407
cg1002882	MAD1L1	NF-Y [T0(	1315	1322	4.867193	ATTGGA(	0.36621	0.35921
cg0231133	MAD1L1	GCF [T00.	644	652	4.846987	GGACGG	0.27466	0.31905
cg1578384	MAD1L1	GCF [T00.	974	982	4.846987	TGGCAG(	0.27466	0.31905

cg1151970	MAD1L1	GCF [T00	1054	1062	4.846987	GGTCGG	0.27466	0.31905
cg1151970	MAD1L1	GCF [T00	1779	1787	4.846987	GGGCAG	0.27466	0.31905
cg1578384	MAD1L1	C/EBPalph	1526	1532	4.845599	AATTGC	0.97656	0.90302
cg0611220	MAD1L1	C/EBPalph	267	273	4.845599	AGCAAT	0.97656	0.90302
cg0372348	MAD1L1	C/EBPalph	368	374	4.845599	ATCAAT	0.97656	0.90302
cg1578384	MAD1L1	HNF-3alph	1637	1644	4.842999	ATAAAA	0.09155	0.07438
cg1578384	MAD1L1	HNF-3alph	1642	1649	4.842999	ATAAAA	0.09155	0.07438
cg0611220	MAD1L1	HNF-3alph	1506	1513	4.842999	AATTTA	0.09155	0.07438
cg0611220	MAD1L1	c-Myb [T0	1232	1239	4.840682	TAACTT	0.30518	0.30087
cg1002882	MAD1L1	HNF-1A [	382	389	4.828753	AACTTA	0.36621	0.34064
cg0231133	MAD1L1	NF-AT1 [	205	214	4.823485	TGGTTT	0.07629	0.07281
cg1002882	MAD1L1	p53 [T006	826	832	4.786849	AGTGCC	0.48828	0.53921
cg0372348	MAD1L1	p53 [T006	550	556	4.786849	GGGCAC	0.48828	0.53921
cg0372348	MAD1L1	p53 [T006	975	981	4.786849	AGTGCC	0.48828	0.53921
cg0372348	MAD1L1	p53 [T006	1768	1774	4.786849	GGGCAC	0.48828	0.53921
cg0372348	MAD1L1	RBP-Jkapp	764	775	4.785186	AACGTG	0.00668	0.00655
cg1151970	MAD1L1	c-Ets-1 [T0	1080	1086	4.782565	CTTCCA	0.48828	0.48026
cg1578384	MAD1L1	C/EBPalph	1071	1077	4.776286	AACAAT	0.97656	0.90302
cg0611220	MAD1L1	C/EBPalph	1603	1609	4.776286	AACAAT	0.97656	0.90302
cg0231133	MAD1L1	FOXP3 [T	123	128	4.756447	GTTGAG	2.92969	2.82
cg0231133	MAD1L1	FOXP3 [T	207	212	4.756447	GTTTTC	2.92969	2.82
cg0231133	MAD1L1	FOXP3 [T	873	878	4.756447	GTTGAG	2.92969	2.82
cg0231133	MAD1L1	FOXP3 [T	944	949	4.756447	CAAAAC	2.92969	2.82
cg0231133	MAD1L1	FOXP3 [T	1478	1483	4.756447	GAAAAC	2.92969	2.82
cg0231133	MAD1L1	FOXP3 [T	1647	1652	4.756447	CAAAAC	2.92969	2.82
cg0231133	MAD1L1	TFII-I [T0	54	59	4.756447	CAATCC	2.92969	2.89715
cg0231133	MAD1L1	TFII-I [T0	808	813	4.756447	GGACTG	2.92969	2.89715
cg0231133	MAD1L1	TFII-I [T0	956	961	4.756447	ATGTCC	2.92969	2.89715
cg0231133	MAD1L1	TFII-I [T0	1179	1184	4.756447	CAATCC	2.92969	2.89715
cg0231133	MAD1L1	TFII-I [T0	1387	1392	4.756447	GGACAT	2.92969	2.89715
cg0231133	MAD1L1	TFII-I [T0	1451	1456	4.756447	GGAAAT	2.92969	2.89715
cg0231133	MAD1L1	TFII-I [T0	1581	1586	4.756447	GGACTG	2.92969	2.89715
cg1578384	MAD1L1	FOXP3 [T	165	170	4.756447	GAAAAC	2.92969	2.82
cg1578384	MAD1L1	FOXP3 [T	1024	1029	4.756447	ATCAAC	2.92969	2.82
cg1578384	MAD1L1	FOXP3 [T	1090	1095	4.756447	GAAAAC	2.92969	2.82
cg1578384	MAD1L1	FOXP3 [T	1192	1197	4.756447	ATCAAC	2.92969	2.82
cg1578384	MAD1L1	FOXP3 [T	1364	1369	4.756447	CTCAAC	2.92969	2.82
cg1578384	MAD1L1	FOXP3 [T	1460	1465	4.756447	CAAAAC	2.92969	2.82
cg1578384	MAD1L1	FOXP3 [T	1807	1812	4.756447	GAAAAC	2.92969	2.82
cg1151970	MAD1L1	FOXP3 [T	204	209	4.756447	GTTGAG	2.92969	2.82
cg1151970	MAD1L1	FOXP3 [T	826	831	4.756447	CAAAAC	2.92969	2.82
cg1151970	MAD1L1	TFII-I [T0	612	617	4.756447	ATGTCC	2.92969	2.89715
cg1151970	MAD1L1	TFII-I [T0	869	874	4.756447	CAATCC	2.92969	2.89715
cg1151970	MAD1L1	TFII-I [T0	1281	1286	4.756447	CATTCC	2.92969	2.89715
cg1151970	MAD1L1	TFII-I [T0	1516	1521	4.756447	ATTTCC	2.92969	2.89715
cg1151970	MAD1L1	TFII-I [T0	1637	1642	4.756447	GGACAT	2.92969	2.89715
cg1151970	MAD1L1	TFII-I [T0	1640	1645	4.756447	CATTCC	2.92969	2.89715
cg1151970	MAD1L1	TFII-I [T0	1802	1807	4.756447	CATTCC	2.92969	2.89715

cg1151970	MAD1L1	TFII-I [T0	1927	1932	4.756447	ATGTCC	2.92969	2.89715
cg1002882	MAD1L1	FOXP3 [T	379	384	4.756447	GAAAAC	2.92969	2.82
cg1002882	MAD1L1	FOXP3 [T	1216	1221	4.756447	GAAAAC	2.92969	2.82
cg1002882	MAD1L1	TFII-I [T0	1030	1035	4.756447	ATTTCC	2.92969	2.89715
cg0611220	MAD1L1	FOXP3 [T	650	655	4.756447	AAAAAC	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	946	951	4.756447	GTTTTT	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	992	997	4.756447	GTTTTG	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1073	1078	4.756447	GTTTTT	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1359	1364	4.756447	GTTTTG	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1364	1369	4.756447	GTTTTT	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1380	1385	4.756447	GTTTTG	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1389	1394	4.756447	GTTTTC	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1535	1540	4.756447	GTTGAC	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1600	1605	4.756447	AAAAAC	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1849	1854	4.756447	CAAAAC	2.92969	2.82
cg0611220	MAD1L1	FOXP3 [T	1916	1921	4.756447	GTTTTG	2.92969	2.82
cg0611220	MAD1L1	TFII-I [T0	792	797	4.756447	GGACTG	2.92969	2.89715
cg0611220	MAD1L1	TFII-I [T0	926	931	4.756447	GGACAT	2.92969	2.89715
cg0611220	MAD1L1	TFII-I [T0	1036	1041	4.756447	GGAATG	2.92969	2.89715
cg0611220	MAD1L1	TFII-I [T0	1240	1245	4.756447	ATTTCC	2.92969	2.89715
cg0611220	MAD1L1	TFII-I [T0	1989	1994	4.756447	GGAATG	2.92969	2.89715
cg0372348	MAD1L1	FOXP3 [T	307	312	4.756447	GTTTTT	2.92969	2.82
cg0372348	MAD1L1	FOXP3 [T	871	876	4.756447	CAAAAC	2.92969	2.82
cg0372348	MAD1L1	FOXP3 [T	1444	1449	4.756447	CTCAAC	2.92969	2.82
cg0372348	MAD1L1	FOXP3 [T	1547	1552	4.756447	CAAAAC	2.92969	2.82
cg0372348	MAD1L1	TFII-I [T0	378	383	4.756447	ATTTCC	2.92969	2.89715
cg0372348	MAD1L1	TFII-I [T0	456	461	4.756447	CATTCC	2.92969	2.89715
cg0372348	MAD1L1	TFII-I [T0	668	673	4.756447	GGATAT	2.92969	2.89715
cg0372348	MAD1L1	TFII-I [T0	1069	1074	4.756447	CAGTCC	2.92969	2.89715
cg0372348	MAD1L1	TFII-I [T0	1156	1161	4.756447	CAGTCC	2.92969	2.89715
cg1578384	MAD1L1	c-Myb [T0	1911	1918	4.754782	GAACTG	0.30518	0.30087
cg0611220	MAD1L1	c-Myb [T0	1283	1290	4.754782	TAACTG	0.30518	0.30087
cg1002882	MAD1L1	Ik-1 [T027	960	972	4.748597	CGAGGT	0.00313	0.00339
cg1151970	MAD1L1	c-Ets-1 [T	106	112	4.74411	ACGGAA	0.85449	0.8381
cg1002882	MAD1L1	NF-kappa	1530	1540	4.735432	GGGGAG	0.03242	0.03571
cg1578384	MAD1L1	USF1 [T0	1975	1984	4.677985	CATACA	0.06866	0.06933
cg1578384	MAD1L1	c-Ets-1 [T	856	862	4.654478	CTGGAA	0.85449	0.8381
cg1151970	MAD1L1	c-Ets-1 [T	1750	1756	4.654478	CTTCCA	0.85449	0.8381
cg1151970	MAD1L1	c-Ets-1 [T	1846	1852	4.654478	CTGGAA	0.85449	0.8381
cg1002882	MAD1L1	c-Ets-1 [T	1339	1345	4.654478	CTGGAA	0.85449	0.8381
cg0611220	MAD1L1	c-Ets-1 [T	44	50	4.654478	CTGGAA	0.85449	0.8381
cg0611220	MAD1L1	c-Ets-1 [T	1748	1754	4.654478	CTTCCA	0.85449	0.8381
cg0372348	MAD1L1	p53 [T006	1231	1237	4.645444	CGCGCC	0.24414	0.28373
cg0372348	MAD1L1	p53 [T006	1626	1632	4.645444	CGCGCC	0.24414	0.28373
cg1151970	MAD1L1	ATF-2 [T0	588	597	4.623667	AGGACG	0.03815	0.03703
cg0231133	MAD1L1	VDR [T00	866	874	4.617121	GTTCAG	0.37384	0.36855
cg1578384	MAD1L1	VDR [T00	300	308	4.617121	GTTCAC	0.37384	0.36855
cg0611220	MAD1L1	VDR [T00	1259	1267	4.617121	ATGTTG	0.37384	0.36855

cg0231133	MAD1L1	c-Ets-1 [T	928	934	4.616023	TTTCCG	0.85449	0.8381
cg0372348	MAD1L1	AP-1 [T00	786	794	4.606866	GTGGAG	0.03052	0.03196
cg1151970	MAD1L1	c-Ets-2 [T	810	818	4.589988	ATGAAG	0.06866	0.06805
cg0372348	MAD1L1	c-Ets-2 [T	1791	1799	4.589988	AGGAAG	0.06866	0.06805
cg1002882	MAD1L1	NF-AT1 [	166	174	4.566689	ATAGTT	0.06866	0.06549
cg0372348	MAD1L1	C/EBPalp	1150	1156	4.560723	GCCAAT	0.24414	0.24373
cg1002882	MAD1L1	AP-1 [T00	452	460	4.553988	TGACTC	0.03052	0.03196
cg0231133	MAD1L1	E2F-1 [T0	1688	1695	4.549709	GCGGTA	0.15259	0.16681
cg0231133	MAD1L1	E2F-1 [T0	708	715	4.545253	GCGGGA	0.15259	0.16681
cg0372348	MAD1L1	E2F-1 [T0	1053	1060	4.545253	GCGGGA	0.15259	0.16681
cg1002882	MAD1L1	c-Ets-1 [T	1249	1255	4.539113	ATTCCT	0.85449	0.8381
cg1578384	MAD1L1	USF2 [T0	1689	1698	4.528187	CAGGTG	0.06866	0.07203
cg1151970	MAD1L1	USF2 [T0	1124	1133	4.528187	TGGGCA	0.06866	0.07203
cg1002882	MAD1L1	c-Ets-1 [T	890	896	4.487936	TTTCCG	0.85449	0.8381
cg0231133	MAD1L1	NF-kappa	981	991	4.48433	TGGACC	0.03242	0.03571
cg1578384	MAD1L1	T3R-beta1	1964	1972	4.481316	TCACCA	0.27466	0.27245
cg1002882	MAD1L1	T3R-beta1	12	20	4.481316	TCACCT	0.27466	0.27245
cg0231133	MAD1L1	PU.1 [T02	1275	1287	4.468786	TGTGAG	0.00131	0.00135
cg0372348	MAD1L1	USF1 [T0	1906	1915	4.464121	GTATCA	0.06866	0.06933
cg1578384	MAD1L1	T3R-beta1	835	843	4.462023	TCACCT	0.27466	0.27245
cg1151970	MAD1L1	T3R-beta1	1700	1708	4.462023	TCCAGG	0.27466	0.27245
cg0231133	MAD1L1	GATA-2 [	189	197	4.444445	GGATAG	0.24414	0.23857
cg0231133	MAD1L1	GATA-2 [	1015	1023	4.444445	GGATAA	0.24414	0.23857
cg0231133	MAD1L1	c-Jun [T00	133	139	4.441904	TCAGTC	0.12207	0.11843
cg1002882	MAD1L1	c-Jun [T00	1953	1959	4.441904	TCAGTC	0.12207	0.11843
cg0231133	MAD1L1	AP-2alpha	1613	1618	4.438035	CTAGGC	0.97656	0.99839
cg0372348	MAD1L1	AP-2alpha	847	852	4.438035	CTAGGC	0.97656	0.99839
cg1151970	MAD1L1	RXR-alph	606	612	4.423008	GGGTGG	0.24414	0.25781
cg1151970	MAD1L1	RXR-alph	1483	1489	4.423008	TCCACC	0.24414	0.25781
cg1151970	MAD1L1	RXR-alph	1558	1564	4.423008	GGGTGG	0.24414	0.25781
cg1002882	MAD1L1	RXR-alph	1414	1420	4.423008	TCCACC	0.24414	0.25781
cg0611220	MAD1L1	RXR-alph	596	602	4.423008	ACAACC	0.24414	0.25781
cg0611220	MAD1L1	RXR-alph	661	667	4.423008	GGGTTG	0.24414	0.25781
cg0231133	MAD1L1	AP-2alpha	1422	1427	4.422424	TAAGGC	0.97656	0.99839
cg0231133	MAD1L1	STAT4 [T	613	618	4.411765	GCTTCC	1.95312	1.99838
cg0231133	MAD1L1	STAT4 [T	687	692	4.411765	GGAACG	1.95312	1.99838
cg0231133	MAD1L1	STAT4 [T	1473	1478	4.411765	GGAACG	1.95312	1.99838
cg1578384	MAD1L1	STAT4 [T	7	12	4.411765	GGAAGC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	333	338	4.411765	TCTTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	362	367	4.411765	TCTTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	388	393	4.411765	TCTTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	631	636	4.411765	CGTTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	644	649	4.411765	GGAACG	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	1079	1084	4.411765	GCTTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	1281	1286	4.411765	CATTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	1448	1453	4.411765	CGTTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	1468	1473	4.411765	TCTTCC	1.95312	1.99838
cg1151970	MAD1L1	STAT4 [T	1640	1645	4.411765	CATTCC	1.95312	1.99838

cg1151970	MAD1L1	STAT4 [T	1802	1807	4.411765	CATTCC	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	431	436	4.411765	GGAAGC	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	684	689	4.411765	GGAACG	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	895	900	4.411765	GGAAGC	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	899	904	4.411765	GCTTCC	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	1091	1096	4.411765	GGAAGC	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	1288	1293	4.411765	GGAAGA	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	1424	1429	4.411765	GGAAGC	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	1803	1808	4.411765	GGAAGC	1.95312	1.99838
cg1002882	MAD1L1	STAT4 [T	1924	1929	4.411765	GGAAGA	1.95312	1.99838
cg0611220	MAD1L1	STAT4 [T	46	51	4.411765	GGAAGA	1.95312	1.99838
cg0611220	MAD1L1	STAT4 [T	974	979	4.411765	GGAAGA	1.95312	1.99838
cg0611220	MAD1L1	STAT4 [T	1036	1041	4.411765	GGAATG	1.95312	1.99838
cg0611220	MAD1L1	STAT4 [T	1551	1556	4.411765	GGAACG	1.95312	1.99838
cg0611220	MAD1L1	STAT4 [T	1989	1994	4.411765	GGAATG	1.95312	1.99838
cg0372348	MAD1L1	STAT4 [T	83	88	4.411765	GGAAGC	1.95312	1.99838
cg0372348	MAD1L1	STAT4 [T	206	211	4.411765	GCTTCC	1.95312	1.99838
cg0372348	MAD1L1	STAT4 [T	456	461	4.411765	CATTCC	1.95312	1.99838
cg0372348	MAD1L1	STAT4 [T	572	577	4.411765	GGAAGC	1.95312	1.99838
cg0372348	MAD1L1	STAT4 [T	859	864	4.411765	CGTTCC	1.95312	1.99838
cg0372348	MAD1L1	STAT4 [T	1796	1801	4.411765	GGAAGA	1.95312	1.99838
cg0611220	MAD1L1	c-Ets-1 [T	856	862	4.411026	ATTCCT	0.85449	0.8381
cg0611220	MAD1L1	c-Ets-1 [T	1769	1775	4.411026	AAGGAA	0.85449	0.8381
cg1578384	MAD1L1	NF-AT2 [	849	858	4.342522	GGAAAC	0.04196	0.03925
cg0231133	MAD1L1	p53 [T006	636	642	4.33696	GGGCCA	0.24414	0.28373
cg0231133	MAD1L1	p53 [T006	1985	1991	4.33696	GGGCCA	0.24414	0.28373
cg1151970	MAD1L1	p53 [T006	485	491	4.33696	CTGGCC	0.24414	0.28373
cg1151970	MAD1L1	p53 [T006	884	890	4.33696	CTGGCC	0.24414	0.28373
cg1151970	MAD1L1	p53 [T006	915	921	4.33696	CTGGCC	0.24414	0.28373
cg1151970	MAD1L1	p53 [T006	1421	1427	4.33696	GGGCCA	0.24414	0.28373
cg0372348	MAD1L1	p53 [T006	1520	1526	4.33696	GGGCCA	0.24414	0.28373
cg0611220	MAD1L1	Sp1 [T007	409	418	4.333247	GATCCG	0.08583	0.0979
cg1578384	MAD1L1	RAR-beta	1531	1540	4.326039	CTTGAA	0.14496	0.14853
cg1578384	MAD1L1	HOXD9 [	898	907	4.321431	AATAAA	0.03433	0.02831
cg1578384	MAD1L1	HOXD9 [	1636	1645	4.321431	AATAAA	0.03433	0.02831
cg1578384	MAD1L1	HOXD9 [	1641	1650	4.321431	AATAAA	0.03433	0.02831
cg1578384	MAD1L1	HOXD10 [	898	907	4.321431	AATAAA	0.03433	0.02831
cg1578384	MAD1L1	HOXD10 [	1636	1645	4.321431	AATAAA	0.03433	0.02831
cg1578384	MAD1L1	HOXD10 [	1641	1650	4.321431	AATAAA	0.03433	0.02831
cg0231133	MAD1L1	PEA3 [T0	414	422	4.30818	TGGATG	0.13733	0.13607
cg0231133	MAD1L1	PEA3 [T0	1262	1270	4.30818	CATCAT	0.13733	0.13607
cg1151970	MAD1L1	PEA3 [T0	609	617	4.30818	TGGATG	0.13733	0.13607
cg1151970	MAD1L1	PEA3 [T0	707	715	4.30818	CATCAT	0.13733	0.13607
cg0372348	MAD1L1	PEA3 [T0	1386	1394	4.30818	GCACAT	0.13733	0.13607
cg0231133	MAD1L1	RAR-beta	395	404	4.289108	GATGAA	0.14496	0.14853
cg1002882	MAD1L1	c-Ets-1 [T	1485	1491	4.282938	GAGGAA	0.85449	0.8381
cg0611220	MAD1L1	c-Ets-1 [T	683	689	4.282938	ATTCCT	0.85449	0.8381
cg0611220	MAD1L1	RAR-beta	357	366	4.252176	AGGGTT	0.14496	0.14853

cg1578384	MAD1L1	RXR-alpha	954	960	4.24113	GGGTCC	0.97656	1.02803
cg1151970	MAD1L1	RXR-alpha	1104	1110	4.24113	GGGTCA	0.97656	1.02803
cg1002882	MAD1L1	RXR-alpha	650	656	4.24113	GGGACC	0.97656	1.02803
cg0372348	MAD1L1	RXR-alpha	628	634	4.24113	GTGACC	0.97656	1.02803
cg0372348	MAD1L1	RXR-alpha	1356	1362	4.24113	GTGACC	0.97656	1.02803
cg0372348	MAD1L1	RXR-alpha	1594	1600	4.24113	GGGACC	0.97656	1.02803
cg1578384	MAD1L1	PXR-1:RX	1533	1540	4.213958	TGAACC	0.12207	0.12474
cg1002882	MAD1L1	AP-2alpha	1230	1235	4.211849	GTAGGC	0.97656	1.02535
cg0231133	MAD1L1	GR-beta [T	5	9	4.201913	AATAG	7.8125	7.23274
cg0231133	MAD1L1	GR-beta [T	309	313	4.201913	CTATT	7.8125	7.23274
cg0231133	MAD1L1	GR-beta [T	449	453	4.201913	AATAA	7.8125	7.23274
cg0231133	MAD1L1	GR-beta [T	1038	1042	4.201913	CGATT	7.8125	7.23274
cg0231133	MAD1L1	GR-beta [T	1109	1113	4.201913	TGATT	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	887	891	4.201913	AATCG	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	898	902	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1009	1013	4.201913	AATAG	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1074	1078	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1136	1140	4.201913	AATCA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1318	1322	4.201913	AATCA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1619	1623	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1622	1626	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1625	1629	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1636	1640	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1641	1645	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1646	1650	4.201913	AATAA	7.8125	7.23274
cg1578384	MAD1L1	GR-beta [T	1652	1656	4.201913	AATAA	7.8125	7.23274
cg1151970	MAD1L1	GR-beta [T	164	168	4.201913	TGATT	7.8125	7.23274
cg1151970	MAD1L1	GR-beta [T	823	827	4.201913	AATCA	7.8125	7.23274
cg1151970	MAD1L1	GR-beta [T	1414	1418	4.201913	TGATT	7.8125	7.23274
cg1151970	MAD1L1	GR-beta [T	1514	1518	4.201913	TGATT	7.8125	7.23274
cg1002882	MAD1L1	GR-beta [T	1024	1028	4.201913	TGATT	7.8125	7.23274
cg1002882	MAD1L1	GR-beta [T	1115	1119	4.201913	TTATT	7.8125	7.23274
cg1002882	MAD1L1	GR-beta [T	1727	1731	4.201913	TGATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	479	483	4.201913	TTATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	519	523	4.201913	AATAA	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	561	565	4.201913	AATAG	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	681	685	4.201913	CGATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	749	753	4.201913	AATAA	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	829	833	4.201913	CTATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1012	1016	4.201913	TTATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1024	1028	4.201913	AATCG	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1302	1306	4.201913	TTATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1370	1374	4.201913	CTATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1399	1403	4.201913	CTATT	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1414	1418	4.201913	AATCG	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1443	1447	4.201913	AATAG	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1558	1562	4.201913	AATAA	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1561	1565	4.201913	AATAA	7.8125	7.23274

cg0611220	MAD1L1	GR-beta [T	1579	1583	4.201913	AATAA	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1588	1592	4.201913	AATAA	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1606	1610	4.201913	AATAA	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1615	1619	4.201913	AATCG	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1646	1650	4.201913	AATAG	7.8125	7.23274
cg0611220	MAD1L1	GR-beta [T	1803	1807	4.201913	AATAA	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	348	352	4.201913	CTATT	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	367	371	4.201913	AATCA	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	376	380	4.201913	TGATT	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	713	717	4.201913	CTATT	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	729	733	4.201913	TTATT	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	1153	1157	4.201913	AATCA	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	1328	1332	4.201913	AATAG	7.8125	7.23274
cg0372348	MAD1L1	GR-beta [T	1528	1532	4.201913	AATCA	7.8125	7.23274
cg0611220	MAD1L1	c-Ets-1 [T	1034	1040	4.154851	CAGGAA	0.24414	0.23719
cg0231133	MAD1L1	c-Fos [T00	1528	1537	4.139091	AGCATG	0.03815	0.03747
cg0372348	MAD1L1	c-Fos [T00	1553	1562	4.139091	AAGATG	0.03815	0.03747
cg0231133	MAD1L1	NF-1 [T00	949	956	4.135372	CGACCC	0.24414	0.25714
cg1578384	MAD1L1	NF-1 [T00	1558	1565	4.135372	TGAGCC	0.24414	0.25714
cg1151970	MAD1L1	NF-1 [T00	1719	1726	4.135372	TGCCCC	0.24414	0.25714
cg1002882	MAD1L1	NF-1 [T00	178	185	4.135372	TGACCC	0.24414	0.25714
cg0611220	MAD1L1	NF-1 [T00	234	241	4.135372	TTGGCT	0.24414	0.25714
cg0611220	MAD1L1	NF-1 [T00	1537	1544	4.135372	TGACCC	0.24414	0.25714
cg1002882	MAD1L1	NF-AT1 [T	291	300	4.134416	TGGAAA	0.08392	0.07965
cg1002882	MAD1L1	c-Jun [T00	850	856	4.1298	CGAGTC	0.24414	0.23729
cg1002882	MAD1L1	c-Jun [T00	1134	1140	4.1298	CGAGTC	0.24414	0.23729
cg0372348	MAD1L1	c-Jun [T00	1557	1563	4.1298	TGACTC	0.24414	0.23729
cg0231133	MAD1L1	p53 [T006	110	116	4.125254	CCGGCC	0.73242	0.82434
cg0231133	MAD1L1	p53 [T006	365	371	4.125254	CAGGCC	0.73242	0.82434
cg0231133	MAD1L1	p53 [T006	1820	1826	4.125254	CAGGCC	0.73242	0.82434
cg1578384	MAD1L1	p53 [T006	1790	1796	4.125254	CAGGCC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	701	707	4.125254	CCGGCC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	1521	1527	4.125254	CAGGCC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	1645	1651	4.125254	CCGGCC	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	537	543	4.125254	CAGGCC	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	743	749	4.125254	CAGGCC	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	1583	1589	4.125254	CAGGCC	0.73242	0.82434
cg0372348	MAD1L1	p53 [T006	682	688	4.125254	GGGCCT	0.73242	0.82434
cg0372348	MAD1L1	p53 [T006	692	698	4.125254	CAGGCC	0.73242	0.82434
cg0372348	MAD1L1	p53 [T006	1062	1068	4.125254	CCGGCC	0.73242	0.82434
cg1002882	MAD1L1	AhR:Arnt	1500	1509	4.117831	GCACGC	0.02289	0.02659
cg0372348	MAD1L1	PXR-1:RX	474	481	4.090374	TGAACC	0.12207	0.12474
cg0231133	MAD1L1	p53 [T006	1256	1262	4.083527	GGTGCC	0.73242	0.82434
cg1578384	MAD1L1	p53 [T006	1691	1697	4.083527	GGTGCC	0.73242	0.82434
cg1578384	MAD1L1	p53 [T006	1950	1956	4.083527	GGGCAC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	689	695	4.083527	GGTGCC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	1125	1131	4.083527	GGGCAC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	1383	1389	4.083527	GGGCAC	0.73242	0.82434

cg1002882	MAD1L1	p53 [T006	494	500	4.083527	GGGCAC	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	576	582	4.083527	GGTGCC	0.73242	0.82434
cg0372348	MAD1L1	p53 [T006	1872	1878	4.083527	GGGCAC	0.73242	0.82434
cg0611220	MAD1L1	IRF-1 [T0	940	948	4.043231	TTTCCAC	0.1297	0.12468
cg1578384	MAD1L1	EBF [T05	1953	1963	4.04219	CACCCA	0.0248	0.02839
cg0372348	MAD1L1	EBF [T05	1628	1638	4.04219	CGCCCA	0.0248	0.02839
cg1151970	MAD1L1	IRF-1 [T0	1322	1330	4.035054	TTTCCCT	0.1297	0.12468
cg0611220	MAD1L1	IRF-1 [T0	1241	1249	4.035054	TTTCCCT	0.1297	0.12468
cg0231133	MAD1L1	C/EBPalph	52	58	4.019783	GGCAAT	0.48828	0.46347
cg1002882	MAD1L1	C/EBPalph	1137	1143	4.019783	GTCAAT	0.48828	0.46347
cg0231133	MAD1L1	RXR-alpha	9	15	4.019014	GGGTCT	0.97656	1.02803
cg0231133	MAD1L1	RXR-alpha	1359	1365	4.019014	GGGTGT	0.97656	1.02803
cg1578384	MAD1L1	RXR-alpha	1853	1859	4.019014	CACACC	0.97656	1.02803
cg0611220	MAD1L1	RXR-alpha	358	364	4.019014	GGGTTT	0.97656	1.02803
cg0611220	MAD1L1	RXR-alpha	1081	1087	4.019014	GAAACC	0.97656	1.02803
cg0372348	MAD1L1	RXR-alpha	218	224	4.019014	CACACC	0.97656	1.02803
cg0372348	MAD1L1	RXR-alpha	1798	1804	4.019014	AAGACC	0.97656	1.02803
cg1151970	MAD1L1	c-Ets-2 [T	1462	1470	4.017001	TTCCTTT	0.16022	0.15061
cg0611220	MAD1L1	c-Ets-2 [T	1766	1774	4.017001	GTAAAG	0.16022	0.15061
cg0372348	MAD1L1	c-Ets-2 [T	835	843	4.017001	TTCCTTT	0.16022	0.15061
cg0611220	MAD1L1	STAT1bet	1240	1249	4.01053	ATTTCCC	0.03433	0.03308
cg0231133	MAD1L1	TFIID [T0	0	6	4.007279	TTATAA	1.09863	0.94722
cg0231133	MAD1L1	Pax-5 [T0	1320	1326	4.007279	GGGCTG	1.09863	1.18533
cg0231133	MAD1L1	Pax-5 [T0	1627	1633	4.007279	GGGCAG	1.09863	1.18533
cg1578384	MAD1L1	TFIID [T0	889	895	4.007279	TCGTAA	1.09863	0.94722
cg1578384	MAD1L1	TFIID [T0	1624	1630	4.007279	TAATAA	1.09863	0.94722
cg1578384	MAD1L1	Pax-5 [T0	907	913	4.007279	AGAGCC	1.09863	1.18533
cg1578384	MAD1L1	Pax-5 [T0	928	934	4.007279	AAAGCC	1.09863	1.18533
cg1578384	MAD1L1	Pax-5 [T0	1327	1333	4.007279	AAGGCC	1.09863	1.18533
cg1578384	MAD1L1	Pax-5 [T0	1656	1662	4.007279	AAAGCC	1.09863	1.18533
cg1151970	MAD1L1	TFIID [T0	859	865	4.007279	TCTTAA	1.09863	0.94722
cg1151970	MAD1L1	Pax-5 [T0	227	233	4.007279	GGGCTG	1.09863	1.18533
cg1151970	MAD1L1	Pax-5 [T0	661	667	4.007279	ACAGCC	1.09863	1.18533
cg1151970	MAD1L1	Pax-5 [T0	791	797	4.007279	AAAGCC	1.09863	1.18533
cg1151970	MAD1L1	Pax-5 [T0	1261	1267	4.007279	GGGCTC	1.09863	1.18533
cg1151970	MAD1L1	Pax-5 [T0	1349	1355	4.007279	AGAGCC	1.09863	1.18533
cg1151970	MAD1L1	Pax-5 [T0	1919	1925	4.007279	ACGGCC	1.09863	1.18533
cg1002882	MAD1L1	TFIID [T0	1168	1174	4.007279	TTTTAAA	1.09863	0.94722
cg1002882	MAD1L1	Pax-5 [T0	235	241	4.007279	GGGCCC	1.09863	1.18533
cg1002882	MAD1L1	Pax-5 [T0	756	762	4.007279	AGGGCC	1.09863	1.18533
cg1002882	MAD1L1	Pax-5 [T0	826	832	4.007279	AGTGCC	1.09863	1.18533
cg1002882	MAD1L1	Pax-5 [T0	985	991	4.007279	GGGCTG	1.09863	1.18533
cg1002882	MAD1L1	Pax-5 [T0	1334	1340	4.007279	GGGCTC	1.09863	1.18533
cg1002882	MAD1L1	Pax-5 [T0	1471	1477	4.007279	GGGCTC	1.09863	1.18533
cg1002882	MAD1L1	Pax-5 [T0	1666	1672	4.007279	GGGCTC	1.09863	1.18533
cg1002882	MAD1L1	Pax-5 [T0	1981	1987	4.007279	GGGCCC	1.09863	1.18533
cg0611220	MAD1L1	TFIID [T0	746	752	4.007279	TTTAAT	1.09863	0.94722
cg0611220	MAD1L1	TFIID [T0	1076	1082	4.007279	TTTAAG	1.09863	0.94722

cg0611220	MAD1L1	TFIID [T0	1560	1566	4.007279	TAATAA	1.09863	0.94722
cg0611220	MAD1L1	Pax-5 [T0(	61	67	4.007279	GGGCTT	1.09863	1.18533
cg0611220	MAD1L1	Pax-5 [T0(	797	803	4.007279	GGGCTC	1.09863	1.18533
cg0372348	MAD1L1	TFIID [T0	310	316	4.007279	TTTACA	1.09863	0.94722
cg0372348	MAD1L1	Pax-5 [T0(	275	281	4.007279	GGGCTG	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	550	556	4.007279	GGGCAC	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	603	609	4.007279	ACGGCC	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	975	981	4.007279	AGTGCC	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	1001	1007	4.007279	GGGCCT	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	1268	1274	4.007279	GGGCTC	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	1321	1327	4.007279	GGGCTC	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	1339	1345	4.007279	AAAGCC	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	1634	1640	4.007279	GGGCTG	1.09863	1.18533
cg0372348	MAD1L1	Pax-5 [T0(	1768	1774	4.007279	GGGCAC	1.09863	1.18533
cg0231133	MAD1L1	USF1 [T0(	1377	1386	3.987093	GCCTCA(	0.08011	0.08435
cg1578384	MAD1L1	AP-2alpha	1002	1007	3.970052	GCCTTG	0.97656	1.02535
cg1578384	MAD1L1	AP-2alpha	1308	1313	3.970052	CAAGGC	0.97656	1.02535
cg1151970	MAD1L1	AP-2alpha	69	74	3.970052	CAAGGC	0.97656	1.02535
cg1151970	MAD1L1	AP-2alpha	474	479	3.970052	CAAGGC	0.97656	1.02535
cg1002882	MAD1L1	AP-2alpha	300	305	3.970052	CAAGGC	0.97656	1.02535
cg0611220	MAD1L1	AP-2alpha	1133	1138	3.970052	CAAGGC	0.97656	1.02535
cg0372348	MAD1L1	AP-2alpha	487	492	3.970052	GCCTTG	0.97656	1.02535
cg0372348	MAD1L1	AP-2alpha	1003	1008	3.970052	GCCTTG	0.97656	1.02535
cg0372348	MAD1L1	AP-2alpha	1211	1216	3.970052	CAAGGC	0.97656	1.02535
cg0372348	MAD1L1	AP-2alpha	1479	1484	3.970052	GCCTTG	0.97656	1.02535
cg0372348	MAD1L1	AP-2alpha	1843	1848	3.970052	CAAGGC	0.97656	1.02535
cg1151970	MAD1L1	NF-AT1 [T	1513	1521	3.917696	ATGATT	0.07629	0.07182
cg0372348	MAD1L1	NF-AT1 [T	375	383	3.917696	ATGATT	0.07629	0.07182
cg0611220	MAD1L1	ATF-2 [T0	750	759	3.88316	ATAACG	0.03433	0.03238
cg0231133	MAD1L1	PPAR-alpl	582	592	3.872523	ACCTGG(	0.02575	0.0279
cg1151970	MAD1L1	PPAR-alpl	288	298	3.872523	CTGACC(	0.02575	0.0279
cg1151970	MAD1L1	PPAR-alpl	1100	1110	3.872523	CCCTGG(	0.02575	0.0279
cg1578384	MAD1L1	c-Ets-1 [T(	1670	1676	3.846637	TAGGAA	0.24414	0.23719
cg0372348	MAD1L1	c-Ets-1 [T(	860	866	3.846637	GTTCCT	0.24414	0.23719
cg0231133	MAD1L1	EBF [T05	367	377	3.842007	GGCCCT(	0.0248	0.02839
cg0231133	MAD1L1	NF-AT2 [T	1101	1110	3.814941	GGAAAA	0.01144	0.01081
cg0611220	MAD1L1	Elk-1 [T00	970	978	3.81032	GCTAGG	0.09155	0.08816
cg0611220	MAD1L1	c-Jun [T00	1250	1256	3.807346	TGACTA	0.24414	0.23729
cg1578384	MAD1L1	NFI/CTF [	102	109	3.793671	CCAATG(	0.18311	0.19063
cg1578384	MAD1L1	NFI/CTF [	1812	1819	3.793671	CCAAAG	0.18311	0.19063
cg1002882	MAD1L1	NFI/CTF [	1547	1554	3.793671	CCAAAG	0.18311	0.19063
cg0231133	MAD1L1	GR [T050	944	950	3.763516	CAAAAC	0.73242	0.6946
cg0231133	MAD1L1	GR [T050	1647	1653	3.763516	CAAAAC	0.73242	0.6946
cg1578384	MAD1L1	GR [T050	1460	1466	3.763516	CAAAAC	0.73242	0.6946
cg1151970	MAD1L1	GR [T050	826	832	3.763516	CAAAAC	0.73242	0.6946
cg0611220	MAD1L1	GR [T050	1358	1364	3.763516	TGTTTC	0.73242	0.6946
cg0611220	MAD1L1	GR [T050	1379	1385	3.763516	AGTTTC	0.73242	0.6946
cg0611220	MAD1L1	GR [T050	1849	1855	3.763516	CAAAAC	0.73242	0.6946

cg0611220	MAD1L1	GR [T050	1915	1921	3.763516	AGTTTTC	0.73242	0.6946
cg0372348	MAD1L1	GR [T050	871	877	3.763516	CAAAAC	0.73242	0.6946
cg0372348	MAD1L1	GR [T050	1547	1553	3.763516	CAAAAC	0.73242	0.6946
cg0231133	MAD1L1	p53 [T006	739	745	3.750231	GGGCTG	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	667	673	3.750231	CCAGCC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	674	680	3.750231	CCAGCC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	741	747	3.750231	GGGCTT	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	964	970	3.750231	GGGCTG	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	973	979	3.750231	CCAGCC	0.73242	0.82434
cg1151970	MAD1L1	p53 [T006	1140	1146	3.750231	GGGCTG	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	2	8	3.750231	GGGCTG	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	64	70	3.750231	GGGCTG	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	305	311	3.750231	CCAGCC	0.73242	0.82434
cg1002882	MAD1L1	p53 [T006	556	562	3.750231	CCAGCC	0.73242	0.82434
cg0372348	MAD1L1	p53 [T006	1313	1319	3.750231	CCAGCC	0.73242	0.82434
cg0372348	MAD1L1	p53 [T006	1895	1901	3.750231	CCAGCC	0.73242	0.82434
cg1578384	MAD1L1	AP-2alpha	995	1000	3.743866	GAAGGC	0.48828	0.5124
cg1578384	MAD1L1	AP-2alpha	1376	1381	3.743866	GAAGGC	0.48828	0.5124
cg1151970	MAD1L1	AP-2alpha	220	225	3.743866	GAAGGC	0.48828	0.5124
cg1151970	MAD1L1	AP-2alpha	932	937	3.743866	GAAGGC	0.48828	0.5124
cg1151970	MAD1L1	AP-2alpha	1343	1348	3.743866	GAAGGC	0.48828	0.5124
cg0611220	MAD1L1	AP-2alpha	36	41	3.743866	GCCTTC	0.48828	0.5124
cg0611220	MAD1L1	AP-2alpha	96	101	3.743866	GCCTTC	0.48828	0.5124
cg0611220	MAD1L1	AP-2alpha	253	258	3.743866	GCCTTC	0.48828	0.5124
cg0372348	MAD1L1	AP-2alpha	45	50	3.743866	GAAGGC	0.48828	0.5124
cg0372348	MAD1L1	AP-2alpha	1224	1229	3.743866	GAAGGC	0.48828	0.5124
cg0372348	MAD1L1	AP-2alpha	1484	1489	3.743866	GCCTTC	0.48828	0.5124
cg0372348	MAD1L1	AP-2alpha	1922	1927	3.743866	GCCTTC	0.48828	0.5124
cg0231133	MAD1L1	NF-Y [T0	950	957	3.732121	GACCCA	0.48828	0.48427
cg1578384	MAD1L1	NF-Y [T0	99	106	3.732121	GACCCA	0.48828	0.48427
cg0611220	MAD1L1	NF-Y [T0	486	493	3.732121	GATCCA	0.48828	0.48427
cg0231133	MAD1L1	CREB [T0	1652	1660	3.729071	CACACG	0.10681	0.10808
cg0611220	MAD1L1	c-Ets-1 [T	1549	1555	3.71855	AAGGAA	0.61035	0.61936
cg0372348	MAD1L1	c-Ets-1 [T	834	840	3.71855	GTTCCTT	0.61035	0.61936
cg1578384	MAD1L1	PEA3 [T0	108	116	3.710864	GTACAT	0.09155	0.08745
cg1578384	MAD1L1	PEA3 [T0	1272	1280	3.710864	TCACAT	0.09155	0.08745
cg0231133	MAD1L1	IRF-1 [T0	431	439	3.689552	CTAGGG	0.06866	0.0661
cg1002882	MAD1L1	c-Fos [T00	851	860	3.637699	GAGTCA	0.05341	0.05266
cg1578384	MAD1L1	CREB [T0	43	51	3.615427	TGCACG	0.10681	0.10808
cg0231133	MAD1L1	c-Ets-1 [T	685	691	3.590463	GAGGAA	0.61035	0.61936
cg0231133	MAD1L1	c-Ets-1 [T	1471	1477	3.590463	GAGGAA	0.61035	0.61936
cg1002882	MAD1L1	c-Ets-1 [T	1972	1978	3.590463	GTTCCTC	0.61035	0.61936
cg0611220	MAD1L1	c-Ets-1 [T	552	558	3.590463	GTTCCTC	0.61035	0.61936
cg0611220	MAD1L1	c-Ets-1 [T	1447	1453	3.590463	GTTCCTC	0.61035	0.61936
cg1151970	MAD1L1	p53 [T006	1232	1238	3.586914	GGGCGA	0.73242	0.80362
cg0372348	MAD1L1	p53 [T006	1560	1566	3.586914	CTCGCC	0.73242	0.80362
cg1151970	MAD1L1	RXR-alpha	532	538	3.574782	GGGTCG	1.09863	1.1653
cg1151970	MAD1L1	NF-AT2 [	755	764	3.571424	GGAAAC	0.03433	0.03138

cg1002882	MAD1L1	NF-kappa	1878	1888	3.568679	GGGGAG	0.01812	0.02061
cg1578384	MAD1L1	C/EBPalp	1315	1321	3.555778	AACAAT	0.24414	0.23261
cg1151970	MAD1L1	C/EBPalp	867	873	3.555778	ACCAAT	0.24414	0.23261
cg1002882	MAD1L1	c-Ets-2 [T	171	179	3.518824	TTCCTTC	0.18311	0.18314
cg0611220	MAD1L1	c-Ets-2 [T	857	865	3.518824	TTCCTTC	0.18311	0.18314
cg0611220	MAD1L1	c-Ets-2 [T	1546	1554	3.518824	CAGAAG	0.18311	0.18314
cg0231133	MAD1L1	p53 [T006	1627	1633	3.516613	GGGCAG	0.73242	0.80362
cg0231133	MAD1L1	HNF-3alp	1	8	3.500065	TATAAA	0.27466	0.23175
cg0231133	MAD1L1	HNF-3alp	445	452	3.500065	AAAAAA	0.27466	0.23175
cg1578384	MAD1L1	HNF-3alp	1615	1622	3.500065	AAAAAA	0.27466	0.23175
cg0611220	MAD1L1	HNF-3alp	515	522	3.500065	AAAAAA	0.27466	0.23175
cg1151970	MAD1L1	VDR [T00	625	633	3.462841	GTTCAA	0.21362	0.21283
cg0372348	MAD1L1	VDR [T00	57	65	3.462841	AGGCTG	0.21362	0.21283
cg0231133	MAD1L1	c-Ets-1 [T	248	254	3.462376	CAGGAA	0.61035	0.61936
cg1578384	MAD1L1	c-Ets-1 [T	122	128	3.462376	CAGGAA	0.61035	0.61936
cg1151970	MAD1L1	c-Ets-1 [T	642	648	3.462376	CAGGAA	0.61035	0.61936
cg1151970	MAD1L1	c-Ets-1 [T	1449	1455	3.462376	GTTCCTC	0.61035	0.61936
cg1002882	MAD1L1	c-Ets-1 [T	908	914	3.462376	CAGGAA	0.61035	0.61936
cg0611220	MAD1L1	c-Ets-1 [T	1485	1491	3.462376	CAGGAA	0.61035	0.61936
cg0372348	MAD1L1	c-Ets-1 [T	1105	1111	3.462376	CAGGAA	0.61035	0.61936
cg0372348	MAD1L1	NF-AT1 [	1015	1024	3.445347	GGAGTT	0.07629	0.07204
cg1151970	MAD1L1	GCF [T00	1059	1067	3.409768	GCGCAG	0.03052	0.03366
cg0372348	MAD1L1	GCF [T00	509	517	3.409768	CACCTG	0.03052	0.03366
cg0611220	MAD1L1	PXR-1:RX	259	266	3.395883	TGGGTT	0.12207	0.11883
cg0231133	MAD1L1	RXR-alph	286	292	3.392904	GGGTCC	1.09863	1.1653
cg0231133	MAD1L1	RXR-alph	818	824	3.392904	GGGTAC	1.09863	1.1653
cg0231133	MAD1L1	RXR-alph	1306	1312	3.392904	CGCACC	1.09863	1.1653
cg0231133	MAD1L1	RXR-alph	1502	1508	3.392904	TGTACC	1.09863	1.1653
cg1578384	MAD1L1	RXR-alph	97	103	3.392904	AGGACC	1.09863	1.1653
cg1578384	MAD1L1	RXR-alph	1828	1834	3.392904	AGGACC	1.09863	1.1653
cg1151970	MAD1L1	RXR-alph	323	329	3.392904	CTCACC	1.09863	1.1653
cg1151970	MAD1L1	RXR-alph	352	358	3.392904	CTCACC	1.09863	1.1653
cg1002882	MAD1L1	RXR-alph	69	75	3.392904	GGGTTC	1.09863	1.1653
cg1002882	MAD1L1	RXR-alph	248	254	3.392904	GGGTAC	1.09863	1.1653
cg1002882	MAD1L1	RXR-alph	467	473	3.392904	GGGTGA	1.09863	1.1653
cg1002882	MAD1L1	RXR-alph	1124	1130	3.392904	GGGTCA	1.09863	1.1653
cg1002882	MAD1L1	RXR-alph	1389	1395	3.392904	AGGACC	1.09863	1.1653
cg0372348	MAD1L1	RXR-alph	92	98	3.392904	GGGTCC	1.09863	1.1653
cg0372348	MAD1L1	RXR-alph	108	114	3.392904	CTCACC	1.09863	1.1653
cg0372348	MAD1L1	RXR-alph	178	184	3.392904	GGGTTA	1.09863	1.1653
cg0372348	MAD1L1	RXR-alph	832	838	3.392904	GGGTTC	1.09863	1.1653
cg0372348	MAD1L1	RXR-alph	1435	1441	3.392904	GGGTCC	1.09863	1.1653
cg0372348	MAD1L1	RXR-alph	1931	1937	3.392904	GGGTAC	1.09863	1.1653
cg0372348	MAD1L1	Elk-1 [T00	1440	1448	3.381796	CTTCCTC	0.04578	0.04517
cg0231133	MAD1L1	p53 [T006	1752	1758	3.375208	CACGCC	0.73242	0.80362
cg1578384	MAD1L1	p53 [T006	1472	1478	3.375208	GGGCGT	0.73242	0.80362
cg1002882	MAD1L1	p53 [T006	24	30	3.375208	CCCGCC	0.73242	0.80362
cg1002882	MAD1L1	p53 [T006	980	986	3.375208	GGGCGG	0.73242	0.80362

cg1002882	MAD1L1	p53 [T006	1370	1376	3.375208	GGGCGG	0.73242	0.80362
cg1002882	MAD1L1	p53 [T006	1501	1507	3.375208	CACGCC	0.73242	0.80362
cg1002882	MAD1L1	T3R-beta1	469	477	3.370634	GTGAGG	0.27466	0.27326
cg0372348	MAD1L1	T3R-beta1	1673	1681	3.370634	AAGTGG	0.27466	0.27326
cg0231133	MAD1L1	GR-beta [T	1129	1133	3.361531	AGATT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	220	224	3.361531	AATCT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	758	762	3.361531	AATAT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	1361	1365	3.361531	AATCT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	1565	1569	3.361531	AGATT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [T	117	121	3.361531	AATCT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [T	151	155	3.361531	AATAT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [T	152	156	3.361531	ATATT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [T	769	773	3.361531	ATATT	3.90625	3.51525
cg1002882	MAD1L1	GR-beta [T	1140	1144	3.361531	AATCT	3.90625	3.51525
cg1002882	MAD1L1	GR-beta [T	1173	1177	3.361531	AATCT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [T	13	17	3.361531	AGATT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [T	230	234	3.361531	AATCT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [T	497	501	3.361531	AGATT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [T	1512	1516	3.361531	AATCT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [T	1565	1569	3.361531	AATAT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [T	1566	1570	3.361531	ATATT	3.90625	3.51525
cg0372348	MAD1L1	GR-beta [T	913	917	3.361531	AATCT	3.90625	3.51525
cg0372348	MAD1L1	GR-beta [T	1377	1381	3.361531	AGATT	3.90625	3.51525
cg1002882	MAD1L1	IRF-1 [T0	1187	1195	3.352297	TTTCCCC	0.06866	0.0661
cg0611220	MAD1L1	GATA-2 [	1755	1763	3.333333	AGATAA	0.30518	0.29349
cg0372348	MAD1L1	T3R-beta1	611	619	3.332047	TCACCA	0.27466	0.27326
cg0231133	MAD1L1	PR B [T00	862	868	3.29756	AAATGT	0.24414	0.21408
cg0231133	MAD1L1	PR A [T01	862	868	3.29756	AAATGT	0.24414	0.21408
cg1151970	MAD1L1	PR B [T00	758	764	3.29756	AACAAT	0.24414	0.21408
cg1151970	MAD1L1	PR A [T01	758	764	3.29756	AACAAT	0.24414	0.21408
cg0231133	MAD1L1	c-Ets-2 [T	682	690	3.2883	AGCGAG	0.18311	0.18314
cg0372348	MAD1L1	c-Ets-2 [T	1441	1449	3.2883	TTCCTCA	0.18311	0.18314
cg0372348	MAD1L1	E2F-1 [T0	699	706	3.288084	TGTGCC	0.15259	0.16507
cg0611220	MAD1L1	HNF-1C [	1800	1808	3.273679	ATTAATA	0.04578	0.04013
cg1578384	MAD1L1	NF-Y [T0	607	614	3.263282	ACGCCA	0.48828	0.48427
cg1578384	MAD1L1	NF-Y [T0	753	760	3.263282	ATGCCA	0.48828	0.48427
cg0231133	MAD1L1	Elk-1 [T00	1276	1284	3.247448	GTGAGG	0.07629	0.07518
cg1151970	MAD1L1	c-Jun [T00	1788	1794	3.244843	AGAGTC	0.24414	0.2435
cg0611220	MAD1L1	RAR-beta	259	268	3.244529	TGGGTT	0.12207	0.12558
cg0231133	MAD1L1	c-Ets-1 [T	480	486	3.231072	GCGGAA	0.24414	0.26272
cg0231133	MAD1L1	AP-2alpha	46	51	3.229049	GCCTCT	0.48828	0.5124
cg0231133	MAD1L1	AP-2alpha	200	205	3.229049	GCCTCT	0.48828	0.5124
cg0231133	MAD1L1	AP-2alpha	1236	1241	3.229049	AGAGGC	0.48828	0.5124
cg1578384	MAD1L1	AP-2alpha	1012	1017	3.229049	AGAGGC	0.48828	0.5124
cg1151970	MAD1L1	AP-2alpha	461	466	3.229049	AGAGGC	0.48828	0.5124
cg1151970	MAD1L1	AP-2alpha	1358	1363	3.229049	AGAGGC	0.48828	0.5124
cg1002882	MAD1L1	AP-2alpha	939	944	3.229049	AGAGGC	0.48828	0.5124
cg1002882	MAD1L1	AP-2alpha	1770	1775	3.229049	GCCTCT	0.48828	0.5124

cg0611220	MAD1L1	AP-2alpha	1937	1942	3.229049	GCCTCT	0.48828	0.5124
cg0372348	MAD1L1	MAZ [T00	257	269	3.189496	GTGGGG	0.00474	0.00544
cg0611220	MAD1L1	RXR-alpha	651	657	3.170788	AAAACC	0.24414	0.24551
cg0611220	MAD1L1	RXR-alpha	990	996	3.170788	GGGTTT	0.24414	0.24551
cg1002882	MAD1L1	MAZ [T00	1685	1697	3.162267	GGCGGG	0.00474	0.00544
cg1151970	MAD1L1	c-Fos [T00	1789	1798	3.154982	GAGTCA	0.06104	0.06233
cg1578384	MAD1L1	TCF-4E [T	142	148	3.151193	ATCAAA	0.24414	0.23169
cg1151970	MAD1L1	TCF-4E [T	946	952	3.151193	TGCAAA	0.24414	0.23169
cg1002882	MAD1L1	TCF-4E [T	1006	1012	3.151193	CTTTGC	0.24414	0.23169
cg0372348	MAD1L1	TCF-4E [T	926	932	3.151193	TGCAAA	0.24414	0.23169
cg0231133	MAD1L1	Elk-1 [T00	779	787	3.121991	TCAAGG	0.07629	0.07518
cg0231133	MAD1L1	Elk-1 [T00	1775	1783	3.121991	TCAAGG	0.07629	0.07518
cg1002882	MAD1L1	Elk-1 [T00	427	435	3.121991	AAAAGG	0.07629	0.07518
cg1002882	MAD1L1	c-Ets-1 [T	893	899	3.102985	CCGGAA	0.24414	0.26272
cg1002882	MAD1L1	NF-AT1 [	1094	1102	3.098758	AGCCTT	0.03052	0.0304
cg1578384	MAD1L1	SRY [T00	140	148	3.088221	AGATCA	0.06104	0.05645
cg1578384	MAD1L1	CREB [T0	1968	1976	3.082031	CAAACG	0.06104	0.05946
cg0231133	MAD1L1	TFIID [T0	1215	1221	3.075094	TTTTGC	0.12207	0.11309
cg1151970	MAD1L1	Pax-5 [T0	1232	1238	3.075094	GGGCGA	0.12207	0.13819
cg0611220	MAD1L1	TFIID [T0	960	966	3.075094	TGCAAA	0.12207	0.11309
cg0372348	MAD1L1	Pax-5 [T0	1560	1566	3.075094	CTCGCC	0.12207	0.13819
cg1578384	MAD1L1	NF-AT1 [	849	857	3.075022	GGAAAC	0.03052	0.0304
cg0231133	MAD1L1	NF-kappa	1451	1461	3.049833	GGAAAT	0.01669	0.01859
cg1151970	MAD1L1	c-Jun [T00	289	295	3.049104	TGACCC	0.24414	0.2435
cg1151970	MAD1L1	c-Jun [T00	1103	1109	3.049104	TGGGTC	0.24414	0.2435
cg1002882	MAD1L1	c-Jun [T00	178	184	3.049104	TGACCC	0.24414	0.2435
cg1002882	MAD1L1	c-Jun [T00	1123	1129	3.049104	TGGGTC	0.24414	0.2435
cg0611220	MAD1L1	c-Jun [T00	1537	1543	3.049104	TGACCC	0.24414	0.2435
cg0372348	MAD1L1	c-Jun [T00	658	664	3.049104	TGACCC	0.24414	0.2435
cg1151970	MAD1L1	p53 [T006	62	68	3.028543	GGGCAC	0.48828	0.53227
cg0231133	MAD1L1	AR [T000	953	961	3.025151	CCAATG	0.06104	0.0627
cg1578384	MAD1L1	p53 [T006	1590	1596	3.024997	GGGCAA	0.48828	0.53227
cg0372348	MAD1L1	p53 [T006	760	766	3.024997	GGGCAA	0.48828	0.53227
cg0611220	MAD1L1	c-Fos [T00	1851	1860	3.022518	AAACTG	0.06104	0.06233
cg1151970	MAD1L1	Elk-1 [T00	1461	1469	2.987643	CTTCCTT	0.07629	0.07518
cg0231133	MAD1L1	C/EBPalph	952	958	2.981957	CCCAAT	0.48828	0.47526
cg1578384	MAD1L1	C/EBPalph	101	107	2.981957	CCCAAT	0.48828	0.47526
cg1002882	MAD1L1	c-Ets-2 [T	373	381	2.945838	CAAAAG	0.06104	0.05567
cg0231133	MAD1L1	STAT4 [T	482	487	2.941176	GGAAGT	2.92969	2.92382
cg0231133	MAD1L1	STAT4 [T	728	733	2.941176	TGTTCC	2.92969	2.92382
cg0231133	MAD1L1	STAT4 [T	914	919	2.941176	GGAAAG	2.92969	2.92382
cg0231133	MAD1L1	STAT4 [T	1280	1285	2.941176	GGAAGT	2.92969	2.92382
cg0231133	MAD1L1	STAT4 [T	1554	1559	2.941176	GGAACC	2.92969	2.92382
cg1578384	MAD1L1	STAT4 [T	124	129	2.941176	GGAACA	2.92969	2.92382
cg1578384	MAD1L1	STAT4 [T	281	286	2.941176	GGAACA	2.92969	2.92382
cg1578384	MAD1L1	STAT4 [T	885	890	2.941176	GGAATC	2.92969	2.92382
cg1578384	MAD1L1	STAT4 [T	916	921	2.941176	GGAACA	2.92969	2.92382
cg1578384	MAD1L1	STAT4 [T	1672	1677	2.941176	GGAACA	2.92969	2.92382

cg1578384	MAD1L1	STAT4 [T	1762	1767	2.941176	GGAAAG	2.92969	2.92382
cg1151970	MAD1L1	STAT4 [T	1064	1069	2.941176	GGTTCC	2.92969	2.92382
cg1151970	MAD1L1	STAT4 [T	1239	1244	2.941176	GGAAGT	2.92969	2.92382
cg1151970	MAD1L1	STAT4 [T	1321	1326	2.941176	CTTTCC	2.92969	2.92382
cg1151970	MAD1L1	STAT4 [T	1749	1754	2.941176	ACTTCC	2.92969	2.92382
cg1151970	MAD1L1	STAT4 [T	1848	1853	2.941176	GGAAGT	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	70	75	2.941176	GGTTCC	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	116	121	2.941176	GGAACC	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	402	407	2.941176	GGAACA	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	910	915	2.941176	GGAACA	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	1097	1102	2.941176	CTTTCC	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	1248	1253	2.941176	GATTCC	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	1487	1492	2.941176	GGAATC	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	1520	1525	2.941176	GGAACC	2.92969	2.92382
cg1002882	MAD1L1	STAT4 [T	1860	1865	2.941176	GATTCC	2.92969	2.92382
cg0611220	MAD1L1	STAT4 [T	441	446	2.941176	GATTCC	2.92969	2.92382
cg0611220	MAD1L1	STAT4 [T	682	687	2.941176	GATTCC	2.92969	2.92382
cg0611220	MAD1L1	STAT4 [T	939	944	2.941176	CTTTCC	2.92969	2.92382
cg0611220	MAD1L1	STAT4 [T	1022	1027	2.941176	GGAATC	2.92969	2.92382
cg0611220	MAD1L1	STAT4 [T	1095	1100	2.941176	GGTTCC	2.92969	2.92382
cg0611220	MAD1L1	STAT4 [T	1270	1275	2.941176	CTTTCC	2.92969	2.92382
cg0611220	MAD1L1	STAT4 [T	1771	1776	2.941176	GGAATA	2.92969	2.92382
cg0372348	MAD1L1	STAT4 [T	365	370	2.941176	GGAATC	2.92969	2.92382
cg0372348	MAD1L1	STAT4 [T	833	838	2.941176	GGTTCC	2.92969	2.92382
cg0372348	MAD1L1	STAT4 [T	838	843	2.941176	CTTTCC	2.92969	2.92382
cg0372348	MAD1L1	STAT4 [T	1088	1093	2.941176	GGAACA	2.92969	2.92382
cg0372348	MAD1L1	STAT4 [T	1164	1169	2.941176	GGAACC	2.92969	2.92382
cg0372348	MAD1L1	STAT4 [T	1300	1305	2.941176	GGAAAG	2.92969	2.92382
cg0372348	MAD1L1	STAT4 [T	1570	1575	2.941176	GGAAGT	2.92969	2.92382
cg1002882	MAD1L1	IRF-1 [T0	170	178	2.890712	TTTCCTT	0.07629	0.07093
cg0231133	MAD1L1	AhR [T01	991	1001	2.82917	CTCACG	0.00572	0.00599
cg0231133	MAD1L1	p53 [T006	21	27	2.813291	GCTGCC	0.48828	0.53227
cg0231133	MAD1L1	p53 [T006	678	684	2.813291	GGGCAG	0.48828	0.53227
cg0231133	MAD1L1	p53 [T006	1843	1849	2.813291	GCTGCC	0.48828	0.53227
cg1151970	MAD1L1	p53 [T006	465	471	2.813291	GCTGCC	0.48828	0.53227
cg1151970	MAD1L1	p53 [T006	1530	1536	2.813291	GATGCC	0.48828	0.53227
cg1151970	MAD1L1	p53 [T006	1779	1785	2.813291	GGGCAG	0.48828	0.53227
cg1151970	MAD1L1	p53 [T006	1893	1899	2.813291	GGGCAG	0.48828	0.53227
cg0372348	MAD1L1	p53 [T006	1348	1354	2.813291	GGGCAG	0.48828	0.53227
cg0372348	MAD1L1	p53 [T006	1888	1894	2.813291	GATGCC	0.48828	0.53227
cg0231133	MAD1L1	NF-1 [T00	939	946	2.813149	GGGGCC	0.24414	0.2566
cg1578384	MAD1L1	PR B [T00	177	183	2.80933	GAATGT	0.73242	0.66711
cg1578384	MAD1L1	PR B [T00	1071	1077	2.80933	AACAAT	0.73242	0.66711
cg1578384	MAD1L1	PR B [T00	1315	1321	2.80933	AACAAT	0.73242	0.66711
cg1578384	MAD1L1	PR A [T01	177	183	2.80933	GAATGT	0.73242	0.66711
cg1578384	MAD1L1	PR A [T01	1071	1077	2.80933	AACAAT	0.73242	0.66711
cg1578384	MAD1L1	PR A [T01	1315	1321	2.80933	AACAAT	0.73242	0.66711
cg1151970	MAD1L1	PR B [T00	1279	1285	2.80933	AACATT	0.73242	0.66711

cg1151970	MAD1L1	PR A [T01	1279	1285	2.80933	AACATT	0.73242	0.66711
cg0611220	MAD1L1	PR B [T00	1603	1609	2.80933	AACAAT	0.73242	0.66711
cg0611220	MAD1L1	PR A [T01	1603	1609	2.80933	AACAAT	0.73242	0.66711
cg0611220	MAD1L1	NF-AT2 [	935	944	2.800326	AATTCT	0.03433	0.03159
cg0611220	MAD1L1	NF-AT1 [	1267	1276	2.756277	CATCTT	0.05913	0.05541
cg0372348	MAD1L1	CTF [T001	1148	1159	2.746279	CAGCCA	0.0062	0.0062
cg1002882	MAD1L1	RXR-alpha	20	26	2.726556	CCAACC	0.85449	0.89683
cg1002882	MAD1L1	RXR-alpha	1630	1636	2.726556	GGGTTG	0.85449	0.89683
cg0231133	MAD1L1	c-Ets-2 [T	1468	1476	2.715313	CTGGAG	0.07629	0.07844
cg1151970	MAD1L1	c-Ets-2 [T	335	343	2.715313	TTCCTCC	0.07629	0.07844
cg1151970	MAD1L1	c-Ets-2 [T	390	398	2.715313	TTCCTCC	0.07629	0.07844
cg1002882	MAD1L1	c-Ets-2 [T	1419	1427	2.715313	CCGGAG	0.07629	0.07844
cg0231133	MAD1L1	NFI/CTF [	38	45	2.683003	CCAACC	0.06104	0.06609
cg0231133	MAD1L1	c-Jun [T00	1833	1839	2.654872	GGAGTC	0.48828	0.48077
cg1002882	MAD1L1	c-Jun [T00	452	458	2.654872	TGACTC	0.48828	0.48077
cg0372348	MAD1L1	c-Jun [T00	788	794	2.654872	GGAGTC	0.48828	0.48077
cg1002882	MAD1L1	PPAR-alph	1833	1843	2.642917	CACTGG	0.00858	0.00898
cg1002882	MAD1L1	Sp1 [T007	22	31	2.617556	AACCCG	0.04005	0.04683
cg1151970	MAD1L1	NF-AT1 [	755	763	2.595974	GGAAAC	0.09155	0.08666
cg0372348	MAD1L1	PXR-1:RX	19	26	2.577808	TGAACT	0.12207	0.11843
cg0231133	MAD1L1	AP-2alpha	168	173	2.550491	GCCTCA	0.48828	0.51216
cg0231133	MAD1L1	AP-2alpha	1377	1382	2.550491	GCCTCA	0.48828	0.51216
cg0231133	MAD1L1	AP-2alpha	1725	1730	2.550491	TGAGGC	0.48828	0.51216
cg1578384	MAD1L1	AP-2alpha	1382	1387	2.550491	TGAGGC	0.48828	0.51216
cg1578384	MAD1L1	AP-2alpha	1509	1514	2.550491	TGAGGC	0.48828	0.51216
cg1578384	MAD1L1	AP-2alpha	1515	1520	2.550491	TGAGGC	0.48828	0.51216
cg1578384	MAD1L1	AP-2alpha	1756	1761	2.550491	GCCTCA	0.48828	0.51216
cg1151970	MAD1L1	AP-2alpha	321	326	2.550491	GCCTCA	0.48828	0.51216
cg1151970	MAD1L1	AP-2alpha	350	355	2.550491	GCCTCA	0.48828	0.51216
cg1151970	MAD1L1	AP-2alpha	376	381	2.550491	GCCTCA	0.48828	0.51216
cg1151970	MAD1L1	AP-2alpha	1045	1050	2.550491	TGAGGC	0.48828	0.51216
cg1151970	MAD1L1	AP-2alpha	1878	1883	2.550491	TGAGGC	0.48828	0.51216
cg1002882	MAD1L1	AP-2alpha	9	14	2.550491	GCCTCA	0.48828	0.51216
cg1002882	MAD1L1	AP-2alpha	475	480	2.550491	TGAGGC	0.48828	0.51216
cg1002882	MAD1L1	AP-2alpha	737	742	2.550491	GCCTCA	0.48828	0.51216
cg1002882	MAD1L1	AP-2alpha	1542	1547	2.550491	TGAGGC	0.48828	0.51216
cg1002882	MAD1L1	AP-2alpha	1791	1796	2.550491	TGAGGC	0.48828	0.51216
cg0611220	MAD1L1	AP-2alpha	279	284	2.550491	GCCTCA	0.48828	0.51216
cg0611220	MAD1L1	AP-2alpha	324	329	2.550491	GCCTCA	0.48828	0.51216
cg0372348	MAD1L1	AP-2alpha	1176	1181	2.550491	TGAGGC	0.48828	0.51216
cg0231133	MAD1L1	RXR-alpha	316	322	2.544678	TTCACC	0.85449	0.89683
cg0231133	MAD1L1	RXR-alpha	1399	1405	2.544678	GGGTGA	0.85449	0.89683
cg1151970	MAD1L1	RXR-alpha	44	50	2.544678	TGCACC	0.85449	0.89683
cg1151970	MAD1L1	RXR-alpha	131	137	2.544678	ATAACC	0.85449	0.89683
cg1151970	MAD1L1	RXR-alpha	1214	1220	2.544678	AGAACC	0.85449	0.89683
cg1151970	MAD1L1	RXR-alpha	1953	1959	2.544678	TGCACC	0.85449	0.89683
cg1002882	MAD1L1	RXR-alpha	1363	1369	2.544678	GGGTTC	0.85449	0.89683
cg1002882	MAD1L1	RXR-alpha	1379	1385	2.544678	GGGTGC	0.85449	0.89683

cg1002882	MAD1L1	RXR-alph	1912	1918	2.544678	TTCACC	0.85449	0.89683
cg0611220	MAD1L1	RXR-alph	1109	1115	2.544678	TGCACC	0.85449	0.89683
cg0611220	MAD1L1	RXR-alph	1703	1709	2.544678	GGGTGC	0.85449	0.89683
cg0231133	MAD1L1	ENKTF-1	1732	1739	2.511511	TGGCGG	0.12207	0.13847
cg0231133	MAD1L1	ENKTF-1	1874	1881	2.511511	TGGCGG	0.12207	0.13847
cg1578384	MAD1L1	ENKTF-1	1890	1897	2.511511	TGGCGG	0.12207	0.13847
cg1002882	MAD1L1	ENKTF-1	951	958	2.511511	TGGCGG	0.12207	0.13847
cg1002882	MAD1L1	ENKTF-1	1684	1691	2.511511	TGGCGG	0.12207	0.13847
cg0231133	MAD1L1	C/EBPalph	1157	1163	2.441016	CATTGA	0.48828	0.47439
cg0231133	MAD1L1	MAZ [T00	526	538	2.392122	GAGGGG	0.00405	0.00469
cg1002882	MAD1L1	MAZ [T00	1743	1755	2.392122	TGGGGG	0.00405	0.00469
cg0611220	MAD1L1	Ik-1 [T027	430	442	2.374299	CAAAGT	0.00063	0.00068
cg0231133	MAD1L1	C/EBPalph	1595	1601	2.371703	AATTGT	0.48828	0.47439
cg0372348	MAD1L1	NF-Y [T0	1148	1155	2.355069	CAGCCA	0.21362	0.20842
cg1002882	MAD1L1	c-Jun [T00	280	286	2.345465	TGTGTC	0.48828	0.48077
cg0611220	MAD1L1	LEF-1 [T0	1897	1904	2.345041	CAGCAA	0.09155	0.09076
cg1002882	MAD1L1	RXR-alph	99	105	2.322562	GGGTCT	0.85449	0.89683
cg1002882	MAD1L1	RXR-alph	253	259	2.322562	CAGACC	0.85449	0.89683
cg1002882	MAD1L1	RXR-alph	729	735	2.322562	CAGACC	0.85449	0.89683
cg0372348	MAD1L1	Elk-1 [T00	1788	1796	2.299314	ACCAGG	0.09155	0.09306
cg0231133	MAD1L1	E2F-1 [T0	927	934	2.294501	TTTTCC	0.06104	0.06262
cg1151970	MAD1L1	NF-kappa	1317	1328	2.285265	GGGACT	0.00441	0.00457
cg1578384	MAD1L1	T3R-beta1	1820	1828	2.259951	AGGAGG	0.03052	0.03203
cg0611220	MAD1L1	T3R-beta1	643	651	2.240658	TCACCA	0.15259	0.15303
cg1578384	MAD1L1	GATA-2 [	715	723	2.222222	AGATAA	0.22888	0.21978
cg1578384	MAD1L1	GATA-2 [	732	740	2.222222	AGATAA	0.22888	0.21978
cg1578384	MAD1L1	GATA-2 [	782	790	2.222222	AGATAA	0.22888	0.21978
cg1151970	MAD1L1	GATA-2 [	511	519	2.222222	AGATAG	0.22888	0.21978
cg0611220	MAD1L1	GATA-2 [	134	142	2.222222	AGATAA	0.22888	0.21978
cg0611220	MAD1L1	GATA-2 [	1452	1460	2.222222	TCTTTAT	0.22888	0.21978
cg0231133	MAD1L1	T3R-beta1	1270	1278	2.221365	TCACCT	0.15259	0.15303
cg1578384	MAD1L1	LEF-1 [T0	1810	1817	2.21836	AACCAA	0.18311	0.17215
cg0231133	MAD1L1	c-Ets-2 [T	1275	1283	2.217136	TGTGAG	0.16785	0.16456
cg1151970	MAD1L1	NF-Y [T0	865	872	2.194008	ACACCA	0.21362	0.20748
cg0231133	MAD1L1	GATA-1 [	188	193	2.176375	AGGATA	3.90625	3.79558
cg0231133	MAD1L1	GATA-1 [	1486	1491	2.176375	TATCCA	3.90625	3.79558
cg1578384	MAD1L1	GATA-1 [	760	765	2.176375	TATCGA	3.90625	3.79558
cg1002882	MAD1L1	GATA-1 [	391	396	2.176375	TATCCT	3.90625	3.79558
cg0611220	MAD1L1	GATA-1 [	844	849	2.176375	TATCCA	3.90625	3.79558
cg1151970	MAD1L1	Elk-1 [T00	363	371	2.164966	CTTCCTC	0.05341	0.05461
cg0372348	MAD1L1	Elk-1 [T00	79	87	2.164966	GAGAGG	0.05341	0.05461
cg0372348	MAD1L1	Elk-1 [T00	568	576	2.164966	GACAGG	0.05341	0.05461
cg1578384	MAD1L1	TCF-4 [T0	140	149	2.160205	AGATCA	0.04196	0.03736
cg1002882	MAD1L1	RAR-beta	125	134	2.144554	GCCAAA	0.07629	0.07711
cg1151970	MAD1L1	c-Ets-2 [T	364	372	2.142327	TTCCTCT	0.16785	0.16456
cg0372348	MAD1L1	c-Ets-2 [T	78	86	2.142327	AGAGAG	0.16785	0.16456
cg0372348	MAD1L1	c-Ets-2 [T	840	848	2.142327	TTCCTCT	0.16785	0.16456
cg0231133	MAD1L1	AP-2alpha	1409	1414	2.098119	GCCTCG	0.97656	1.07805

cg0231133	MAD1L1	AP-2alpha	1666	1671	2.098119	CGAGGC	0.97656	1.07805
cg1151970	MAD1L1	AP-2alpha	478	483	2.098119	GCCTCG	0.97656	1.07805
cg1151970	MAD1L1	AP-2alpha	1810	1815	2.098119	GCCTCG	0.97656	1.07805
cg1002882	MAD1L1	AP-2alpha	1039	1044	2.098119	CGAGGC	0.97656	1.07805
cg1002882	MAD1L1	AP-2alpha	1238	1243	2.098119	CGAGGC	0.97656	1.07805
cg1002882	MAD1L1	AP-2alpha	1242	1247	2.098119	GCCTCG	0.97656	1.07805
cg0372348	MAD1L1	AP-2alpha	384	389	2.098119	CGAGGC	0.97656	1.07805
cg0231133	MAD1L1	NF-1 [T00	1068	1075	2.067686	TTGGGA	0.12207	0.12476
cg1151970	MAD1L1	NF-1 [T00	143	150	2.067686	TGTCCC	0.12207	0.12476
cg0372348	MAD1L1	NF-1 [T00	1007	1014	2.067686	TGTGCC	0.12207	0.12476
cg0231133	MAD1L1	NF-AT1 [T	1450	1459	2.067208	TGGAAA	0.03815	0.03545
cg0611220	MAD1L1	CREB [T0	750	758	2.017477	ATAACG	0.03052	0.02887
cg0231133	MAD1L1	GATA-1 [	1014	1019	2.001358	GGGATA	3.90625	3.79558
cg1002882	MAD1L1	GATA-1 [	163	168	2.001358	GGGATA	3.90625	3.79558
cg1002882	MAD1L1	GATA-1 [	837	842	2.001358	GCGATA	3.90625	3.79558
cg1002882	MAD1L1	NF-AT1 [T	378	386	1.970716	GGAAAA	0.06866	0.0623
cg0611220	MAD1L1	p53 [T006	1499	1505	1.970013	GGGCAA	0.36621	0.38097
cg1578384	MAD1L1	GATA-1 [	1338	1343	1.896347	CGGATA	3.90625	3.79558
cg0372348	MAD1L1	GATA-1 [	667	672	1.896347	CGGATA	3.90625	3.79558
cg1578384	MAD1L1	PR B [T00	1078	1084	1.892895	AAGTGT	0.12207	0.1127
cg1578384	MAD1L1	PR B [T00	1367	1373	1.892895	AACACT	0.12207	0.1127
cg1578384	MAD1L1	PR A [T01	1078	1084	1.892895	AAGTGT	0.12207	0.1127
cg1578384	MAD1L1	PR A [T01	1367	1373	1.892895	AACACT	0.12207	0.1127
cg1151970	MAD1L1	RXR-alpha	173	179	1.87833	TCAACC	0.12207	0.12517
cg1002882	MAD1L1	c-Ets-2 [T	426	434	1.874674	TAAAAG	0.16785	0.16456
cg0231133	MAD1L1	AP-2alpha	71	76	1.871933	GCCTCC	0.97656	1.07805
cg0231133	MAD1L1	AP-2alpha	698	703	1.871933	GGAGGC	0.97656	1.07805
cg0231133	MAD1L1	AP-2alpha	762	767	1.871933	GCCTCC	0.97656	1.07805
cg0231133	MAD1L1	AP-2alpha	1739	1744	1.871933	GGAGGC	0.97656	1.07805
cg0231133	MAD1L1	AP-2alpha	1924	1929	1.871933	GCCTCC	0.97656	1.07805
cg1578384	MAD1L1	AP-2alpha	865	870	1.871933	GGAGGC	0.97656	1.07805
cg1578384	MAD1L1	AP-2alpha	1541	1546	1.871933	GGAGGC	0.97656	1.07805
cg1151970	MAD1L1	AP-2alpha	382	387	1.871933	GCCTCC	0.97656	1.07805
cg1151970	MAD1L1	AP-2alpha	1095	1100	1.871933	GGAGGC	0.97656	1.07805
cg1151970	MAD1L1	AP-2alpha	1606	1611	1.871933	GCCTCC	0.97656	1.07805
cg1151970	MAD1L1	AP-2alpha	1660	1665	1.871933	GGAGGC	0.97656	1.07805
cg1002882	MAD1L1	AP-2alpha	1532	1537	1.871933	GGAGGC	0.97656	1.07805
cg1002882	MAD1L1	AP-2alpha	1880	1885	1.871933	GGAGGC	0.97656	1.07805
cg1002882	MAD1L1	AP-2alpha	1895	1900	1.871933	GCCTCC	0.97656	1.07805
cg0611220	MAD1L1	AP-2alpha	285	290	1.871933	GCCTCC	0.97656	1.07805
cg0611220	MAD1L1	AP-2alpha	891	896	1.871933	GGAGGC	0.97656	1.07805
cg0372348	MAD1L1	AP-2alpha	55	60	1.871933	GGAGGC	0.97656	1.07805
cg0372348	MAD1L1	AP-2alpha	234	239	1.871933	GCCTCC	0.97656	1.07805
cg0372348	MAD1L1	AP-2alpha	851	856	1.871933	GCCTCC	0.97656	1.07805
cg0372348	MAD1L1	AP-2alpha	1248	1253	1.871933	GCCTCC	0.97656	1.07805
cg0372348	MAD1L1	AP-2alpha	1726	1731	1.871933	GGAGGC	0.97656	1.07805
cg1002882	MAD1L1	PPAR-alph	1120	1130	1.869153	GACTGG	0.00668	0.00699
cg0231133	MAD1L1	NF-kappa	1450	1461	1.858427	TGGAAA	0.00322	0.0034

cg0611220	MAD1L1	TCF-4 [T0	97	106	1.850015	CCTTCA	0.04196	0.03736
cg1578384	MAD1L1	HIF-1 [T0	41	49	1.839875	TGTGCA	0.1297	0.13373
cg0231133	MAD1L1	TFII-I [T0	336	341	1.824994	GGAGAG	0.48828	0.51201
cg0231133	MAD1L1	TFII-I [T0	390	395	1.824994	GGAGAG	0.48828	0.51201
cg0231133	MAD1L1	TFII-I [T0	1234	1239	1.824994	GGAGAG	0.48828	0.51201
cg0231133	MAD1L1	TFII-I [T0	1433	1438	1.824994	CTCTCC	0.48828	0.51201
cg1578384	MAD1L1	FOXP3 [T	1292	1297	1.824994	TACAAC	0.48828	0.46414
cg1151970	MAD1L1	FOXP3 [T	190	195	1.824994	TACAAC	0.48828	0.46414
cg1151970	MAD1L1	TFII-I [T0	367	372	1.824994	CTCTCC	0.48828	0.51201
cg1151970	MAD1L1	TFII-I [T0	1026	1031	1.824994	CTCTCC	0.48828	0.51201
cg1151970	MAD1L1	TFII-I [T0	1111	1116	1.824994	GGAGAG	0.48828	0.51201
cg1002882	MAD1L1	TFII-I [T0	502	507	1.824994	GGAGAG	0.48828	0.51201
cg1002882	MAD1L1	TFII-I [T0	935	940	1.824994	GGAGAG	0.48828	0.51201
cg1002882	MAD1L1	TFII-I [T0	1345	1350	1.824994	GGAGAG	0.48828	0.51201
cg1002882	MAD1L1	TFII-I [T0	1752	1757	1.824994	GGAGAG	0.48828	0.51201
cg1002882	MAD1L1	TFII-I [T0	1772	1777	1.824994	CTCTCC	0.48828	0.51201
cg0611220	MAD1L1	TFII-I [T0	1121	1126	1.824994	CTCTCC	0.48828	0.51201
cg0372348	MAD1L1	FOXP3 [T	340	345	1.824994	TACAAC	0.48828	0.46414
cg0372348	MAD1L1	TFII-I [T0	38	43	1.824994	CTCTCC	0.48828	0.51201
cg0372348	MAD1L1	TFII-I [T0	97	102	1.824994	CTCTCC	0.48828	0.51201
cg0372348	MAD1L1	TFII-I [T0	752	757	1.824994	GGAGAG	0.48828	0.51201
cg0372348	MAD1L1	TFII-I [T0	1470	1475	1.824994	GGAGAG	0.48828	0.51201
cg0372348	MAD1L1	TFII-I [T0	1701	1706	1.824994	CTCTCC	0.48828	0.51201
cg0372348	MAD1L1	TFII-I [T0	1720	1725	1.824994	GGAGAG	0.48828	0.51201
cg0372348	MAD1L1	TFII-I [T0	1818	1823	1.824994	GGAGAG	0.48828	0.51201
cg0372348	MAD1L1	TFII-I [T0	1867	1872	1.824994	GGAGAG	0.48828	0.51201
cg0372348	MAD1L1	Elk-1 [T00	352	360	1.779702	TGTAGG	0.05341	0.05461
cg0611220	MAD1L1	C/EBPalp	558	564	1.761449	CCCAAT	0.48828	0.46352
cg1002882	MAD1L1	PXR-1:RX	1261	1268	1.759733	TGAACT	0.06104	0.05771
cg0372348	MAD1L1	PXR-1:RX	903	910	1.759733	ACAGTT	0.06104	0.05771
cg0231133	MAD1L1	p53 [T006	587	593	1.758307	GGGCAG	0.36621	0.38097
cg1578384	MAD1L1	p53 [T006	194	200	1.758307	GGGCAG	0.36621	0.38097
cg1151970	MAD1L1	p53 [T006	1374	1380	1.758307	GGGCAG	0.36621	0.38097
cg1002882	MAD1L1	p53 [T006	45	51	1.758307	GGGCAG	0.36621	0.38097
cg1002882	MAD1L1	p53 [T006	1463	1469	1.758307	GGGCAG	0.36621	0.38097
cg0231133	MAD1L1	RXR-alpha	1051	1057	1.696452	GGGTCA	0.48828	0.52093
cg1578384	MAD1L1	RXR-alpha	1914	1920	1.696452	CTGACC	0.48828	0.52093
cg1151970	MAD1L1	RXR-alpha	240	246	1.696452	CTGACC	0.48828	0.52093
cg1151970	MAD1L1	RXR-alpha	288	294	1.696452	CTGACC	0.48828	0.52093
cg1151970	MAD1L1	RXR-alpha	539	545	1.696452	GGGTCA	0.48828	0.52093
cg1002882	MAD1L1	RXR-alpha	177	183	1.696452	CTGACC	0.48828	0.52093
cg1002882	MAD1L1	RXR-alpha	442	448	1.696452	GGGTCA	0.48828	0.52093
cg1002882	MAD1L1	RXR-alpha	1641	1647	1.696452	GGGTCA	0.48828	0.52093
cg0611220	MAD1L1	RXR-alpha	1964	1970	1.696452	CGGACC	0.48828	0.52093
cg0372348	MAD1L1	RXR-alpha	657	663	1.696452	CTGACC	0.48828	0.52093
cg0372348	MAD1L1	RXR-alpha	1037	1043	1.696452	CTGACC	0.48828	0.52093
cg0372348	MAD1L1	RXR-alpha	1653	1659	1.696452	GGGTCA	0.48828	0.52093
cg0231133	MAD1L1	GR-beta [T	1062	1066	1.680765	GAATT	3.90625	3.70067

cg0231133	MAD1L1	GR-beta [T	1063	1067	1.680765	AATTC	3.90625	3.70067
cg0231133	MAD1L1	GR-beta [T	1156	1160	1.680765	GCATT	3.90625	3.70067
cg0231133	MAD1L1	GR-beta [T	1454	1458	1.680765	AATTC	3.90625	3.70067
cg0231133	MAD1L1	GR-beta [T	1594	1598	1.680765	GAATT	3.90625	3.70067
cg0231133	MAD1L1	GR-beta [T	1886	1890	1.680765	GAATT	3.90625	3.70067
cg0231133	MAD1L1	GR-beta [T	1887	1891	1.680765	AATTC	3.90625	3.70067
cg1578384	MAD1L1	GR-beta [T	291	295	1.680765	GCATT	3.90625	3.70067
cg1578384	MAD1L1	GR-beta [T	612	616	1.680765	AATGC	3.90625	3.70067
cg1578384	MAD1L1	GR-beta [T	769	773	1.680765	AATGC	3.90625	3.70067
cg1578384	MAD1L1	GR-beta [T	808	812	1.680765	AATGC	3.90625	3.70067
cg1578384	MAD1L1	GR-beta [T	824	828	1.680765	AATGC	3.90625	3.70067
cg1578384	MAD1L1	GR-beta [T	1203	1207	1.680765	AATTC	3.90625	3.70067
cg1578384	MAD1L1	GR-beta [T	1525	1529	1.680765	GAATT	3.90625	3.70067
cg1151970	MAD1L1	GR-beta [T	122	126	1.680765	GAATT	3.90625	3.70067
cg1151970	MAD1L1	GR-beta [T	761	765	1.680765	AATTC	3.90625	3.70067
cg1151970	MAD1L1	GR-beta [T	1116	1120	1.680765	GCATT	3.90625	3.70067
cg1002882	MAD1L1	GR-beta [T	1845	1849	1.680765	AATGC	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	270	274	1.680765	AATTC	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	541	545	1.680765	GCATT	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	854	858	1.680765	GAATT	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	855	859	1.680765	AATTC	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	934	938	1.680765	GAATT	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	935	939	1.680765	AATTC	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	1038	1042	1.680765	AATGC	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	1238	1242	1.680765	GCATT	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	1656	1660	1.680765	GAATT	3.90625	3.70067
cg0611220	MAD1L1	GR-beta [T	1991	1995	1.680765	AATGC	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	9	13	1.680765	GCATT	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	423	427	1.680765	AATTC	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	452	456	1.680765	AATGC	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	455	459	1.680765	GCATT	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	880	884	1.680765	GAATT	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	1542	1546	1.680765	GAATT	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	1543	1547	1.680765	AATTC	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	1614	1618	1.680765	GCATT	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	1621	1625	1.680765	GAATT	3.90625	3.70067
cg0372348	MAD1L1	GR-beta [T	1622	1626	1.680765	AATTC	3.90625	3.70067
cg1002882	MAD1L1	c-Ets-2 [TC	1482	1490	1.64415	GAGGAG	0.04578	0.04602
cg1002882	MAD1L1	c-Ets-2 [TC	1973	1981	1.64415	TTCCTCC	0.04578	0.04602
cg0611220	MAD1L1	c-Ets-2 [TC	553	561	1.64415	TTCCTCC	0.04578	0.04602
cg0611220	MAD1L1	c-Ets-2 [TC	684	692	1.64415	TTCCTCC	0.04578	0.04602
cg1151970	MAD1L1	c-Ets-1 [TC	813	819	1.641124	AAGGAA	0.36621	0.35197
cg1002882	MAD1L1	c-Ets-1 [TC	170	176	1.641124	TTTCCTT	0.36621	0.35197
cg1002882	MAD1L1	c-Ets-1 [TC	376	382	1.641124	AAGGAA	0.36621	0.35197
cg0611220	MAD1L1	c-Ets-1 [TC	1687	1693	1.641124	AAGGAA	0.36621	0.35197
cg0231133	MAD1L1	C/EBPbeta	38	41	1.639871	CCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	76	79	1.639871	CCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	84	87	1.639871	TTGG	15.625	15.23827

cg0231133	MAD1L1	C/EBPbeta	475	478	1.639871	TTGG	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	766	769	1.639871	CCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	943	946	1.639871	CCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	953	956	1.639871	CCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	1068	1071	1.639871	TTGG	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	1347	1350	1.639871	CCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	1507	1510	1.639871	CCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	1545	1548	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	0	3	1.639871	TTGG	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	102	105	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	150	153	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	360	363	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	392	395	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	424	427	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	472	475	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	488	491	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	610	613	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	616	619	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	640	643	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	756	759	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	812	815	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1116	1119	1.639871	TTGG	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1373	1376	1.639871	TTGG	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1426	1429	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1562	1565	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1661	1664	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1752	1755	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1812	1815	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1859	1862	1.639871	CCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1967	1970	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	147	150	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	569	572	1.639871	TTGG	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	788	791	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	796	799	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	820	823	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	868	871	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	891	894	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	938	941	1.639871	TTGG	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	1050	1053	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	1616	1619	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	1723	1726	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	1745	1748	1.639871	CCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	1966	1969	1.639871	CCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	20	23	1.639871	CCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	126	129	1.639871	CCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	182	185	1.639871	CCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	398	401	1.639871	TTGG	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	439	442	1.639871	TTGG	15.625	15.23827

cg1002882	MAD1L1	C/EBPbeta	465	468	1.639871	TTGG	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	1196	1199	1.639871	TTGG	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	1316	1319	1.639871	TTGG	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	1547	1550	1.639871	CCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	1633	1636	1.639871	TTGG	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	1990	1993	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	234	237	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	290	293	1.639871	CCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	489	492	1.639871	CCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	505	508	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	559	562	1.639871	CCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	950	953	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1306	1309	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1526	1529	1.639871	CCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1541	1544	1.639871	CCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1633	1636	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1681	1684	1.639871	CCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1685	1688	1.639871	CCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1721	1724	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1848	1851	1.639871	CCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	175	178	1.639871	TTGG	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	583	586	1.639871	CCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	893	896	1.639871	TTGG	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1011	1014	1.639871	CCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1151	1154	1.639871	CCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1274	1277	1.639871	TTGG	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1381	1384	1.639871	TTGG	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1416	1419	1.639871	CCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1928	1931	1.639871	TTGG	15.625	15.23827
cg0611220	MAD1L1	PXR-1:RX	1192	1199	1.63615	TGAACT	0.06104	0.05484
cg1151970	MAD1L1	AR [T000	1637	1645	1.620358	GGACAT	0.09155	0.09239
cg1578384	MAD1L1	IRF-1 [T0	845	853	1.616539	ACAGGG	0.04578	0.04268
cg1578384	MAD1L1	HNF-4alph	144	156	1.594935	CAAAGT	0.00083	0.00077
cg0231133	MAD1L1	XBP-1 [T	89	94	1.583727	ATGACA	0.97656	0.94995
cg0231133	MAD1L1	XBP-1 [T	149	154	1.583727	TGTCAT	0.97656	0.94995
cg0231133	MAD1L1	XBP-1 [T	1226	1231	1.583727	ATGACC	0.97656	0.94995
cg0231133	MAD1L1	XBP-1 [T	1538	1543	1.583727	ATGACA	0.97656	0.94995
cg0231133	MAD1L1	XBP-1 [T	1958	1963	1.583727	ATGACA	0.97656	0.94995
cg1578384	MAD1L1	XBP-1 [T	74	79	1.583727	TGTCAT	0.97656	0.94995
cg1578384	MAD1L1	XBP-1 [T	208	213	1.583727	ATGACA	0.97656	0.94995
cg1002882	MAD1L1	XBP-1 [T	1125	1130	1.583727	GGTCAT	0.97656	0.94995
cg0611220	MAD1L1	XBP-1 [T	1050	1055	1.583727	GGTCAT	0.97656	0.94995
cg0611220	MAD1L1	XBP-1 [T	1287	1292	1.583727	TGTCAT	0.97656	0.94995
cg0372348	MAD1L1	XBP-1 [T	417	422	1.583727	ATGACA	0.97656	0.94995
cg0372348	MAD1L1	MAZ [T00	220	232	1.581133	CACCCT	0.00143	0.00166
cg1578384	MAD1L1	c-Fos [T00	1137	1146	1.540603	ATCATG	0.00763	0.00739
cg0231133	MAD1L1	TFIID [T0	208	214	1.537547	TTTTCCA	0.73242	0.65627
cg0231133	MAD1L1	TFIID [T0	884	890	1.537547	TTCAAA	0.73242	0.65627

cg0231133	MAD1L1	Pax-5 [T0	636	642	1.537547	GGGCCA	0.73242	0.83087
cg0231133	MAD1L1	Pax-5 [T0	1752	1758	1.537547	CACGCC	0.73242	0.83087
cg0231133	MAD1L1	Pax-5 [T0	1985	1991	1.537547	GGGCCA	0.73242	0.83087
cg1578384	MAD1L1	TFIID [T0	1214	1220	1.537547	TGAAAA	0.73242	0.65627
cg1578384	MAD1L1	TFIID [T0	1458	1464	1.537547	TACAAA	0.73242	0.65627
cg1578384	MAD1L1	TFIID [T0	1730	1736	1.537547	TGTAAA	0.73242	0.65627
cg1578384	MAD1L1	Pax-5 [T0	1472	1478	1.537547	GGGCGT	0.73242	0.83087
cg1151970	MAD1L1	TFIID [T0	180	186	1.537547	TTCAAA	0.73242	0.65627
cg1151970	MAD1L1	Pax-5 [T0	485	491	1.537547	CTGGCC	0.73242	0.83087
cg1151970	MAD1L1	Pax-5 [T0	884	890	1.537547	CTGGCC	0.73242	0.83087
cg1151970	MAD1L1	Pax-5 [T0	915	921	1.537547	CTGGCC	0.73242	0.83087
cg1151970	MAD1L1	Pax-5 [T0	1421	1427	1.537547	GGGCCA	0.73242	0.83087
cg1002882	MAD1L1	TFIID [T0	1194	1200	1.537547	TTTTGGA	0.73242	0.65627
cg1002882	MAD1L1	Pax-5 [T0	24	30	1.537547	CCCGCC	0.73242	0.83087
cg1002882	MAD1L1	Pax-5 [T0	568	574	1.537547	GGGCAA	0.73242	0.83087
cg1002882	MAD1L1	Pax-5 [T0	980	986	1.537547	GGGCGG	0.73242	0.83087
cg1002882	MAD1L1	Pax-5 [T0	1351	1357	1.537547	GGGCAA	0.73242	0.83087
cg1002882	MAD1L1	Pax-5 [T0	1370	1376	1.537547	GGGCGG	0.73242	0.83087
cg1002882	MAD1L1	Pax-5 [T0	1501	1507	1.537547	CACGCC	0.73242	0.83087
cg0611220	MAD1L1	TFIID [T0	65	71	1.537547	TTTTACA	0.73242	0.65627
cg0611220	MAD1L1	TFIID [T0	336	342	1.537547	TTTTGTA	0.73242	0.65627
cg0611220	MAD1L1	TFIID [T0	1917	1923	1.537547	TTTTGAA	0.73242	0.65627
cg0372348	MAD1L1	TFIID [T0	309	315	1.537547	TTTTACA	0.73242	0.65627
cg0372348	MAD1L1	TFIID [T0	907	913	1.537547	TTCAAA	0.73242	0.65627
cg0372348	MAD1L1	TFIID [T0	1545	1551	1.537547	TTCAAA	0.73242	0.65627
cg0372348	MAD1L1	TFIID [T0	1617	1623	1.537547	TTTTGAA	0.73242	0.65627
cg0372348	MAD1L1	Pax-5 [T0	1231	1237	1.537547	CGCGCC	0.73242	0.83087
cg0372348	MAD1L1	Pax-5 [T0	1308	1314	1.537547	CTTGCC	0.73242	0.83087
cg0372348	MAD1L1	Pax-5 [T0	1520	1526	1.537547	GGGCCA	0.73242	0.83087
cg0372348	MAD1L1	Pax-5 [T0	1626	1632	1.537547	CGCGCC	0.73242	0.83087
cg0372348	MAD1L1	Pax-5 [T0	1840	1846	1.537547	GGGCAA	0.73242	0.83087
cg1002882	MAD1L1	Sp1 [T007	1369	1378	1.523913	TGGGCG	0.03242	0.03924
cg0372348	MAD1L1	c-Ets-1 [T	839	845	1.513038	TTTCCTC	0.36621	0.35197
cg0611220	MAD1L1	POU2F1 [	755	765	1.509618	GTCATG	0.00811	0.00748
cg0231133	MAD1L1	E2F-1 [T0	1012	1019	1.490375	GCGGGA	0.06104	0.0656
cg1002882	MAD1L1	RXR-alph	127	133	1.474336	CAAACC	0.48828	0.52093
cg0611220	MAD1L1	RXR-alph	1884	1890	1.474336	TAGACC	0.48828	0.52093
cg0231133	MAD1L1	STAT4 [T	208	213	1.470588	TTTTCC	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	250	255	1.470588	GGAACT	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	435	440	1.470588	GGAAAC	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	600	605	1.470588	GGAAAA	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	927	932	1.470588	TTTTCC	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	1061	1066	1.470588	GGAATT	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	1101	1106	1.470588	GGAAAA	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	1414	1419	1.470588	GGAAAC	1.95312	1.90161
cg0231133	MAD1L1	STAT4 [T	1454	1459	1.470588	AATTCC	1.95312	1.90161
cg1578384	MAD1L1	STAT4 [T	849	854	1.470588	GGAAAC	1.95312	1.90161
cg1578384	MAD1L1	STAT4 [T	1203	1208	1.470588	AATTCC	1.95312	1.90161

cg1578384	MAD1L1	STAT4 [T	1910	1915	1.470588	GGAACT	1.95312	1.90161
cg1151970	MAD1L1	STAT4 [T	108	113	1.470588	GGAAAC	1.95312	1.90161
cg1151970	MAD1L1	STAT4 [T	597	602	1.470588	AGTTCC	1.95312	1.90161
cg1151970	MAD1L1	STAT4 [T	724	729	1.470588	GTTTCC	1.95312	1.90161
cg1151970	MAD1L1	STAT4 [T	755	760	1.470588	GGAAAC	1.95312	1.90161
cg1151970	MAD1L1	STAT4 [T	815	820	1.470588	GGAAAC	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	169	174	1.470588	GTTTCC	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	200	205	1.470588	GGAAAC	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	292	297	1.470588	GGAAAC	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	378	383	1.470588	GGAAAA	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	889	894	1.470588	GTTTCC	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	1186	1191	1.470588	TTTTCC	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	1300	1305	1.470588	GGAACT	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	1938	1943	1.470588	GGAAAC	1.95312	1.90161
cg1002882	MAD1L1	STAT4 [T	1971	1976	1.470588	AGTTCC	1.95312	1.90161
cg0611220	MAD1L1	STAT4 [T	551	556	1.470588	AGTTCC	1.95312	1.90161
cg0611220	MAD1L1	STAT4 [T	855	860	1.470588	AATTCC	1.95312	1.90161
cg0611220	MAD1L1	STAT4 [T	1446	1451	1.470588	AGTTCC	1.95312	1.90161
cg0611220	MAD1L1	STAT4 [T	1487	1492	1.470588	GGAACT	1.95312	1.90161
cg0611220	MAD1L1	STAT4 [T	1689	1694	1.470588	GGAAAC	1.95312	1.90161
cg0372348	MAD1L1	STAT4 [T	268	273	1.470588	GGAAAA	1.95312	1.90161
cg0372348	MAD1L1	STAT4 [T	423	428	1.470588	AATTCC	1.95312	1.90161
cg0372348	MAD1L1	STAT4 [T	770	775	1.470588	GGAAAC	1.95312	1.90161
cg0372348	MAD1L1	STAT4 [T	879	884	1.470588	GGAATT	1.95312	1.90161
cg0372348	MAD1L1	STAT4 [T	1018	1023	1.470588	GTTTCC	1.95312	1.90161
cg0372348	MAD1L1	STAT4 [T	1107	1112	1.470588	GGAACT	1.95312	1.90161
cg0611220	MAD1L1	GR [T050	649	655	1.444018	CAAAAA	0.12207	0.11476
cg0611220	MAD1L1	GR [T050	946	952	1.444018	GTTTTC	0.12207	0.11476
cg0611220	MAD1L1	GR [T050	1599	1605	1.444018	CAAAAA	0.12207	0.11476
cg0231133	MAD1L1	NF-AT1 [	1101	1109	1.437145	GGAAAA	0.00763	0.00705
cg0231133	MAD1L1	USF1 [T0	1381	1390	1.431084	CACGTG	0.0248	0.02734
cg0231133	MAD1L1	PR B [T00	1044	1050	1.404665	AACACT	0.36621	0.35143
cg0231133	MAD1L1	PR A [T01	1044	1050	1.404665	AACACT	0.36621	0.35143
cg1578384	MAD1L1	PR B [T00	852	858	1.404665	AACACT	0.36621	0.35143
cg1578384	MAD1L1	PR A [T01	852	858	1.404665	AACACT	0.36621	0.35143
cg1151970	MAD1L1	PR B [T00	1618	1624	1.404665	AACACT	0.36621	0.35143
cg1151970	MAD1L1	PR A [T01	1618	1624	1.404665	AACACT	0.36621	0.35143
cg1002882	MAD1L1	PR B [T00	809	815	1.404665	AACACT	0.36621	0.35143
cg1002882	MAD1L1	PR A [T01	809	815	1.404665	AACACT	0.36621	0.35143
cg0231133	MAD1L1	c-Ets-1 [T	1099	1105	1.384951	CAGGAA	0.36621	0.35197
cg1578384	MAD1L1	c-Ets-1 [T	1760	1766	1.384951	CAGGAA	0.36621	0.35197
cg1151970	MAD1L1	c-Ets-1 [T	753	759	1.384951	CAGGAA	0.36621	0.35197
cg1002882	MAD1L1	c-Ets-1 [T	1936	1942	1.384951	CAGGAA	0.36621	0.35197
cg0231133	MAD1L1	C/EBPbeta	124	127	1.366559	TTGA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	427	430	1.366559	TCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	779	782	1.366559	TCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	874	877	1.366559	TTGA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	885	888	1.366559	TCAA	15.625	15.23827

cg0231133	MAD1L1	C/EBPbeta	1042	1045	1.366559	TCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	1146	1149	1.366559	TCAA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	1159	1162	1.366559	TTGA	15.625	15.23827
cg0231133	MAD1L1	C/EBPbeta	1775	1778	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	49	52	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	88	91	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	143	146	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	183	186	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	238	241	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	267	270	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	344	347	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	664	667	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1025	1028	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1145	1148	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1193	1196	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1258	1261	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1365	1368	1.366559	TCAA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1532	1535	1.366559	TTGA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1568	1571	1.366559	TTGA	15.625	15.23827
cg1578384	MAD1L1	C/EBPbeta	1613	1616	1.366559	TCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	163	166	1.366559	TTGA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	173	176	1.366559	TCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	181	184	1.366559	TCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	205	208	1.366559	TTGA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	404	407	1.366559	TCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	594	597	1.366559	TCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	627	630	1.366559	TCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	745	748	1.366559	TTGA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	825	828	1.366559	TCAA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	1432	1435	1.366559	TTGA	15.625	15.23827
cg1151970	MAD1L1	C/EBPbeta	1981	1984	1.366559	TCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	372	375	1.366559	TCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	854	857	1.366559	TCAA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	1118	1121	1.366559	TTGA	15.625	15.23827
cg1002882	MAD1L1	C/EBPbeta	1138	1141	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	100	103	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	179	182	1.366559	TTGA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	264	267	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	403	406	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	429	432	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	484	487	1.366559	TTGA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	623	626	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	833	836	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1198	1201	1.366559	TTGA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1262	1265	1.366559	TTGA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1383	1386	1.366559	TTGA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1516	1519	1.366559	TTGA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1536	1539	1.366559	TTGA	15.625	15.23827

cg0611220	MAD1L1	C/EBPbeta	1621	1624	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1659	1662	1.366559	TTGA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1859	1862	1.366559	TCAA	15.625	15.23827
cg0611220	MAD1L1	C/EBPbeta	1919	1922	1.366559	TTGA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	319	322	1.366559	TCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	369	372	1.366559	TCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	718	721	1.366559	TTGA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	733	736	1.366559	TTGA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	908	911	1.366559	TCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1119	1122	1.366559	TCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1445	1448	1.366559	TCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1546	1549	1.366559	TCAA	15.625	15.23827
cg0372348	MAD1L1	C/EBPbeta	1619	1622	1.366559	TTGA	15.625	15.23827
cg0231133	MAD1L1	AP-2alpha	92	97	1.357116	ACAGGC	0.48828	0.51319
cg1578384	MAD1L1	AP-2alpha	116	121	1.357116	ACAGGC	0.48828	0.51319
cg1578384	MAD1L1	AP-2alpha	1228	1233	1.357116	ACAGGC	0.48828	0.51319
cg1578384	MAD1L1	AP-2alpha	1355	1360	1.357116	GCCTGT	0.48828	0.51319
cg1578384	MAD1L1	AP-2alpha	1488	1493	1.357116	GCCTGT	0.48828	0.51319
cg1578384	MAD1L1	AP-2alpha	1682	1687	1.357116	GCCTGT	0.48828	0.51319
cg1578384	MAD1L1	AP-2alpha	1789	1794	1.357116	ACAGGC	0.48828	0.51319
cg1151970	MAD1L1	AP-2alpha	1251	1256	1.357116	ACAGGC	0.48828	0.51319
cg1151970	MAD1L1	AP-2alpha	1989	1994	1.357116	ACAGGC	0.48828	0.51319
cg1002882	MAD1L1	AP-2alpha	606	611	1.357116	ACAGGC	0.48828	0.51319
cg1002882	MAD1L1	AP-2alpha	742	747	1.357116	ACAGGC	0.48828	0.51319
cg0611220	MAD1L1	AP-2alpha	722	727	1.357116	ACAGGC	0.48828	0.51319
cg0372348	MAD1L1	AP-2alpha	691	696	1.357116	ACAGGC	0.48828	0.51319
cg0372348	MAD1L1	AP-2alpha	961	966	1.357116	ACAGGC	0.48828	0.51319
cg0372348	MAD1L1	AP-2alpha	1751	1756	1.357116	ACAGGC	0.48828	0.51319
cg0372348	MAD1L1	AP-2alpha	1761	1766	1.357116	ACAGGC	0.48828	0.51319
cg1578384	MAD1L1	HNF-3alp	1632	1639	1.342935	TTAAAA	0.03052	0.02477
cg1002882	MAD1L1	IRF-1 [T0	374	382	1.274173	AAAAGG	0.04578	0.04268
cg1151970	MAD1L1	p53 [T006	102	108	1.270236	GGGCAC	0.12207	0.13816
cg1151970	MAD1L1	p53 [T006	1717	1723	1.270236	CGTGCC	0.12207	0.13816
cg0231133	MAD1L1	GCF [T00	649	657	1.26923	GCGCAG	0.03052	0.03542
cg1151970	MAD1L1	ENKTF-1	1206	1213	1.255756	TGGCGT	0.24414	0.27027
cg1002882	MAD1L1	ENKTF-1	1439	1446	1.255756	TGGCGT	0.24414	0.27027
cg1002882	MAD1L1	ENKTF-1	1634	1641	1.255756	TGGCGT	0.24414	0.27027
cg1002882	MAD1L1	ENKTF-1	1897	1904	1.255756	CTCCGC	0.24414	0.27027
cg0372348	MAD1L1	ENKTF-1	1688	1695	1.255756	TGGCGC	0.24414	0.27027
cg0231133	MAD1L1	RelA [T00	1452	1462	1.207015	GAAATT	0.00381	0.00384
cg1578384	MAD1L1	GATA-2 [	765	773	1.111111	AGATAA	0.09155	0.08894
cg1002882	MAD1L1	T3R-beta1	446	454	1.110682	CAGAGG	0.07629	0.07886
cg0611220	MAD1L1	c-Ets-2 [T	1448	1456	1.071163	TTCCTCT	0.06104	0.0583
cg1151970	MAD1L1	GCF [T00	560	568	1.070269	GCGCTG	0.18311	0.21473
cg1151970	MAD1L1	GCF [T00	1817	1825	1.070269	AGCCCG	0.18311	0.21473
cg0231133	MAD1L1	GATA-1 [	1144	1149	1.038567	TATCAA	1.95312	1.80234
cg1578384	MAD1L1	GATA-1 [	342	347	1.038567	TATCAA	1.95312	1.80234
cg0611220	MAD1L1	GATA-1 [	614	619	1.038567	ATGATA	1.95312	1.80234

cg0372348	MAD1L1	GATA-1 [	1984	1989	1.038567	ATGATA	1.95312	1.80234
cg1151970	MAD1L1	CREB [T0	588	596	0.989089	AGGACG	0.05341	0.05499
cg1151970	MAD1L1	NF-kappaI	1636	1647	0.986122	GGGACA	0.00095	0.001
cg1578384	MAD1L1	TBP [T007	1056	1065	0.935771	AACATA	0.12207	0.10448
cg0611220	MAD1L1	TBP [T007	508	517	0.935771	GAGCTA	0.12207	0.10448
cg0372348	MAD1L1	TBP [T007	444	453	0.935771	GCTGTA	0.12207	0.10448
cg1002882	MAD1L1	GATA-1 [	841	846	0.863549	TATCAC	1.95312	1.80234
cg0611220	MAD1L1	GATA-1 [	592	597	0.863549	TATCAC	1.95312	1.80234
cg0611220	MAD1L1	GATA-1 [	732	737	0.863549	TATCAC	1.95312	1.80234
cg0372348	MAD1L1	GATA-1 [	1907	1912	0.863549	TATCAC	1.95312	1.80234
cg1578384	MAD1L1	RXR-alpha	85	91	0.848226	GGGTCA	0.48828	0.51313
cg1151970	MAD1L1	RXR-alpha	570	576	0.848226	TGGACC	0.48828	0.51313
cg1002882	MAD1L1	RXR-alpha	217	223	0.848226	GGGTCC	0.48828	0.51313
cg0611220	MAD1L1	RXR-alpha	1536	1542	0.848226	TTGACC	0.48828	0.51313
cg0231133	MAD1L1	GR-beta [T	313	317	0.840383	TCATT	7.8125	7.2174
cg0231133	MAD1L1	GR-beta [T	412	416	0.840383	AATGG	7.8125	7.2174
cg0231133	MAD1L1	GR-beta [T	1166	1170	0.840383	AATGA	7.8125	7.2174
cg0231133	MAD1L1	GR-beta [T	1192	1196	0.840383	AATGG	7.8125	7.2174
cg0231133	MAD1L1	GR-beta [T	1595	1599	0.840383	AATTG	7.8125	7.2174
cg0231133	MAD1L1	GR-beta [T	1957	1961	0.840383	AATGA	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	104	108	0.840383	AATGG	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	207	211	0.840383	AATGA	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	255	259	0.840383	AATTA	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	275	279	0.840383	AATGG	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	1320	1324	0.840383	TCATT	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	1526	1530	0.840383	AATTG	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	1573	1577	0.840383	CCATT	7.8125	7.2174
cg1578384	MAD1L1	GR-beta [T	1630	1634	0.840383	AATTA	7.8125	7.2174
cg1151970	MAD1L1	GR-beta [T	760	764	0.840383	CAATT	7.8125	7.2174
cg1151970	MAD1L1	GR-beta [T	1801	1805	0.840383	CCATT	7.8125	7.2174
cg1151970	MAD1L1	GR-beta [T	1862	1866	0.840383	AATGG	7.8125	7.2174
cg1151970	MAD1L1	GR-beta [T	1976	1980	0.840383	CCATT	7.8125	7.2174
cg1002882	MAD1L1	GR-beta [T	354	358	0.840383	AATGG	7.8125	7.2174
cg1002882	MAD1L1	GR-beta [T	513	517	0.840383	AATGG	7.8125	7.2174
cg1002882	MAD1L1	GR-beta [T	1028	1032	0.840383	TAATT	7.8125	7.2174
cg1002882	MAD1L1	GR-beta [T	1127	1131	0.840383	TCATT	7.8125	7.2174
cg1002882	MAD1L1	GR-beta [T	1259	1263	0.840383	AATGA	7.8125	7.2174
cg1002882	MAD1L1	GR-beta [T	1313	1317	0.840383	TAATT	7.8125	7.2174
cg1002882	MAD1L1	GR-beta [T	1314	1318	0.840383	AATTG	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	138	142	0.840383	AATGA	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	196	200	0.840383	TCATT	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	269	273	0.840383	CAATT	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	331	335	0.840383	TAATT	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	490	494	0.840383	CAATT	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	491	495	0.840383	AATTA	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	613	617	0.840383	AATGA	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	763	767	0.840383	AATGG	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	954	958	0.840383	CCATT	7.8125	7.2174

cg0611220	MAD1L1	GR-beta [T	1255	1259	0.840383	AATGA	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	1344	1348	0.840383	TAATT	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	1345	1349	0.840383	AATTA	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	1657	1661	0.840383	AATTG	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	1799	1803	0.840383	AATTA	7.8125	7.2174
cg0611220	MAD1L1	GR-beta [T	1817	1821	0.840383	AATGA	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	314	318	0.840383	CAATT	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	370	374	0.840383	CAATT	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	371	375	0.840383	AATTA	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	389	393	0.840383	CAATT	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	432	436	0.840383	TCATT	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	881	885	0.840383	AATTA	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	1045	1049	0.840383	TCATT	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	1120	1124	0.840383	CAATT	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	1121	1125	0.840383	AATTA	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	1129	1133	0.840383	AATGA	7.8125	7.2174
cg0372348	MAD1L1	GR-beta [T	1409	1413	0.840383	CCATT	7.8125	7.2174
cg0372348	MAD1L1	Elk-1 [T00	1792	1800	0.822677	GGAAGG	0.03052	0.03046
cg1578384	MAD1L1	HNF-1A [	1984	1991	0.781639	GTTAAA	0.48828	0.45029
cg0611220	MAD1L1	HNF-1A [	1228	1235	0.781639	GTTTTA	0.48828	0.45029
cg0372348	MAD1L1	GATA-1 [	326	331	0.758539	CTGATA	1.95312	1.80234
cg0372348	MAD1L1	GATA-1 [	865	870	0.758539	TATCAG	1.95312	1.80234
cg0372348	MAD1L1	USF1 [T0	242	251	0.690892	CACCCA	0.01335	0.01451
cg1151970	MAD1L1	AP-2alpha	583	588	0.678558	GCCTGA	0.48828	0.51196
cg1151970	MAD1L1	AP-2alpha	1669	1674	0.678558	GCCTGA	0.48828	0.51196
cg1151970	MAD1L1	AP-2alpha	1792	1797	0.678558	TCAGGC	0.48828	0.51196
cg0611220	MAD1L1	AP-2alpha	463	468	0.678558	GCCTGA	0.48828	0.51196
cg0372348	MAD1L1	AP-2alpha	655	660	0.678558	GCCTGA	0.48828	0.51196
cg0372348	MAD1L1	AP-2alpha	684	689	0.678558	GCCTGA	0.48828	0.51196
cg0372348	MAD1L1	AP-2alpha	816	821	0.678558	GCCTGA	0.48828	0.51196
cg0372348	MAD1L1	AP-2alpha	1656	1661	0.678558	TCAGGC	0.48828	0.51196
cg0611220	MAD1L1	NF-AT1 [T	936	944	0.648993	ATTCTTT	0.02289	0.02115
cg0231133	MAD1L1	C/EBPalph	1177	1183	0.540941	CACAAT	0.24414	0.24432
cg0611220	MAD1L1	C/EBPalph	227	233	0.540941	CACAAT	0.24414	0.24432
cg1002882	MAD1L1	POU2F2 (	1727	1737	0.501684	TGATTT	0.01287	0.01128
cg1578384	MAD1L1	AP-1 [T00	1141	1149	0.489074	TGACTC	0.09155	0.08806
cg0611220	MAD1L1	HNF-1A [	905	912	0.431647	TGTTTA	0.24414	0.21942
cg0611220	MAD1L1	c-Ets-1 [T	972	978	0.384261	TAGGAA	0.24414	0.23743
cg0372348	MAD1L1	c-Ets-1 [T	354	360	0.384261	TAGGAA	0.24414	0.23743
cg0611220	MAD1L1	AP-1 [T00	1855	1863	0.314596	TGACTC	0.09155	0.08806
cg1578384	MAD1L1	GATA-1 [	306	311	0.280028	AAGATA	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	346	351	0.280028	AAGATA	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	362	367	0.280028	AAGATA	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	426	431	0.280028	AAGATA	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	474	479	0.280028	AAGATA	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	642	647	0.280028	AAGATA	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	666	671	0.280028	AAGATA	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	814	819	0.280028	AAGATA	0.97656	0.8795

cg1578384	MAD1L1	GATA-1 [	1103	1108	0.280028	TATCTT	0.97656	0.8795
cg1578384	MAD1L1	GATA-1 [	1240	1245	0.280028	AAGATA	0.97656	0.8795
cg1151970	MAD1L1	GATA-1 [	838	843	0.280028	AAGATA	0.97656	0.8795
cg0611220	MAD1L1	GATA-1 [	625	630	0.280028	AAGATA	0.97656	0.8795
cg0611220	MAD1L1	GATA-1 [	1326	1331	0.280028	TATCTT	0.97656	0.8795
cg0231133	MAD1L1	AP-1 [T00	1532	1540	0.261718	TGACTC	0.09155	0.08806
cg0231133	MAD1L1	c-Ets-1 [T	781	787	0.256174	AAGGAA	0.24414	0.23743
cg0231133	MAD1L1	c-Ets-1 [T	1777	1783	0.256174	AAGGAA	0.24414	0.23743
cg1151970	MAD1L1	c-Ets-1 [T	1461	1467	0.256174	CTTCCT	0.24414	0.23743
cg1002882	MAD1L1	c-Ets-1 [T	429	435	0.256174	AAGGAA	0.24414	0.23743
cg0372348	MAD1L1	c-Ets-1 [T	1794	1800	0.256174	AAGGAA	0.24414	0.23743
cg0231133	MAD1L1	AP-2alpha	26	31	0.226186	CCAGGC	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	351	356	0.226186	GCCTGG	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	364	369	0.226186	CCAGGC	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	1819	1824	0.226186	CCAGGC	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	1848	1853	0.226186	CCAGGC	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	1853	1858	0.226186	CCAGGC	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	1857	1862	0.226186	GCCTGG	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	1988	1993	0.226186	CCAGGC	0.97656	1.07867
cg1578384	MAD1L1	AP-2alpha	1586	1591	0.226186	GCCTGG	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	257	262	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	317	322	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	372	377	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	397	402	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	483	488	0.226186	GCCTGG	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	980	985	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	1187	1192	0.226186	GCCTGG	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	1285	1290	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	1336	1341	0.226186	GCCTGG	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	1424	1429	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	1520	1525	0.226186	CCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	1775	1780	0.226186	GCCTGG	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	724	729	0.226186	CCAGGC	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	943	948	0.226186	GCCTGG	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	1431	1436	0.226186	GCCTGG	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	1509	1514	0.226186	GCCTGG	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	1582	1587	0.226186	CCAGGC	0.97656	1.07867
cg0611220	MAD1L1	AP-2alpha	208	213	0.226186	CCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	67	72	0.226186	CCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	132	137	0.226186	CCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	302	307	0.226186	GCCTGG	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	988	993	0.226186	CCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	1084	1089	0.226186	GCCTGG	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	1264	1269	0.226186	GCCTGG	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	1584	1589	0.226186	CCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	1716	1721	0.226186	GCCTGG	0.97656	1.07867
cg1002882	MAD1L1	p53 [T006	568	574	0.211706	GGGCAA	0.36621	0.40082
cg1002882	MAD1L1	p53 [T006	1351	1357	0.211706	GGGCAA	0.36621	0.40082

cg0372348	MAD1L1	p53 [T006'	1308	1314	0.211706	CTTGCCC	0.36621	0.40082
cg0372348	MAD1L1	p53 [T006'	1840	1846	0.211706	GGGCAA	0.36621	0.40082
cg0231133	MAD1L1	GR-alpha [	47	51	0.207689	CCTCT	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	201	205	0.207689	CCTCT	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	338	342	0.207689	AGAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	548	552	0.207689	AAAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	657	661	0.207689	AGAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	1236	1240	0.207689	AGAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	1432	1436	0.207689	CCTCT	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	1640	1644	0.207689	AGAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	1699	1703	0.207689	AGAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	259	263	0.207689	AAAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1012	1016	0.207689	AGAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1064	1068	0.207689	AAAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1326	1330	0.207689	AAAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1663	1667	0.207689	AAAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1814	1818	0.207689	AAAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	285	289	0.207689	CCTCT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	331	335	0.207689	CCTCT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	360	364	0.207689	CCTCT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	366	370	0.207689	CCTCT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	386	390	0.207689	CCTCT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	461	465	0.207689	AGAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	774	778	0.207689	AGAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	881	885	0.207689	CCTCT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1358	1362	0.207689	AGAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1464	1468	0.207689	CCTTT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1600	1604	0.207689	AGAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1693	1697	0.207689	CCTCT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1969	1973	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	375	379	0.207689	AAAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	394	398	0.207689	CCTTT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	428	432	0.207689	AAAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	447	451	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	565	569	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	585	589	0.207689	CCTCT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	706	710	0.207689	CCTCT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	817	821	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	939	943	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1078	1082	0.207689	CCTCT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1087	1091	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1096	1100	0.207689	CCTTT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1192	1196	0.207689	CCTTT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1291	1295	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1347	1351	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1549	1553	0.207689	AAAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1771	1775	0.207689	CCTCT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1799	1803	0.207689	AGAGG	7.8125	7.79817

cg0611220	MAD1L1	GR-alpha [	77	81	0.207689	AGAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	110	114	0.207689	AGAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	425	429	0.207689	CCTCT	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	743	747	0.207689	CCTTT	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	982	986	0.207689	CCTCT	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1313	1317	0.207689	AAAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1450	1454	0.207689	CCTCT	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1700	1704	0.207689	AGAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1759	1763	0.207689	AAAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1768	1772	0.207689	AAAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1938	1942	0.207689	CCTCT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	80	84	0.207689	AGAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	96	100	0.207689	CCTCT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	114	118	0.207689	CCTCT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	200	204	0.207689	CCTCT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	271	275	0.207689	AAAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	323	327	0.207689	CCTCT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	749	753	0.207689	AAAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	837	841	0.207689	CCTTT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	842	846	0.207689	CCTCT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1196	1200	0.207689	CCTTT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1722	1726	0.207689	AGAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1869	1873	0.207689	AGAGG	7.8125	7.79817
cg1002882	MAD1L1	Elk-1 [T00	1420	1428	0.134348	CGGAGG	0.06104	0.06399
cg0231133	MAD1L1	c-Ets-1 [T	1278	1284	0.128087	GAGGAA	0.24414	0.24982
cg1151970	MAD1L1	c-Ets-1 [T	334	340	0.128087	CTTCCTC	0.24414	0.24982
cg1151970	MAD1L1	c-Ets-1 [T	363	369	0.128087	CTTCCTC	0.24414	0.24982
cg1151970	MAD1L1	c-Ets-1 [T	389	395	0.128087	CTTCCTC	0.24414	0.24982
cg1002882	MAD1L1	c-Ets-1 [T	1422	1428	0.128087	GAGGAA	0.24414	0.24982
cg0372348	MAD1L1	c-Ets-1 [T	81	87	0.128087	GAGGAA	0.24414	0.24982
cg0372348	MAD1L1	c-Ets-1 [T	1440	1446	0.128087	CTTCCTC	0.24414	0.24982
cg1578384	MAD1L1	GATA-1 [	322	327	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	378	383	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	410	415	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	442	447	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	458	463	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	506	511	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	522	527	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	538	543	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	554	559	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	570	575	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	586	591	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	602	607	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	626	631	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	682	687	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	698	703	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	714	719	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	731	736	0.105011	GAGATA	0.97656	0.92541

cg1578384	MAD1L1	GATA-1 [	748	753	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	764	769	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	781	786	0.105011	GAGATA	0.97656	0.92541
cg1578384	MAD1L1	GATA-1 [	798	803	0.105011	GAGATA	0.97656	0.92541
cg1002882	MAD1L1	GATA-1 [	505	510	0.105011	GAGATA	0.97656	0.92541
cg0611220	MAD1L1	GATA-1 [	133	138	0.105011	GAGATA	0.97656	0.92541
cg0611220	MAD1L1	GATA-1 [	1456	1461	0.105011	TATCTC	0.97656	0.92541
cg0611220	MAD1L1	GATA-1 [	1754	1759	0.105011	GAGATA	0.97656	0.92541
cg1151970	MAD1L1	EBF [T05	1675	1685	0.10398	GCCCCT	0.00381	0.00466
cg0231133	MAD1L1	GR-beta [T	829	833	0	AATGT	3.90625	3.51525
cg0231133	MAD1L1	GR-beta [T	863	867	0	AATGT	3.90625	3.51525
cg0231133	MAD1L1	GR-beta [T	955	959	0	AATGT	3.90625	3.51525
cg0231133	MAD1L1	GR-beta [T	1446	1450	0	AATGT	3.90625	3.51525
cg0231133	MAD1L1	GR-beta [T	1453	1457	0	AAATT	3.90625	3.51525
cg0231133	MAD1L1	XBP-1 [T	1531	1536	0	ATGACT	0.97656	0.94838
cg0231133	MAD1L1	XBP-1 [T	1656	1661	0	CGTCAT	0.97656	0.94838
cg0231133	MAD1L1	TFIID [T0	424	430	0	TTTTCA	1.09863	0.95175
cg0231133	MAD1L1	TFIID [T0	444	450	0	TAAAAA	1.09863	0.95175
cg0231133	MAD1L1	TFIID [T0	882	888	0	TTTTCA	1.09863	0.95175
cg0231133	MAD1L1	TFIID [T0	885	891	0	TCAAAA	1.09863	0.95175
cg0231133	MAD1L1	TFIID [T0	1132	1138	0	TTTAAA	1.09863	0.95175
cg0231133	MAD1L1	TFIID [T0	1187	1193	0	TCGAAA	1.09863	0.95175
cg0231133	MAD1L1	c-Jun [T00	1532	1538	0	TGACTC	0.12207	0.11843
cg0231133	MAD1L1	GR-alpha [	6	10	0	ATAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	60	64	0	CCTGT	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	92	96	0	ACAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	162	166	0	ACAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	695	699	0	ACAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	1098	1102	0	ACAGG	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	1273	1277	0	CCTGT	7.8125	7.79817
cg0231133	MAD1L1	GR-alpha [	1902	1906	0	CCTGT	7.8125	7.79817
cg0231133	MAD1L1	FOXP3 [T	1516	1521	0	CACAAC	1.46484	1.44953
cg0231133	MAD1L1	PR B [T00	463	469	0	AACAGT	0.36621	0.35051
cg0231133	MAD1L1	PR A [T01	463	469	0	AACAGT	0.36621	0.35051
cg0231133	MAD1L1	C/EBPbeta	14	17	0	TTGC	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	53	56	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	148	151	0	TTGT	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	159	162	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	271	274	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	420	423	0	TTGC	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	461	464	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	822	825	0	ACAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	826	829	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	892	895	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	902	905	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1073	1076	0	ACAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1178	1181	0	ACAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1217	1220	0	TTGC	15.625	15.26275

cg0231133	MAD1L1	C/EBPbeta	1244	1247	0	ACAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1393	1396	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1493	1496	0	ACAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1501	1504	0	TTGT	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1517	1520	0	ACAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1597	1600	0	TTGT	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1646	1649	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1705	1708	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1828	1831	0	GCAA	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1919	1922	0	TTGT	15.625	15.26275
cg0231133	MAD1L1	C/EBPbeta	1922	1925	0	TTGC	15.625	15.26275
cg0231133	MAD1L1	YY1 [T00	153	156	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	388	391	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	413	416	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	522	525	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	793	796	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	1087	1090	0	CCAT	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	1193	1196	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	1261	1264	0	CCAT	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	1660	1663	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	1731	1734	0	ATGG	7.8125	7.79459
cg0231133	MAD1L1	YY1 [T00	1896	1899	0	CCAT	7.8125	7.79459
cg0231133	MAD1L1	TFII-I [T0	189	194	0	GGATAG	1.46484	1.48598
cg0231133	MAD1L1	TFII-I [T0	621	626	0	GGACAG	1.46484	1.48598
cg0231133	MAD1L1	TFII-I [T0	914	919	0	GGAAAG	1.46484	1.48598
cg0231133	MAD1L1	TFII-I [T0	1674	1679	0	GGACAG	1.46484	1.48598
cg0231133	MAD1L1	STAT4 [T	1451	1456	0	GGAAAT	0.48828	0.46235
cg0231133	MAD1L1	ER-alpha [	672	676	0	GGTCA	1.95312	1.99744
cg0231133	MAD1L1	ER-alpha [	1052	1056	0	GGTCA	1.95312	1.99744
cg0231133	MAD1L1	ER-alpha [	1227	1231	0	TGACC	1.95312	1.99744
cg0231133	MAD1L1	ER-alpha [	1327	1331	0	GGTCA	1.95312	1.99744
cg0231133	MAD1L1	RXR-alpha	397	403	0	TGAACC	0.24414	0.24342
cg0231133	MAD1L1	NFI/CTF [	1507	1514	0	CCAAAC	0.18311	0.191
cg0231133	MAD1L1	GR [T050	886	892	0	CAAAAA	0.36621	0.33174
cg0231133	MAD1L1	GR [T050	1546	1552	0	CAAAAA	0.36621	0.33174
cg0231133	MAD1L1	c-Myc [T0	1381	1386	0	CACGTG	0.48828	0.51196
cg0231133	MAD1L1	GATA-1 [	440	445	0	CAGATA	0.97656	0.92541
cg0231133	MAD1L1	Pax-5 [T0	110	116	0	CCGGCC	1.09863	1.24633
cg0231133	MAD1L1	Pax-5 [T0	219	225	0	CGAGCC	1.09863	1.24633
cg0231133	MAD1L1	Pax-5 [T0	365	371	0	CAGGCC	1.09863	1.24633
cg0231133	MAD1L1	Pax-5 [T0	404	410	0	CCTGCC	1.09863	1.24633
cg0231133	MAD1L1	Pax-5 [T0	739	745	0	GGGCTG	1.09863	1.24633
cg0231133	MAD1L1	Pax-5 [T0	1820	1826	0	CAGGCC	1.09863	1.24633
cg0231133	MAD1L1	Pax-5 [T0	1897	1903	0	CATGCC	1.09863	1.24633
cg0231133	MAD1L1	p53 [T006	404	410	0	CCTGCC	0.36621	0.40082
cg0231133	MAD1L1	p53 [T006	1897	1903	0	CATGCC	0.36621	0.40082
cg0231133	MAD1L1	AP-2alpha	651	656	0	GCAGGC	0.97656	1.07867
cg0231133	MAD1L1	AP-2alpha	758	763	0	GCCTGC	0.97656	1.07867

cg0231133	MAD1L1	AP-2alpha	1286	1291	0	GCAGGC	0.97656	1.07867
cg0231133	MAD1L1	GCF [T00	107	115	0	GCGCCG	0.09155	0.10999
cg0231133	MAD1L1	IRF-2 [T01	894	899	0	AAGTGA	0.48828	0.46235
cg0231133	MAD1L1	IRF-2 [T01	1106	1111	0	AAGTGA	0.48828	0.46235
cg0231133	MAD1L1	c-Fos [T00	1834	1843	0	GAGTCA	0.01144	0.01148
cg1578384	MAD1L1	GR-beta [T	90	94	0	AATGT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	178	182	0	AATGT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	254	258	0	AAATT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	792	796	0	AATGT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	1202	1206	0	AAATT	3.90625	3.51525
cg1578384	MAD1L1	GR-beta [T	1629	1633	0	AAATT	3.90625	3.51525
cg1578384	MAD1L1	XBP-1 [T0	1140	1145	0	ATGACT	0.97656	0.94838
cg1578384	MAD1L1	XBP-1 [T0	1972	1977	0	CGTCAT	0.97656	0.94838
cg1578384	MAD1L1	ENKTF-1	977	984	0	CAGCGC	0.12207	0.13179
cg1578384	MAD1L1	TFIID [T0	900	906	0	TAAAAA	1.09863	0.95175
cg1578384	MAD1L1	TFIID [T0	1060	1066	0	TATAAA	1.09863	0.95175
cg1578384	MAD1L1	TFIID [T0	1613	1619	0	TCAAAA	1.09863	0.95175
cg1578384	MAD1L1	c-Jun [T00	1141	1147	0	TGACTC	0.12207	0.11843
cg1578384	MAD1L1	GR-alpha [	116	120	0	ACAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	845	849	0	ACAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1228	1232	0	ACAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1356	1360	0	CCTGT	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1489	1493	0	CCTGT	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1683	1687	0	CCTGT	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1789	1793	0	ACAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1862	1866	0	ACAGG	7.8125	7.79817
cg1578384	MAD1L1	GR-alpha [	1919	1923	0	CCTAT	7.8125	7.79817
cg1578384	MAD1L1	FOXP3 [T	72	77	0	GTTGTC	1.46484	1.44953
cg1578384	MAD1L1	FOXP3 [T	157	162	0	GACAAC	1.46484	1.44953
cg1578384	MAD1L1	FOXP3 [T	1109	1114	0	CACAAC	1.46484	1.44953
cg1578384	MAD1L1	FOXP3 [T	1772	1777	0	AACAAC	1.46484	1.44953
cg1578384	MAD1L1	PR B [T00	1128	1134	0	GACTGT	0.36621	0.35051
cg1578384	MAD1L1	PR A [T01	1128	1134	0	GACTGT	0.36621	0.35051
cg1578384	MAD1L1	HNF-3alph	1452	1459	0	TAAAAA	0.09155	0.07727
cg1578384	MAD1L1	HNF-3alph	1648	1655	0	TAAAAA	0.09155	0.07727
cg1578384	MAD1L1	C/EBPbeta	67	70	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	73	76	0	TTGT	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	158	161	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	244	247	0	TTGC	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	304	307	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	869	872	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	895	898	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1005	1008	0	TTGC	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1007	1010	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1045	1048	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1054	1057	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1072	1075	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1110	1113	0	ACAA	15.625	15.26275

cg1578384	MAD1L1	C/EBPbeta	1123	1126	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1163	1166	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1221	1224	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1261	1264	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1293	1296	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1307	1310	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1312	1315	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1316	1319	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1459	1462	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1528	1531	0	TTGC	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1576	1579	0	TTGC	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1592	1595	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1773	1776	0	ACAA	15.625	15.26275
cg1578384	MAD1L1	C/EBPbeta	1946	1949	0	GCAA	15.625	15.26275
cg1578384	MAD1L1	YY1 [T00	13	16	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	105	108	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	235	238	0	CCAT	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	264	267	0	CCAT	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	276	279	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	297	300	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	883	886	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	912	915	0	CCAT	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	914	917	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	971	974	0	CCAT	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	973	976	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	1431	1434	0	ATGG	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	1442	1445	0	CCAT	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	1573	1576	0	CCAT	7.8125	7.79459
cg1578384	MAD1L1	YY1 [T00	1848	1851	0	CCAT	7.8125	7.79459
cg1578384	MAD1L1	C/EBPalph	1566	1572	0	GATTGA	0.24414	0.24342
cg1578384	MAD1L1	TFII-I [T0	1684	1689	0	CTGTCC	1.46484	1.48598
cg1578384	MAD1L1	TFII-I [T0	1762	1767	0	GGAAAG	1.46484	1.48598
cg1578384	MAD1L1	HOXD9 [T	1625	1634	0	AATAAA	0.01144	0.00905
cg1578384	MAD1L1	HOXD9 [T	1646	1655	0	AATAAA	0.01144	0.00905
cg1578384	MAD1L1	HOXD10 [	1625	1634	0	AATAAA	0.01144	0.00905
cg1578384	MAD1L1	HOXD10 [	1646	1655	0	AATAAA	0.01144	0.00905
cg1578384	MAD1L1	ER-alpha [	86	90	0	GGTCA	1.95312	1.99744
cg1578384	MAD1L1	ER-alpha [	1401	1405	0	GGTCA	1.95312	1.99744
cg1578384	MAD1L1	ER-alpha [	1915	1919	0	TGACC	1.95312	1.99744
cg1578384	MAD1L1	RXR-alpha	1533	1539	0	TGAACC	0.24414	0.24342
cg1578384	MAD1L1	NFI/CTF [	1967	1974	0	CCAAAC	0.18311	0.191
cg1578384	MAD1L1	GR [T050	1614	1620	0	CAAAAA	0.36621	0.33174
cg1578384	MAD1L1	c-Myc [T0	1979	1984	0	CACGTG	0.48828	0.51196
cg1578384	MAD1L1	LEF-1 [T0	141	148	0	GATCAA	0.03052	0.02895
cg1578384	MAD1L1	Pax-5 [T0	1790	1796	0	CAGGCC	1.09863	1.24633
cg1578384	MAD1L1	Pax-5 [T0	1933	1939	0	GGGCAT	1.09863	1.24633
cg1578384	MAD1L1	Pax-5 [T0	1936	1942	0	CATGCC	1.09863	1.24633
cg1578384	MAD1L1	p53 [T006	1933	1939	0	GGGCAT	0.36621	0.40082

cg1578384	MAD1L1	p53 [T006	1936	1942	0	CATGCC	0.36621	0.40082
cg1578384	MAD1L1	AP-2alpha	1119	1124	0	GCAGGC	0.97656	1.07867
cg1578384	MAD1L1	AP-2alpha	1386	1391	0	GCAGGC	0.97656	1.07867
cg1578384	MAD1L1	GCF [T00	1939	1947	0	GCCCAG	0.09155	0.10999
cg1151970	MAD1L1	GR-beta [	123	127	0	AATTT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [	186	190	0	AATGT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [	1280	1284	0	ACATT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [	1639	1643	0	ACATT	3.90625	3.51525
cg1151970	MAD1L1	GR-beta [	1831	1835	0	ACATT	3.90625	3.51525
cg1151970	MAD1L1	ENKTF-1	564	571	0	TGGCGT	0.12207	0.13179
cg1151970	MAD1L1	TFIID [T0	181	187	0	TCAAAA	1.09863	0.95175
cg1151970	MAD1L1	GR-alpha [	513	517	0	ATAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	873	877	0	CCTGT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1251	1255	0	ACAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1495	1499	0	CCTGT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1554	1558	0	ACAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1710	1714	0	ACAGG	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1871	1875	0	CCTGT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1924	1928	0	CCTAT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1931	1935	0	CCTAT	7.8125	7.79817
cg1151970	MAD1L1	GR-alpha [	1989	1993	0	ACAGG	7.8125	7.79817
cg1151970	MAD1L1	PR B [T00	893	899	0	AACAGT	0.36621	0.35051
cg1151970	MAD1L1	PR A [T01	893	899	0	AACAGT	0.36621	0.35051
cg1151970	MAD1L1	C/EBPbeta	39	42	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	68	71	0	ACAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	191	194	0	ACAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	250	253	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	473	476	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	523	526	0	TTGC	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	620	623	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	759	762	0	ACAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	947	950	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	986	989	0	TTGT	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	1183	1186	0	ACAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	1277	1280	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	1626	1629	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	1936	1939	0	ACAA	15.625	15.26275
cg1151970	MAD1L1	C/EBPbeta	1996	1999	0	GCAA	15.625	15.26275
cg1151970	MAD1L1	NF-1 [T00	1612	1619	0	TGGGCC	0.12207	0.13147
cg1151970	MAD1L1	YY1 [T00	79	82	0	ATGG	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	454	457	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	706	709	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	736	739	0	ATGG	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1158	1161	0	ATGG	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1196	1199	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1274	1277	0	ATGG	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1456	1459	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1480	1483	0	CCAT	7.8125	7.79459

cg1151970	MAD1L1	YY1 [T00	1504	1507	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1575	1578	0	ATGG	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1801	1804	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1806	1809	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1863	1866	0	ATGG	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1911	1914	0	ATGG	7.8125	7.79459
cg1151970	MAD1L1	YY1 [T00	1976	1979	0	CCAT	7.8125	7.79459
cg1151970	MAD1L1	TFII-I [T0	1249	1254	0	GGACAG	1.46484	1.48598
cg1151970	MAD1L1	TFII-I [T0	1321	1326	0	CTTTCC	1.46484	1.48598
cg1151970	MAD1L1	TFII-I [T0	1500	1505	0	CTGTCC	1.46484	1.48598
cg1151970	MAD1L1	STAT4 [T	1516	1521	0	ATTTCC	0.48828	0.46235
cg1151970	MAD1L1	ER-alpha [	241	245	0	TGACC	1.95312	1.99744
cg1151970	MAD1L1	ER-alpha [	289	293	0	TGACC	1.95312	1.99744
cg1151970	MAD1L1	ER-alpha [	451	455	0	TGACC	1.95312	1.99744
cg1151970	MAD1L1	ER-alpha [	540	544	0	GGTCA	1.95312	1.99744
cg1151970	MAD1L1	ER-alpha [	1105	1109	0	GGTCA	1.95312	1.99744
cg1151970	MAD1L1	ER-alpha [	1168	1172	0	TGACC	1.95312	1.99744
cg1151970	MAD1L1	ER-alpha [	1433	1437	0	TGACC	1.95312	1.99744
cg1151970	MAD1L1	ER-alpha [	1767	1771	0	TGACC	1.95312	1.99744
cg1151970	MAD1L1	GR [T050	182	188	0	CAAAAA	0.36621	0.33174
cg1151970	MAD1L1	GATA-1 [	128	133	0	CAGATA	0.97656	0.92541
cg1151970	MAD1L1	GATA-1 [	510	515	0	CAGATA	0.97656	0.92541
cg1151970	MAD1L1	PXR-1:RX	1308	1315	0	TAAGTT	0.12207	0.11255
cg1151970	MAD1L1	Pax-5 [T0	11	17	0	CCTGCC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	102	108	0	GGGCAC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	639	645	0	GGGCAG	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	667	673	0	CCAGCC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	674	680	0	CCAGCC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	701	707	0	CCGGCC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	741	747	0	GGGCTT	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	964	970	0	GGGCTG	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	973	979	0	CCAGCC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	1140	1146	0	GGGCTG	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	1521	1527	0	CAGGCC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	1645	1651	0	CCGGCC	1.09863	1.24633
cg1151970	MAD1L1	Pax-5 [T0	1717	1723	0	CGTGCC	1.09863	1.24633
cg1151970	MAD1L1	p53 [T006	11	17	0	CCTGCC	0.36621	0.40082
cg1151970	MAD1L1	p53 [T006	639	645	0	GGGCAG	0.36621	0.40082
cg1151970	MAD1L1	AP-2alpha	346	351	0	GCAGGC	0.97656	1.07867
cg1151970	MAD1L1	AP-2alpha	1756	1761	0	GCCTGC	0.97656	1.07867
cg1151970	MAD1L1	GCF [T00	555	563	0	GCCCAG	0.09155	0.10999
cg1151970	MAD1L1	Elk-1 [T00	334	342	0	CTTCCT	0.06104	0.06399
cg1151970	MAD1L1	Elk-1 [T00	389	397	0	CTTCCT	0.06104	0.06399
cg1002882	MAD1L1	GR-beta [	1029	1033	0	AATTT	3.90625	3.51525
cg1002882	MAD1L1	GR-beta [	1227	1231	0	AATGT	3.90625	3.51525
cg1002882	MAD1L1	XBP-1 [T	1955	1960	0	AGTCAT	0.97656	0.94838
cg1002882	MAD1L1	TFIID [T0	1130	1136	0	TTTTCG	1.09863	0.95175
cg1002882	MAD1L1	GR-alpha [	15	19	0	CCTGT	7.8125	7.79817

cg1002882	MAD1L1	GR-alpha [	310	314	0	CCTGT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	389	393	0	CCTAT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	460	464	0	CCTGT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	606	610	0	ACAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	655	659	0	CCTGT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	742	746	0	ACAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	762	766	0	CCTGT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1178	1182	0	CCTGT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1252	1256	0	CCTAT	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1331	1335	0	ACAGG	7.8125	7.79817
cg1002882	MAD1L1	GR-alpha [	1918	1922	0	CCTAT	7.8125	7.79817
cg1002882	MAD1L1	C/EBPbeta	92	95	0	TTGT	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	299	302	0	GCAA	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	351	354	0	GCAA	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	570	573	0	GCAA	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1008	1011	0	TTGC	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1045	1048	0	TTGC	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1156	1159	0	GCAA	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1353	1356	0	GCAA	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1591	1594	0	TTGC	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1647	1650	0	GCAA	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1784	1787	0	ACAA	15.625	15.26275
cg1002882	MAD1L1	C/EBPbeta	1843	1846	0	GCAA	15.625	15.26275
cg1002882	MAD1L1	YY1 [T00	32	35	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	120	123	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	122	125	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	225	228	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	329	332	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	333	336	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	355	358	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	514	517	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	581	584	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	665	668	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	1457	1460	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	1612	1615	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	1713	1716	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	1742	1745	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	1902	1905	0	CCAT	7.8125	7.79459
cg1002882	MAD1L1	YY1 [T00	1921	1924	0	ATGG	7.8125	7.79459
cg1002882	MAD1L1	TFII-I [T0	16	21	0	CTGTCC	1.46484	1.48598
cg1002882	MAD1L1	TFII-I [T0	164	169	0	GGATAG	1.46484	1.48598
cg1002882	MAD1L1	TFII-I [T0	390	395	0	CTATCC	1.46484	1.48598
cg1002882	MAD1L1	TFII-I [T0	1097	1102	0	CTTTCC	1.46484	1.48598
cg1002882	MAD1L1	STAT4 [T	1030	1035	0	ATTTCC	0.48828	0.46235
cg1002882	MAD1L1	ER-alpha [	178	182	0	TGACC	1.95312	1.99744
cg1002882	MAD1L1	ER-alpha [	443	447	0	GGTCA	1.95312	1.99744
cg1002882	MAD1L1	ER-alpha [	862	866	0	TGACC	1.95312	1.99744
cg1002882	MAD1L1	ER-alpha [	1125	1129	0	GGTCA	1.95312	1.99744

cg1002882	MAD1L1	ER-alpha [	1642	1646	0	GGTCA	1.95312	1.99744
cg1002882	MAD1L1	GATA-1 [	1270	1275	0	CAGATA	0.97656	0.92541
cg1002882	MAD1L1	Pax-5 [T0	2	8	0	GGGCTG	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	64	70	0	GGGCTG	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	305	311	0	CCAGCC	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	359	365	0	GGGCAT	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	537	543	0	CAGGCC	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	556	562	0	CCAGCC	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	743	749	0	CAGGCC	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	914	920	0	CATGCC	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	1071	1077	0	CGAGCC	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	1583	1589	0	CAGGCC	1.09863	1.24633
cg1002882	MAD1L1	Pax-5 [T0	1958	1964	0	CATGCC	1.09863	1.24633
cg1002882	MAD1L1	p53 [T006	359	365	0	GGGCAT	0.36621	0.40082
cg1002882	MAD1L1	p53 [T006	914	920	0	CATGCC	0.36621	0.40082
cg1002882	MAD1L1	p53 [T006	1958	1964	0	CATGCC	0.36621	0.40082
cg1002882	MAD1L1	AP-2alpha	479	484	0	GCAGGC	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	536	541	0	GCAGGC	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	767	772	0	GCAGGC	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	1066	1071	0	GCAGGC	0.97656	1.07867
cg1002882	MAD1L1	AP-2alpha	1848	1853	0	GCAGGC	0.97656	1.07867
cg1002882	MAD1L1	Sp1 [T007	979	988	0	GGGGCG	0.00191	0.00246
cg0611220	MAD1L1	GR-beta [	332	336	0	AATTT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [	635	639	0	ACATT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [	1505	1509	0	AAATT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [	1506	1510	0	AATTT	3.90625	3.51525
cg0611220	MAD1L1	GR-beta [	1798	1802	0	AAATT	3.90625	3.51525
cg0611220	MAD1L1	XBP-1 [T	148	153	0	ATGACT	0.97656	0.94838
cg0611220	MAD1L1	XBP-1 [T	754	759	0	CGTCAT	0.97656	0.94838
cg0611220	MAD1L1	XBP-1 [T	1249	1254	0	ATGACT	0.97656	0.94838
cg0611220	MAD1L1	TFIID [T	176	182	0	TTTTTGA	1.09863	0.95175
cg0611220	MAD1L1	TFIID [T	512	518	0	TATAAA	1.09863	0.95175
cg0611220	MAD1L1	TFIID [T	514	520	0	TAAAAA	1.09863	0.95175
cg0611220	MAD1L1	TFIID [T	1074	1080	0	TTTTTAA	1.09863	0.95175
cg0611220	MAD1L1	TFIID [T	1366	1372	0	TTTTCTA	1.09863	0.95175
cg0611220	MAD1L1	c-Jun [T00	1855	1861	0	TGACTC	0.12207	0.11843
cg0611220	MAD1L1	GR-alpha [	355	359	0	ACAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	689	693	0	CCTGT	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	722	726	0	ACAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1114	1118	0	CCTGT	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1201	1205	0	ACAGG	7.8125	7.79817
cg0611220	MAD1L1	GR-alpha [	1484	1488	0	ACAGG	7.8125	7.79817
cg0611220	MAD1L1	FOXP3 [T	576	581	0	CACAAC	1.46484	1.44953
cg0611220	MAD1L1	FOXP3 [T	595	600	0	CACAAC	1.46484	1.44953
cg0611220	MAD1L1	FOXP3 [T	663	668	0	GTTGTC	1.46484	1.44953
cg0611220	MAD1L1	FOXP3 [T	903	908	0	GTTGTT	1.46484	1.44953
cg0611220	MAD1L1	FOXP3 [T	1873	1878	0	GACAAC	1.46484	1.44953
cg0611220	MAD1L1	FOXP3 [T	1982	1987	0	CACAAC	1.46484	1.44953

cg0611220	MAD1L1	HNF-3alp	341	348	0	TATTTTT	0.09155	0.07727
cg0611220	MAD1L1	HNF-3alp	480	487	0	TATTTTC	0.09155	0.07727
cg0611220	MAD1L1	C/EBPbeta	17	20	0	TTGC	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	115	118	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	228	231	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	244	247	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	268	271	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	306	309	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	338	341	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	534	537	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	565	568	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	577	580	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	596	599	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	611	614	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	648	651	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	664	667	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	760	763	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	904	907	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	961	964	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	995	998	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1132	1135	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1236	1239	0	TTGC	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1332	1335	0	TTGC	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1336	1339	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1340	1343	0	TTGC	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1362	1365	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1411	1414	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1422	1425	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1438	1441	0	TTGC	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1440	1443	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1466	1469	0	TTGT	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1501	1504	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1574	1577	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1598	1601	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1604	1607	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1650	1653	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1693	1696	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1822	1825	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1838	1841	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1874	1877	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1899	1902	0	GCAA	15.625	15.26275
cg0611220	MAD1L1	C/EBPbeta	1983	1986	0	ACAA	15.625	15.26275
cg0611220	MAD1L1	NF-1 [T00	1677	1684	0	TGGGCC	0.12207	0.13147
cg0611220	MAD1L1	YY1 [T00	366	369	0	CCAT	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	380	383	0	ATGG	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	445	448	0	CCAT	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	716	719	0	CCAT	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	764	767	0	ATGG	7.8125	7.79459

cg0611220	MAD1L1	YY1 [T00	912	915	0	CCAT	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	954	957	0	CCAT	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	1056	1059	0	ATGG	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	1126	1129	0	CCAT	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	1146	1149	0	ATGG	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	1178	1181	0	ATGG	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	1519	1522	0	ATGG	7.8125	7.79459
cg0611220	MAD1L1	YY1 [T00	1949	1952	0	CCAT	7.8125	7.79459
cg0611220	MAD1L1	TFII-I [T0	939	944	0	CTTTCC	1.46484	1.48598
cg0611220	MAD1L1	TFII-I [T0	1270	1275	0	CTTTCC	1.46484	1.48598
cg0611220	MAD1L1	STAT4 [T	1240	1245	0	ATTTCC	0.48828	0.46235
cg0611220	MAD1L1	ER-alpha [	398	402	0	TGACC	1.95312	1.99744
cg0611220	MAD1L1	ER-alpha [	1050	1054	0	GGTCA	1.95312	1.99744
cg0611220	MAD1L1	ER-alpha [	1537	1541	0	TGACC	1.95312	1.99744
cg0611220	MAD1L1	ER-alpha [	1619	1623	0	GGTCA	1.95312	1.99744
cg0611220	MAD1L1	ER-alpha [	1744	1748	0	TGACC	1.95312	1.99744
cg0611220	MAD1L1	RXR-alpha	260	266	0	GGGTTC	0.24414	0.24342
cg0611220	MAD1L1	TCF-4E [T	1898	1904	0	AGCAAA	0.12207	0.11933
cg0611220	MAD1L1	GR [T050	175	181	0	TTTTTTG	0.36621	0.33174
cg0611220	MAD1L1	GR [T050	334	340	0	TTTTTTG	0.36621	0.33174
cg0611220	MAD1L1	GR [T050	1502	1508	0	CAAAAA	0.36621	0.33174
cg0611220	MAD1L1	GR [T050	1575	1581	0	CAAAAA	0.36621	0.33174
cg0611220	MAD1L1	GATA-1 [	1405	1410	0	CAGATA	0.97656	0.92541
cg0611220	MAD1L1	GATA-1 [	1426	1431	0	CAGATA	0.97656	0.92541
cg0611220	MAD1L1	T3R-beta1	915	923	0	TCACCA	0.01526	0.01642
cg0611220	MAD1L1	T3R-beta1	1808	1816	0	CGGAGG	0.01526	0.01642
cg0611220	MAD1L1	AP-2alpha	1930	1935	0	GCCTGC	0.97656	1.07867
cg0611220	MAD1L1	IRF-2 [T0	405	410	0	AAGTGA	0.48828	0.46235
cg0611220	MAD1L1	IRF-2 [T0	501	506	0	TCACTT	0.48828	0.46235
cg0611220	MAD1L1	IRF-2 [T0	734	739	0	TCACTT	0.48828	0.46235
cg0611220	MAD1L1	IRF-2 [T0	1582	1587	0	AAGTGA	0.48828	0.46235
cg0372348	MAD1L1	GR-beta [T	315	319	0	AATTT	3.90625	3.51525
cg0372348	MAD1L1	GR-beta [T	390	394	0	AATTT	3.90625	3.51525
cg0372348	MAD1L1	GR-beta [T	400	404	0	ACATT	3.90625	3.51525
cg0372348	MAD1L1	GR-beta [T	422	426	0	AAATT	3.90625	3.51525
cg0372348	MAD1L1	XBP-1 [T	519	524	0	ATGACG	0.97656	0.94838
cg0372348	MAD1L1	XBP-1 [T	1556	1561	0	ATGACT	0.97656	0.94838
cg0372348	MAD1L1	TFIID [T0	908	914	0	TCAAAA	1.09863	0.95175
cg0372348	MAD1L1	TFIID [T0	1123	1129	0	TTAAAA	1.09863	0.95175
cg0372348	MAD1L1	TFIID [T0	1124	1130	0	TAAAAA	1.09863	0.95175
cg0372348	MAD1L1	GR-alpha [	347	351	0	CCTAT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	569	573	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	691	695	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	697	701	0	CCTGT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	736	740	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	741	745	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	863	867	0	CCTAT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	875	879	0	ACAGG	7.8125	7.79817

cg0372348	MAD1L1	GR-alpha [	961	965	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1074	1078	0	CCTGT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1096	1100	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1599	1603	0	CCTGT	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1751	1755	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1761	1765	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	GR-alpha [	1814	1818	0	ACAGG	7.8125	7.79817
cg0372348	MAD1L1	HNF-3alph	714	721	0	TATTTTC	0.09155	0.07727
cg0372348	MAD1L1	C/EBPbeta	298	301	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	313	316	0	ACAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	341	344	0	ACAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	351	354	0	TTGT	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	388	391	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	420	423	0	ACAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	436	439	0	TTGT	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	490	493	0	TTGT	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	637	640	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	762	765	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	870	873	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	927	930	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	1006	1009	0	TTGT	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	1210	1213	0	ACAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	1309	1312	0	TTGC	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	1482	1485	0	TTGC	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	1551	1554	0	ACAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	1671	1674	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	C/EBPbeta	1842	1845	0	GCAA	15.625	15.26275
cg0372348	MAD1L1	YY1 [T00	16	19	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	561	564	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	577	580	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	672	675	0	ATGG	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	678	681	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	680	683	0	ATGG	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	707	710	0	ATGG	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	887	890	0	ATGG	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1022	1025	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1144	1147	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1278	1281	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1392	1395	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1394	1397	0	ATGG	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1409	1412	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1565	1568	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1567	1570	0	ATGG	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1829	1832	0	ATGG	7.8125	7.79459
cg0372348	MAD1L1	YY1 [T00	1982	1985	0	CCAT	7.8125	7.79459
cg0372348	MAD1L1	TFII-I [T0	739	744	0	GGACAG	1.46484	1.48598
cg0372348	MAD1L1	TFII-I [T0	838	843	0	CTTTCC	1.46484	1.48598
cg0372348	MAD1L1	TFII-I [T0	1075	1080	0	CTGTCC	1.46484	1.48598

cg0372348	MAD1L1	TFII-I [T0	1300	1305	0	GGAAAG	1.46484	1.48598
cg0372348	MAD1L1	TFII-I [T0	1759	1764	0	GGACAG	1.46484	1.48598
cg0372348	MAD1L1	STAT4 [T	378	383	0	ATTTCC	0.48828	0.46235
cg0372348	MAD1L1	c-Ets-1 [T	207	213	0	CTTCCTC	0.24414	0.24982
cg0372348	MAD1L1	c-Ets-1 [T	570	576	0	CAGGAA	0.24414	0.24982
cg0372348	MAD1L1	c-Ets-1 [T	1790	1796	0	CAGGAA	0.24414	0.24982
cg0372348	MAD1L1	ER-alpha [	629	633	0	TGACC	1.95312	1.99744
cg0372348	MAD1L1	ER-alpha [	658	662	0	TGACC	1.95312	1.99744
cg0372348	MAD1L1	ER-alpha [	1038	1042	0	TGACC	1.95312	1.99744
cg0372348	MAD1L1	ER-alpha [	1357	1361	0	TGACC	1.95312	1.99744
cg0372348	MAD1L1	ER-alpha [	1654	1658	0	GGTCA	1.95312	1.99744
cg0372348	MAD1L1	GR [T050	909	915	0	CAAAAA	0.36621	0.33174
cg0372348	MAD1L1	c-Myc [T0	246	251	0	CACGTG	0.48828	0.51196
cg0372348	MAD1L1	c-Myc [T0	1910	1915	0	CACGTG	0.48828	0.51196
cg0372348	MAD1L1	Pax-5 [T0	158	164	0	CCTGCC	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	682	688	0	GGGCCT	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	692	698	0	CAGGCC	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	1062	1068	0	CCGGCC	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	1291	1297	0	GGGCAG	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	1313	1319	0	CCAGCC	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	1402	1408	0	GGGCAG	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	1832	1838	0	GGGCAG	1.09863	1.24633
cg0372348	MAD1L1	Pax-5 [T0	1895	1901	0	CCAGCC	1.09863	1.24633
cg0372348	MAD1L1	p53 [T006	158	164	0	CCTGCC	0.36621	0.40082
cg0372348	MAD1L1	p53 [T006	1291	1297	0	GGGCAG	0.36621	0.40082
cg0372348	MAD1L1	p53 [T006	1402	1408	0	GGGCAG	0.36621	0.40082
cg0372348	MAD1L1	p53 [T006	1832	1838	0	GGGCAG	0.36621	0.40082
cg0372348	MAD1L1	AP-2alpha	119	124	0	GCCTGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	965	970	0	GCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	1180	1185	0	GCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	1404	1409	0	GCAGGC	0.97656	1.07867
cg0372348	MAD1L1	AP-2alpha	1696	1701	0	GCCTGC	0.97656	1.07867
cg0372348	MAD1L1	WT1 [T00	1848	1856	0	CGCCCC	0.00763	0.00958
cg0372348	MAD1L1	GCF [T00	1690	1698	0	GCGCCG	0.09155	0.10999
cg0372348	MAD1L1	Elk-1 [T00	207	215	0	CTTCCTC	0.06104	0.06399
cg1662289	MAFK	c-Ets-1 [T	961	967	9.969337	TGGGAA	0.24414	0.2459
cg1662289	MAFK	LEF-1 [T0	1829	1836	9.937995	CTTTGG	0.12207	0.12154
cg1662289	MAFK	STAT1bet	1081	1090	9.807397	ACATGG	0.14877	0.1495
cg1662289	MAFK	XBP-1 [T	336	341	9.789909	CGACAT	1.95312	1.95208
cg1662289	MAFK	XBP-1 [T	1009	1014	9.789909	ATGTCG	1.95312	1.95208
cg1662289	MAFK	XBP-1 [T	1704	1709	9.789909	ATGTCT	1.95312	1.95208
cg1662289	MAFK	XBP-1 [T	1792	1797	9.789909	CGCCAT	1.95312	1.95208
cg1662289	MAFK	c-Jun [T00	515	521	9.717135	TGACCT	0.73242	0.73031
cg1662289	MAFK	c-Jun [T00	1718	1724	9.717135	TGACCT	0.73242	0.73031
cg1662289	MAFK	RAR-beta	415	424	9.622793	TGGGTT	0.21362	0.21243
cg1662289	MAFK	NF-AT2 [	94	103	9.5654	CACGCT	0.04578	0.04604
cg1662289	MAFK	Pax-5 [T0	41	47	9.552105	GTAGCC	1.46484	1.43083
cg1662289	MAFK	Pax-5 [T0	73	79	9.552105	GGGCGT	1.46484	1.43083

cg1662289	MAFK	Pax-5 [T0	667	673	9.552105	GTAGCC	1.46484	1.43083
cg1662289	MAFK	Pax-5 [T0	716	722	9.552105	GGGCGC	1.46484	1.43083
cg1662289	MAFK	Pax-5 [T0	717	723	9.552105	GGCGCC	1.46484	1.43083
cg1662289	MAFK	Pax-5 [T0	879	885	9.552105	TCCGCC	1.46484	1.43083
cg1662289	MAFK	Pax-5 [T0	1892	1898	9.552105	GGGCGG	1.46484	1.43083
cg1662289	MAFK	Pax-5 [T0	1938	1944	9.552105	GGGCGG	1.46484	1.43083
cg1662289	MAFK	Pax-5 [T0	1988	1994	9.552105	GCCGCC	1.46484	1.43083
cg1662289	MAFK	TFIID [T0	292	298	9.552105	TTCCAA	1.46484	1.48472
cg1662289	MAFK	TFIID [T0	1092	1098	9.552105	TTTCTCA	1.46484	1.48472
cg1662289	MAFK	NF-1 [T00	1520	1527	9.535536	CTGACC	0.73242	0.73053
cg1662289	MAFK	NF-1 [T00	1587	1594	9.513281	TTGGGG	0.73242	0.73053
cg1662289	MAFK	TFII-I [T0	290	295	9.512894	CCTTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	358	363	9.512894	GGATTT	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	399	404	9.512894	CCATCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	404	409	9.512894	CCATCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	450	455	9.512894	CCGTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	853	858	9.512894	CGGTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	870	875	9.512894	CCTTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	876	881	9.512894	TTTTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1085	1090	9.512894	GGAAAA	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1219	1224	9.512894	CCGTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1228	1233	9.512894	GGACCG	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1241	1246	9.512894	CCATCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1410	1415	9.512894	GGATTT	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1470	1475	9.512894	GGACGG	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1528	1533	9.512894	GGACAC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1651	1656	9.512894	CCGTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1731	1736	9.512894	GGATCG	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1752	1757	9.512894	GTTTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1780	1785	9.512894	CGGTCC	7.32422	7.29728
cg1662289	MAFK	TFII-I [T0	1883	1888	9.512894	GGACGG	7.32422	7.29728
cg1662289	MAFK	FOXP3 [T	242	247	9.512894	GTTGCT	7.32422	7.35678
cg1662289	MAFK	FOXP3 [T	675	680	9.512894	GGCAAC	7.32422	7.35678
cg1662289	MAFK	FOXP3 [T	980	985	9.512894	GTAAAC	7.32422	7.35678
cg1662289	MAFK	FOXP3 [T	1364	1369	9.512894	GTTGCG	7.32422	7.35678
cg1662289	MAFK	FOXP3 [T	1798	1803	9.512894	GGCAAC	7.32422	7.35678
cg1662289	MAFK	c-Jun [T00	304	310	9.442241	GCTGTC	0.73242	0.73031
cg1662289	MAFK	EBF [T05	1433	1443	9.441272	GGCCCA	0.06866	0.06676
cg1662289	MAFK	NFI/CTF [	1280	1287	9.352332	GGCCTT	0.54932	0.54821
cg1662289	MAFK	NFI/CTF [	1524	1531	9.352332	CCAAGG	0.54932	0.54821
cg1662289	MAFK	NFI/CTF [	1785	1792	9.352332	CCAAGG	0.54932	0.54821
cg1662289	MAFK	c-Ets-1 [T	1567	1573	9.276861	TGGGAA	0.36621	0.36441
cg1662289	MAFK	ATF [T00	828	839	9.257019	ACACGT	0.07725	0.07724
cg1662289	MAFK	ATF [T00	1027	1038	9.257019	GCACTG	0.07725	0.07724
cg1662289	MAFK	ATF [T00	1255	1266	9.257019	CTACGT	0.07725	0.07724
cg1662289	MAFK	USF2 [T0	27	36	9.056375	CAGGTG	0.1545	0.15287
cg1662289	MAFK	E2F-1 [T0	1900	1907	9.028527	GCGGGG	0.27466	0.26875
cg1662289	MAFK	NF-AT2 [	780	789	9.016873	GGAAAG	0.05341	0.05386

cg1662289	MAFK	c-Jun [T00	829	835	9.013496	CACGTC	0.61035	0.61059
cg1662289	MAFK	c-Jun [T00	1031	1037	9.013496	TGACGT	0.61035	0.61059
cg1662289	MAFK	c-Jun [T00	1079	1085	9.013496	TGACAT	0.61035	0.61059
cg1662289	MAFK	GR [T050	295	301	8.971049	CAAAAG	0.61035	0.61632
cg1662289	MAFK	GR [T050	1583	1589	8.971049	GTATTT	0.61035	0.61632
cg1662289	MAFK	Elk-1 [T00	1048	1056	8.931691	AGCTGG	0.24414	0.24034
cg1662289	MAFK	IRF-1 [T0	877	885	8.916359	TTTCCG	0.09155	0.09147
cg1662289	MAFK	p53 [T006	605	611	8.912104	AGGGCC	0.12207	0.11837
cg1662289	MAFK	T3R-beta1	833	841	8.885459	TCACCG	0.2594	0.25766
cg1662289	MAFK	ETF [T002	1068	1078	8.876947	GCCCCT	0.02384	0.02303
cg1662289	MAFK	c-Jun [T00	224	230	8.807683	GTCGTC	0.61035	0.61059
cg1662289	MAFK	c-Jun [T00	1759	1765	8.807683	TGACAA	0.61035	0.61059
cg1662289	MAFK	NF-1 [T00	1284	1291	8.790071	TTGGCA	0.24414	0.24467
cg1662289	MAFK	XBP-1 [T	1094	1099	8.75604	TCTCAT	2.92969	2.9674
cg1662289	MAFK	XBP-1 [T	1813	1818	8.75604	GCTCAT	2.92969	2.9674
cg1662289	MAFK	XBP-1 [T	1842	1847	8.75604	TTTCAT	2.92969	2.9674
cg1662289	MAFK	STAT1bet	98	107	8.695301	CTTTCC	0.22316	0.22446
cg1662289	MAFK	STAT1bet	776	785	8.695301	TAGTGG	0.22316	0.22446
cg1662289	MAFK	RAR-beta	637	646	8.578216	GGGGTT	0.26703	0.26657
cg1662289	MAFK	RAR-beta	204	213	8.55975	ACAAAA	0.26703	0.26657
cg1662289	MAFK	NF-AT1 [	873	881	8.532897	TCCTTTT	0.10681	0.10725
cg1662289	MAFK	USF2 [T0	617	626	8.532138	CAGGTG	0.103	0.10183
cg1662289	MAFK	c-Myb [T0	238	245	8.443873	ATCAGT	0.30518	0.30924
cg1662289	MAFK	E2F-1 [T0	1483	1490	8.336446	TCACCC	0.15259	0.14963
cg1662289	MAFK	GR-alpha [	0	4	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	51	55	8.281568	CCTTG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	178	182	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	290	294	8.281568	CCTTC	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	386	390	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	496	500	8.281568	CCTCG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	524	528	8.281568	CAAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	527	531	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	625	629	8.281568	CCTCG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	680	684	8.281568	CCTTG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	686	690	8.281568	CCTCC	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	709	713	8.281568	CCTCC	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	738	742	8.281568	CCTCC	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	763	767	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	870	874	8.281568	CCTTC	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	934	938	8.281568	CCTTG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	946	950	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1071	1075	8.281568	CCTCC	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1141	1145	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1196	1200	8.281568	GAAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1282	1286	8.281568	CCTTG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1387	1391	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1399	1403	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1406	1410	8.281568	GGAGG	7.8125	7.72956

cg1662289	MAFK	GR-alpha [	1421	1425	8.281568	CGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1447	1451	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1467	1471	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1513	1517	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1525	1529	8.281568	CAAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1639	1643	8.281568	CCTTC	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1697	1701	8.281568	CCTCG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1786	1790	8.281568	CAAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1808	1812	8.281568	GGAGG	7.8125	7.72956
cg1662289	MAFK	GR-alpha [	1955	1959	8.281568	CCTCC	7.8125	7.72956
cg1662289	MAFK	c-Jun [T00	683	689	8.242207	TGACCT	0.48828	0.49076
cg1662289	MAFK	p53 [T006	606	612	8.208781	GGGCCC	0.48828	0.47377
cg1662289	MAFK	p53 [T006	917	923	8.208781	GGGGCC	0.48828	0.47377
cg1662289	MAFK	p53 [T006	1151	1157	8.208781	GGGCCC	0.48828	0.47377
cg1662289	MAFK	p53 [T006	1375	1381	8.208781	GGGGCC	0.48828	0.47377
cg1662289	MAFK	p53 [T006	1376	1382	8.208781	GGGCCC	0.48828	0.47377
cg1662289	MAFK	ENKTF-1	168	175	8.19852	TGGCGG	0.73242	0.71737
cg1662289	MAFK	ENKTF-1	442	449	8.19852	TGGCTG	0.73242	0.71737
cg1662289	MAFK	ENKTF-1	1285	1292	8.19852	TGGCAG	0.73242	0.71737
cg1662289	MAFK	ENKTF-1	1461	1468	8.19852	TGGCAG	0.73242	0.71737
cg1662289	MAFK	ENKTF-1	1789	1796	8.19852	GGTCGC	0.73242	0.71737
cg1662289	MAFK	ENKTF-1	1832	1839	8.19852	TGGCTG	0.73242	0.71737
cg1662289	MAFK	ENKTF-1	1911	1918	8.19852	TCCCGC	0.73242	0.71737
cg1662289	MAFK	ENKTF-1	1968	1975	8.19852	TGGCTG	0.73242	0.71737
cg1662289	MAFK	NF-1 [T00	1740	1747	8.191058	TTGGGC	0.24414	0.24409
cg1662289	MAFK	p53 [T006	1262	1268	8.162057	AGCGCC	0.48828	0.47377
cg1662289	MAFK	GR-alpha [	26	30	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	47	51	8.073878	CCTGC	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	89	93	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	105	109	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	137	141	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	175	179	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	471	475	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	488	492	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	518	522	8.073878	CCTGC	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	538	542	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	567	571	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	576	580	8.073878	CCTGC	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	586	590	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	616	620	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	672	676	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	689	693	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	712	716	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	807	811	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	922	926	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1123	1127	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1182	1186	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1203	1207	8.073878	CCTGG	7.8125	7.72238

cg1662289	MAFK	GR-alpha [	1214	1218	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1287	1291	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1309	1313	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1315	1319	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1391	1395	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1430	1434	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1436	1440	8.073878	CCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1454	1458	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1463	1467	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1689	1693	8.073878	CCTGC	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1935	1939	8.073878	GCAGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1959	1963	8.073878	CCTGG	7.8125	7.72238
cg1662289	MAFK	GR-alpha [	1985	1989	8.073878	CCTGC	7.8125	7.72238
cg1662289	MAFK	Pax-5 [T0	54	60	8.014558	TGGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	170	176	8.014558	GCGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	561	567	8.014558	GGGCCG	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	571	577	8.014558	GGAGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	606	612	8.014558	GGGCCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	649	655	8.014558	GGGCAC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	754	760	8.014558	GGGCAT	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	801	807	8.014558	TCTGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	909	915	8.014558	TGGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	917	923	8.014558	GGGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	918	924	8.014558	GGGCCA	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	947	953	8.014558	GAGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1058	1064	8.014558	GGTGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1065	1071	8.014558	GCGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1150	1156	8.014558	TGGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1151	1157	8.014558	GGGCCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1206	1212	8.014558	GGAGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1291	1297	8.014558	GGGCAG	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1336	1342	8.014558	GCGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1375	1381	8.014558	GGGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1376	1382	8.014558	GGGCCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1415	1421	8.014558	TGGGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1424	1430	8.014558	GGGCTC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1497	1503	8.014558	GATGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1628	1634	8.014558	GCTGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1642	1648	8.014558	TCTGCC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1742	1748	8.014558	GGGCTT	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1811	1817	8.014558	GGGCTC	2.19727	2.14502
cg1662289	MAFK	Pax-5 [T0	1973	1979	8.014558	GCGGCC	2.19727	2.14502
cg1662289	MAFK	TFIID [T0	202	208	8.014558	TCACAA	2.19727	2.24348
cg1662289	MAFK	TFIID [T0	248	254	8.014558	TTACAA	2.19727	2.24348
cg1662289	MAFK	USF2 [T0	1208	1217	8.007902	AGCCCA	0.01717	0.01695
cg1662289	MAFK	MAZ [T00	1068	1080	7.990706	GCCCCT	0.00915	0.009
cg1662289	MAFK	AR [T000	1501	1509	7.97308	CCCATG	0.19836	0.19634
cg1662289	MAFK	ETF [T002	574	584	7.870358	GCCCTG	0.07153	0.06862

cg1662289	MAFK	ETF [T002	911	921	7.870358	GGCCCG	0.07153	0.06862
cg1662289	MAFK	ETF [T002	1061	1071	7.870358	GCCCGC	0.07153	0.06862
cg1662289	MAFK	ETF [T002	1369	1379	7.870358	GGGGGT	0.07153	0.06862
cg1662289	MAFK	ETF [T002	1976	1986	7.870358	GCCCCC	0.07153	0.06862
cg1662289	MAFK	c-Ets-2 [T	419	427	7.84116	TTCCTG	0.32043	0.32298
cg1662289	MAFK	p53 [T006	571	577	7.833758	GGAGCC	0.48828	0.47377
cg1662289	MAFK	p53 [T006	1206	1212	7.833758	GGAGCC	0.48828	0.47377
cg1662289	MAFK	p53 [T006	1424	1430	7.833758	GGGCTC	0.48828	0.47377
cg1662289	MAFK	RXR-alpha	62	68	7.815913	GGGTAG	0.24414	0.24104
cg1662289	MAFK	RXR-alpha	703	709	7.815913	GCCACC	0.24414	0.24104
cg1662289	MAFK	T3R-beta1	996	1004	7.813363	TCACCG	0.27466	0.27236
cg1662289	MAFK	T3R-beta1	1483	1491	7.813363	TCACCC	0.27466	0.27236
cg1662289	MAFK	T3R-beta1	1171	1179	7.79407	TCACCC	0.27466	0.27236
cg1662289	MAFK	c-Ets-2 [T	1561	1569	7.76635	TTCCTGT	0.32043	0.32298
cg1662289	MAFK	p53 [T006	447	453	7.641867	GGGCCG	0.73242	0.7186
cg1662289	MAFK	NFI/CTF [	294	301	7.587343	CCAAAA	0.36621	0.36674
cg1662289	MAFK	GR [T050	430	436	7.527031	AGCTTTC	1.83105	1.86007
cg1662289	MAFK	GR [T050	1827	1833	7.527031	TGCTTTC	1.83105	1.86007
cg1662289	MAFK	RAR-beta	1836	1845	7.459774	TGGGTTT	0.24414	0.24343
cg1662289	MAFK	p53 [T006	716	722	7.458735	GGGCGC	0.73242	0.7186
cg1662289	MAFK	p53 [T006	717	723	7.458735	GGCGCC	0.73242	0.7186
cg1662289	MAFK	E2F-1 [T0	1985	1992	7.336545	CCTGCC	0.45776	0.44878
cg1662289	MAFK	IRF-1 [T0	776	784	7.299819	TAGTGG	0.14496	0.14449
cg1662289	MAFK	SRY [T00	432	440	7.175614	CTTTGCT	0.30518	0.30739
cg1662289	MAFK	XBP-1 [T	592	597	7.172312	CCTCAT	2.92969	2.97018
cg1662289	MAFK	XBP-1 [T	1495	1500	7.172312	ATGATG	2.92969	2.97018
cg1662289	MAFK	XBP-1 [T	1846	1851	7.172312	ATGAAT	2.92969	2.97018
cg1662289	MAFK	XBP-1 [T	1850	1855	7.172312	ATGATT	2.92969	2.97018
cg1662289	MAFK	p53 [T006	54	60	7.153797	TGGGCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	909	915	7.153797	TGGGCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	918	924	7.153797	GGGCCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	1150	1156	7.153797	TGGGCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	1415	1421	7.153797	TGGGCC	1.09863	1.07125
cg1662289	MAFK	AR [T000	1614	1622	7.107265	CCCCTGT	0.23651	0.23551
cg1662289	MAFK	c-Jun [T00	1683	1689	7.096776	TGACTG	0.73242	0.73173
cg1662289	MAFK	ATF-2 [T0	1254	1263	7.05714	TCTACGT	0.01907	0.01886
cg1662289	MAFK	NFI/CTF [	637	644	7.014249	GGGGTT	0.73242	0.73214
cg1662289	MAFK	HNF-3alph	229	236	7.000129	CATTTTT	0.82397	0.84946
cg1662289	MAFK	EBF [T05	172	182	6.976098	GGCCCTC	0.03052	0.02964
cg1662289	MAFK	NF-1 [T00	641	648	6.948522	TTGGAG	0.48828	0.4856
cg1662289	MAFK	c-Ets-1 [T	99	105	6.943262	TTTCCCC	0.73242	0.73099
cg1662289	MAFK	ENKTF-1	388	395	6.942764	AGGCGC	1.46484	1.44228
cg1662289	MAFK	ENKTF-1	581	588	6.942764	GTCCGC	1.46484	1.44228
cg1662289	MAFK	ENKTF-1	816	823	6.942764	TGGCCG	1.46484	1.44228
cg1662289	MAFK	ENKTF-1	1775	1782	6.942764	TGGCTC	1.46484	1.44228
cg1662289	MAFK	p53 [T006	170	176	6.938545	GCGGCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	561	567	6.938545	GGGCCG	1.09863	1.07125
cg1662289	MAFK	p53 [T006	947	953	6.938545	GAGGCC	1.09863	1.07125

cg1662289	MAFK	p53 [T006	1065	1071	6.938545	GCGGCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	1336	1342	6.938545	GCGGCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	1973	1979	6.938545	GCGGCC	1.09863	1.07125
cg1662289	MAFK	VDR [T00	200	208	6.925682	GTTCAC	0.42725	0.43062
cg1662289	MAFK	STAT1bet	1752	1761	6.908963	GTTTCC	0.103	0.10372
cg1662289	MAFK	EBF [T05	1264	1274	6.87365	CGCCCT	0.03052	0.02964
cg1662289	MAFK	c-Jun [T00	1521	1527	6.856451	TGACCA	0.73242	0.73173
cg1662289	MAFK	PEA3 [T0	107	115	6.824411	TGGATG	0.22888	0.22933
cg1662289	MAFK	PEA3 [T0	1239	1247	6.824411	TGCCAT	0.22888	0.22933
cg1662289	MAFK	NF-AT1 [	780	788	6.799037	GGAAAG	0.15259	0.1548
cg1662289	MAFK	NFI/CTF [	437	444	6.786076	CTGCTT	0.73242	0.73214
cg1662289	MAFK	p53 [T006	1811	1817	6.778774	GGGCTC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	41	47	6.775228	GTAGCC	1.09863	1.07125
cg1662289	MAFK	p53 [T006	667	673	6.775228	GTAGCC	1.09863	1.07125
cg1662289	MAFK	ATF3 [T0	1864	1871	6.744803	TGACAC	0.27466	0.27656
cg1662289	MAFK	POU2F2 (	244	254	6.735173	TGCTTTA	0.04292	0.04408
cg1662289	MAFK	NF-1 [T00	519	526	6.722386	CTGCCC	0.24414	0.24147
cg1662289	MAFK	NF-kappa	1942	1952	6.69019	GGCGGC	0.03052	0.02976
cg1662289	MAFK	TFII-I [T0	1597	1602	6.581441	GGAGTG	0.97656	0.97366
cg1662289	MAFK	RXR-alph	112	118	6.563693	GACACC	0.24414	0.2434
cg1662289	MAFK	RXR-alph	1529	1535	6.563693	GACACC	0.24414	0.2434
cg1662289	MAFK	p53 [T006	1742	1748	6.563521	GGGCTT	0.48828	0.47541
cg1662289	MAFK	XBP-1 [T	754	759	6.478682	GGGCAT	0.97656	0.97062
cg1662289	MAFK	XBP-1 [T	809	814	6.478682	TGGCAT	0.97656	0.97062
cg1662289	MAFK	XBP-1 [T	1498	1503	6.478682	ATGCCC	0.97656	0.97062
cg1662289	MAFK	E2F-1 [T0	646	653	6.47044	GCGGGG	0.12207	0.12031
cg1662289	MAFK	c-Jun [T00	696	702	6.462218	GTAGTC	0.61035	0.60769
cg1662289	MAFK	RAR-beta	1353	1362	6.452127	GGGGTT	0.18311	0.183
cg1662289	MAFK	NF-kappa	1216	1226	6.434233	TGGCCG	0.03052	0.02976
cg1662289	MAFK	ATF-2 [T0	1030	1039	6.398573	CTGACG	0.05722	0.05698
cg1662289	MAFK	c-Ets-1 [T	1083	1089	6.295602	ATGGAA	0.48828	0.48798
cg1662289	MAFK	c-Ets-1 [T	1753	1759	6.295602	TTTCCAT	0.48828	0.48798
cg1662289	MAFK	GR-alpha [	119	123	6.263098	TAAGG	3.90625	3.91061
cg1662289	MAFK	GR-alpha [	188	192	6.263098	TGAGG	3.90625	3.91061
cg1662289	MAFK	GR-alpha [	347	351	6.263098	TAAGG	3.90625	3.91061
cg1662289	MAFK	GR-alpha [	592	596	6.263098	CCTCA	3.90625	3.91061
cg1662289	MAFK	GR-alpha [	1175	1179	6.263098	CCTCA	3.90625	3.91061
cg1662289	MAFK	GR-alpha [	1880	1884	6.263098	TGAGG	3.90625	3.91061
cg1662289	MAFK	GR-alpha [	1994	1998	6.263098	CCTCA	3.90625	3.91061
cg1662289	MAFK	NF-AT1 [	1749	1758	6.201624	TCGGTTT	0.03815	0.03846
cg1662289	MAFK	p53 [T006	73	79	6.188498	GGGCGT	0.61035	0.594
cg1662289	MAFK	p53 [T006	1892	1898	6.188498	GGGCGG	0.61035	0.594
cg1662289	MAFK	p53 [T006	1938	1944	6.188498	GGGCGG	0.61035	0.594
cg1662289	MAFK	p53 [T006	1988	1994	6.188498	GCCGCC	0.61035	0.594
cg1662289	MAFK	c-Ets-1 [T	778	784	6.167515	GTGGAA	0.36621	0.36731
cg1662289	MAFK	NF-kappa	1445	1455	6.144028	GGGGAG	0.04053	0.03971
cg1662289	MAFK	RXR-alph	83	89	6.119461	GCGACC	0.73242	0.72249
cg1662289	MAFK	GR-alpha [	117	121	6.055408	CCTAA	3.90625	3.9065

cg1662289	MAFK	GR-alpha [	216	220	6.055408	TTAGG	3.90625	3.9065
cg1662289	MAFK	GR-alpha [	341	345	6.055408	TTAGG	3.90625	3.9065
cg1662289	MAFK	GR-alpha [	421	425	6.055408	CCTGA	3.90625	3.9065
cg1662289	MAFK	GR-alpha [	1267	1271	6.055408	CCTGA	3.90625	3.9065
cg1662289	MAFK	GR-alpha [	1716	1720	6.055408	CCTGA	3.90625	3.9065
cg1662289	MAFK	GR-alpha [	1721	1725	6.055408	CCTGA	3.90625	3.9065
cg1662289	MAFK	GR-alpha [	1728	1732	6.055408	TCAGG	3.90625	3.9065
cg1662289	MAFK	AR [T000	855	863	5.953985	GTCCTG	0.24414	0.24229
cg1662289	MAFK	RXR-alph	1170	1176	5.937582	GTCACC	0.73242	0.72249
cg1662289	MAFK	RXR-alph	1482	1488	5.937582	GTCACC	0.73242	0.72249
cg1662289	MAFK	GCF [T00	970	978	5.917256	GCGCGG	0.64087	0.6219
cg1662289	MAFK	GCF [T00	1258	1266	5.917256	CGTCAG	0.64087	0.6219
cg1662289	MAFK	STAT4 [T	290	295	5.882353	CCTTCC	0.48828	0.48408
cg1662289	MAFK	STAT4 [T	870	875	5.882353	CCTTCC	0.48828	0.48408
cg1662289	MAFK	PXR-1:RX	1610	1617	5.850108	TGAACC	0.06104	0.06035
cg1662289	MAFK	VDR [T00	1606	1614	5.771401	GCTGTG	0.42725	0.42999
cg1662289	MAFK	HNF-1A [	345	352	5.754274	GTTAAG	0.24414	0.24409
cg1662289	MAFK	ENKTF-1	133	140	5.687009	TGGCCC	0.73242	0.7249
cg1662289	MAFK	ENKTF-1	1246	1253	5.687009	CTGTGC	0.73242	0.7249
cg1662289	MAFK	ENKTF-1	1279	1286	5.687009	TGGCCT	0.73242	0.7249
cg1662289	MAFK	ENKTF-1	1432	1439	5.687009	TGGCCC	0.73242	0.7249
cg1662289	MAFK	AR [T000	1528	1536	5.644986	GGACAC	0.05341	0.05229
cg1662289	MAFK	c-Jun [T00	745	751	5.590308	AGTGTC	0.48828	0.48665
cg1662289	MAFK	IRF-1 [T0	1753	1761	5.564062	TTTCCA	0.22888	0.23087
cg1662289	MAFK	NFI/CTF [	6	13	5.558661	GAGCTT	0.54932	0.55038
cg1662289	MAFK	T3R-beta1	1177	1185	5.553412	TCACCC	0.21362	0.21287
cg1662289	MAFK	Pax-5 [T0	1262	1268	5.544826	AGCGCC	0.73242	0.72046
cg1662289	MAFK	p53 [T006	55	61	5.39549	GGGCCC	0.61035	0.59991
cg1662289	MAFK	p53 [T006	910	916	5.39549	GGGCCC	0.61035	0.59991
cg1662289	MAFK	p53 [T006	1416	1422	5.39549	GGGCCC	0.61035	0.59991
cg1662289	MAFK	RAR-beta	1608	1617	5.389083	TGTGAA	0.15259	0.15189
cg1662289	MAFK	PPAR-alp	606	616	5.285833	GGGCCC	0.03529	0.03451
cg1662289	MAFK	RXR-alph	141	147	5.271235	GGGTGG	0.61035	0.6044
cg1662289	MAFK	RXR-alph	941	947	5.271235	GGGTGG	0.61035	0.6044
cg1662289	MAFK	RXR-alph	1362	1368	5.271235	GGGTTG	0.61035	0.6044
cg1662289	MAFK	RXR-alph	1371	1377	5.271235	GGGTGG	0.61035	0.6044
cg1662289	MAFK	GR [T050	205	211	5.207533	CAAAAC	0.24414	0.24606
cg1662289	MAFK	AhR:Arnt	653	662	5.196125	ACAGGC	0.00572	0.00556
cg1662289	MAFK	c-Jun [T00	1724	1730	5.193102	GAAGTC	0.61035	0.61057
cg1662289	MAFK	p53 [T006	879	885	5.133514	TCCGCC	0.48828	0.47747
cg1662289	MAFK	RXR-alph	1602	1608	5.089356	GGGTGC	0.48828	0.484
cg1662289	MAFK	USF2 [T0	1325	1334	5.052423	GTCTCA	0.103	0.10178
cg1662289	MAFK	GR-beta [	358	362	5.042296	GGATT	3.90625	3.95351
cg1662289	MAFK	GR-beta [	1410	1414	5.042296	GGATT	3.90625	3.95351
cg1662289	MAFK	GR-beta [	1583	1587	5.042296	GTATT	3.90625	3.95351
cg1662289	MAFK	E2F-1 [T0	1909	1916	5.042045	ACTCCC	0.18311	0.17901
cg1662289	MAFK	c-Ets-1 [T	291	297	5.038739	CTTCCA	0.48828	0.49031
cg1662289	MAFK	p53 [T006	820	826	5.020467	CGAGCC	0.48828	0.47747

cg1662289	MAFK	c-Jun [T00	111	117	5.000337	TGACAC	0.61035	0.61057
cg1662289	MAFK	NF-AT2 [	1085	1094	4.979362	GGAAAA	0.03815	0.03879
cg1662289	MAFK	IRF-1 [T0	99	107	4.968836	TTTCCC	0.1297	0.1302
cg1662289	MAFK	ATF3 [T0	1255	1262	4.941398	CTACGT	0.09155	0.09183
cg1662289	MAFK	XBP-1 [T	765	770	4.894955	AGGCAT	0.97656	0.96979
cg1662289	MAFK	XBP-1 [T	1115	1120	4.894955	CGGCAT	0.97656	0.96979
cg1662289	MAFK	XBP-1 [T	1817	1822	4.894955	ATGCCG	0.97656	0.96979
cg1662289	MAFK	PPAR-alp	1431	1441	4.88658	CTGGCC	0.01717	0.01681
cg1662289	MAFK	c-Jun [T00	1256	1262	4.883696	TACGTC	0.61035	0.61057
cg1662289	MAFK	NF-1 [T00	1781	1788	4.880836	GGTCCC	0.24414	0.24398
cg1662289	MAFK	RXR-alph	1590	1596	4.86724	GGGTAT	0.48828	0.484
cg1662289	MAFK	Sp1 [T007	877	886	4.81072	TTTCCG	0.06485	0.06365
cg1662289	MAFK	TFII-I [T0	286	291	4.756447	ATGTCC	2.92969	2.93695
cg1662289	MAFK	TFII-I [T0	963	968	4.756447	GGAATG	2.92969	2.93695
cg1662289	MAFK	TFII-I [T0	1504	1509	4.756447	ATGTCC	2.92969	2.93695
cg1662289	MAFK	FOXP3 [T	205	210	4.756447	CAAAAC	2.92969	2.96063
cg1662289	MAFK	FOXP3 [T	270	275	4.756447	CAAAAC	2.92969	2.96063
cg1662289	MAFK	FOXP3 [T	1681	1686	4.756447	GTTGAC	2.92969	2.96063
cg1662289	MAFK	FOXP3 [T	1839	1844	4.756447	GTTTTT	2.92969	2.96063
cg1662289	MAFK	c-Myb [T0	196	203	4.754782	GACAGT	0.30518	0.30568
cg1662289	MAFK	c-Ets-1 [T	690	696	4.654478	CTGGAA	0.85449	0.85764
cg1662289	MAFK	c-Ets-1 [T	1050	1056	4.654478	CTGGAA	0.85449	0.85764
cg1662289	MAFK	VDR [T00	792	800	4.617121	ACGCTG	0.37384	0.37445
cg1662289	MAFK	c-Ets-1 [T	877	883	4.616023	TTTCCG	0.85449	0.85764
cg1662289	MAFK	E2F-1 [T0	451	458	4.545253	CGTCCC	0.15259	0.14941
cg1662289	MAFK	T3R-beta1	986	994	4.481316	ATCTGG	0.27466	0.27551
cg1662289	MAFK	RXR-alph	1402	1408	4.423008	GGGTGG	0.24414	0.24292
cg1662289	MAFK	AP-2alpha	119	124	4.422424	TAAGGC	0.97656	0.96979
cg1662289	MAFK	AP-2alpha	347	352	4.422424	TAAGGC	0.97656	0.96979
cg1662289	MAFK	STAT4 [T	492	497	4.411765	GCTTCC	1.95312	1.94235
cg1662289	MAFK	STAT4 [T	963	968	4.411765	GGAATG	1.95312	1.94235
cg1662289	MAFK	STAT4 [T	1052	1057	4.411765	GGAAGC	1.95312	1.94235
cg1662289	MAFK	p53 [T006	132	138	4.33696	CTGGCC	0.24414	0.23584
cg1662289	MAFK	p53 [T006	1431	1437	4.33696	CTGGCC	0.24414	0.23584
cg1662289	MAFK	CREB [T0	1254	1262	4.299974	TCTACG	0.04578	0.04561
cg1662289	MAFK	RAR-beta	1674	1683	4.289108	TGGGTT	0.14496	0.1447
cg1662289	MAFK	GR-beta [	362	366	4.201913	TTATT	7.8125	7.94607
cg1662289	MAFK	GR-beta [	1851	1855	4.201913	TGATT	7.8125	7.94607
cg1662289	MAFK	p53 [T006	1058	1064	4.083527	GGTGCC	0.73242	0.71379
cg1662289	MAFK	NF-AT1 [	95	103	4.056854	ACGCTT	0.07629	0.07734
cg1662289	MAFK	RXR-alph	954	960	4.019014	GGGTGT	0.97656	0.9671
cg1662289	MAFK	RXR-alph	1439	1445	4.019014	GGGTGT	0.97656	0.9671
cg1662289	MAFK	Pax-5 [T0	219	225	4.007279	GGGCAG	1.09863	1.07975
cg1662289	MAFK	Pax-5 [T0	447	453	4.007279	GGGCCG	1.09863	1.07975
cg1662289	MAFK	Pax-5 [T0	605	611	4.007279	AGGGCC	1.09863	1.07975
cg1662289	MAFK	Pax-5 [T0	903	909	4.007279	GGGCAG	1.09863	1.07975
cg1662289	MAFK	TFIID [T0	247	253	4.007279	TTTACA	1.09863	1.13456
cg1662289	MAFK	AP-2alpha	50	55	3.970052	GCCTTG	0.97656	0.96469

cg1662289	MAFK	AP-2alpha	1281	1286	3.970052	GCCTTG	0.97656	0.96469
cg1662289	MAFK	GR [T050	270	276	3.763516	CAAAAC	0.73242	0.74251
cg1662289	MAFK	p53 [T006	1394	1400	3.750231	GGGCTG	0.73242	0.71379
cg1662289	MAFK	p53 [T006	1457	1463	3.750231	GGGCTG	0.73242	0.71379
cg1662289	MAFK	p53 [T006	1771	1777	3.750231	GGGCTG	0.73242	0.71379
cg1662289	MAFK	AP-2alpha	1638	1643	3.743866	GCCTTC	0.48828	0.48238
cg1662289	MAFK	CREB [T0	827	835	3.729071	CACACG	0.10681	0.10641
cg1662289	MAFK	Sp1 [T007	1986	1995	3.623596	CTGCCG	0.07439	0.07186
cg1662289	MAFK	CREB [T0	1031	1039	3.577247	TGACGT	0.10681	0.10641
cg1662289	MAFK	p53 [T006	219	225	3.516613	GGGCAG	0.73242	0.7189
cg1662289	MAFK	p53 [T006	903	909	3.516613	GGGCAG	0.73242	0.7189
cg1662289	MAFK	c-Ets-1 [T	418	424	3.462376	GTTCCT	0.61035	0.60765
cg1662289	MAFK	c-Ets-1 [T	1560	1566	3.462376	GTTCCT	0.61035	0.60765
cg1662289	MAFK	NF-AT1 [	1084	1093	3.445347	TGGAAA	0.07629	0.07722
cg1662289	MAFK	RXR-alph	416	422	3.392904	GGGTTC	1.09863	1.08572
cg1662289	MAFK	RXR-alph	930	936	3.392904	GGGTCC	1.09863	1.08572
cg1662289	MAFK	RXR-alph	1176	1182	3.392904	CTCACC	1.09863	1.08572
cg1662289	MAFK	RXR-alph	1317	1323	3.392904	AGGACC	1.09863	1.08572
cg1662289	MAFK	RXR-alph	1450	1456	3.392904	GGGTCC	1.09863	1.08572
cg1662289	MAFK	p53 [T006	1486	1492	3.375208	CCCGCC	0.73242	0.7189
cg1662289	MAFK	p53 [T006	1646	1652	3.375208	CCCGCC	0.73242	0.7189
cg1662289	MAFK	Sp1 [T007	1937	1946	3.305137	AGGGCG	0.07439	0.07186
cg1662289	MAFK	c-Ets-2 [T	494	502	3.2883	TTCCTC	0.18311	0.18304
cg1662289	MAFK	AP-2alpha	319	324	3.229049	GCCTCT	0.48828	0.48238
cg1662289	MAFK	AP-2alpha	1159	1164	3.229049	GCCTCT	0.48828	0.48238
cg1662289	MAFK	RXR-alph	206	212	3.170788	AAAACC	0.24414	0.24522
cg1662289	MAFK	RXR-alph	1837	1843	3.170788	GGGTTT	0.24414	0.24522
cg1662289	MAFK	IRF-1 [T0	1081	1089	3.145547	ACATGG	0.07629	0.07756
cg1662289	MAFK	Elk-1 [T00	871	879	3.121991	CTTCCT	0.07629	0.07656
cg1662289	MAFK	c-Fos [T00	988	997	3.081206	CTGGTG	0.06104	0.06065
cg1662289	MAFK	ATF-2 [T0	827	836	3.04901	CACACG	0.06104	0.0608
cg1662289	MAFK	p53 [T006	649	655	3.028543	GGGCAC	0.48828	0.47786
cg1662289	MAFK	C/EBPalp	1867	1873	2.981957	CACAAT	0.48828	0.4911
cg1662289	MAFK	c-Ets-2 [T	872	880	2.945838	TTCCTT	0.06104	0.06231
cg1662289	MAFK	STAT4 [T	98	103	2.941176	CTTTCC	2.92969	2.929
cg1662289	MAFK	STAT4 [T	417	422	2.941176	GGTTCC	2.92969	2.929
cg1662289	MAFK	STAT4 [T	692	697	2.941176	GGAAGT	2.92969	2.929
cg1662289	MAFK	STAT4 [T	780	785	2.941176	GGAAAG	2.92969	2.929
cg1662289	MAFK	STAT4 [T	1559	1564	2.941176	TGTTCC	2.92969	2.929
cg1662289	MAFK	STAT4 [T	1569	1574	2.941176	GGAACC	2.92969	2.929
cg1662289	MAFK	p53 [T006	754	760	2.813291	GGGCAT	0.48828	0.47786
cg1662289	MAFK	p53 [T006	1291	1297	2.813291	GGGCAG	0.48828	0.47786
cg1662289	MAFK	p53 [T006	1497	1503	2.813291	GATGCC	0.48828	0.47786
cg1662289	MAFK	p53 [T006	1628	1634	2.813291	GCTGCC	0.48828	0.47786
cg1662289	MAFK	NF-1 [T00	53	60	2.813149	TTGGGC	0.24414	0.24101
cg1662289	MAFK	NF-1 [T00	1414	1421	2.813149	TTGGGC	0.24414	0.24101
cg1662289	MAFK	RXR-alph	638	644	2.726556	GGGTTG	0.85449	0.84796
cg1662289	MAFK	MAZ [T00	1442	1454	2.655656	TGTGGG	0.00405	0.00399

cg1662289	MAFK	RXR-alph	1665	1671	2.544678	GGGTGC	0.85449	0.84796
cg1662289	MAFK	Sp1 [T007	1891	1900	2.491373	GGGGCG	0.04005	0.03892
cg1662289	MAFK	AR [T0004	283	291	2.484092	TGAATG	0.11444	0.11507
cg1662289	MAFK	c-Jun [T00	1864	1870	2.345465	TGACAC	0.48828	0.48929
cg1662289	MAFK	LEF-1 [T0	432	439	2.345041	CTTTGCT	0.09155	0.09192
cg1662289	MAFK	GCF [T00	1313	1321	2.339499	GCGCAG	0.06104	0.05925
cg1662289	MAFK	RXR-alph	840	846	2.322562	GGGTCT	0.85449	0.84796
cg1662289	MAFK	Elk-1 [T00	493	501	2.299314	CTTCCTC	0.09155	0.09114
cg1662289	MAFK	E2F-1 [T0	876	883	2.294501	TTTTCC	0.06104	0.06059
cg1662289	MAFK	T3R-beta1	1328	1336	2.221365	TCACCT	0.15259	0.15262
cg1662289	MAFK	Sp1 [T007	1644	1653	2.203247	TGCCCG	0.03624	0.0349
cg1662289	MAFK	AP-2alpha	624	629	2.098119	GCCTCG	0.97656	0.95407
cg1662289	MAFK	AP-2alpha	1696	1701	2.098119	GCCTCG	0.97656	0.95407
cg1662289	MAFK	NF-AT1 [	779	788	2.067208	TGGAAA	0.03815	0.03874
cg1662289	MAFK	NF-AT1 [	1085	1093	1.970716	GGAAAA	0.06866	0.07012
cg1662289	MAFK	HIF-1 [T0	1033	1041	1.911603	ACGTGC	0.1297	0.12851
cg1662289	MAFK	GATA-1 [	1804	1809	1.896347	TATCGG	3.90625	3.92756
cg1662289	MAFK	AP-2alpha	178	183	1.871933	GGAGGC	0.97656	0.95407
cg1662289	MAFK	AP-2alpha	386	391	1.871933	GGAGGC	0.97656	0.95407
cg1662289	MAFK	AP-2alpha	737	742	1.871933	GCCTCC	0.97656	0.95407
cg1662289	MAFK	AP-2alpha	763	768	1.871933	GGAGGC	0.97656	0.95407
cg1662289	MAFK	AP-2alpha	946	951	1.871933	GGAGGC	0.97656	0.95407
cg1662289	MAFK	AP-2alpha	1141	1146	1.871933	GGAGGC	0.97656	0.95407
cg1662289	MAFK	AP-2alpha	1387	1392	1.871933	GGAGGC	0.97656	0.95407
cg1662289	MAFK	TFII-I [T0	380	385	1.824994	GGAGAG	0.48828	0.48408
cg1662289	MAFK	TFII-I [T0	467	472	1.824994	CTCTCC	0.48828	0.48408
cg1662289	MAFK	TFII-I [T0	1161	1166	1.824994	CTCTCC	0.48828	0.48408
cg1662289	MAFK	PXR-1:RX	197	204	1.759733	ACAGTT	0.06104	0.06168
cg1662289	MAFK	PXR-1:RX	796	803	1.759733	TGAACT	0.06104	0.06168
cg1662289	MAFK	p53 [T006	801	807	1.758307	TCTGCC	0.36621	0.36261
cg1662289	MAFK	p53 [T006	1642	1648	1.758307	TCTGCC	0.36621	0.36261
cg1662289	MAFK	GR-beta [	35	39	1.680765	AATGC	3.90625	3.94936
cg1662289	MAFK	GR-beta [	965	969	1.680765	AATGC	3.90625	3.94936
cg1662289	MAFK	GR-beta [	1117	1121	1.680765	GCATT	3.90625	3.94936
cg1662289	MAFK	GR-beta [	1870	1874	1.680765	AATGC	3.90625	3.94936
cg1662289	MAFK	GR-beta [	1927	1931	1.680765	AATGC	3.90625	3.94936
cg1662289	MAFK	C/EBPbeta	10	13	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	53	56	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	294	297	1.639871	CCAA	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	356	359	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	441	444	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	523	526	1.639871	CCAA	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	641	644	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1284	1287	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1414	1417	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1524	1527	1.639871	CCAA	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1587	1590	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1740	1743	1.639871	TTGG	15.625	15.72563

cg1662289	MAFK	C/EBPbeta	1785	1788	1.639871	CCAA	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1831	1834	1.639871	TTGG	15.625	15.72563
cg1662289	MAFK	XBP-1 [T	110	115	1.583727	ATGACA	0.97656	0.98146
cg1662289	MAFK	XBP-1 [T	306	311	1.583727	TGTCAT	0.97656	0.98146
cg1662289	MAFK	XBP-1 [T	1758	1763	1.583727	ATGACA	0.97656	0.98146
cg1662289	MAFK	Sp1 [T007	1484	1493	1.566059	CACCCG	0.03242	0.03129
cg1662289	MAFK	Pax-5 [T0	132	138	1.537547	CTGGCC	0.73242	0.71311
cg1662289	MAFK	Pax-5 [T0	1431	1437	1.537547	CTGGCC	0.73242	0.71311
cg1662289	MAFK	Pax-5 [T0	1486	1492	1.537547	CCCGCC	0.73242	0.71311
cg1662289	MAFK	Pax-5 [T0	1646	1652	1.537547	CCCGCC	0.73242	0.71311
cg1662289	MAFK	TFIID [T0	268	274	1.537547	TACAAA	0.73242	0.75096
cg1662289	MAFK	TFIID [T0	293	299	1.537547	TCCAAA	0.73242	0.75096
cg1662289	MAFK	TFIID [T0	1084	1090	1.537547	TGGAAA	0.73242	0.75096
cg1662289	MAFK	TFIID [T0	1840	1846	1.537547	TTTTCA	0.73242	0.75096
cg1662289	MAFK	RXR-alpha	1354	1360	1.474336	GGGTTT	0.48828	0.48222
cg1662289	MAFK	RXR-alpha	1675	1681	1.474336	GGGTTT	0.48828	0.48222
cg1662289	MAFK	STAT4 [T	876	881	1.470588	TTTTCC	1.95312	1.96333
cg1662289	MAFK	STAT4 [T	1085	1090	1.470588	GGAAAA	1.95312	1.96333
cg1662289	MAFK	STAT4 [T	1752	1757	1.470588	GTTTCC	1.95312	1.96333
cg1662289	MAFK	C/EBPbeta	682	685	1.366559	TTGA	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1682	1685	1.366559	TTGA	15.625	15.72563
cg1662289	MAFK	C/EBPbeta	1924	1927	1.366559	TCAA	15.625	15.72563
cg1662289	MAFK	AP-2alpha	653	658	1.357116	ACAGGC	0.48828	0.48203
cg1662289	MAFK	AP-2alpha	1021	1026	1.357116	GCCTGT	0.48828	0.48203
cg1662289	MAFK	ENKTF-1	1137	1144	1.255756	TGGCGG	0.24414	0.23904
cg1662289	MAFK	EBF [T05	134	144	1.088777	GGCCCT	0.00763	0.00736
cg1662289	MAFK	AR [T000	195	203	1.006056	GGACAG	0.03815	0.03779
cg1662289	MAFK	E2F-1 [T0	1618	1625	0.993583	TGTCCC	0.03052	0.02978
cg1662289	MAFK	GR-beta [T	212	216	0.840383	CCATT	7.8125	7.94706
cg1662289	MAFK	GR-beta [T	228	232	0.840383	TCATT	7.8125	7.94706
cg1662289	MAFK	GR-beta [T	594	598	0.840383	TCATT	7.8125	7.94706
cg1662289	MAFK	GR-beta [T	1672	1676	0.840383	AATGG	7.8125	7.94706
cg1662289	MAFK	GR-beta [T	1849	1853	0.840383	AATGA	7.8125	7.94706
cg1662289	MAFK	c-Ets-1 [T	871	877	0.256174	CTTCCTT	0.24414	0.24569
cg1662289	MAFK	AP-2alpha	89	94	0.226186	CCAGGC	0.97656	0.95305
cg1662289	MAFK	AP-2alpha	471	476	0.226186	CCAGGC	0.97656	0.95305
cg1662289	MAFK	AP-2alpha	488	493	0.226186	CCAGGC	0.97656	0.95305
cg1662289	MAFK	AP-2alpha	566	571	0.226186	GCCTGG	0.97656	0.95305
cg1662289	MAFK	AP-2alpha	1202	1207	0.226186	GCCTGG	0.97656	0.95305
cg1662289	MAFK	AP-2alpha	1308	1313	0.226186	GCCTGG	0.97656	0.95305
cg1662289	MAFK	GR-alpha [	320	324	0.207689	CCTCT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	382	386	0.207689	AGAGG	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	603	607	0.207689	AGAGG	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	874	878	0.207689	CCTTT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1075	1079	0.207689	CCTCT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1160	1164	0.207689	CCTCT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1341	1345	0.207689	CCTCT	7.8125	7.81264
cg1662289	MAFK	c-Ets-1 [T	493	499	0.128087	CTTCCTC	0.24414	0.2429

cg1662289	MAFK	AP-1 [T00	992	1000	0.052878	TGACTC	0.03052	0.03051
cg1662289	MAFK	GR-alpha [	653	657	0	ACAGG	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	751	755	0	ACAGG	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	857	861	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1022	1026	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1245	1249	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1322	1326	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1331	1335	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1563	1567	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1573	1577	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	GR-alpha [	1616	1620	0	CCTGT	7.8125	7.81264
cg1662289	MAFK	AP-2alpha	538	543	0	GCAGGC	0.97656	0.95305
cg1662289	MAFK	AP-2alpha	1688	1693	0	GCCTGC	0.97656	0.95305
cg1662289	MAFK	XBP-1 [T0	226	231	0	CGTCAT	0.97656	0.98127
cg1662289	MAFK	RXR-alph	1610	1616	0	TGAACC	0.24414	0.2444
cg1662289	MAFK	Pax-5 [T0	55	61	0	GGGCCC	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	518	524	0	CCTGCC	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	536	542	0	GGGCAG	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	820	826	0	CGAGCC	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	910	916	0	GGGCCC	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	1394	1400	0	GGGCTG	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	1416	1422	0	GGGCCC	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	1457	1463	0	GGGCTG	1.09863	1.06846
cg1662289	MAFK	Pax-5 [T0	1771	1777	0	GGGCTG	1.09863	1.06846
cg1662289	MAFK	p53 [T006	518	524	0	CCTGCC	0.36621	0.35912
cg1662289	MAFK	p53 [T006	536	542	0	GGGCAG	0.36621	0.35912
cg1662289	MAFK	ENKTF-1	1311	1318	0	TGGCGC	0.12207	0.1201
cg1662289	MAFK	TFII-I [T0	98	103	0	CTTTCC	1.46484	1.45997
cg1662289	MAFK	TFII-I [T0	195	200	0	GGACAG	1.46484	1.45997
cg1662289	MAFK	TFII-I [T0	780	785	0	GGAAAG	1.46484	1.45997
cg1662289	MAFK	TFII-I [T0	858	863	0	CTGTCC	1.46484	1.45997
cg1662289	MAFK	TFII-I [T0	1617	1622	0	CTGTCC	1.46484	1.45997
cg1662289	MAFK	YY1 [T00	183	186	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	212	215	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	373	376	0	ATGG	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	399	402	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	404	407	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1083	1086	0	ATGG	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1098	1101	0	ATGG	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1241	1244	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1251	1254	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1382	1385	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1493	1496	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1502	1505	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1594	1597	0	ATGG	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1673	1676	0	ATGG	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1756	1759	0	CCAT	7.8125	7.81711
cg1662289	MAFK	YY1 [T00	1794	1797	0	CCAT	7.8125	7.81711

cg1662289	MAFK	YY1 [T00	1796	1799	0	ATGG	7.8125	7.81711
cg1662289	MAFK	GCF [T00	1631	1639	0	GCCCGG	0.09155	0.08765
cg1662289	MAFK	ER-alpha [	23	27	0	TGACC	1.95312	1.9404
cg1662289	MAFK	ER-alpha [	515	519	0	TGACC	1.95312	1.9404
cg1662289	MAFK	ER-alpha [	683	687	0	TGACC	1.95312	1.9404
cg1662289	MAFK	ER-alpha [	1481	1485	0	GGTCA	1.95312	1.9404
cg1662289	MAFK	ER-alpha [	1521	1525	0	TGACC	1.95312	1.9404
cg1662289	MAFK	ER-alpha [	1718	1722	0	TGACC	1.95312	1.9404
cg1662289	MAFK	ER-alpha [	1922	1926	0	GGTCA	1.95312	1.9404
cg1662289	MAFK	C/EBPbeta	204	207	0	ACAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	243	246	0	TTGC	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	250	253	0	ACAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	261	264	0	TTGT	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	269	272	0	ACAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	300	303	0	GCAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	317	320	0	TTGC	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	434	437	0	TTGC	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	544	547	0	TTGC	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	676	679	0	GCAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	936	939	0	TTGC	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1121	1124	0	TTGC	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1345	1348	0	TTGT	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1348	1351	0	TTGT	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1358	1361	0	TTGT	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1365	1368	0	TTGC	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1669	1672	0	GCAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1679	1682	0	TTGT	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1712	1715	0	GCAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1761	1764	0	ACAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1799	1802	0	GCAA	15.625	15.71349
cg1662289	MAFK	C/EBPbeta	1868	1871	0	ACAA	15.625	15.71349
cg1662289	MAFK	c-Jun [T00	992	998	0	TGACTC	0.12207	0.12266
cg1662289	MAFK	NFI/CTF [	1736	1743	0	GCGTTT	0.18311	0.18147
cg1662289	MAFK	TFIID [T0	232	238	0	TTTTAG	1.09863	1.13474
cg1662289	MAFK	FOXP3 [T	1347	1352	0	GTTGTG	1.46484	1.47315
cg1662289	MAFK	FOXP3 [T	1760	1765	0	GACAAC	1.46484	1.47315
cg1662289	MAFK	GR-beta [	285	289	0	AATGT	3.90625	3.99611
cg1662289	MAFK	GR-beta [	338	342	0	ACATT	3.90625	3.99611
cg1662289	MAFK	GR-beta [	1858	1862	0	AATGT	3.90625	3.99611
cg1662289	MAFK	GR [T050	257	263	0	TTTTTTG	0.36621	0.37562
cg1662289	MAFK	TCF-4E [	432	438	0	CTTTGC	0.12207	0.12262
cg1662289	MAFK	WT1 [T00	1888	1896	0	GCGGGG	0.00763	0.00729
cg1911297	MGC1612	MAZ [T00	1373	1385	9.826821	GCCCGG	0.00435	0.00423
cg1911297	MGC1612	XBP-1 [T	395	400	9.789909	ATGTCG	1.95312	1.95208
cg1911297	MGC1612	XBP-1 [T	1062	1067	9.789909	ATGGCG	1.95312	1.95208
cg1911297	MGC1612	NF-AT2 [	257	266	9.755755	GGAAAA	0.08774	0.08903
cg1911297	MGC1612	RAR-beta	1475	1484	9.641259	TCGGAA	0.21362	0.21243
cg1911297	MGC1612	RAR-beta	1759	1768	9.641259	TCGGAA	0.21362	0.21243

cg1911297	MGC1612	Pax-5 [T0	442	448	9.552105	GGGCCA	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	912	918	9.552105	GGGCAA	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	970	976	9.552105	GCCGCC	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	1173	1179	9.552105	GGGCGT	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	1339	1345	9.552105	GGGCGG	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	1343	1349	9.552105	GGCGCC	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	1390	1396	9.552105	GCCGCC	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	1715	1721	9.552105	TTAGCC	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	1752	1758	9.552105	GGGCAA	1.46484	1.43083
cg1911297	MGC1612	Pax-5 [T0	1988	1994	9.552105	GGGCGC	1.46484	1.43083
cg1911297	MGC1612	TFIID [T0	40	46	9.552105	TTTCCC	1.46484	1.48472
cg1911297	MGC1612	TFIID [T0	108	114	9.552105	TTTGGG	1.46484	1.48472
cg1911297	MGC1612	TFIID [T0	526	532	9.552105	TGAGAA	1.46484	1.48472
cg1911297	MGC1612	TFIID [T0	1500	1506	9.552105	TGGGAA	1.46484	1.48472
cg1911297	MGC1612	TFIID [T0	1600	1606	9.552105	TGACAA	1.46484	1.48472
cg1911297	MGC1612	TFIID [T0	1612	1618	9.552105	TGGGAA	1.46484	1.48472
cg1911297	MGC1612	NF-1 [T00	1490	1497	9.513281	CACCCC	0.73242	0.73053
cg1911297	MGC1612	TFII-I [T0	19	24	9.512894	GGACTT	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	112	117	9.512894	GGACAC	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	208	213	9.512894	GTGTCC	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	257	262	9.512894	GGAAAA	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	518	523	9.512894	GGAAAA	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	703	708	9.512894	GGAACG	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	770	775	9.512894	TTGTCC	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	781	786	9.512894	GGAAAA	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	806	811	9.512894	GGATCG	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1060	1065	9.512894	GGATGG	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1084	1089	9.512894	GGAAGG	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1135	1140	9.512894	GGACGG	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1310	1315	9.512894	GGATTT	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1502	1507	9.512894	GGAAAC	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1769	1774	9.512894	GTTTCC	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1807	1812	9.512894	GGATGG	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1865	1870	9.512894	GGACTT	7.32422	7.29728
cg1911297	MGC1612	TFII-I [T0	1957	1962	9.512894	GGAATT	7.32422	7.29728
cg1911297	MGC1612	FOXP3 [T	46	51	9.512894	AATAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	222	227	9.512894	GCCAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	250	255	9.512894	GTTGGG	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	352	357	9.512894	GTTTAT	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	458	463	9.512894	ATAAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	503	508	9.512894	AATAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	513	518	9.512894	GTTGGG	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	640	645	9.512894	AGCAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	939	944	9.512894	GGCAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	976	981	9.512894	CCCAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	1006	1011	9.512894	CCCAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	1753	1758	9.512894	GGCAAC	7.32422	7.35678
cg1911297	MGC1612	FOXP3 [T	1851	1856	9.512894	AGCAAC	7.32422	7.35678

cg1911297	MGC1612	TCF-4E [T	167	173	9.453578	CTTTGA	0.48828	0.49215
cg1911297	MGC1612	NFI/CTF [	772	779	9.352332	GTCCTT	0.54932	0.54821
cg1911297	MGC1612	SRY [T00	1203	1211	9.264664	AGTGCA	0.12207	0.12265
cg1911297	MGC1612	c-Ets-1 [T	1955	1961	9.19359	TTGGAA	0.85449	0.85523
cg1911297	MGC1612	PPAR-alp	1915	1925	9.158357	CCCTGG	0.0515	0.04986
cg1911297	MGC1612	NFI/CTF [	223	230	9.042931	CCAACA	0.48828	0.48804
cg1911297	MGC1612	E2F-1 [T0	216	223	9.028527	GTCCCC	0.27466	0.26875
cg1911297	MGC1612	E2F-1 [T0	1222	1229	9.028527	GCGGGG	0.27466	0.26875
cg1911297	MGC1612	E2F-1 [T0	1363	1370	9.028527	GTCCCC	0.27466	0.26875
cg1911297	MGC1612	c-Ets-1 [T	1122	1128	9.020687	GGGGAA	0.85449	0.85523
cg1911297	MGC1612	AP-1 [T00	836	844	9.002849	TTTAAG	0.24414	0.24693
cg1911297	MGC1612	RBP-Jkap	39	50	8.942683	ATTTCC	0.00763	0.00768
cg1911297	MGC1612	c-Ets-1 [T	1620	1626	8.937416	ATTCCA	0.85449	0.85523
cg1911297	MGC1612	Elk-1 [T00	1147	1155	8.931691	AGGGGG	0.24414	0.24034
cg1911297	MGC1612	p53 [T006	1267	1273	8.912104	GGGCCC	0.12207	0.11837
cg1911297	MGC1612	PR B [T00	1228	1234	8.827054	ACCTGT	0.36621	0.36944
cg1911297	MGC1612	PR A [T01	1228	1234	8.827054	ACCTGT	0.36621	0.36944
cg1911297	MGC1612	NF-1 [T00	40	47	8.790071	TTTCCC	0.24414	0.24467
cg1911297	MGC1612	XBP-1 [T	28	33	8.75604	GATCAT	2.92969	2.9674
cg1911297	MGC1612	XBP-1 [T	525	530	8.75604	ATGAGA	2.92969	2.9674
cg1911297	MGC1612	XBP-1 [T	1848	1853	8.75604	ATGAGC	2.92969	2.9674
cg1911297	MGC1612	STAT1bet	39	48	8.695301	ATTTCC	0.22316	0.22446
cg1911297	MGC1612	STAT1bet	534	543	8.695301	TAGTGG	0.22316	0.22446
cg1911297	MGC1612	STAT1bet	777	786	8.695301	TGGAGG	0.22316	0.22446
cg1911297	MGC1612	STAT1bet	1498	1507	8.695301	ACTGGG	0.22316	0.22446
cg1911297	MGC1612	IRF-1 [T	777	785	8.661524	TGGAGG	0.20599	0.20664
cg1911297	MGC1612	IRF-1 [T	1770	1778	8.661524	TTTCCT	0.20599	0.20664
cg1911297	MGC1612	RAR-beta	1951	1960	8.578216	CGGGTT	0.26703	0.26657
cg1911297	MGC1612	EBF [T05	1115	1125	8.453294	GCTCCA	0.03052	0.02952
cg1911297	MGC1612	HNF-3alp	144	151	8.343064	TTAAAA	0.27466	0.28528
cg1911297	MGC1612	HNF-3alp	320	327	8.343064	TTTAAA	0.27466	0.28528
cg1911297	MGC1612	HNF-3alp	656	663	8.343064	AATTTA	0.27466	0.28528
cg1911297	MGC1612	HNF-3alp	745	752	8.343064	CTAAAA	0.27466	0.28528
cg1911297	MGC1612	HNF-3alp	1676	1683	8.343064	ATTAAA	0.27466	0.28528
cg1911297	MGC1612	PR B [T00	194	200	8.338824	AACAGG	1.09863	1.10009
cg1911297	MGC1612	PR A [T01	194	200	8.338824	AACAGG	1.09863	1.10009
cg1911297	MGC1612	GR-alpha	15	19	8.281568	CCTTG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	101	105	8.281568	CCTTC	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	296	300	8.281568	CCTTC	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	547	551	8.281568	CCTCC	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	550	554	8.281568	CCTTG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	554	558	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	774	778	8.281568	CCTTG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	778	782	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	826	830	8.281568	CAAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	936	940	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	962	966	8.281568	CCTTG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha	1050	1054	8.281568	GGAGG	7.8125	7.72956

cg1911297	MGC1612	GR-alpha [	1085	1089	8.281568	GAAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1108	1112	8.281568	CCTTC	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1169	1173	8.281568	GAAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1181	1185	8.281568	CAAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1291	1295	8.281568	CGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1378	1382	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1415	1419	8.281568	CAAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1628	1632	8.281568	CCTCC	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1632	1636	8.281568	CCTCC	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1780	1784	8.281568	GAAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1789	1793	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1811	1815	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1881	1885	8.281568	GAAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1982	1986	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	GR-alpha [	1985	1989	8.281568	GGAGG	7.8125	7.72956
cg1911297	MGC1612	NFI/CTF [	1951	1958	8.241664	CGGGTT	0.18311	0.1823
cg1911297	MGC1612	p53 [T006	1266	1272	8.208781	GGGGCC	0.48828	0.47377
cg1911297	MGC1612	p53 [T006	1513	1519	8.208781	GGGGCC	0.48828	0.47377
cg1911297	MGC1612	ENKTF-1	1641	1648	8.19852	GCCCGC	0.73242	0.71737
cg1911297	MGC1612	LEF-1 [T0	167	174	8.117221	CTTTGA	0.12207	0.1241
cg1911297	MGC1612	c-Ets-1 [T	701	707	8.116854	CTGGAA	0.24414	0.2425
cg1911297	MGC1612	c-Ets-1 [T	1542	1548	8.116854	GTTCCA	0.24414	0.2425
cg1911297	MGC1612	GR-alpha [	135	139	8.073878	CCTAG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	212	216	8.073878	CCAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	365	369	8.073878	CCTGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	432	436	8.073878	CCTAG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	788	792	8.073878	CTAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	993	997	8.073878	CCTGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1027	1031	8.073878	CCTGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1034	1038	8.073878	CCTGC	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1037	1041	8.073878	GCAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1118	1122	8.073878	CCAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1212	1216	8.073878	GCAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1246	1250	8.073878	CCTGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1271	1275	8.073878	CCTGC	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1316	1320	8.073878	CTAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1510	1514	8.073878	CTAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1523	1527	8.073878	CCTGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1545	1549	8.073878	CCAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1862	1866	8.073878	CCAGG	7.8125	7.72238
cg1911297	MGC1612	GR-alpha [	1916	1920	8.073878	CCTGG	7.8125	7.72238
cg1911297	MGC1612	Pax-5 [T0	850	856	8.014558	GGGCAT	2.19727	2.14502
cg1911297	MGC1612	Pax-5 [T0	1102	1108	8.014558	GGGCTT	2.19727	2.14502
cg1911297	MGC1612	Pax-5 [T0	1266	1272	8.014558	GGGGCC	2.19727	2.14502
cg1911297	MGC1612	Pax-5 [T0	1443	1449	8.014558	GGGCCG	2.19727	2.14502
cg1911297	MGC1612	Pax-5 [T0	1513	1519	8.014558	GGGGCC	2.19727	2.14502
cg1911297	MGC1612	Pax-5 [T0	1514	1520	8.014558	GGGCCC	2.19727	2.14502
cg1911297	MGC1612	Pax-5 [T0	1534	1540	8.014558	GAAGCC	2.19727	2.14502

cg1911297	MGC1612	Pax-5 [T0(	1549	1555	8.014558	GCAGCC(	2.19727	2.14502
cg1911297	MGC1612	Pax-5 [T0(	1884	1890	8.014558	GGGCTC(	2.19727	2.14502
cg1911297	MGC1612	TFIID [T0	168	174	8.014558	TTTGAG/	2.19727	2.24348
cg1911297	MGC1612	TFIID [T0	355	361	8.014558	TATCAA/	2.19727	2.24348
cg1911297	MGC1612	TFIID [T0	498	504	8.014558	TAACAA.	2.19727	2.24348
cg1911297	MGC1612	TFIID [T0	842	848	8.014558	TCAGAA.	2.19727	2.24348
cg1911297	MGC1612	TFIID [T0	1670	1676	8.014558	TTTCAG/	2.19727	2.24348
cg1911297	MGC1612	C/EBPalpł	468	474	8.006685	TACAAT(	0.24414	0.24674
cg1911297	MGC1612	c-Jun [T00	1726	1732	7.937147	CTAGTC/	0.48828	0.49076
cg1911297	MGC1612	ETF [T002	1981	1991	7.870358	GGGAGG	0.07153	0.06862
cg1911297	MGC1612	c-Ets-2 [T(	430	438	7.84116	TTCCTAC	0.32043	0.32298
cg1911297	MGC1612	c-Ets-2 [T(	1079	1087	7.84116	TTTCAG(	0.32043	0.32298
cg1911297	MGC1612	p53 [T006'	1884	1890	7.833758	GGGCTC(	0.48828	0.47377
cg1911297	MGC1612	NF-AT1 [T	538	546	7.744746	GGAAAG	0.19836	0.19941
cg1911297	MGC1612	POU2F2 ((	834	844	7.738542	GTTTTA/	0.00715	0.0074
cg1911297	MGC1612	NFI/CTF [	114	121	7.587343	ACACTT(	0.36621	0.36674
cg1911297	MGC1612	NFI/CTF [	1200	1207	7.587343	CCAAGT(	0.36621	0.36674
cg1911297	MGC1612	E2F [T002	218	227	7.575186	CCCCGC(	0.00763	0.00747
cg1911297	MGC1612	GR [T050'	105	111	7.527031	CTATTTC	1.83105	1.86007
cg1911297	MGC1612	GR [T050'	358	364	7.527031	CAAACA.	1.83105	1.86007
cg1911297	MGC1612	GR [T050'	501	507	7.527031	CAAATA.	1.83105	1.86007
cg1911297	MGC1612	GR [T050'	737	743	7.527031	ATGTTTC	1.83105	1.86007
cg1911297	MGC1612	GR [T050'	915	921	7.527031	CAAAAG	1.83105	1.86007
cg1911297	MGC1612	GR [T050'	1867	1873	7.527031	ACTTTTC	1.83105	1.86007
cg1911297	MGC1612	GR [T050'	1993	1999	7.527031	CAAAGC.	1.83105	1.86007
cg1911297	MGC1612	C/EBPalpł	128	134	7.465744	TTCAAT(	0.48828	0.49653
cg1911297	MGC1612	p53 [T006'	1343	1349	7.458735	GGCGCC(	0.73242	0.7186
cg1911297	MGC1612	RXR-alpha	368	374	7.411919	GGGTAT(	0.12207	0.12139
cg1911297	MGC1612	LEF-1 [T0	1204	1211	7.396545	GTGCAA.	0.21362	0.21302
cg1911297	MGC1612	LEF-1 [T0	1990	1997	7.396545	GCGCAA.	0.21362	0.21302
cg1911297	MGC1612	IRF-1 [T0(	253	261	7.387351	GGGGGG	0.14496	0.14449
cg1911297	MGC1612	IRF-1 [T0(	514	522	7.387351	TTGGGG/	0.14496	0.14449
cg1911297	MGC1612	IRF-1 [T0(	534	542	7.299819	TAGTGG/	0.14496	0.14449
cg1911297	MGC1612	HOXD9 [T	503	512	7.270719	AATAAC.	0.06866	0.07152
cg1911297	MGC1612	HOXD10 [	503	512	7.270719	AATAAC.	0.06866	0.07152
cg1911297	MGC1612	p53 [T006'	868	874	7.266844	GGGCTG'	0.73242	0.7186
cg1911297	MGC1612	c-Ets-1 [T(	930	936	7.257837	ATTCCG(	0.48828	0.4878
cg1911297	MGC1612	c-Ets-1 [T(	40	46	7.199436	TTTCCCA	0.73242	0.73099
cg1911297	MGC1612	c-Ets-1 [T(	1500	1506	7.199436	TGGGAA.	0.73242	0.73099
cg1911297	MGC1612	c-Ets-1 [T(	1612	1618	7.199436	TGGGAA.	0.73242	0.73099
cg1911297	MGC1612	c-Jun [T00	568	574	7.178905	CGGGTC/	0.73242	0.73173
cg1911297	MGC1612	SRY [T00!	1922	1930	7.175614	GCGACA.	0.30518	0.30739
cg1911297	MGC1612	XBP-1 [T(	176	181	7.172312	ATGATT	2.92969	2.97018
cg1911297	MGC1612	XBP-1 [T(	627	632	7.172312	ATGATG	2.92969	2.97018
cg1911297	MGC1612	XBP-1 [T(	1844	1849	7.172312	ACTCAT	2.92969	2.97018
cg1911297	MGC1612	p53 [T006'	1514	1520	7.153797	GGGCCC.	1.09863	1.07125
cg1911297	MGC1612	p53 [T006'	442	448	7.150251	GGGCCA(	1.09863	1.07125
cg1911297	MGC1612	c-Myb [T0	277	284	7.127234	TAACTG(	0.18311	0.18399

cg1911297	MGC1612	c-Jun [T00	859	865	7.096776	GCAGTC	0.73242	0.73173
cg1911297	MGC1612	TFIID [T0	637	643	7.082373	TTTAGC	0.12207	0.12407
cg1911297	MGC1612	HNF-1B [	494	502	7.037014	TCACTA	0.07629	0.07762
cg1911297	MGC1612	C/EBPalph	1645	1651	7.00174	GCCAAT	0.73242	0.74337
cg1911297	MGC1612	HNF-3alph	51	58	7.000129	CATTTTT	0.82397	0.84946
cg1911297	MGC1612	HNF-3alph	154	161	7.000129	TATAAA	0.82397	0.84946
cg1911297	MGC1612	HNF-3alph	331	338	7.000129	AAAAAA	0.82397	0.84946
cg1911297	MGC1612	HNF-3alph	589	596	7.000129	TATAAA	0.82397	0.84946
cg1911297	MGC1612	HNF-3alph	691	698	7.000129	AATTTA	0.82397	0.84946
cg1911297	MGC1612	IRF-1 [T0	1610	1618	6.968314	TGTGGG	0.1297	0.13036
cg1911297	MGC1612	RXR-alph	120	126	6.967687	GGGTGG	0.36621	0.36214
cg1911297	MGC1612	c-Ets-1 [T	1475	1481	6.949623	TCGGAA	0.73242	0.73099
cg1911297	MGC1612	c-Ets-1 [T	1759	1765	6.949623	TCGGAA	0.73242	0.73099
cg1911297	MGC1612	NF-1 [T00	804	811	6.948522	TTGGAT	0.48828	0.4856
cg1911297	MGC1612	c-Ets-1 [T	255	261	6.943262	GGGGAA	0.73242	0.73099
cg1911297	MGC1612	c-Ets-1 [T	516	522	6.943262	GGGGAA	0.73242	0.73099
cg1911297	MGC1612	ENKTF-1	1095	1102	6.942764	TGGCAC	1.46484	1.44228
cg1911297	MGC1612	ENKTF-1	1525	1532	6.942764	TGGCCC	1.46484	1.44228
cg1911297	MGC1612	p53 [T006	1443	1449	6.938545	GGGCCG	1.09863	1.07125
cg1911297	MGC1612	VDR [T00	341	349	6.925682	GTTCAA	0.42725	0.43062
cg1911297	MGC1612	HNF-1B [	681	689	6.912308	TGTTAA	0.07629	0.07762
cg1911297	MGC1612	p53 [T006	942	948	6.891821	AACGCC	1.09863	1.07125
cg1911297	MGC1612	C/EBPalph	342	348	6.85549	TTCAAT	0.73242	0.74337
cg1911297	MGC1612	C/EBPalph	709	715	6.85549	AATTGC	0.73242	0.74337
cg1911297	MGC1612	E2F-1 [T0	1750	1757	6.846071	GCGGGC	0.30518	0.29782
cg1911297	MGC1612	E2F-1 [T0	1943	1950	6.839754	CGTGCC	0.30518	0.29782
cg1911297	MGC1612	c-Ets-1 [T	1014	1020	6.821536	GTTCCG	0.73242	0.73099
cg1911297	MGC1612	AR [T000	1658	1666	6.817719	TACCTG	0.23651	0.23551
cg1911297	MGC1612	NFI/CTF [	1494	1501	6.786076	CCAAAC	0.73242	0.73214
cg1911297	MGC1612	AR [T000	767	775	6.760234	TTTTTGT	0.23651	0.23551
cg1911297	MGC1612	ATF3 [T0	837	844	6.744803	TTAAGT	0.27466	0.27656
cg1911297	MGC1612	c-Myb [T0	675	682	6.719843	GGGAGT	0.30518	0.3056
cg1911297	MGC1612	c-Ets-2 [T	311	319	6.695187	TTCCTGT	0.09155	0.09289
cg1911297	MGC1612	c-Jun [T00	950	956	6.668031	CAAGTC	0.61035	0.60769
cg1911297	MGC1612	T3R-beta1	1775	1783	6.664094	TCACCG	0.21362	0.21147
cg1911297	MGC1612	E2F [T002	1641	1650	6.649462	GCCCGC	0.02289	0.02238
cg1911297	MGC1612	TFII-I [T0	282	287	6.581441	GGAGAT	0.97656	0.97366
cg1911297	MGC1612	TFII-I [T0	1249	1254	6.581441	GGAGAT	0.97656	0.97366
cg1911297	MGC1612	TFII-I [T0	1519	1524	6.581441	CACTCC	0.97656	0.97366
cg1911297	MGC1612	FOXP3 [T	33	38	6.581441	TAAAAC	0.97656	0.99397
cg1911297	MGC1612	FOXP3 [T	141	146	6.581441	GTTTTA	0.97656	0.99397
cg1911297	MGC1612	FOXP3 [T	834	839	6.581441	GTTTTA	0.97656	0.99397
cg1911297	MGC1612	RXR-alph	1575	1581	6.563693	GGGTGT	0.24414	0.2434
cg1911297	MGC1612	p53 [T006	1102	1108	6.563521	GGGCTT	0.48828	0.47541
cg1911297	MGC1612	p53 [T006	1534	1540	6.563521	GAAGCC	0.48828	0.47541
cg1911297	MGC1612	p53 [T006	1549	1555	6.563521	GCAGCC	0.48828	0.47541
cg1911297	MGC1612	PXR-1:RX	338	345	6.5446	TATGTT	0.24414	0.24672
cg1911297	MGC1612	c-Myb [T0	800	807	6.539977	CAACTT	0.30518	0.3056

cg1911297	MGC1612	XBP-1 [T	472	477	6.478682	ATGCCA	0.97656	0.97062
cg1911297	MGC1612	XBP-1 [T	850	855	6.478682	GGGCAT	0.97656	0.97062
cg1911297	MGC1612	c-Myb [T0	1496	1503	6.422836	AAACTG	0.30518	0.3056
cg1911297	MGC1612	p53 [T006	1988	1994	6.403751	GGGCGC	0.48828	0.47541
cg1911297	MGC1612	p53 [T006	1826	1832	6.400205	GGGCGA	0.48828	0.47541
cg1911297	MGC1612	p53 [T006	1920	1926	6.400205	GGGCGA	0.48828	0.47541
cg1911297	MGC1612	TCF-4E [T	246	252	6.302385	CTTTGT	0.61035	0.61344
cg1911297	MGC1612	TCF-4E [T	1991	1997	6.302385	CGCAAA	0.61035	0.61344
cg1911297	MGC1612	GR-alpha [	439	443	6.263098	TAAGG	3.90625	3.91061
cg1911297	MGC1612	GR-alpha [	492	496	6.263098	CCTCA	3.90625	3.91061
cg1911297	MGC1612	GR-alpha [	670	674	6.263098	CCTTA	3.90625	3.91061
cg1911297	MGC1612	GR-alpha [	1263	1267	6.263098	TGAGG	3.90625	3.91061
cg1911297	MGC1612	GR-alpha [	1358	1362	6.263098	TGAGG	3.90625	3.91061
cg1911297	MGC1612	GR-alpha [	1595	1599	6.263098	TAAGG	3.90625	3.91061
cg1911297	MGC1612	GR-alpha [	1773	1777	6.263098	CCTCA	3.90625	3.91061
cg1911297	MGC1612	GR-alpha [	1803	1807	6.263098	TGAGG	3.90625	3.91061
cg1911297	MGC1612	p53 [T006	970	976	6.188498	GCCGCC	0.61035	0.594
cg1911297	MGC1612	p53 [T006	1173	1179	6.188498	GGGCGT	0.61035	0.594
cg1911297	MGC1612	p53 [T006	1339	1345	6.188498	GGGCGG	0.61035	0.594
cg1911297	MGC1612	p53 [T006	1390	1396	6.188498	GCCGCC	0.61035	0.594
cg1911297	MGC1612	c-Ets-1 [T	536	542	6.167515	GTGGAA	0.36621	0.36731
cg1911297	MGC1612	c-Myb [T0	383	390	6.157321	CAACTT	0.21362	0.21535
cg1911297	MGC1612	c-Jun [T00	1600	1606	6.152811	TGACAA	0.36621	0.37082
cg1911297	MGC1612	GR-alpha [	672	676	6.055408	TTAGG	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	863	867	6.055408	TCAGG	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	954	958	6.055408	TCAGG	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	985	989	6.055408	TCAGG	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	1081	1085	6.055408	TCAGG	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	1261	1265	6.055408	CCTGA	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	1356	1360	6.055408	CCTGA	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	1746	1750	6.055408	TCAGG	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	1786	1790	6.055408	TCAGG	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	1889	1893	6.055408	CCTGA	3.90625	3.9065
cg1911297	MGC1612	GR-alpha [	1904	1908	6.055408	TCAGG	3.90625	3.9065
cg1911297	MGC1612	RXR-alph	96	102	5.937582	ATTACC	0.73242	0.72249
cg1911297	MGC1612	STAT4 [T	1084	1089	5.882353	GGAAGG	0.48828	0.48408
cg1911297	MGC1612	C/EBPalp	571	577	5.850545	GTCAAT	0.97656	0.99
cg1911297	MGC1612	C/EBPalp	724	730	5.850545	AATTGA	0.97656	0.99
cg1911297	MGC1612	STAT1bet	1610	1619	5.796867	TGTGGG	0.1545	0.1557
cg1911297	MGC1612	AR [T000	205	213	5.754178	TCTGTG	0.24414	0.24229
cg1911297	MGC1612	p53 [T006	1715	1721	5.720243	TTAGCC	0.61035	0.59991
cg1911297	MGC1612	ENKTF-1	470	477	5.687009	CAATGC	0.73242	0.7249
cg1911297	MGC1612	C/EBPalp	178	184	5.565669	GATTGT	0.73242	0.74391
cg1911297	MGC1612	NFI/CTF [	737	744	5.558661	ATGTTT	0.54932	0.55038
cg1911297	MGC1612	NFI/CTF [	1069	1076	5.558661	GGGCTT	0.54932	0.55038
cg1911297	MGC1612	NFI/CTF [	1569	1576	5.558661	GAGTTT	0.54932	0.55038
cg1911297	MGC1612	c-Ets-1 [T	1149	1155	5.558311	GGGGAA	0.36621	0.3623
cg1911297	MGC1612	Pax-5 [T0	942	948	5.544826	AACGCC	0.73242	0.72046

cg1911297	MGC1612	TFIID [T0	353	359	5.544826	TTTATCA	0.73242	0.75085
cg1911297	MGC1612	TFIID [T0	681	687	5.544826	TGTTAA	0.73242	0.75085
cg1911297	MGC1612	NF-kappa	1358	1368	5.475772	TGAGGG	0.02384	0.0233
cg1911297	MGC1612	c-Ets-1 [T	1531	1537	5.430224	CGGGAA	0.36621	0.3623
cg1911297	MGC1612	C/EBPalp	653	659	5.38654	AACAAT	0.73242	0.74391
cg1911297	MGC1612	RXR-alph	1193	1199	5.271235	CCCACC	0.61035	0.6044
cg1911297	MGC1612	RXR-alph	1488	1494	5.271235	CCCACC	0.61035	0.6044
cg1911297	MGC1612	NF-AT2 [	781	790	5.231211	GGAAAA	0.03815	0.03879
cg1911297	MGC1612	c-Jun [T00	1873	1879	5.193102	GAAGTC	0.61035	0.61057
cg1911297	MGC1612	c-Myb [T0	1538	1545	5.137438	CCCAGT	0.30518	0.30568
cg1911297	MGC1612	NF-AT1 [	257	265	5.125037	GGAAAA	0.05341	0.05402
cg1911297	MGC1612	HNF-1A [	1737	1744	5.116518	GTTAAG	0.36621	0.37179
cg1911297	MGC1612	AP-2alpha	165	170	5.100982	GCCTTT	0.97656	0.97567
cg1911297	MGC1612	AP-2alpha	917	922	5.100982	AAAGGC	0.97656	0.97567
cg1911297	MGC1612	AP-2alpha	1208	1213	5.100982	AAAGGC	0.97656	0.97567
cg1911297	MGC1612	USF2 [T0	1021	1030	5.052423	GTCTCA	0.103	0.10178
cg1911297	MGC1612	GR-beta [	10	14	5.042296	GGATT	3.90625	3.95351
cg1911297	MGC1612	GR-beta [	182	186	5.042296	GTATT	3.90625	3.95351
cg1911297	MGC1612	GR-beta [	666	670	5.042296	AATAC	3.90625	3.95351
cg1911297	MGC1612	GR-beta [	928	932	5.042296	GGATT	3.90625	3.95351
cg1911297	MGC1612	GR-beta [	1310	1314	5.042296	GGATT	3.90625	3.95351
cg1911297	MGC1612	E2F-1 [T0	1295	1302	5.042045	GCGGGA	0.18311	0.17901
cg1911297	MGC1612	C/EBPalp	712	718	5.024728	TGCAAT	0.97656	0.99332
cg1911297	MGC1612	c-Jun [T00	1174	1180	5.000337	GGCGTC	0.61035	0.61057
cg1911297	MGC1612	NF-AT2 [	35	44	4.979362	AAACAT	0.03815	0.03879
cg1911297	MGC1612	XBP-1 [T	132	137	4.894955	ATGCCT	0.97656	0.96979
cg1911297	MGC1612	XBP-1 [T	293	298	4.894955	ATGCCT	0.97656	0.96979
cg1911297	MGC1612	HNF-1C [	493	501	4.875677	CTCACT	0.04578	0.04693
cg1911297	MGC1612	RXR-alph	905	911	4.86724	GAGACC	0.48828	0.484
cg1911297	MGC1612	GCF [T00	1339	1347	4.846987	GGGCGG	0.27466	0.26486
cg1911297	MGC1612	C/EBPalp	593	599	4.845599	AATTGA	0.97656	0.99332
cg1911297	MGC1612	p53 [T006	1857	1863	4.786849	AGTGCC	0.48828	0.47747
cg1911297	MGC1612	TFII-I [T0	39	44	4.756447	ATTTCC	2.92969	2.93695
cg1911297	MGC1612	TFII-I [T0	309	314	4.756447	CATTCC	2.92969	2.93695
cg1911297	MGC1612	TFII-I [T0	829	834	4.756447	GGAATG	2.92969	2.93695
cg1911297	MGC1612	FOXP3 [T	125	130	4.756447	GTTTTC	2.92969	2.96063
cg1911297	MGC1612	FOXP3 [T	231	236	4.756447	GTTGAT	2.92969	2.96063
cg1911297	MGC1612	FOXP3 [T	304	309	4.756447	AAAAAC	2.92969	2.96063
cg1911297	MGC1612	FOXP3 [T	650	655	4.756447	AAAAAC	2.92969	2.96063
cg1911297	MGC1612	IRF-1 [T0	40	48	4.549799	TTTCCCA	0.05341	0.05405
cg1911297	MGC1612	IRF-1 [T0	1498	1506	4.549799	ACTGGG	0.05341	0.05405
cg1911297	MGC1612	E2F-1 [T0	1907	1914	4.545253	GGTCCC	0.15259	0.14941
cg1911297	MGC1612	T3R-beta1	1594	1602	4.462023	TTAAGG	0.27466	0.27551
cg1911297	MGC1612	HNF-1C [	682	690	4.443787	GTTAAA	0.07629	0.07843
cg1911297	MGC1612	AP-2alpha	134	139	4.438035	GCCTAG	0.97656	0.96979
cg1911297	MGC1612	AP-2alpha	788	793	4.438035	CTAGGC	0.97656	0.96979
cg1911297	MGC1612	AP-2alpha	1316	1321	4.438035	CTAGGC	0.97656	0.96979
cg1911297	MGC1612	STAT4 [T	309	314	4.411765	CATTCC	1.95312	1.94235

cg1911297	MGC1612	STAT4 [T	428	433	4.411765	TCTTCC	1.95312	1.94235
cg1911297	MGC1612	STAT4 [T	488	493	4.411765	GCTTCC	1.95312	1.94235
cg1911297	MGC1612	STAT4 [T	703	708	4.411765	GGAACG	1.95312	1.94235
cg1911297	MGC1612	STAT4 [T	829	834	4.411765	GGAATG	1.95312	1.94235
cg1911297	MGC1612	STAT4 [T	1053	1058	4.411765	GGAAGC	1.95312	1.94235
cg1911297	MGC1612	STAT4 [T	1104	1109	4.411765	GCTTCC	1.95312	1.94235
cg1911297	MGC1612	STAT4 [T	1151	1156	4.411765	GGAAGC	1.95312	1.94235
cg1911297	MGC1612	STAT4 [T	1533	1538	4.411765	GGAAGC	1.95312	1.94235
cg1911297	MGC1612	c-Ets-1 [T	12	18	4.411026	ATTCCT	0.85449	0.85764
cg1911297	MGC1612	c-Ets-1 [T	827	833	4.411026	AAGGAA	0.85449	0.85764
cg1911297	MGC1612	p53 [T006	1524	1530	4.33696	CTGGCC	0.24414	0.23584
cg1911297	MGC1612	RXR-alph	1361	1367	4.24113	GGGTCC	0.97656	0.9671
cg1911297	MGC1612	RXR-alph	1381	1387	4.24113	GGGACC	0.97656	0.9671
cg1911297	MGC1612	C/EBPalph	751	757	4.235345	TATTGC	0.48828	0.49358
cg1911297	MGC1612	PXR-1:RX	1450	1457	4.213958	TGAACC	0.12207	0.12119
cg1911297	MGC1612	GR-beta [	46	50	4.201913	AATAA	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	83	87	4.201913	TGATT	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	87	91	4.201913	TGATT	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	105	109	4.201913	CTATT	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	177	181	4.201913	TGATT	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	265	269	4.201913	AATCA	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	317	321	4.201913	TGATT	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	457	461	4.201913	AATAA	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	503	507	4.201913	AATAA	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	532	536	4.201913	AATAG	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	578	582	4.201913	AATCA	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	596	600	4.201913	TGATT	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	758	762	4.201913	TTATT	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	816	820	4.201913	AATAA	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	1680	1684	4.201913	AATAA	7.8125	7.94607
cg1911297	MGC1612	GR-beta [	1894	1898	4.201913	AATCG	7.8125	7.94607
cg1911297	MGC1612	NF-Y [T0	41	48	4.186615	TTCCCA	0.18311	0.1853
cg1911297	MGC1612	c-Ets-1 [T	310	316	4.154851	ATTCCT	0.24414	0.24526
cg1911297	MGC1612	NF-AT1 [	537	546	4.134416	TGGAAA	0.08392	0.08485
cg1911297	MGC1612	p53 [T006	1258	1264	4.125254	GGGCCT	0.73242	0.71379
cg1911297	MGC1612	p53 [T006	1370	1376	4.125254	CCGGCC	0.73242	0.71379
cg1911297	MGC1612	p53 [T006	1483	1489	4.125254	CCGGCC	0.73242	0.71379
cg1911297	MGC1612	c-Ets-2 [T	13	21	4.091811	TTCCTT	0.16022	0.16243
cg1911297	MGC1612	c-Ets-2 [T	243	251	4.017001	TTCCTT	0.16022	0.16243
cg1911297	MGC1612	Pax-5 [T0	868	874	4.007279	GGGCTG	1.09863	1.07975
cg1911297	MGC1612	Pax-5 [T0	1267	1273	4.007279	GGGCCC	1.09863	1.07975
cg1911297	MGC1612	Pax-5 [T0	1403	1409	4.007279	ACTGCC	1.09863	1.07975
cg1911297	MGC1612	Pax-5 [T0	1857	1863	4.007279	AGTGCC	1.09863	1.07975
cg1911297	MGC1612	TFIID [T0	30	36	4.007279	TCATAA	1.09863	1.13456
cg1911297	MGC1612	TFIID [T0	54	60	4.007279	TTTTAA	1.09863	1.13456
cg1911297	MGC1612	TFIID [T0	142	148	4.007279	TTTTAA	1.09863	1.13456
cg1911297	MGC1612	TFIID [T0	327	333	4.007279	TTTTAA	1.09863	1.13456
cg1911297	MGC1612	TFIID [T0	456	462	4.007279	TAATAA	1.09863	1.13456

cg1911297	MGC1612	Elk-1 [T00	429	437	3.944668	CTTCCTA	0.09155	0.09227
cg1911297	MGC1612	NF-AT1 [	36	44	3.917696	AACATT	0.07629	0.07734
cg1911297	MGC1612	TCF-4 [T0	166	175	3.876591	CCTTTGA	0.01144	0.01138
cg1911297	MGC1612	AR [T000	112	120	3.814754	GGACAC	0.06866	0.06828
cg1911297	MGC1612	NFI/CTF [	1646	1653	3.793671	CCAATG	0.18311	0.18109
cg1911297	MGC1612	p53 [T006	1069	1075	3.750231	GGGCTT	0.73242	0.71379
cg1911297	MGC1612	p53 [T006	1331	1337	3.750231	GGGCTG	0.73242	0.71379
cg1911297	MGC1612	p53 [T006	1794	1800	3.750231	CCAGCC	0.73242	0.71379
cg1911297	MGC1612	AP-2alpha	295	300	3.743866	GCCTTC	0.48828	0.48238
cg1911297	MGC1612	AP-2alpha	1085	1090	3.743866	GAAGGC	0.48828	0.48238
cg1911297	MGC1612	AP-2alpha	1780	1785	3.743866	GAAGGC	0.48828	0.48238
cg1911297	MGC1612	c-Ets-1 [T	242	248	3.71855	GTTCCTT	0.61035	0.60765
cg1911297	MGC1612	p53 [T006	1288	1294	3.586914	GGGCGA	0.73242	0.7189
cg1911297	MGC1612	RXR-alpha	1326	1332	3.574782	GGGTCG	1.09863	1.08572
cg1911297	MGC1612	USF1 [T0	476	485	3.561955	CACGTG	0.0515	0.05082
cg1911297	MGC1612	c-Ets-2 [T	1106	1114	3.518824	TTCCTTC	0.18311	0.18304
cg1911297	MGC1612	p53 [T006	1403	1409	3.516613	ACTGCC	0.73242	0.7189
cg1911297	MGC1612	HNF-3alph	183	190	3.500065	TATTTC	0.27466	0.28532
cg1911297	MGC1612	HNF-3alph	324	331	3.500065	AATTTTT	0.27466	0.28532
cg1911297	MGC1612	HNF-3alph	528	535	3.500065	AGAAAA	0.27466	0.28532
cg1911297	MGC1612	HNF-3alph	812	819	3.500065	TGTAAA	0.27466	0.28532
cg1911297	MGC1612	NF-Y [T0	1643	1650	3.490142	CCGCCA	0.48828	0.48904
cg1911297	MGC1612	c-Myb [T0	1830	1837	3.469384	GACAGT	0.12207	0.12203
cg1911297	MGC1612	VDR [T00	1446	1454	3.462841	CCGCTG	0.21362	0.21341
cg1911297	MGC1612	RXR-alpha	1030	1036	3.392904	GGGTCC	1.09863	1.08572
cg1911297	MGC1612	RXR-alpha	1477	1483	3.392904	GGAACC	1.09863	1.08572
cg1911297	MGC1612	RXR-alpha	1761	1767	3.392904	GGAACC	1.09863	1.08572
cg1911297	MGC1612	Sp1 [T007	1388	1397	3.383855	GAGCCG	0.07439	0.07186
cg1911297	MGC1612	Elk-1 [T00	1080	1088	3.381796	TTCAGG	0.04578	0.04588
cg1911297	MGC1612	p53 [T006	1638	1644	3.375208	CACGCC	0.73242	0.7189
cg1911297	MGC1612	p53 [T006	1910	1916	3.375208	CCCGCC	0.73242	0.7189
cg1911297	MGC1612	p53 [T006	1940	1946	3.375208	GGGCGT	0.73242	0.7189
cg1911297	MGC1612	T3R-beta1	1154	1162	3.370634	AGCTGG	0.27466	0.2755
cg1911297	MGC1612	GR-beta [	69	73	3.361531	AATAT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	70	74	3.361531	ATATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	94	98	3.361531	ATATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	407	411	3.361531	AGATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	715	719	3.361531	AATCT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	749	753	3.361531	AATAT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	750	754	3.361531	ATATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	785	789	3.361531	AATCT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	1251	1255	3.361531	AGATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	1618	1622	3.361531	AGATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	1674	1678	3.361531	AGATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	1695	1699	3.361531	AGATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	1971	1975	3.361531	AGATT	3.90625	3.99611
cg1911297	MGC1612	T3R-beta1	1024	1032	3.332047	TCACCT	0.27466	0.2755
cg1911297	MGC1612	PR B [T00	36	42	3.29756	AACATT	0.24414	0.25122

cg1911297	MGC1612	PR B [T00	49	55	3.29756	AACATT	0.24414	0.25122
cg1911297	MGC1612	PR B [T00	653	659	3.29756	AACAAT	0.24414	0.25122
cg1911297	MGC1612	PR B [T00	735	741	3.29756	AAATGT	0.24414	0.25122
cg1911297	MGC1612	PR A [T01	36	42	3.29756	AACATT	0.24414	0.25122
cg1911297	MGC1612	PR A [T01	49	55	3.29756	AACATT	0.24414	0.25122
cg1911297	MGC1612	PR A [T01	653	659	3.29756	AACAAT	0.24414	0.25122
cg1911297	MGC1612	PR A [T01	735	741	3.29756	AAATGT	0.24414	0.25122
cg1911297	MGC1612	c-Ets-2 [T	490	498	3.2883	TTCCTC	0.18311	0.18304
cg1911297	MGC1612	c-Ets-2 [T	1771	1779	3.2883	TTCCTC	0.18311	0.18304
cg1911297	MGC1612	Elk-1 [T00	489	497	3.247448	CTTCCTC	0.07629	0.07656
cg1911297	MGC1612	AP-2alpha	1162	1167	3.229049	AGAGGC	0.48828	0.48238
cg1911297	MGC1612	RAR-beta	1448	1457	3.226064	GCTGAA	0.12207	0.12169
cg1911297	MGC1612	MAZ [T00	1629	1641	3.175881	CTCCCTC	0.00474	0.00467
cg1911297	MGC1612	TCF-4E [T	1205	1211	3.151193	TGCAAA	0.24414	0.24672
cg1911297	MGC1612	Sp1 [T007	1338	1347	3.103976	TGGGCG	0.03433	0.03306
cg1911297	MGC1612	Pax-5 [T0	1288	1294	3.075094	GGGCGA	0.12207	0.11895
cg1911297	MGC1612	p53 [T006	1752	1758	3.024997	GGGCAA	0.48828	0.47786
cg1911297	MGC1612	c-Ets-2 [T	824	832	3.020647	TACAAG	0.06104	0.06231
cg1911297	MGC1612	C/EBPalph	84	90	3.014837	GATTGA	0.48828	0.4911
cg1911297	MGC1612	HOXD9 [T	46	55	2.949288	AATAAC	0.02289	0.02401
cg1911297	MGC1612	HOXD10 [	46	55	2.949288	AATAAC	0.02289	0.02401
cg1911297	MGC1612	STAT4 [T	11	16	2.941176	GATTCC	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	241	246	2.941176	TGTTCC	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	538	543	2.941176	GGAAAG	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	929	934	2.941176	GATTCC	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	1013	1018	2.941176	GGTTCC	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	1124	1129	2.941176	GGAACC	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	1477	1482	2.941176	GGAACC	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	1614	1619	2.941176	GGAAAG	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	1619	1624	2.941176	GATTCC	2.92969	2.929
cg1911297	MGC1612	STAT4 [T	1761	1766	2.941176	GGAACC	2.92969	2.929
cg1911297	MGC1612	USF1 [T0	472	481	2.862167	ATGCCA	0.06294	0.06201
cg1911297	MGC1612	p53 [T006	850	856	2.813291	GGGCAT	0.48828	0.47786
cg1911297	MGC1612	AhR:Arnt	1637	1646	2.810335	CCACGC	0.01717	0.01648
cg1911297	MGC1612	AhR:Arnt	1938	1947	2.810335	GGGGGC	0.01717	0.01648
cg1911297	MGC1612	PR B [T00	307	313	2.80933	AACATT	0.73242	0.74818
cg1911297	MGC1612	PR B [T00	830	836	2.80933	GAATGT	0.73242	0.74818
cg1911297	MGC1612	PR A [T01	307	313	2.80933	AACATT	0.73242	0.74818
cg1911297	MGC1612	PR A [T01	830	836	2.80933	GAATGT	0.73242	0.74818
cg1911297	MGC1612	NF-AT2 [	518	527	2.800326	GGAAAA	0.03433	0.03494
cg1911297	MGC1612	Sp1 [T007	968	977	2.729105	TCGCCG	0.04005	0.03892
cg1911297	MGC1612	RXR-alph	1952	1958	2.726556	GGGTTG	0.85449	0.84796
cg1911297	MGC1612	c-Ets-2 [T	1048	1056	2.715313	CTGGAG	0.07629	0.07593
cg1911297	MGC1612	NFI/CTF [	977	984	2.683003	CCAACC	0.06104	0.06008
cg1911297	MGC1612	NFI/CTF [	1007	1014	2.683003	CCAACC	0.06104	0.06008
cg1911297	MGC1612	c-Jun [T00	838	844	2.538231	TAAGTC	0.48828	0.48929
cg1911297	MGC1612	ENKTF-1	218	225	2.511511	CCCCGC	0.12207	0.11894
cg1911297	MGC1612	NF-AT1 [	781	789	2.449764	GGAAAA	0.09155	0.0926

cg1911297	MGC1612	C/EBPalph	1959	1965	2.371703	AATTGT	0.48828	0.49114
cg1911297	MGC1612	c-Jun [T00	727	733	2.345465	TGACAC	0.48828	0.48929
cg1911297	MGC1612	LEF-1 [T0	246	253	2.345041	CTTTGTT	0.09155	0.09192
cg1911297	MGC1612	AP-2alpha	1291	1296	2.098119	CGAGGC	0.97656	0.95407
cg1911297	MGC1612	NF-1 [T00	109	116	2.067686	TTGGGA	0.12207	0.12133
cg1911297	MGC1612	SRY [T00	246	254	1.998343	CTTTGTT	0.03052	0.03106
cg1911297	MGC1612	p53 [T006	912	918	1.970013	GGGCAA	0.36621	0.36261
cg1911297	MGC1612	AP-2alpha	546	551	1.871933	GCCTCC	0.97656	0.95407
cg1911297	MGC1612	AP-2alpha	936	941	1.871933	GGAGGC	0.97656	0.95407
cg1911297	MGC1612	AP-2alpha	1789	1794	1.871933	GGAGGC	0.97656	0.95407
cg1911297	MGC1612	TBP [T007	150	159	1.871542	TGCATA	0.18311	0.18942
cg1911297	MGC1612	TBP [T007	585	594	1.871542	TGAGTA	0.18311	0.18942
cg1911297	MGC1612	TBP [T007	604	613	1.871542	TTTATAC	0.18311	0.18942
cg1911297	MGC1612	TBP [T007	693	702	1.871542	TTTATAC	0.18311	0.18942
cg1911297	MGC1612	C/EBPalph	884	890	1.830762	CTCAAT	0.48828	0.49438
cg1911297	MGC1612	TFII-I [T0	5	10	1.824994	GGAGAG	0.48828	0.48408
cg1911297	MGC1612	TFII-I [T0	1189	1194	1.824994	CTCTCC	0.48828	0.48408
cg1911297	MGC1612	TFII-I [T0	1427	1432	1.824994	GGAGAG	0.48828	0.48408
cg1911297	MGC1612	C/EBPalph	43	49	1.761449	CCCAAT	0.48828	0.49438
cg1911297	MGC1612	GR-beta [	131	135	1.680765	AATGC	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	148	152	1.680765	AATGC	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	345	349	1.680765	AATTC	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	400	404	1.680765	GAATT	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	471	475	1.680765	AATGC	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	690	694	1.680765	GAATT	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	708	712	1.680765	GAATT	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	1712	1716	1.680765	GAATT	3.90625	3.94936
cg1911297	MGC1612	GR-beta [	1958	1962	1.680765	GAATT	3.90625	3.94936
cg1911297	MGC1612	c-Ets-2 [T	776	784	1.64415	TTGGAG	0.04578	0.04579
cg1911297	MGC1612	C/EBPbeta	17	20	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	44	47	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	109	112	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	118	121	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	223	226	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	251	254	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	514	517	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	552	555	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	741	744	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	776	779	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	804	807	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	926	929	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	949	952	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	977	980	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1007	1010	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1073	1076	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1200	1203	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1494	1497	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1573	1576	1.639871	TTGG	15.625	15.72563

cg1911297	MGC1612	C/EBPbeta	1646	1649	1.639871	CCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1936	1939	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1955	1958	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1977	1980	1.639871	TTGG	15.625	15.72563
cg1911297	MGC1612	EBF [T05	1913	1923	1.581175	GCCCCT	0.00381	0.00363
cg1911297	MGC1612	HIF-1 [T0	477	485	1.549104	ACGTGC	0.09155	0.0902
cg1911297	MGC1612	Pax-5 [T0	1524	1530	1.537547	CTGGCC	0.73242	0.71311
cg1911297	MGC1612	Pax-5 [T0	1638	1644	1.537547	CACGCC	0.73242	0.71311
cg1911297	MGC1612	Pax-5 [T0	1910	1916	1.537547	CCCGCC	0.73242	0.71311
cg1911297	MGC1612	Pax-5 [T0	1940	1946	1.537547	GGGCGT	0.73242	0.71311
cg1911297	MGC1612	TFIID [T0	648	654	1.537547	TGAAAA	0.73242	0.75096
cg1911297	MGC1612	TFIID [T0	1869	1875	1.537547	TTTTGA	0.73242	0.75096
cg1911297	MGC1612	c-Ets-1 [T	779	785	1.513038	GAGGAA	0.36621	0.36952
cg1911297	MGC1612	c-Ets-1 [T	1770	1776	1.513038	TTTCCTC	0.36621	0.36952
cg1911297	MGC1612	STAT4 [T	257	262	1.470588	GGAAAA	1.95312	1.96333
cg1911297	MGC1612	STAT4 [T	518	523	1.470588	GGAAAA	1.95312	1.96333
cg1911297	MGC1612	STAT4 [T	781	786	1.470588	GGAAAA	1.95312	1.96333
cg1911297	MGC1612	STAT4 [T	1502	1507	1.470588	GGAAAC	1.95312	1.96333
cg1911297	MGC1612	STAT4 [T	1541	1546	1.470588	AGTTCC	1.95312	1.96333
cg1911297	MGC1612	STAT4 [T	1769	1774	1.470588	GTTTCC	1.95312	1.96333
cg1911297	MGC1612	STAT4 [T	1957	1962	1.470588	GGAATT	1.95312	1.96333
cg1911297	MGC1612	PR B [T00	227	233	1.404665	CAGTGT	0.36621	0.37023
cg1911297	MGC1612	PR B [T00	238	244	1.404665	TAGTGT	0.36621	0.37023
cg1911297	MGC1612	PR A [T01	227	233	1.404665	CAGTGT	0.36621	0.37023
cg1911297	MGC1612	PR A [T01	238	244	1.404665	TAGTGT	0.36621	0.37023
cg1911297	MGC1612	C/EBPbeta	86	89	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	129	132	1.366559	TCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	169	172	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	190	193	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	232	235	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	299	302	1.366559	TCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	343	346	1.366559	TCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	357	360	1.366559	TCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	572	575	1.366559	TCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	595	598	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	726	729	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	885	888	1.366559	TCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1241	1244	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1690	1693	1.366559	TCAA	15.625	15.72563
cg1911297	MGC1612	C/EBPbeta	1871	1874	1.366559	TTGA	15.625	15.72563
cg1911297	MGC1612	GCF [T00	1269	1277	1.26923	GCCCTG	0.03052	0.02943
cg1911297	MGC1612	ENKTF-1	1063	1070	1.255756	TGGCGC	0.24414	0.23904
cg1911297	MGC1612	NFI/CTF [	922	929	1.227415	CCGCTT	0.18311	0.18127
cg1911297	MGC1612	Sp1 [T007	1908	1917	1.132223	GTCCCG	0.01335	0.01279
cg1911297	MGC1612	GCF [T00	1065	1073	1.070269	GCGCGG	0.18311	0.17647
cg1911297	MGC1612	GCF [T00	1394	1402	1.070269	CCCCCG	0.18311	0.17647
cg1911297	MGC1612	GCF [T00	1407	1415	1.070269	CCCCGG	0.18311	0.17647
cg1911297	MGC1612	GATA-1 [	355	360	1.038567	TATCAA	1.95312	1.98662

cg1911297	MGC1612	POU2F2 ((	317	327	1.003369	TGATTTA	0.00286	0.00299
cg1911297	MGC1612	Elk-1 [T00	1105	1113	0.957025	CTTCCTT	0.03052	0.03057
cg1911297	MGC1612	TBP [T007	464	473	0.935771	TTTATAC	0.12207	0.12628
cg1911297	MGC1612	RXR-alpha	569	575	0.848226	GGGTCA	0.48828	0.48333
cg1911297	MGC1612	GR-beta [T	158	162	0.840383	AATTA	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	335	339	0.840383	AATTA	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	344	348	0.840383	CAATT	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	524	528	0.840383	AATGA	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	573	577	0.840383	CAATT	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	574	578	0.840383	AATTA	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	593	597	0.840383	AATTG	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	655	659	0.840383	CAATT	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	709	713	0.840383	AATTG	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	723	727	0.840383	TAATT	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	724	728	0.840383	AATTG	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	886	890	0.840383	CAATT	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	1305	1309	0.840383	AATGG	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	1554	1558	0.840383	CCATT	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	1648	1652	0.840383	AATGG	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	1682	1686	0.840383	TAATT	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	1683	1687	0.840383	AATTA	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	1713	1717	0.840383	AATTA	7.8125	7.94706
cg1911297	MGC1612	GR-beta [T	1959	1963	0.840383	AATTG	7.8125	7.94706
cg1911297	MGC1612	NF-AT2 [T	1614	1623	0.771098	GGAAAG	0.00763	0.00779
cg1911297	MGC1612	AP-2alpha	1260	1265	0.678558	GCCTGA	0.48828	0.48199
cg1911297	MGC1612	AP-2alpha	1355	1360	0.678558	GCCTGA	0.48828	0.48199
cg1911297	MGC1612	AP-2alpha	1746	1751	0.678558	TCAGGC	0.48828	0.48199
cg1911297	MGC1612	NF-AT1 [T	1614	1622	0.648993	GGAAAG	0.02289	0.02328
cg1911297	MGC1612	PEA3 [T0(	60	68	0.597316	AGGATG'	0.04578	0.04629
cg1911297	MGC1612	c-Ets-1 [T(	429	435	0.384261	CTTCCTA	0.24414	0.24569
cg1911297	MGC1612	HNF-1A ['	682	689	0.287765	GTTAAA(	0.24414	0.24974
cg1911297	MGC1612	GATA-1 ['	371	376	0.280028	TATCTT	0.97656	0.99875
cg1911297	MGC1612	c-Ets-1 [T(	1105	1111	0.256174	CTTCCTT	0.24414	0.24569
cg1911297	MGC1612	AP-2alpha	1245	1250	0.226186	GCCTGG	0.97656	0.95305
cg1911297	MGC1612	AP-2alpha	1545	1550	0.226186	CCAGGC	0.97656	0.95305
cg1911297	MGC1612	GR-alpha [	7	11	0.207689	AGAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	58	62	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	166	170	0.207689	CCTTT	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	245	249	0.207689	CCTTT	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	540	544	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	819	823	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	847	851	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	917	921	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1145	1149	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1162	1166	0.207689	AGAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1208	1212	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1565	1569	0.207689	AGAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1654	1658	0.207689	CCTTT	7.8125	7.81264

cg1911297	MGC1612	GR-alpha [	1720	1724	0.207689	CCTTT	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1823	1827	0.207689	AGAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1927	1931	0.207689	AAAGG	7.8125	7.81264
cg1911297	MGC1612	Elk-1 [T00	1049	1057	0.134348	TGGAGG.	0.06104	0.06047
cg1911297	MGC1612	c-Ets-1 [T(	489	495	0.128087	CTTCCTC	0.24414	0.2429
cg1911297	MGC1612	c-Ets-1 [T(	1051	1057	0.128087	GAGGAA	0.24414	0.2429
cg1911297	MGC1612	GR-alpha [	195	199	0	ACAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	313	317	0	CCTGT	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1132	1136	0	ACAGG	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1229	1233	0	CCTGT	7.8125	7.81264
cg1911297	MGC1612	GR-alpha [	1660	1664	0	CCTGT	7.8125	7.81264
cg1911297	MGC1612	AP-2alpha	1037	1042	0	GCAGGC	0.97656	0.95305
cg1911297	MGC1612	AP-2alpha	1212	1217	0	GCAGGC	0.97656	0.95305
cg1911297	MGC1612	RXR-alpha	1450	1456	0	TGAACC(	0.24414	0.2444
cg1911297	MGC1612	Pax-5 [T0(	1069	1075	0	GGGCTT(	1.09863	1.06846
cg1911297	MGC1612	Pax-5 [T0(	1258	1264	0	GGGCCT(	1.09863	1.06846
cg1911297	MGC1612	Pax-5 [T0(	1331	1337	0	GGGCTG(	1.09863	1.06846
cg1911297	MGC1612	Pax-5 [T0(	1370	1376	0	CCGGCC(	1.09863	1.06846
cg1911297	MGC1612	Pax-5 [T0(	1483	1489	0	CCGGCC(	1.09863	1.06846
cg1911297	MGC1612	Pax-5 [T0(	1794	1800	0	CCAGCC(	1.09863	1.06846
cg1911297	MGC1612	TFII-I [T0(	538	543	0	GGAAAG	1.46484	1.45997
cg1911297	MGC1612	TFII-I [T0(	1614	1619	0	GGAAAG	1.46484	1.45997
cg1911297	MGC1612	TFII-I [T0(	1661	1666	0	CTGTCC	1.46484	1.45997
cg1911297	MGC1612	STAT4 [T(	39	44	0	ATTTCC	0.48828	0.49387
cg1911297	MGC1612	c-Ets-1 [T(	1082	1088	0	CAGGAA	0.24414	0.2429
cg1911297	MGC1612	YY1 [T00!	1062	1065	0	ATGG	7.8125	7.81711
cg1911297	MGC1612	YY1 [T00!	1306	1309	0	ATGG	7.8125	7.81711
cg1911297	MGC1612	YY1 [T00!	1554	1557	0	CCAT	7.8125	7.81711
cg1911297	MGC1612	YY1 [T00!	1649	1652	0	ATGG	7.8125	7.81711
cg1911297	MGC1612	YY1 [T00!	1665	1668	0	CCAT	7.8125	7.81711
cg1911297	MGC1612	YY1 [T00!	1809	1812	0	ATGG	7.8125	7.81711
cg1911297	MGC1612	GCF [T00:	1274	1282	0	GCGCTG(	0.09155	0.08765
cg1911297	MGC1612	ER-alpha [	570	574	0	GGTCA	1.95312	1.9404
cg1911297	MGC1612	ER-alpha [	983	987	0	GGTCA	1.95312	1.9404
cg1911297	MGC1612	C/EBPbeta	180	183	0	TTGT	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	248	251	0	TTGT	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	361	364	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	375	378	0	TTGT	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	382	385	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	469	472	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	500	503	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	609	612	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	641	644	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	654	657	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	680	683	0	TTGT	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	711	714	0	TTGC	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	713	716	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	753	756	0	TTGC	15.625	15.71349

cg1911297	MGC1612	C/EBPbeta	770	773	0	TTGT	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	799	802	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	825	828	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	914	917	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	940	943	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	964	967	0	TTGC	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1180	1183	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1206	1209	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1254	1257	0	TTGC	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1414	1417	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1602	1605	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1699	1702	0	TTGC	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1754	1757	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1835	1838	0	TTGT	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1852	1855	0	GCAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1925	1928	0	ACAA	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1961	1964	0	TTGT	15.625	15.71349
cg1911297	MGC1612	C/EBPbeta	1992	1995	0	GCAA	15.625	15.71349
cg1911297	MGC1612	TFIID [T0	53	59	0	TTTTTAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	126	132	0	TTTTCAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	143	149	0	TTTAAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	326	332	0	TTTTTAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	328	334	0	TTTAAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	329	335	0	TTAAAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	330	336	0	TAAAAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	403	409	0	TTTTAGA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	658	664	0	TTTAAA	1.09863	1.13474
cg1911297	MGC1612	TFIID [T0	1722	1728	0	TTTTCTA	1.09863	1.13474
cg1911297	MGC1612	FOXP3 [T	360	365	0	AACAAC	1.46484	1.47315
cg1911297	MGC1612	FOXP3 [T	381	386	0	CACAAC	1.46484	1.47315
cg1911297	MGC1612	FOXP3 [T	679	684	0	GTTGTT	1.46484	1.47315
cg1911297	MGC1612	FOXP3 [T	1834	1839	0	GTTGTG	1.46484	1.47315
cg1911297	MGC1612	GR-beta [T	37	41	0	ACATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	50	54	0	ACATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	157	161	0	AAATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	308	312	0	ACATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	323	327	0	AAATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	324	328	0	AATTT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	334	338	0	AAATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	394	398	0	AATGT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	401	405	0	AATTT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	592	596	0	AAATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	622	626	0	ACATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	634	638	0	ACATT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	656	660	0	AATTT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	691	695	0	AATTT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	736	740	0	AATGT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [T	764	768	0	ACATT	3.90625	3.99611

cg1911297	MGC1612	GR-beta [	831	835	0	AATGT	3.90625	3.99611
cg1911297	MGC1612	GR-beta [	887	891	0	AATTT	3.90625	3.99611
cg1911297	MGC1612	C/EBPalp	1252	1258	0	GATTGC	0.24414	0.2444
cg1911297	MGC1612	NF-AT1 [	518	526	0	GGAAAA	0.01526	0.01569
cg1911297	MGC1612	PR B [T00	225	231	0	AACAGT	0.36621	0.36944
cg1911297	MGC1612	PR B [T00	1733	1739	0	GACTGT	0.36621	0.36944
cg1911297	MGC1612	PR B [T00	1854	1860	0	AACAGT	0.36621	0.36944
cg1911297	MGC1612	PR A [T01	225	231	0	AACAGT	0.36621	0.36944
cg1911297	MGC1612	PR A [T01	1733	1739	0	GACTGT	0.36621	0.36944
cg1911297	MGC1612	PR A [T01	1854	1860	0	AACAGT	0.36621	0.36944
cg1911297	MGC1612	GR [T050	766	772	0	ATTTTT	0.36621	0.37562
cg1911297	MGC1612	GR [T050	1603	1609	0	CAAAAA	0.36621	0.37562
cg1911297	MGC1612	GR [T050	1973	1979	0	ATTTTT	0.36621	0.37562
cg1911297	MGC1612	WT1 [T00	1392	1400	0	CGCCCC	0.00763	0.00729
cg1911297	MGC1612	IRF-2 [T0	600	605	0	TCACTT	0.48828	0.49387
cg1911297	MGC1612	c-Myc [T0	476	481	0	CACGTG	0.48828	0.48199
cg2454155	MRVI1	c-Ets-1 [T	1185	1191	9.969337	TGGGAA	0.24414	0.2459
cg2454155	MRVI1	LEF-1 [T0	372	379	9.937995	TGCCAA	0.12207	0.12154
cg2454155	MRVI1	STAT1bet	941	950	9.807397	GCAGGG	0.14877	0.1495
cg2454155	MRVI1	NF-1 [T00	1592	1599	9.761671	AGCTCC	0.24414	0.24405
cg2454155	MRVI1	NF-1 [T00	1877	1884	9.761671	TTGGAG	0.24414	0.24405
cg2454155	MRVI1	PR B [T00	221	227	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	PR B [T00	1456	1462	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	PR B [T00	1719	1725	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	PR B [T00	1916	1922	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	PR A [T01	221	227	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	PR A [T01	1456	1462	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	PR A [T01	1719	1725	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	PR A [T01	1916	1922	9.743489	AACACA	1.09863	1.10292
cg2454155	MRVI1	c-Jun [T00	275	281	9.717135	CAGGTC	0.73242	0.73031
cg2454155	MRVI1	Pax-5 [T0	306	312	9.552105	GGGCGT	1.46484	1.43083
cg2454155	MRVI1	TFIID [T0	31	37	9.552105	TTTGGA	1.46484	1.48472
cg2454155	MRVI1	TFIID [T0	1911	1917	9.552105	TGGCAA	1.46484	1.48472
cg2454155	MRVI1	NF-1 [T00	1819	1826	9.535536	TTGGCC	0.73242	0.73053
cg2454155	MRVI1	NF-AT1 [	1518	1526	9.521781	GGAAAT	0.16785	0.1682
cg2454155	MRVI1	TFII-I [T0	25	30	9.512894	TTTTCC	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	34	39	9.512894	GGAAAA	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	145	150	9.512894	GGAAGG	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	227	232	9.512894	GGATGG	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	232	237	9.512894	GGAAGG	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	630	635	9.512894	CCATCC	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	882	887	9.512894	GGACTT	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	933	938	9.512894	GGATAA	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	1025	1030	9.512894	GTATCC	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	1070	1075	9.512894	GGACAC	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	1086	1091	9.512894	GGACGG	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	1520	1525	9.512894	AAATCC	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	1620	1625	9.512894	GGACTT	7.32422	7.29728

cg2454155	MRVI1	TFII-I [T0	1689	1694	9.512894	GGACAC	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	1707	1712	9.512894	GGATTT	7.32422	7.29728
cg2454155	MRVI1	TFII-I [T0	1799	1804	9.512894	AAATCC	7.32422	7.29728
cg2454155	MRVI1	FOXP3 [T	218	223	9.512894	AAGAAC	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	394	399	9.512894	GTTGCC	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	555	560	9.512894	AGCAAC	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	587	592	9.512894	CCCAAC	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	619	624	9.512894	GTTTAG	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	695	700	9.512894	GTTATT	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	733	738	9.512894	GTTATT	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	845	850	9.512894	CAGAAC	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	1054	1059	9.512894	GGCAAC	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	1671	1676	9.512894	GTTGCT	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	1716	1721	9.512894	ATAAAC	7.32422	7.35678
cg2454155	MRVI1	FOXP3 [T	1747	1752	9.512894	GTTATT	7.32422	7.35678
cg2454155	MRVI1	Ik-1 [T027	1261	1273	9.497194	GAATGG	0.02941	0.02907
cg2454155	MRVI1	Ik-1 [T027	1884	1896	9.497194	TCCCAG	0.02941	0.02907
cg2454155	MRVI1	TCF-4E [T	30	36	9.453578	CTTTGG	0.48828	0.49215
cg2454155	MRVI1	EBF [T05	1004	1014	9.441272	CACCCT	0.06866	0.06676
cg2454155	MRVI1	EBF [T05	1159	1169	9.441272	GACCCT	0.06866	0.06676
cg2454155	MRVI1	PPAR-alph	980	990	9.39865	GGCTGG	0.00286	0.0028
cg2454155	MRVI1	NFI/CTF [	374	381	9.352332	CCAAAG	0.54932	0.54821
cg2454155	MRVI1	NFI/CTF [	1574	1581	9.352332	CCAAGG	0.54932	0.54821
cg2454155	MRVI1	POU2F2 (	1451	1461	9.350233	TGTTTA	0.03433	0.03518
cg2454155	MRVI1	AP-1 [T00	1440	1448	9.3434	TGTTAG	0.09155	0.09305
cg2454155	MRVI1	LEF-1 [T0	988	995	9.313676	CTTTGG	0.21362	0.2139
cg2454155	MRVI1	AP-1 [T00	1771	1779	9.203282	AATTAG	0.24414	0.24693
cg2454155	MRVI1	HNF-1C [	613	621	9.170047	GTTAAA	0.12207	0.12495
cg2454155	MRVI1	c-Ets-1 [T	665	671	9.148774	GTTCCC	0.85449	0.85523
cg2454155	MRVI1	LEF-1 [T0	398	405	9.099721	CCACAA	0.54932	0.55326
cg2454155	MRVI1	c-Myb [T0	726	733	9.024874	AAACTG	0.39673	0.40028
cg2454155	MRVI1	LEF-1 [T0	30	37	8.973041	CTTTGG	0.54932	0.55326
cg2454155	MRVI1	GR [T050	592	598	8.971049	CAAAGC	0.61035	0.61632
cg2454155	MRVI1	GR [T050	1815	1821	8.971049	GCTTTC	0.61035	0.61632
cg2454155	MRVI1	GR [T050	1914	1920	8.971049	CAAACA	0.61035	0.61632
cg2454155	MRVI1	c-Ets-2 [T	61	69	8.912323	CTCTAG	0.27466	0.27495
cg2454155	MRVI1	c-Ets-2 [T	1513	1521	8.912323	GCCCAG	0.27466	0.27495
cg2454155	MRVI1	c-Ets-1 [T	1089	1095	8.8926	CGGGAA	0.85449	0.85523
cg2454155	MRVI1	c-Ets-1 [T	1804	1810	8.8926	CGGGAA	0.85449	0.85523
cg2454155	MRVI1	T3R-beta1	1003	1011	8.885459	TCACCC	0.2594	0.25766
cg2454155	MRVI1	c-Jun [T00	792	798	8.832178	AAGGTC	0.61035	0.61059
cg2454155	MRVI1	NFI/CTF [	1174	1181	8.814757	CCAAGA	0.48828	0.48804
cg2454155	MRVI1	NF-1 [T00	370	377	8.790071	CTTGCC	0.24414	0.24467
cg2454155	MRVI1	XBP-1 [T	1396	1401	8.75604	ATGATA	2.92969	2.9674
cg2454155	MRVI1	XBP-1 [T	1434	1439	8.75604	ATGAGA	2.92969	2.9674
cg2454155	MRVI1	XBP-1 [T	1471	1476	8.75604	TCTCAT	2.92969	2.9674
cg2454155	MRVI1	XBP-1 [T	1496	1501	8.75604	ATGAGC	2.92969	2.9674
cg2454155	MRVI1	XBP-1 [T	1584	1589	8.75604	GATCAT	2.92969	2.9674

cg2454155	MRVI1	STAT1bet	604	613	8.695301	CCCTGG	0.22316	0.22446
cg2454155	MRVI1	STAT1bet	742	751	8.695301	CTTTCCT	0.22316	0.22446
cg2454155	MRVI1	STAT1bet	1382	1391	8.695301	AAGTGG	0.22316	0.22446
cg2454155	MRVI1	HNF-1B [	1440	1448	8.688037	TGTTAGT	0.11444	0.11669
cg2454155	MRVI1	NF-AT1 [	22	30	8.599808	GGCTTTT	0.10681	0.10725
cg2454155	MRVI1	HNF-1B [	1451	1459	8.56333	TGTTTAA	0.11444	0.11669
cg2454155	MRVI1	c-Myb [T0	1949	1956	8.443873	ATCAGTT	0.30518	0.30924
cg2454155	MRVI1	RAR-beta:	406	417	8.434402	GGGCCC	0.00954	0.00939
cg2454155	MRVI1	PPAR-alph	877	887	8.384593	GGCTGG	0.02003	0.01963
cg2454155	MRVI1	HNF-3alph	1698	1705	8.343064	TTTAAAT	0.27466	0.28528
cg2454155	MRVI1	c-Ets-2 [T	1502	1510	8.339336	TTCCTGC	0.13733	0.13681
cg2454155	MRVI1	PR B [T00	203	209	8.338824	AACAGG	1.09863	1.10009
cg2454155	MRVI1	PR B [T00	1334	1340	8.338824	AACAGC	1.09863	1.10009
cg2454155	MRVI1	PR A [T01	203	209	8.338824	AACAGG	1.09863	1.10009
cg2454155	MRVI1	PR A [T01	1334	1340	8.338824	AACAGC	1.09863	1.10009
cg2454155	MRVI1	GR-alpha [	90	94	8.281568	GGAGG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	146	150	8.281568	GAAGG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	233	237	8.281568	GAAGG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	296	300	8.281568	CAAGG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	661	665	8.281568	GAAGG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	669	673	8.281568	CCTCC	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	713	717	8.281568	GGAGG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	746	750	8.281568	CCTCC	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	850	854	8.281568	CCTCG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	863	867	8.281568	CCTCC	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	1015	1019	8.281568	CCTCC	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	1131	1135	8.281568	CCTCC	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	1318	1322	8.281568	CCTTG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	1325	1329	8.281568	CCTCC	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	1555	1559	8.281568	CCTTG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	1575	1579	8.281568	CAAGG	7.8125	7.72956
cg2454155	MRVI1	GR-alpha [	1631	1635	8.281568	CCTTC	7.8125	7.72956
cg2454155	MRVI1	EBF [T05	969	979	8.272615	GGCTCA	0.03052	0.02952
cg2454155	MRVI1	NF-AT1 [	945	953	8.223794	GGAAAG	0.1297	0.12988
cg2454155	MRVI1	p53 [T006	405	411	8.208781	GGGGCC	0.48828	0.47377
cg2454155	MRVI1	p53 [T006	1010	1016	8.208781	GGGCCC	0.48828	0.47377
cg2454155	MRVI1	ENKTF-1	939	946	8.19852	TGGCAG	0.73242	0.71737
cg2454155	MRVI1	ENKTF-1	1938	1945	8.19852	CCTGGC	0.73242	0.71737
cg2454155	MRVI1	IRF-1 [T0	30	38	8.151819	CTTTGG	0.25177	0.25263
cg2454155	MRVI1	IRF-1 [T0	476	484	8.151819	TTTCCA	0.25177	0.25263
cg2454155	MRVI1	GR-alpha [	63	67	8.073878	CTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	87	91	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	98	102	8.073878	GCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	134	138	8.073878	CTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	141	145	8.073878	GCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	158	162	8.073878	CCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	256	260	8.073878	GCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	289	293	8.073878	CCAGG	7.8125	7.72238

cg2454155	MRVI1	GR-alpha [	310	314	8.073878	GTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	421	425	8.073878	CTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	605	609	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	691	695	8.073878	GCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	701	705	8.073878	CTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	922	926	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	941	945	8.073878	GCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	977	981	8.073878	GCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1007	1011	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1079	1083	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1104	1108	8.073878	CCTGC	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1124	1128	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1150	1154	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1162	1166	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1201	1205	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1216	1220	8.073878	GCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1267	1271	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1305	1309	8.073878	CCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1414	1418	8.073878	CTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1504	1508	8.073878	CCTGC	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1510	1514	8.073878	CCTGC	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1515	1519	8.073878	CCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1551	1555	8.073878	CCTGC	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1569	1573	8.073878	CCTAC	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1580	1584	8.073878	CCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1661	1665	8.073878	CCTAG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1662	1666	8.073878	CTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1811	1815	8.073878	CCTAG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1870	1874	8.073878	CTAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1886	1890	8.073878	CCAGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1909	1913	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1938	1942	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	GR-alpha [	1986	1990	8.073878	CCTGG	7.8125	7.72238
cg2454155	MRVI1	Pax-5 [T0	82	88	8.014558	GGAGCC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	117	123	8.014558	GGGCAC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	149	155	8.014558	GGGCAC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	236	242	8.014558	GGGCAG	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	405	411	8.014558	GGGGCC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	406	412	8.014558	GGGCCC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	907	913	8.014558	GGAGCC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	968	974	8.014558	GGGCTC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	1009	1015	8.014558	TGGGCC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	1010	1016	8.014558	GGGCCC	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	1220	1226	8.014558	GGGCTG	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	1566	1572	8.014558	GGGCCT	2.19727	2.14502
cg2454155	MRVI1	Pax-5 [T0	1625	1631	8.014558	TCAGCC	2.19727	2.14502
cg2454155	MRVI1	TFIID [T0	32	38	8.014558	TTGGAA	2.19727	2.24348
cg2454155	MRVI1	TFIID [T0	476	482	8.014558	TTTCCA	2.19727	2.24348

cg2454155	MRVI1	TFIID [T0	1710	1716	8.014558	TTTCAG	2.19727	2.24348
cg2454155	MRVI1	TFIID [T0	1755	1761	8.014558	TCTGAA	2.19727	2.24348
cg2454155	MRVI1	TFIID [T0	1793	1799	8.014558	TTTGAT	2.19727	2.24348
cg2454155	MRVI1	MEF-2A [	242	252	7.982343	AGACAG	0.04005	0.04149
cg2454155	MRVI1	MEF-2A [	1785	1795	7.982343	TATTTTT	0.04005	0.04149
cg2454155	MRVI1	HNF-1C [	1441	1449	7.930275	GTTAGT	0.19836	0.20224
cg2454155	MRVI1	p53 [T006	82	88	7.833758	GGAGCC	0.48828	0.47377
cg2454155	MRVI1	p53 [T006	907	913	7.833758	GGAGCC	0.48828	0.47377
cg2454155	MRVI1	RXR-alph	583	589	7.815913	GCCACC	0.24414	0.24104
cg2454155	MRVI1	RXR-alph	1832	1838	7.815913	GCCACC	0.24414	0.24104
cg2454155	MRVI1	c-Ets-2 [T	330	338	7.76635	ACACAG	0.32043	0.32298
cg2454155	MRVI1	c-Ets-2 [T	410	418	7.76635	CCACAG	0.32043	0.32298
cg2454155	MRVI1	c-Ets-2 [T	1194	1202	7.76635	TTCCTG	0.32043	0.32298
cg2454155	MRVI1	NF-AT1 [	415	423	7.744746	GGAAAG	0.19836	0.19941
cg2454155	MRVI1	NF-AT1 [	608	616	7.744746	GGAAAG	0.19836	0.19941
cg2454155	MRVI1	NF-AT1 [	739	747	7.744746	CTCCTTT	0.19836	0.19941
cg2454155	MRVI1	IRF-1 [T0	604	612	7.732782	CCCTGG	0.14496	0.14449
cg2454155	MRVI1	p53 [T006	984	990	7.641867	GGGCCT	0.73242	0.7186
cg2454155	MRVI1	AR [T000	1725	1733	7.588908	GGACAT	0.25177	0.25079
cg2454155	MRVI1	NFI/CTF [	1241	1248	7.587343	ACTCTT	0.36621	0.36674
cg2454155	MRVI1	NFI/CTF [	1815	1822	7.587343	GCTTTT	0.36621	0.36674
cg2454155	MRVI1	NF-AT1 [	34	42	7.587189	GGAAAA	0.19836	0.19941
cg2454155	MRVI1	c-Jun [T00	1310	1316	7.538568	GATGTC	0.48828	0.48775
cg2454155	MRVI1	GR [T050	175	181	7.527031	CAAAAG	1.83105	1.86007
cg2454155	MRVI1	GR [T050	375	381	7.527031	CAAAGC	1.83105	1.86007
cg2454155	MRVI1	GR [T050	490	496	7.527031	CAAAAG	1.83105	1.86007
cg2454155	MRVI1	GR [T050	1790	1796	7.527031	TTGTTT	1.83105	1.86007
cg2454155	MRVI1	HNF-1C [	1450	1458	7.498386	GTGTTT	0.08392	0.08549
cg2454155	MRVI1	RAR-beta	1804	1813	7.47824	CGGGAA	0.24414	0.24343
cg2454155	MRVI1	IRF-1 [T0	1514	1522	7.477948	CCCAGG	0.14496	0.14449
cg2454155	MRVI1	c-Myb [T0	609	616	7.442719	GAAAGT	0.42725	0.43114
cg2454155	MRVI1	RXR-alph	1023	1029	7.411919	GGGTAT	0.12207	0.12139
cg2454155	MRVI1	SRY [T00	397	405	7.175614	GCCACA	0.30518	0.30739
cg2454155	MRVI1	XBP-1 [T	1371	1376	7.172312	CCTCAT	2.92969	2.97018
cg2454155	MRVI1	XBP-1 [T	1492	1497	7.172312	ATGAAT	2.92969	2.97018
cg2454155	MRVI1	XBP-1 [T	1824	1829	7.172312	CATCAT	2.92969	2.97018
cg2454155	MRVI1	p53 [T006	406	412	7.153797	GGGCCC	1.09863	1.07125
cg2454155	MRVI1	p53 [T006	1009	1015	7.153797	TGGGCC	1.09863	1.07125
cg2454155	MRVI1	Ik-1 [T027	872	884	7.122895	AGAGGG	0.01064	0.01049
cg2454155	MRVI1	TFIID [T0	620	626	7.082373	TTTAGC	0.12207	0.12407
cg2454155	MRVI1	c-Ets-1 [T	943	949	7.071349	AGGGAA	0.73242	0.73099
cg2454155	MRVI1	HOXD9 [	1730	1739	7.030183	TACTTG	0.07629	0.0789
cg2454155	MRVI1	HOXD10 [	1730	1739	7.030183	TACTTG	0.07629	0.0789
cg2454155	MRVI1	HNF-3alp	451	458	7.000129	CATTT	0.82397	0.84946
cg2454155	MRVI1	HNF-3alp	1385	1392	7.000129	TGGAAA	0.82397	0.84946
cg2454155	MRVI1	HNF-3alp	1785	1792	7.000129	TATTTTT	0.82397	0.84946
cg2454155	MRVI1	NF-1 [T00	1170	1177	6.948522	AGCGCC	0.48828	0.4856
cg2454155	MRVI1	ENKTF-1	809	816	6.942764	TGGCTC	1.46484	1.44228

cg2454155	MRVI1	ENKTF-1	924	931	6.942764	TGGCTC	1.46484	1.44228
cg2454155	MRVI1	ENKTF-1	1264	1271	6.942764	TGGCCT	1.46484	1.44228
cg2454155	MRVI1	ENKTF-1	1460	1467	6.942764	CACTGC	1.46484	1.44228
cg2454155	MRVI1	VDR [T00	293	301	6.925682	GTTCAA	0.42725	0.43062
cg2454155	MRVI1	EBF [T05	84	94	6.872118	AGCCCT	0.03052	0.02964
cg2454155	MRVI1	HOXD9 [	1389	1398	6.852796	AATAAT	0.07629	0.0789
cg2454155	MRVI1	HOXD10 [	1389	1398	6.852796	AATAAT	0.07629	0.0789
cg2454155	MRVI1	PEA3 [T0	226	234	6.824411	AGGATG	0.22888	0.22933
cg2454155	MRVI1	PEA3 [T0	1308	1316	6.824411	GGGATG	0.22888	0.22933
cg2454155	MRVI1	AR [T000	1194	1202	6.817719	TTCCTGT	0.23651	0.23551
cg2454155	MRVI1	NFI/CTF [	1596	1603	6.786076	CCAAGC	0.73242	0.73214
cg2454155	MRVI1	p53 [T006	968	974	6.778774	GGGCTC	1.09863	1.07125
cg2454155	MRVI1	POU2F2 (	1734	1744	6.735173	TGTATT	0.04292	0.04408
cg2454155	MRVI1	AR [T000	1528	1536	6.675397	ACCCTG	0.19836	0.19597
cg2454155	MRVI1	TFII-I [T0	914	919	6.581441	CACTCC	0.97656	0.97366
cg2454155	MRVI1	TFII-I [T0	1111	1116	6.581441	ATCTCC	0.97656	0.97366
cg2454155	MRVI1	TFII-I [T0	1271	1276	6.581441	GGAGAT	0.97656	0.97366
cg2454155	MRVI1	FOXP3 [T	74	79	6.581441	TTCAAC	0.97656	0.99397
cg2454155	MRVI1	FOXP3 [T	542	547	6.581441	TAAAAC	0.97656	0.99397
cg2454155	MRVI1	FOXP3 [T	724	729	6.581441	TAAAAC	0.97656	0.99397
cg2454155	MRVI1	RXR-alph	1690	1696	6.563693	GACACC	0.24414	0.2434
cg2454155	MRVI1	p53 [T006	1220	1226	6.563521	GGGCTG	0.48828	0.47541
cg2454155	MRVI1	PPAR-alph	1300	1310	6.51544	CAGCCC	0.03719	0.03639
cg2454155	MRVI1	AR [T000	1689	1697	6.50872	GGACAC	0.19836	0.19597
cg2454155	MRVI1	XBP-1 [T	281	286	6.478682	ATGCCA	0.97656	0.97062
cg2454155	MRVI1	XBP-1 [T	581	586	6.478682	ATGCCA	0.97656	0.97062
cg2454155	MRVI1	XBP-1 [T	1402	1407	6.478682	ATGCCC	0.97656	0.97062
cg2454155	MRVI1	c-Jun [T00	1418	1424	6.462218	GTAGTC	0.61035	0.60769
cg2454155	MRVI1	c-Jun [T00	1851	1857	6.462218	GTAGTC	0.61035	0.60769
cg2454155	MRVI1	C/EBPalph	795	801	6.460799	GTCAAT	0.48828	0.49071
cg2454155	MRVI1	c-Ets-1 [T	32	38	6.423689	TTGGAA	0.48828	0.48798
cg2454155	MRVI1	c-Ets-1 [T	476	482	6.423689	TTTCCA	0.48828	0.48798
cg2454155	MRVI1	c-Myb [T0	1181	1188	6.422836	AAACTG	0.30518	0.3056
cg2454155	MRVI1	RAR-beta	1654	1663	6.378264	GAGAAA	0.18311	0.183
cg2454155	MRVI1	TCF-4E [T	590	596	6.302385	AACAAA	0.61035	0.61344
cg2454155	MRVI1	TCF-4E [T	1093	1099	6.302385	AACAAA	0.61035	0.61344
cg2454155	MRVI1	GR-alpha [	263	267	6.263098	TAAGG	3.90625	3.91061
cg2454155	MRVI1	GR-alpha [	652	656	6.263098	TAAGG	3.90625	3.91061
cg2454155	MRVI1	GR-alpha [	791	795	6.263098	TAAGG	3.90625	3.91061
cg2454155	MRVI1	GR-alpha [	963	967	6.263098	CCTCA	3.90625	3.91061
cg2454155	MRVI1	GR-alpha [	1362	1366	6.263098	CCTCA	3.90625	3.91061
cg2454155	MRVI1	GR-alpha [	1371	1375	6.263098	CCTCA	3.90625	3.91061
cg2454155	MRVI1	GR-alpha [	1898	1902	6.263098	CCTCA	3.90625	3.91061
cg2454155	MRVI1	GR-alpha [	1924	1928	6.263098	CCTTA	3.90625	3.91061
cg2454155	MRVI1	NF-AT2 [	471	480	6.245826	CACACT	0.04196	0.04255
cg2454155	MRVI1	IRF-1 [T0	743	751	6.24301	TTTCCTC	0.16785	0.16909
cg2454155	MRVI1	HNF-1B [	1746	1754	6.211503	TGTTATT	0.09918	0.10196
cg2454155	MRVI1	NF-kappa	1041	1051	6.209705	TGGCAG	0.04053	0.03971

cg2454155	MRVI1	c-Ets-1 [T	1384	1390	6.167515	GTGGAA	0.36621	0.36731
cg2454155	MRVI1	RXR-alph	1569	1575	6.119461	CCTACC	0.73242	0.72249
cg2454155	MRVI1	GR-alpha [	441	445	6.055408	TCAGG	3.90625	3.9065
cg2454155	MRVI1	GR-alpha [	460	464	6.055408	CCTGA	3.90625	3.9065
cg2454155	MRVI1	GR-alpha [	514	518	6.055408	TTAGG	3.90625	3.9065
cg2454155	MRVI1	GR-alpha [	722	726	6.055408	CCTAA	3.90625	3.9065
cg2454155	MRVI1	GR-alpha [	965	969	6.055408	TCAGG	3.90625	3.9065
cg2454155	MRVI1	GR-alpha [	972	976	6.055408	TCAGG	3.90625	3.9065
cg2454155	MRVI1	GR-alpha [	1422	1426	6.055408	TCAGG	3.90625	3.9065
cg2454155	MRVI1	c-Ets-1 [T	606	612	6.039428	CTGGAA	0.36621	0.36731
cg2454155	MRVI1	E2F [T002	1169	1178	5.945058	CAGCGC	0.04578	0.04499
cg2454155	MRVI1	p53 [T006	1566	1572	5.883561	GGGCCT	0.61035	0.594
cg2454155	MRVI1	STAT4 [T	145	150	5.882353	GGAAGG	0.48828	0.48408
cg2454155	MRVI1	STAT4 [T	232	237	5.882353	GGAAGG	0.48828	0.48408
cg2454155	MRVI1	IRF-1 [T0	411	419	5.861409	CACAGG	0.16785	0.16909
cg2454155	MRVI1	c-Ets-1 [T	230	236	5.814485	TGGGAA	0.36621	0.36731
cg2454155	MRVI1	c-Ets-1 [T	675	681	5.814485	CTTCCC	0.36621	0.36731
cg2454155	MRVI1	STAT1bet	1514	1523	5.796867	CCCAGG	0.1545	0.1557
cg2454155	MRVI1	VDR [T00	45	53	5.771401	GTTCAA	0.42725	0.42999
cg2454155	MRVI1	ENKTF-1	592	599	5.687009	CAAAGC	0.73242	0.7249
cg2454155	MRVI1	ENKTF-1	1163	1170	5.687009	CTGGGC	0.73242	0.7249
cg2454155	MRVI1	ENKTF-1	1575	1582	5.687009	CAAGGC	0.73242	0.7249
cg2454155	MRVI1	c-Ets-1 [T	143	149	5.686398	AGGGAA	0.36621	0.3623
cg2454155	MRVI1	AP-2alpha	1890	1895	5.568965	GCCTAT	0.48828	0.4878
cg2454155	MRVI1	C/EBPalp	1875	1881	5.565669	GATTGG	0.73242	0.74391
cg2454155	MRVI1	NFI/CTF [	1873	1880	5.558661	GGGATT	0.54932	0.55038
cg2454155	MRVI1	c-Ets-1 [T	161	167	5.558311	GGGGAA	0.36621	0.3623
cg2454155	MRVI1	GATA-2 [	933	941	5.555555	GGATAA	0.18311	0.1835
cg2454155	MRVI1	TFIID [T0	782	788	5.544826	TTTACC	0.73242	0.75085
cg2454155	MRVI1	TFIID [T0	1453	1459	5.544826	TTTAAC	0.73242	0.75085
cg2454155	MRVI1	TFIID [T0	1795	1801	5.544826	TGATAA	0.73242	0.75085
cg2454155	MRVI1	p53 [T006	1625	1631	5.508538	TCAGCC	0.61035	0.59991
cg2454155	MRVI1	HNF-1A [	1345	1352	5.466509	GTCTTA	0.24414	0.2469
cg2454155	MRVI1	EBF [T05	1302	1312	5.295103	GCCCCA	0.01907	0.0183
cg2454155	MRVI1	RXR-alph	425	431	5.271235	GGGTTG	0.61035	0.6044
cg2454155	MRVI1	RXR-alph	1116	1122	5.271235	CCCACC	0.61035	0.6044
cg2454155	MRVI1	NFI/CTF [	479	486	5.249259	CCAACG	0.24414	0.24103
cg2454155	MRVI1	p53 [T006	306	312	5.133514	GGGCGT	0.48828	0.47747
cg2454155	MRVI1	AR [T000	190	198	5.104816	GGACAG	0.11444	0.11247
cg2454155	MRVI1	AR [T000	316	324	5.104816	GGACAG	0.11444	0.11247
cg2454155	MRVI1	AP-2alpha	986	991	5.100982	GCCTTT	0.97656	0.97567
cg2454155	MRVI1	RXR-alph	623	629	5.089356	AGCACC	0.48828	0.484
cg2454155	MRVI1	RXR-alph	637	643	5.089356	AGCACC	0.48828	0.484
cg2454155	MRVI1	USF2 [T0	1545	1554	5.052423	TCTTCAC	0.103	0.10178
cg2454155	MRVI1	GR-beta [	1206	1210	5.042296	GGATT	3.90625	3.95351
cg2454155	MRVI1	GR-beta [	1248	1252	5.042296	GGATT	3.90625	3.95351
cg2454155	MRVI1	GR-beta [	1427	1431	5.042296	GGATT	3.90625	3.95351
cg2454155	MRVI1	GR-beta [	1521	1525	5.042296	AATCC	3.90625	3.95351

cg2454155	MRVI1	GR-beta [T	1707	1711	5.042296	GGATT	3.90625	3.95351
cg2454155	MRVI1	GR-beta [T	1735	1739	5.042296	GTATT	3.90625	3.95351
cg2454155	MRVI1	GR-beta [T	1800	1804	5.042296	AATCC	3.90625	3.95351
cg2454155	MRVI1	GR-beta [T	1874	1878	5.042296	GGATT	3.90625	3.95351
cg2454155	MRVI1	HOXD9 [T	1743	1752	5.035116	GACTGT	0.00763	0.00785
cg2454155	MRVI1	HOXD10 [	1743	1752	5.035116	GACTGT	0.00763	0.00785
cg2454155	MRVI1	C/EBPalph	429	435	5.024728	TGCAAT	0.97656	0.99332
cg2454155	MRVI1	NFI/CTF [	28	35	5.021086	TCCTTTC	0.24414	0.24103
cg2454155	MRVI1	RAR-beta:	968	979	4.98533	GGGCTC	0.00966	0.00942
cg2454155	MRVI1	PPAR-alph	1161	1171	4.88658	CCCTGG	0.01717	0.01681
cg2454155	MRVI1	IRF-1 [T0	1382	1390	4.881305	AAGTGG	0.1297	0.1302
cg2454155	MRVI1	NF-1 [T00	1293	1300	4.880836	TTGGCA	0.24414	0.24398
cg2454155	MRVI1	RXR-alpha	1525	1531	4.86724	CATACC	0.48828	0.484
cg2454155	MRVI1	NF-Y [T0	1876	1883	4.867193	ATTGGA	0.36621	0.36847
cg2454155	MRVI1	HNF-1A [	508	515	4.828753	GTTAAG	0.36621	0.37179
cg2454155	MRVI1	NF-AT1 [T	1385	1394	4.823485	TGGAAA	0.07629	0.07704
cg2454155	MRVI1	c-Ets-1 [T	14	20	4.782565	CTTCCA	0.48828	0.49031
cg2454155	MRVI1	C/EBPalph	558	564	4.776286	AACAAT	0.97656	0.99332
cg2454155	MRVI1	TFII-I [T0	208	213	4.756447	GGACTG	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	517	522	4.756447	GGACTG	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	704	709	4.756447	GGATAT	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1044	1049	4.756447	CAGTCC	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1187	1192	4.756447	GGAATG	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1248	1253	4.756447	GGATTG	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1386	1391	4.756447	GGAAAT	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1518	1523	4.756447	GGAAAT	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1725	1730	4.756447	GGACAT	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1874	1879	4.756447	GGATTG	2.92969	2.93695
cg2454155	MRVI1	TFII-I [T0	1920	1925	4.756447	CAGTCC	2.92969	2.93695
cg2454155	MRVI1	FOXP3 [T	200	205	4.756447	AAAAAC	2.92969	2.96063
cg2454155	MRVI1	FOXP3 [T	1313	1318	4.756447	GTCAAC	2.92969	2.96063
cg2454155	MRVI1	FOXP3 [T	1840	1845	4.756447	GAAAAC	2.92969	2.96063
cg2454155	MRVI1	Ik-1 [T027	633	645	4.748597	TCCCAG	0.00313	0.00308
cg2454155	MRVI1	c-Ets-1 [T	64	70	4.539113	TAGGAA	0.85449	0.85764
cg2454155	MRVI1	STAT4 [T	13	18	4.411765	GCTTCC	1.95312	1.94235
cg2454155	MRVI1	STAT4 [T	163	168	4.411765	GGAAGC	1.95312	1.94235
cg2454155	MRVI1	STAT4 [T	335	340	4.411765	GGAAGC	1.95312	1.94235
cg2454155	MRVI1	STAT4 [T	655	660	4.411765	GGAAGA	1.95312	1.94235
cg2454155	MRVI1	STAT4 [T	674	679	4.411765	GCTTCC	1.95312	1.94235
cg2454155	MRVI1	STAT4 [T	1187	1192	4.411765	GGAATG	1.95312	1.94235
cg2454155	MRVI1	STAT4 [T	1500	1505	4.411765	GCTTCC	1.95312	1.94235
cg2454155	MRVI1	p53 [T006	1165	1171	4.33696	GGGCCA	0.24414	0.23584
cg2454155	MRVI1	p53 [T006	1987	1993	4.33696	CTGGCC	0.24414	0.23584
cg2454155	MRVI1	PEA3 [T0	1775	1783	4.30818	AGTCAT	0.13733	0.13791
cg2454155	MRVI1	RXR-alpha	1099	1105	4.24113	GGGACC	0.97656	0.9671
cg2454155	MRVI1	EBF [T05	962	972	4.230426	GCCTCA	0.0248	0.02398
cg2454155	MRVI1	AP-2alpha	1568	1573	4.211849	GCCTAC	0.97656	0.96469
cg2454155	MRVI1	Elk-1 [T00	651	659	4.204473	TTAAGG	0.09155	0.09227

cg2454155	MRVI1	GR-beta [T	68	72	4.201913	AATCG	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	249	253	4.201913	AATAG	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	432	436	4.201913	AATCG	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	537	541	4.201913	TGATT	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	561	565	4.201913	AATAA	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	696	700	4.201913	TTATT	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	734	738	4.201913	TTATT	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	1389	1393	4.201913	AATAA	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	1392	1396	4.201913	AATAA	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	1748	1752	4.201913	TTATT	7.8125	7.94607
cg2454155	MRVI1	GR-beta [T	1784	1788	4.201913	CTATT	7.8125	7.94607
cg2454155	MRVI1	NF-1 [T00	990	997	4.135372	TTGGGG	0.24414	0.24154
cg2454155	MRVI1	p53 [T006	101	107	4.125254	GGGCCG	0.73242	0.71379
cg2454155	MRVI1	p53 [T006	112	118	4.125254	GGGCCG	0.73242	0.71379
cg2454155	MRVI1	c-Ets-2 [T	650	658	4.091811	TTTAAG	0.16022	0.16243
cg2454155	MRVI1	PXR-1:RX	290	297	4.090374	CAGGTT	0.12207	0.12119
cg2454155	MRVI1	NF-AT1 [T	472	480	4.056854	ACACTT	0.07629	0.07734
cg2454155	MRVI1	IRF-1 [T0	941	949	4.035054	GCAGGG	0.1297	0.13087
cg2454155	MRVI1	C/EBPalph	1249	1255	4.019783	GATTGC	0.48828	0.49358
cg2454155	MRVI1	RXR-alpha	383	389	4.019014	AAGACC	0.97656	0.9671
cg2454155	MRVI1	RXR-alpha	1157	1163	4.019014	AAGACC	0.97656	0.9671
cg2454155	MRVI1	RXR-alpha	1559	1565	4.019014	GGGTAT	0.97656	0.9671
cg2454155	MRVI1	RXR-alpha	1656	1662	4.019014	GAAACC	0.97656	0.9671
cg2454155	MRVI1	c-Ets-2 [T	27	35	4.017001	TTCCTTT	0.16022	0.16243
cg2454155	MRVI1	Pax-5 [T0	984	990	4.007279	GGGCCT	1.09863	1.07975
cg2454155	MRVI1	Pax-5 [T0	993	999	4.007279	GGGCAG	1.09863	1.07975
cg2454155	MRVI1	Pax-5 [T0	1401	1407	4.007279	AATGCC	1.09863	1.07975
cg2454155	MRVI1	TFIID [T0	1736	1742	4.007279	TATTAA	1.09863	1.13456
cg2454155	MRVI1	AP-2alpha	296	301	3.970052	CAAGGC	0.97656	0.96469
cg2454155	MRVI1	AP-2alpha	1554	1559	3.970052	GCCTTG	0.97656	0.96469
cg2454155	MRVI1	AP-2alpha	1575	1580	3.970052	CAAGGC	0.97656	0.96469
cg2454155	MRVI1	AhR:Arnt	858	867	3.888628	GCACGC	0.02289	0.02208
cg2454155	MRVI1	c-Jun [T00	1442	1448	3.807346	TTAGTC	0.24414	0.24526
cg2454155	MRVI1	c-Jun [T00	1773	1779	3.807346	TTAGTC	0.24414	0.24526
cg2454155	MRVI1	NFI/CTF [	986	993	3.793671	GCCTTT	0.18311	0.18109
cg2454155	MRVI1	p53 [T006	284	290	3.750231	CCAGCC	0.73242	0.71379
cg2454155	MRVI1	p53 [T006	876	882	3.750231	GGGCTG	0.73242	0.71379
cg2454155	MRVI1	p53 [T006	1299	1305	3.750231	CCAGCC	0.73242	0.71379
cg2454155	MRVI1	NF-AT2 [T	1386	1395	3.571424	GGAAAT	0.03433	0.03499
cg2454155	MRVI1	p53 [T006	993	999	3.516613	GGGCAG	0.73242	0.7189
cg2454155	MRVI1	p53 [T006	1401	1407	3.516613	AATGCC	0.73242	0.7189
cg2454155	MRVI1	c-Ets-1 [T	1193	1199	3.462376	GTTCCT	0.61035	0.60765
cg2454155	MRVI1	NF-AT1 [T	472	481	3.445347	ACACTT	0.07629	0.07722
cg2454155	MRVI1	NF-AT1 [T	607	616	3.445347	TGGAAA	0.07629	0.07722
cg2454155	MRVI1	RXR-alpha	443	449	3.392904	AGGACC	1.09863	1.08572
cg2454155	MRVI1	RXR-alpha	1002	1008	3.392904	CTCACC	1.09863	1.08572
cg2454155	MRVI1	RXR-alpha	1806	1812	3.392904	GGAACC	1.09863	1.08572
cg2454155	MRVI1	T3R-beta1	1548	1556	3.370634	TCACCT	0.27466	0.2755

cg2454155	MRVI1	GR-beta [T	502	506	3.361531	AATCT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [T	526	530	3.361531	AGATT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [T	1273	1277	3.361531	AGATT	3.90625	3.99611
cg2454155	MRVI1	IRF-1 [T0	26	34	3.347186	TTTCCTT	0.06866	0.06927
cg2454155	MRVI1	AP-2alpha	6	11	3.229049	GCCTCT	0.48828	0.48238
cg2454155	MRVI1	AP-2alpha	252	257	3.229049	AGAGGC	0.48828	0.48238
cg2454155	MRVI1	AP-2alpha	687	692	3.229049	AGAGGC	0.48828	0.48238
cg2454155	MRVI1	AP-2alpha	759	764	3.229049	GCCTCT	0.48828	0.48238
cg2454155	MRVI1	AP-2alpha	834	839	3.229049	GCCTCT	0.48828	0.48238
cg2454155	MRVI1	RXR-alph	124	130	3.170788	TACACC	0.24414	0.24522
cg2454155	MRVI1	p53 [T006	117	123	3.028543	GGGCAC	0.48828	0.47786
cg2454155	MRVI1	p53 [T006	149	155	3.028543	GGGCAC	0.48828	0.47786
cg2454155	MRVI1	STAT4 [T	66	71	2.941176	GGAATC	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	415	420	2.941176	GGAAAG	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	475	480	2.941176	CTTTCC	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	608	613	2.941176	GGAAAG	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	664	669	2.941176	GGTTCC	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	742	747	2.941176	CTTTCC	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	945	950	2.941176	GGAAAG	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	1091	1096	2.941176	GGAACA	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	1192	1197	2.941176	GGTTCC	2.92969	2.929
cg2454155	MRVI1	STAT4 [T	1806	1811	2.941176	GGAACC	2.92969	2.929
cg2454155	MRVI1	PR B [T00	558	564	2.80933	AACAAT	0.73242	0.74818
cg2454155	MRVI1	PR B [T00	797	803	2.80933	CAATGT	0.73242	0.74818
cg2454155	MRVI1	PR B [T00	1843	1849	2.80933	AACATT	0.73242	0.74818
cg2454155	MRVI1	PR A [T01	558	564	2.80933	AACAAT	0.73242	0.74818
cg2454155	MRVI1	PR A [T01	797	803	2.80933	CAATGT	0.73242	0.74818
cg2454155	MRVI1	PR A [T01	1843	1849	2.80933	AACATT	0.73242	0.74818
cg2454155	MRVI1	AP-2alpha	962	967	2.550491	GCCTCA	0.48828	0.48266
cg2454155	MRVI1	AP-2alpha	1361	1366	2.550491	GCCTCA	0.48828	0.48266
cg2454155	MRVI1	AP-2alpha	1897	1902	2.550491	GCCTCA	0.48828	0.48266
cg2454155	MRVI1	RXR-alph	455	461	2.544678	TTCACC	0.85449	0.84796
cg2454155	MRVI1	POU2F2 (	537	547	2.508421	TGATTT	0.01001	0.0104
cg2454155	MRVI1	AR [T000	1070	1078	2.37683	GGACAC	0.11444	0.11507
cg2454155	MRVI1	HNF-1C [	1747	1755	2.372238	GTTATT	0.04578	0.04709
cg2454155	MRVI1	LEF-1 [T0	589	596	2.345041	CAACAA	0.09155	0.09192
cg2454155	MRVI1	Elk-1 [T00	331	339	2.299314	CACAGG	0.09155	0.09114
cg2454155	MRVI1	GATA-2 [	1397	1405	2.222222	TGATAA	0.22888	0.23091
cg2454155	MRVI1	GATA-1 [	703	708	2.176375	AGGATA	3.90625	3.92756
cg2454155	MRVI1	GATA-1 [	1026	1031	2.176375	TATCCA	3.90625	3.92756
cg2454155	MRVI1	c-Myb [T0	41	48	2.152744	GCCAGT	0.06104	0.06059
cg2454155	MRVI1	GATA-1 [	932	937	2.001358	GGGATA	3.90625	3.92756
cg2454155	MRVI1	SRY [T00	588	596	1.998343	CCAACA	0.03052	0.03106
cg2454155	MRVI1	NF-AT1 [	1386	1394	1.94698	GGAAAT	0.06866	0.07012
cg2454155	MRVI1	PR B [T00	1448	1454	1.892895	AAGTGT	0.12207	0.12429
cg2454155	MRVI1	PR A [T01	1448	1454	1.892895	AAGTGT	0.12207	0.12429
cg2454155	MRVI1	AP-2alpha	713	718	1.871933	GGAGGC	0.97656	0.95407
cg2454155	MRVI1	AP-2alpha	862	867	1.871933	GCCTCC	0.97656	0.95407

cg2454155	MRVI1	AP-2alpha	1130	1135	1.871933	GCCTCC	0.97656	0.95407
cg2454155	MRVI1	TFII-I [T0	1905	1910	1.824994	CTCTCC	0.48828	0.48408
cg2454155	MRVI1	TFII-I [T0	1974	1979	1.824994	CTCTCC	0.48828	0.48408
cg2454155	MRVI1	p53 [T006	236	242	1.758307	GGGCAG	0.36621	0.36261
cg2454155	MRVI1	AR [T000	1072	1080	1.727468	ACACTG	0.09155	0.09119
cg2454155	MRVI1	GR-beta [	580	584	1.680765	AATGC	3.90625	3.94936
cg2454155	MRVI1	GR-beta [	1401	1405	1.680765	AATGC	3.90625	3.94936
cg2454155	MRVI1	GR-beta [	1760	1764	1.680765	AATTC	3.90625	3.94936
cg2454155	MRVI1	c-Ets-2 [T	744	752	1.64415	TTCCTC	0.04578	0.04579
cg2454155	MRVI1	c-Ets-1 [T	26	32	1.641124	TTTCCTT	0.36621	0.36952
cg2454155	MRVI1	C/EBPbeta	32	35	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	374	377	1.639871	CCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	479	482	1.639871	CCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	588	591	1.639871	CCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	990	993	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1174	1177	1.639871	CCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1245	1248	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1293	1296	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1557	1560	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1574	1577	1.639871	CCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1596	1599	1.639871	CCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1705	1708	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1819	1822	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1877	1880	1.639871	TTGG	15.625	15.72563
cg2454155	MRVI1	XBP-1 [T	277	282	1.583727	GGTCAT	0.97656	0.98146
cg2454155	MRVI1	Pax-5 [T0	1165	1171	1.537547	GGGCCA	0.73242	0.71311
cg2454155	MRVI1	Pax-5 [T0	1605	1611	1.537547	GGGCAA	0.73242	0.71311
cg2454155	MRVI1	Pax-5 [T0	1987	1993	1.537547	CTGGCC	0.73242	0.71311
cg2454155	MRVI1	TFIID [T0	33	39	1.537547	TGGAAA	0.73242	0.75096
cg2454155	MRVI1	c-Ets-1 [T	743	749	1.513038	TTTCCT	0.36621	0.36952
cg2454155	MRVI1	STAT4 [T	25	30	1.470588	TTTTCC	1.95312	1.96333
cg2454155	MRVI1	STAT4 [T	34	39	1.470588	GGAAAA	1.95312	1.96333
cg2454155	MRVI1	c-Ets-1 [T	413	419	1.384951	CAGGAA	0.36621	0.36952
cg2454155	MRVI1	c-Ets-1 [T	1516	1522	1.384951	CAGGAA	0.36621	0.36952
cg2454155	MRVI1	NF-AT1 [	33	42	1.378139	TGGAAA	0.01907	0.0194
cg2454155	MRVI1	C/EBPbeta	47	50	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	75	78	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	295	298	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	796	799	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1314	1317	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1446	1449	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1763	1766	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1794	1797	1.366559	TTGA	15.625	15.72563
cg2454155	MRVI1	C/EBPbeta	1900	1903	1.366559	TCAA	15.625	15.72563
cg2454155	MRVI1	AP-2alpha	153	158	1.357116	ACAGGC	0.48828	0.48203
cg2454155	MRVI1	AP-2alpha	436	441	1.357116	GCCTGT	0.48828	0.48203
cg2454155	MRVI1	AP-2alpha	1338	1343	1.357116	GCCTGT	0.48828	0.48203
cg2454155	MRVI1	p53 [T006	106	112	1.270236	GGGCAC	0.12207	0.11849

cg2454155	MRVI1	T3R-beta1	89	97	1.129976	TGGAGG'	0.07629	0.07585
cg2454155	MRVI1	GATA-1 ['	1396	1401	1.038567	ATGATA	1.95312	1.98662
cg2454155	MRVI1	GATA-1 ['	1794	1799	1.038567	TTGATA	1.95312	1.98662
cg2454155	MRVI1	PXR-1:RX	42	49	0.941658	CCAGTT(	0.12207	0.12266
cg2454155	MRVI1	GR-beta []	50	54	0.840383	AATGG	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	786	790	0.840383	CCATT	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	937	941	0.840383	AATGG	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1189	1193	0.840383	AATGG	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1262	1266	0.840383	AATGG	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1328	1332	0.840383	CCATT	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1395	1399	0.840383	AATGA	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1433	1437	0.840383	AATGA	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1495	1499	0.840383	AATGA	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1682	1686	0.840383	AATTA	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1695	1699	0.840383	CCATT	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1770	1774	0.840383	TAATT	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1771	1775	0.840383	AATTA	7.8125	7.94706
cg2454155	MRVI1	GR-beta []	1826	1830	0.840383	TCATT	7.8125	7.94706
cg2454155	MRVI1	LEF-1 [T0	1092	1099	0.641865	GAACAA	0.06104	0.06131
cg2454155	MRVI1	C/EBPalpl	499	505	0.540941	CACAAT(	0.24414	0.24507
cg2454155	MRVI1	HNF-1A ['	1236	1243	0.431647	GTTAAA(	0.24414	0.24974
cg2454155	MRVI1	HNF-1A ['	1451	1458	0.431647	TGTTTAA	0.24414	0.24974
cg2454155	MRVI1	HNF-1A ['	613	620	0.287765	GTTAAA(	0.24414	0.24974
cg2454155	MRVI1	GATA-1 ['	565	570	0.280028	AAGATA	0.97656	0.99875
cg2454155	MRVI1	GATA-1 ['	1676	1681	0.280028	TAGATA	0.97656	0.99875
cg2454155	MRVI1	c-Ets-1 [T(	653	659	0.256174	AAGGAA	0.24414	0.24569
cg2454155	MRVI1	AP-2alpha	921	926	0.226186	GCCTGG	0.97656	0.95305
cg2454155	MRVI1	AP-2alpha	1123	1128	0.226186	GCCTGG	0.97656	0.95305
cg2454155	MRVI1	AP-2alpha	1149	1154	0.226186	GCCTGG	0.97656	0.95305
cg2454155	MRVI1	AP-2alpha	1266	1271	0.226186	GCCTGG	0.97656	0.95305
cg2454155	MRVI1	AP-2alpha	1886	1891	0.226186	CCAGGC	0.97656	0.95305
cg2454155	MRVI1	AP-2alpha	1985	1990	0.226186	GCCTGG	0.97656	0.95305
cg2454155	MRVI1	p53 [T006'	1605	1611	0.211706	GGGCAA	0.36621	0.35912
cg2454155	MRVI1	GR-alpha [	7	11	0.207689	CCTCT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	29	33	0.207689	CCTTT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	131	135	0.207689	CCTCT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	179	183	0.207689	AGAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	252	256	0.207689	AGAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	302	306	0.207689	AGAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	343	347	0.207689	AGAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	402	406	0.207689	AAAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	492	496	0.207689	AAAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	648	652	0.207689	CCTTT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	687	691	0.207689	AGAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	741	745	0.207689	CCTTT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	749	753	0.207689	CCTCT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	760	764	0.207689	CCTCT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	835	839	0.207689	CCTCT	7.8125	7.81264

cg2454155	MRVI1	GR-alpha [	866	870	0.207689	CCTCT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	872	876	0.207689	AGAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	901	905	0.207689	CCTCT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	987	991	0.207689	CCTTT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1096	1100	0.207689	AAAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1781	1785	0.207689	CCTCT	7.8125	7.81264
cg2454155	MRVI1	GATA-1 [	195	200	0.105011	GAGATA	0.97656	0.98738
cg2454155	MRVI1	GR-alpha [	153	157	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	186	190	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	204	208	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	224	228	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	274	278	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	332	336	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	412	416	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	437	441	0	CCTGT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	642	646	0	CCTGT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	708	712	0	ATAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1196	1200	0	CCTGT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1339	1343	0	CCTGT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1530	1534	0	CCTGT	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1563	1567	0	ATAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1686	1690	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1722	1726	0	ACAGG	7.8125	7.81264
cg2454155	MRVI1	GR-alpha [	1891	1895	0	CCTAT	7.8125	7.81264
cg2454155	MRVI1	AP-2alpha	256	261	0	GCAGGC	0.97656	0.95305
cg2454155	MRVI1	AP-2alpha	977	982	0	GCAGGC	0.97656	0.95305
cg2454155	MRVI1	XBP-1 [T(	1775	1780	0	AGTCAT	0.97656	0.98127
cg2454155	MRVI1	XBP-1 [T(	1853	1858	0	AGTCAT	0.97656	0.98127
cg2454155	MRVI1	Pax-5 [T0(	101	107	0	GGGCCG	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	106	112	0	GGGCAC	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	112	118	0	GGGCCG	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	284	290	0	CCAGCC(	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	876	882	0	GGGCTG	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	975	981	0	GGGCAG	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	1214	1220	0	GGGCAG	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	1299	1305	0	CCAGCC(	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	1504	1510	0	CCTGCC(	1.09863	1.06846
cg2454155	MRVI1	Pax-5 [T0(	1510	1516	0	CCTGCC(	1.09863	1.06846
cg2454155	MRVI1	p53 [T006'	975	981	0	GGGCAG	0.36621	0.35912
cg2454155	MRVI1	p53 [T006'	1214	1220	0	GGGCAG	0.36621	0.35912
cg2454155	MRVI1	p53 [T006'	1504	1510	0	CCTGCC(	0.36621	0.35912
cg2454155	MRVI1	p53 [T006'	1510	1516	0	CCTGCC(	0.36621	0.35912
cg2454155	MRVI1	ENKTF-1	1169	1176	0	CAGCGC	0.12207	0.1201
cg2454155	MRVI1	TFII-I [T0	190	195	0	GGACAG	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	316	321	0	GGACAG	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	415	420	0	GGAAAG	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	475	480	0	CTTTCC	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	608	613	0	GGAAAG	1.46484	1.45997

cg2454155	MRVI1	TFII-I [T0	742	747	0	CTTTCC	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	945	950	0	GGAAAG	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	1075	1080	0	CTGTCC	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	1197	1202	0	CTGTCC	1.46484	1.45997
cg2454155	MRVI1	TFII-I [T0	1531	1536	0	CTGTCC	1.46484	1.45997
cg2454155	MRVI1	STAT4 [T	1386	1391	0	GGAAAT	0.48828	0.49387
cg2454155	MRVI1	STAT4 [T	1518	1523	0	GGAAAT	0.48828	0.49387
cg2454155	MRVI1	c-Ets-1 [T	333	339	0	CAGGAA	0.24414	0.2429
cg2454155	MRVI1	c-Ets-1 [T	1501	1507	0	CTTCCTC	0.24414	0.2429
cg2454155	MRVI1	YY1 [T00	51	54	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	229	232	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	630	633	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	786	789	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	938	941	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1021	1024	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1040	1043	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1050	1053	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1052	1055	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1190	1193	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1263	1266	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1328	1331	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1524	1527	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1535	1538	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1588	1591	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1616	1619	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1695	1698	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1823	1826	0	CCAT	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1857	1860	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	YY1 [T00	1894	1897	0	ATGG	7.8125	7.81711
cg2454155	MRVI1	Elk-1 [T00	1501	1509	0	CTTCCTC	0.06104	0.06047
cg2454155	MRVI1	GCF [T00	1166	1174	0	GGCCAG	0.09155	0.08765
cg2454155	MRVI1	ER-alpha [	277	281	0	GGTCA	1.95312	1.9404
cg2454155	MRVI1	ER-alpha [	794	798	0	GGTCA	1.95312	1.9404
cg2454155	MRVI1	GATA-1 [	1713	1718	0	CAGATA	0.97656	0.98738
cg2454155	MRVI1	GATA-1 [	1753	1758	0	TATCTG	0.97656	0.98738
cg2454155	MRVI1	C/EBPbeta	174	177	0	ACAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	216	219	0	ACAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	371	374	0	TTGC	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	395	398	0	TTGC	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	400	403	0	ACAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	428	431	0	TTGC	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	430	433	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	485	488	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	489	492	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	500	503	0	ACAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	523	526	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	556	559	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	559	562	0	ACAA	15.625	15.71349

cg2454155	MRVI1	C/EBPbeta	591	594	0	ACAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1055	1058	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1094	1097	0	ACAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1137	1140	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1251	1254	0	TTGC	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1320	1323	0	TTGC	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1607	1610	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1672	1675	0	TTGC	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1733	1736	0	TTGT	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1790	1793	0	TTGT	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1913	1916	0	GCAA	15.625	15.71349
cg2454155	MRVI1	C/EBPbeta	1954	1957	0	TTGT	15.625	15.71349
cg2454155	MRVI1	TFIID [T0	540	546	0	TTTAAA	1.09863	1.13474
cg2454155	MRVI1	FOXP3 [T	1953	1958	0	GTTGTG	1.46484	1.47315
cg2454155	MRVI1	GR-beta [	450	454	0	ACATT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	798	802	0	AATGT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	1681	1685	0	AAATT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	1701	1705	0	AAATT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	1702	1706	0	AATTT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	1759	1763	0	AAATT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	1765	1769	0	AAATT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	1766	1770	0	AATTT	3.90625	3.99611
cg2454155	MRVI1	GR-beta [	1844	1848	0	ACATT	3.90625	3.99611
cg2454155	MRVI1	PR B [T00	390	396	0	CACTGT	0.36621	0.36944
cg2454155	MRVI1	PR B [T00	1743	1749	0	GACTGT	0.36621	0.36944
cg2454155	MRVI1	PR A [T01	390	396	0	CACTGT	0.36621	0.36944
cg2454155	MRVI1	PR A [T01	1743	1749	0	GACTGT	0.36621	0.36944
cg2454155	MRVI1	GR [T050	1786	1792	0	ATTTTTC	0.36621	0.37562
cg2454155	MRVI1	SRY [T00	1091	1099	0	GGAACA	0.03052	0.03101
cg2454155	MRVI1	IRF-2 [T0	530	535	0	TCACTT	0.48828	0.49387
cg2264768	NAV2	c-Ets-1 [T	445	451	9.969337	ATTCCC	0.24414	0.2459
cg0273928	NAV2	PEA3 [T0	1386	1394	9.937959	TGGATG	0.18311	0.18304
cg0273928	NAV2	GATA-3 [	1015	1026	9.927126	GTGGCT	0.01037	0.01047
cg2264768	NAV2	NF-kappa	1127	1137	9.916075	TGCCTA	0.02289	0.0224
cg2264768	NAV2	c-Ets-1 [T	1082	1088	9.841249	ATTCCC	0.24414	0.2459
cg2264768	NAV2	c-Ets-1 [T	1875	1881	9.841249	ATTCCC	0.24414	0.2459
cg0273928	NAV2	STAT1bet	1946	1955	9.807397	TTTTCCA	0.14877	0.1495
cg2264768	NAV2	STAT1bet	1801	1810	9.807397	TGAAGG	0.14877	0.1495
cg0273928	NAV2	XBP-1 [T	125	130	9.789909	AGACAT	1.95312	1.95208
cg0273928	NAV2	XBP-1 [T	135	140	9.789909	ATGGCT	1.95312	1.95208
cg0273928	NAV2	XBP-1 [T	566	571	9.789909	ATGTCT	1.95312	1.95208
cg0273928	NAV2	XBP-1 [T	783	788	9.789909	AGACAT	1.95312	1.95208
cg0273928	NAV2	XBP-1 [T	907	912	9.789909	ATGTCG	1.95312	1.95208
cg2264768	NAV2	XBP-1 [T	346	351	9.789909	AGACAT	1.95312	1.95208
cg2264768	NAV2	XBP-1 [T	637	642	9.789909	AGCCAT	1.95312	1.95208
cg2264768	NAV2	XBP-1 [T	676	681	9.789909	ATGTCT	1.95312	1.95208
cg2264768	NAV2	XBP-1 [T	1764	1769	9.789909	ATGGCT	1.95312	1.95208
cg2264768	NAV2	NF-AT2 [	1420	1429	9.787971	GGAAAA	0.08774	0.08903

cg2264768	NAV2	NF-1 [T00	656	663	9.761671	TTGGAT	0.24414	0.24405
cg0273928	NAV2	NF-AT2 [	1584	1593	9.755755	GGAAAA	0.08774	0.08903
cg2264768	NAV2	NF-AT2 [	276	285	9.755755	TTTTTTT	0.08774	0.08903
cg0273928	NAV2	PR B [T00	406	412	9.743489	AACACA	1.09863	1.10292
cg0273928	NAV2	PR B [T00	995	1001	9.743489	AACACC	1.09863	1.10292
cg0273928	NAV2	PR B [T00	1035	1041	9.743489	AACACG	1.09863	1.10292
cg0273928	NAV2	PR B [T00	1640	1646	9.743489	TTGTGT	1.09863	1.10292
cg0273928	NAV2	PR B [T00	1831	1837	9.743489	TTGTGT	1.09863	1.10292
cg0273928	NAV2	PR A [T01	406	412	9.743489	AACACA	1.09863	1.10292
cg0273928	NAV2	PR A [T01	995	1001	9.743489	AACACC	1.09863	1.10292
cg0273928	NAV2	PR A [T01	1035	1041	9.743489	AACACG	1.09863	1.10292
cg0273928	NAV2	PR A [T01	1640	1646	9.743489	TTGTGT	1.09863	1.10292
cg0273928	NAV2	PR A [T01	1831	1837	9.743489	TTGTGT	1.09863	1.10292
cg2264768	NAV2	PR B [T00	451	457	9.743489	AACACA	1.09863	1.10292
cg2264768	NAV2	PR B [T00	1537	1543	9.743489	TTGTGT	1.09863	1.10292
cg2264768	NAV2	PR A [T01	451	457	9.743489	AACACA	1.09863	1.10292
cg2264768	NAV2	PR A [T01	1537	1543	9.743489	TTGTGT	1.09863	1.10292
cg2105276	NAV2	PR B [T00	1569	1575	9.743489	TGGTGT	1.09863	1.10292
cg2105276	NAV2	PR B [T00	1625	1631	9.743489	TCGTGT	1.09863	1.10292
cg2105276	NAV2	PR B [T00	1752	1758	9.743489	TGGTGT	1.09863	1.10292
cg2105276	NAV2	PR A [T01	1569	1575	9.743489	TGGTGT	1.09863	1.10292
cg2105276	NAV2	PR A [T01	1625	1631	9.743489	TCGTGT	1.09863	1.10292
cg2105276	NAV2	PR A [T01	1752	1758	9.743489	TGGTGT	1.09863	1.10292
cg2264768	NAV2	c-Myb [T0	944	951	9.729271	AACAGT	0.36621	0.37054
cg2264768	NAV2	c-Myb [T0	1674	1681	9.729271	TAACTG	0.36621	0.37054
cg2264768	NAV2	LEF-1 [T0	1462	1469	9.72404	TGGCAA	0.21362	0.2139
cg2105276	NAV2	LEF-1 [T0	968	975	9.72404	TGGCAA	0.21362	0.2139
cg2264768	NAV2	c-Jun [T00	842	848	9.717135	CAGGTC	0.73242	0.73031
cg2264768	NAV2	c-Ets-1 [T	1913	1919	9.713162	ATTCCC	0.36621	0.36441
cg2105276	NAV2	RelA [T00	326	336	9.694004	TTGGGA	0.02813	0.0279
cg2264768	NAV2	NF-AT1 [	1183	1191	9.691726	TAAGTT	0.16785	0.1682
cg2105276	NAV2	NF-AT1 [	1412	1420	9.691726	TTAGTT	0.16785	0.1682
cg0273928	NAV2	Elk-1 [T00	498	506	9.62002	GGATGG	0.07629	0.07577
cg2105276	NAV2	HNF-1C [	580	588	9.576203	GTTAAG	0.19836	0.20229
cg0273928	NAV2	Pax-5 [T0	1137	1143	9.552105	GTGGCC	1.46484	1.43083
cg0273928	NAV2	TFIID [T0	396	402	9.552105	TTCCAA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	517	523	9.552105	TGTCAA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	790	796	9.552105	TGAGAA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	990	996	9.552105	TCCGAA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	1055	1061	9.552105	TGTGAA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	1409	1415	9.552105	TGGGAA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	1510	1516	9.552105	TTTCTCA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	1615	1621	9.552105	TGGGAA	1.46484	1.48472
cg0273928	NAV2	TFIID [T0	1735	1741	9.552105	TCCCAA	1.46484	1.48472
cg2264768	NAV2	Pax-5 [T0	71	77	9.552105	GTGGCC	1.46484	1.43083
cg2264768	NAV2	Pax-5 [T0	101	107	9.552105	GTGGCC	1.46484	1.43083
cg2264768	NAV2	TFIID [T0	171	177	9.552105	TTCCAA	1.46484	1.48472
cg2264768	NAV2	TFIID [T0	1064	1070	9.552105	TTTGTCA	1.46484	1.48472

cg2264768	NAV2	TFIID [T0	1462	1468	9.552105	TGGCAA	1.46484	1.48472
cg2264768	NAV2	TFIID [T0	1862	1868	9.552105	TGAGAA	1.46484	1.48472
cg2264768	NAV2	TFIID [T0	1900	1906	9.552105	TTCGAA	1.46484	1.48472
cg2105276	NAV2	Pax-5 [T0	1051	1057	9.552105	TTGGCC	1.46484	1.43083
cg2105276	NAV2	Pax-5 [T0	1085	1091	9.552105	GTGGCC	1.46484	1.43083
cg2105276	NAV2	Pax-5 [T0	1263	1269	9.552105	GTGGCC	1.46484	1.43083
cg2105276	NAV2	Pax-5 [T0	1378	1384	9.552105	GGGCCA	1.46484	1.43083
cg2105276	NAV2	TFIID [T0	327	333	9.552105	TGGGAA	1.46484	1.48472
cg2105276	NAV2	TFIID [T0	968	974	9.552105	TGGCAA	1.46484	1.48472
cg2105276	NAV2	TFIID [T0	1019	1025	9.552105	TTTCTCA	1.46484	1.48472
cg2105276	NAV2	TFIID [T0	1528	1534	9.552105	TTTCTCA	1.46484	1.48472
cg2105276	NAV2	TFIID [T0	1828	1834	9.552105	TGAGAA	1.46484	1.48472
cg2264768	NAV2	NF-1 [T00	123	130	9.535536	TTGGGC	0.73242	0.73053
cg2264768	NAV2	NF-1 [T00	891	898	9.535536	GTGGCC	0.73242	0.73053
cg2264768	NAV2	NF-1 [T00	1847	1854	9.535536	GTGGCC	0.73242	0.73053
cg2105276	NAV2	NF-AT1 [	329	337	9.521781	GGAAAT	0.16785	0.1682
cg0273928	NAV2	HNF-1B [	1275	1283	9.513548	TATCTA	0.09155	0.09374
cg0273928	NAV2	TFII-I [T0	86	91	9.512894	CCATCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	146	151	9.512894	GGACCG	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	414	419	9.512894	TTTTCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	498	503	9.512894	GGATGG	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	540	545	9.512894	TTTTCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	593	598	9.512894	GGAAAA	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	609	614	9.512894	TTTTCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	726	731	9.512894	TTATCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	825	830	9.512894	GGAAAA	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	886	891	9.512894	TTTTCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1097	1102	9.512894	GGAATT	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1242	1247	9.512894	GGAAAC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1411	1416	9.512894	GGAAAA	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1584	1589	9.512894	GGAAAA	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1617	1622	9.512894	GGAAAC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1630	1635	9.512894	TTATCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1691	1696	9.512894	GTGTCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1946	1951	9.512894	TTTTCC	7.32422	7.29728
cg0273928	NAV2	TFII-I [T0	1959	1964	9.512894	GGAATT	7.32422	7.29728
cg0273928	NAV2	FOXP3 [T	194	199	9.512894	GTTGGG	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	215	220	9.512894	AATAAC	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	633	638	9.512894	CTAAAC	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	948	953	9.512894	GTTCTT	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	981	986	9.512894	AGCAAC	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	1032	1037	9.512894	GAGAAC	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	1260	1265	9.512894	GTTTAT	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	1326	1331	9.512894	AATAAC	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	1629	1634	9.512894	GTTATC	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	1644	1649	9.512894	GTTTAG	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	1777	1782	9.512894	GTTATG	7.32422	7.35678
cg0273928	NAV2	FOXP3 [T	1916	1921	9.512894	GTTGGT	7.32422	7.35678

cg2264768	NAV2	TFII-I [T0	280	285	9.512894	TTTTCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	314	319	9.512894	GGACAC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	335	340	9.512894	GTGTCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	444	449	9.512894	AATTCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	503	508	9.512894	GGAAGG	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	554	559	9.512894	GGAAGG	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	559	564	9.512894	GGAAAC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	596	601	9.512894	GGATGG	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	780	785	9.512894	AAATCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	832	837	9.512894	GGAAAC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	851	856	9.512894	GGACAA	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1186	1191	9.512894	GTTTCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1334	1339	9.512894	GTGTCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1420	1425	9.512894	GGAAAA	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1580	1585	9.512894	GGAAGG	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1786	1791	9.512894	TTATCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1805	1810	9.512894	GGAAAA	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1866	1871	9.512894	AAATCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1874	1879	9.512894	AATTCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1904	1909	9.512894	AAATCC	7.32422	7.29728
cg2264768	NAV2	TFII-I [T0	1986	1991	9.512894	TTTTCC	7.32422	7.29728
cg2264768	NAV2	FOXP3 [T	402	407	9.512894	AGCAAC	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	448	453	9.512894	CCCAAC	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	485	490	9.512894	GGCAAC	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	542	547	9.512894	GTTGGG	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	626	631	9.512894	GTTTAT	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	689	694	9.512894	GTTCTT	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	941	946	9.512894	GCCAAC	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	1000	1005	9.512894	CGCAAC	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	1249	1254	9.512894	GTTTAT	7.32422	7.35678
cg2264768	NAV2	FOXP3 [T	1523	1528	9.512894	CAGAAC	7.32422	7.35678
cg2105276	NAV2	TFII-I [T0	343	348	9.512894	GTTTCC	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	505	510	9.512894	CCTTCC	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	618	623	9.512894	GGACGG	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	642	647	9.512894	GGAAGG	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	817	822	9.512894	GGACAA	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	957	962	9.512894	GGAAAA	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	1097	1102	9.512894	CCTTCC	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	1398	1403	9.512894	GGAATT	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	1415	1420	9.512894	GTTTCC	7.32422	7.29728
cg2105276	NAV2	TFII-I [T0	1821	1826	9.512894	GGAATT	7.32422	7.29728
cg2105276	NAV2	FOXP3 [T	29	34	9.512894	GTTCTC	7.32422	7.35678
cg2105276	NAV2	FOXP3 [T	594	599	9.512894	AGCAAC	7.32422	7.35678
cg2105276	NAV2	FOXP3 [T	854	859	9.512894	GCCAAC	7.32422	7.35678
cg2105276	NAV2	FOXP3 [T	1123	1128	9.512894	GTTGGT	7.32422	7.35678
cg2105276	NAV2	FOXP3 [T	1321	1326	9.512894	CAGAAC	7.32422	7.35678
cg2105276	NAV2	FOXP3 [T	1629	1634	9.512894	GTTGGG	7.32422	7.35678
cg2105276	NAV2	FOXP3 [T	1650	1655	9.512894	GTTCTT	7.32422	7.35678

cg2105276	NAV2	FOXP3 [T	1789	1794	9.512894	GTTTAC	7.32422	7.35678
cg2264768	NAV2	c-Jun [T00	201	207	9.511322	GTGGTC	0.73242	0.73031
cg2264768	NAV2	c-Jun [T00	1439	1445	9.511322	GTGGTC	0.73242	0.73031
cg0273928	NAV2	TCF-4E [T	422	428	9.453578	CTCAAA	0.48828	0.49215
cg0273928	NAV2	TCF-4E [T	469	475	9.453578	CTTTGTA	0.48828	0.49215
cg0273928	NAV2	TCF-4E [T	480	486	9.453578	CTTTGA	0.48828	0.49215
cg0273928	NAV2	TCF-4E [T	1383	1389	9.453578	CTTTGG	0.48828	0.49215
cg2264768	NAV2	TCF-4E [T	358	364	9.453578	CTTTGA	0.48828	0.49215
cg2264768	NAV2	TCF-4E [T	1969	1975	9.453578	CTTTGA	0.48828	0.49215
cg2105276	NAV2	c-Jun [T00	270	276	9.442241	GCTGTC	0.73242	0.73031
cg2105276	NAV2	c-Jun [T00	835	841	9.442241	GCTGTC	0.73242	0.73031
cg2105276	NAV2	c-Jun [T00	1011	1017	9.442241	TGACAG	0.73242	0.73031
cg2105276	NAV2	EBF [T05	1437	1447	9.441272	CTCCCT	0.06866	0.06676
cg2264768	NAV2	NF-AT2 [	1182	1191	9.386314	ATAAGT	0.04578	0.04604
cg0273928	NAV2	NFI/CTF [	202	209	9.352332	ATCCTT	0.54932	0.54821
cg0273928	NAV2	NFI/CTF [	960	967	9.352332	AGCATT	0.54932	0.54821
cg0273928	NAV2	NFI/CTF [	1381	1388	9.352332	AGCTTT	0.54932	0.54821
cg2105276	NAV2	NFI/CTF [	21	28	9.352332	GGCCTT	0.54932	0.54821
cg0273928	NAV2	POU2F2 (	1719	1729	9.350233	TGTTTA	0.03433	0.03518
cg2105276	NAV2	AP-1 [T00	935	943	9.3434	TGTCAG	0.09155	0.09305
cg2264768	NAV2	EBF [T05	103	113	9.337292	GGCCCA	0.06866	0.06676
cg2264768	NAV2	HNF-1B [	605	613	9.308068	TTTATA	0.09155	0.09374
cg0273928	NAV2	SRY [T00	480	488	9.264664	CTTTGA	0.12207	0.12265
cg2264768	NAV2	SRY [T00	1969	1977	9.264664	CTTTGA	0.12207	0.12265
cg2264768	NAV2	RelA [T00	775	785	9.195844	CAGGGA	0.02432	0.0241
cg2105276	NAV2	PPAR-alph	1086	1096	9.158357	TGGCCC	0.0515	0.04986
cg0273928	NAV2	c-Ets-1 [T	386	392	9.148774	AGGGAA	0.85449	0.85523
cg2264768	NAV2	c-Myb [T0	903	910	9.142015	CTAAGT	0.39673	0.40028
cg2264768	NAV2	NF-kappa	440	451	9.123759	AAGAAA	0.01872	0.01846
cg0273928	NAV2	LEF-1 [T0	1568	1575	9.099721	CCACAA	0.54932	0.55326
cg2105276	NAV2	HNF-1C [	1886	1894	9.094725	GTTAGC	0.12207	0.12495
cg2264768	NAV2	HNF-1B [	348	356	9.06748	ACATTA	0.08392	0.0857
cg0273928	NAV2	c-Ets-1 [T	1316	1322	9.065503	ATGGAA	0.85449	0.85523
cg2105276	NAV2	c-Ets-1 [T	1819	1825	9.065503	ATGGAA	0.85449	0.85523
cg2264768	NAV2	USF2 [T0	1886	1895	9.056375	TTTCCA	0.1545	0.15287
cg0273928	NAV2	NFI/CTF [	191	198	9.042931	ACAGTT	0.48828	0.48804
cg2264768	NAV2	NFI/CTF [	942	949	9.042931	CCAACA	0.48828	0.48804
cg2105276	NAV2	NFI/CTF [	855	862	9.042931	CCAACA	0.48828	0.48804
cg0273928	NAV2	NF-AT1 [	263	271	9.042733	GGAAAT	0.22888	0.22959
cg2105276	NAV2	c-Ets-1 [T	102	108	9.020687	GTTCCC	0.85449	0.85523
cg2264768	NAV2	AP-1 [T00	1257	1265	9.002849	TGACTT	0.24414	0.24693
cg2264768	NAV2	PXR-1:RX	288	295	8.998824	TGAACG	0.24414	0.2439
cg2105276	NAV2	PXR-1:RX	921	928	8.998824	GTTGTT	0.24414	0.2439
cg0273928	NAV2	LEF-1 [T0	1383	1390	8.973041	CTTTGG	0.54932	0.55326
cg2264768	NAV2	LEF-1 [T0	1044	1051	8.973041	CTTTGG	0.54932	0.55326
cg0273928	NAV2	GR [T050	278	284	8.971049	CAAAGC	0.61035	0.61632
cg0273928	NAV2	GR [T050	1106	1112	8.971049	GTGTTT	0.61035	0.61632
cg0273928	NAV2	GR [T050	1161	1167	8.971049	GTATTT	0.61035	0.61632

cg0273928	NAV2	GR [T050	1247	1253	8.971049	CAAAAT	0.61035	0.61632
cg0273928	NAV2	GR [T050	1743	1749	8.971049	GTATTT	0.61035	0.61632
cg2264768	NAV2	GR [T050	1735	1741	8.971049	CAAATA	0.61035	0.61632
cg2264768	NAV2	c-Myb [T0	352	359	8.947824	TAACTT	0.39673	0.40028
cg0273928	NAV2	c-Ets-1 [T	295	301	8.937416	ATTCCA	0.85449	0.85523
cg2105276	NAV2	c-Ets-1 [T	1396	1402	8.937416	GTGGAA	0.85449	0.85523
cg2264768	NAV2	Elk-1 [T00	244	252	8.931691	CTTCCA	0.24414	0.24034
cg2264768	NAV2	Elk-1 [T00	550	558	8.931691	TGGGGG	0.24414	0.24034
cg2105276	NAV2	Elk-1 [T00	1554	1562	8.931691	AGCTGG	0.24414	0.24034
cg0273928	NAV2	IRF-1 [T0	1926	1934	8.916359	TTTCCA	0.09155	0.09147
cg0273928	NAV2	c-Ets-2 [T	588	596	8.912323	ACTTAG	0.27466	0.27495
cg0273928	NAV2	c-Ets-2 [T	1237	1245	8.912323	CCTTAG	0.27466	0.27495
cg2264768	NAV2	c-Ets-2 [T	498	506	8.912323	ACTCAG	0.27466	0.27495
cg2264768	NAV2	c-Ets-2 [T	1188	1196	8.912323	TTCCTG	0.27466	0.27495
cg2264768	NAV2	c-Ets-2 [T	1199	1207	8.912323	CCTCAG	0.27466	0.27495
cg2264768	NAV2	c-Ets-2 [T	1575	1583	8.912323	GCTTAG	0.27466	0.27495
cg2105276	NAV2	ELF-1 [T0	1478	1490	8.853261	GTACTT	0.01085	0.01094
cg0273928	NAV2	POU2F2 (	207	217	8.848549	TGGATT	0.01144	0.01182
cg2105276	NAV2	AP-1 [T00	670	678	8.82837	TGACTT	0.24414	0.24693
cg0273928	NAV2	PR B [T00	24	30	8.827054	AACAGC	0.36621	0.36944
cg0273928	NAV2	PR A [T01	24	30	8.827054	AACAGC	0.36621	0.36944
cg2264768	NAV2	PR B [T00	934	940	8.827054	AACAGA	0.36621	0.36944
cg2264768	NAV2	PR A [T01	934	940	8.827054	AACAGA	0.36621	0.36944
cg0273928	NAV2	NFI/CTF [	487	494	8.814757	CCAAAA	0.48828	0.48804
cg2105276	NAV2	NFI/CTF [	15	22	8.814757	TCTCTT	0.48828	0.48804
cg2105276	NAV2	NFI/CTF [	1372	1379	8.814757	CCAAGT	0.48828	0.48804
cg2105276	NAV2	NFI/CTF [	1484	1491	8.814757	CCTCTT	0.48828	0.48804
cg2105276	NAV2	c-Jun [T00	1149	1155	8.807683	GTTGTC	0.61035	0.61059
cg0273928	NAV2	NF-AT2 [	410	419	8.794303	CACGTT	0.05341	0.05386
cg2105276	NAV2	NF-1 [T00	326	333	8.790071	TTGGGA	0.24414	0.24467
cg0273928	NAV2	AP-1 [T00	301	309	8.775493	CCTAAG	0.24414	0.24693
cg2105276	NAV2	E2F-1 [T0	864	871	8.76494	TGCTCC	0.27466	0.26875
cg2264768	NAV2	AR [T000	851	859	8.762682	GGACAA	0.04578	0.04533
cg0273928	NAV2	LEF-1 [T0	275	282	8.759086	ATGCAA	0.54932	0.55326
cg0273928	NAV2	LEF-1 [T0	469	476	8.759086	CTTTGT	0.54932	0.55326
cg0273928	NAV2	XBP-1 [T	112	117	8.75604	ATGAGA	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	267	272	8.75604	ATGAGA	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	475	480	8.75604	ATGATC	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	622	627	8.75604	GTTCAT	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	806	811	8.75604	ATGATC	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	808	813	8.75604	GATCAT	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	1460	1465	8.75604	ATGAAA	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	1512	1517	8.75604	TCTCAT	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	1762	1767	8.75604	TATCAT	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	1801	1806	8.75604	TTTCAT	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	1821	1826	8.75604	GCTCAT	2.92969	2.9674
cg0273928	NAV2	XBP-1 [T	1839	1844	8.75604	TCTCAT	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T	8	13	8.75604	ATGAGA	2.92969	2.9674

cg2264768	NAV2	XBP-1 [T0	40	45	8.75604	GCTCAT	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T0	207	212	8.75604	ATGATC	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T0	968	973	8.75604	TTTCAT	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T0	1171	1176	8.75604	ATGATA	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T0	1178	1183	8.75604	TCTCAT	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T0	1625	1630	8.75604	ATGATA	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T0	1722	1727	8.75604	TTTCAT	2.92969	2.9674
cg2264768	NAV2	XBP-1 [T0	1963	1968	8.75604	ATGAAA	2.92969	2.9674
cg2105276	NAV2	XBP-1 [T0	822	827	8.75604	ATGAGC	2.92969	2.9674
cg2264768	NAV2	c-Myb [T0	1311	1318	8.728118	AAACTTA	0.30518	0.30924
cg2264768	NAV2	HNF-1B [T	262	270	8.696557	TCTGTAA	0.11444	0.11669
cg0273928	NAV2	STAT1beta	540	549	8.695301	TTTTCCA	0.22316	0.22446
cg2264768	NAV2	STAT1beta	828	837	8.695301	TGTTGGA	0.22316	0.22446
cg2264768	NAV2	STAT1beta	1608	1617	8.695301	ATTTCC	0.22316	0.22446
cg2264768	NAV2	STAT1beta	1885	1894	8.695301	CTTTCCA	0.22316	0.22446
cg2105276	NAV2	STAT1beta	1103	1112	8.695301	CCTTGGA	0.22316	0.22446
cg2105276	NAV2	STAT1beta	1449	1458	8.695301	ATTTCCT	0.22316	0.22446
cg0273928	NAV2	IRF-1 [T0	259	267	8.661524	GTGAGG	0.20599	0.20664
cg0273928	NAV2	c-Jun [T00	69	75	8.571705	TGACTG	0.12207	0.12139
cg2105276	NAV2	IRF-1 [T0	344	352	8.570857	TTTCCA	0.20599	0.20664
cg2264768	NAV2	RAR-beta	1099	1108	8.55975	ACCTAA	0.26703	0.26657
cg0273928	NAV2	NF-AT2 [T	605	614	8.550786	TAGCTTT	0.04959	0.05001
cg0273928	NAV2	NF-AT2 [T	1762	1771	8.550786	TATCATT	0.04959	0.05001
cg2105276	NAV2	AR [T000	178	186	8.547269	GGACAT	0.10681	0.10625
cg2105276	NAV2	p53 [T006	1001	1007	8.537081	GGGCTCT	0.12207	0.11986
cg2105276	NAV2	p53 [T006	1028	1034	8.537081	GGGCTCT	0.12207	0.11986
cg0273928	NAV2	NF-AT1 [T	1943	1951	8.532897	CCATTTT	0.10681	0.10725
cg2264768	NAV2	USF2 [T0	451	460	8.532138	AACACA	0.103	0.10183
cg2105276	NAV2	NF-AT1 [T	1446	1454	8.509162	CCTATTT	0.10681	0.10725
cg2264768	NAV2	c-Ets-1 [T0	170	176	8.501115	GTTCCAA	0.24414	0.24529
cg2264768	NAV2	NF-AT2 [T	559	568	8.497624	GGAAAC	0.04959	0.05001
cg2264768	NAV2	IRF-1 [T0	828	836	8.497322	TGTTGGA	0.20599	0.20664
cg2264768	NAV2	LEF-1 [T0	358	365	8.457856	CTTTGA	0.15259	0.15214
cg2105276	NAV2	LEF-1 [T0	1653	1660	8.457856	CTTCAAA	0.15259	0.15214
cg0273928	NAV2	c-Myb [T0	1505	1512	8.412632	TCCAGTT	0.30518	0.30924
cg2264768	NAV2	c-Myb [T0	834	841	8.412632	AAACTG	0.30518	0.30924
cg0273928	NAV2	PPAR-alph	1532	1542	8.384593	AAGCCC	0.02003	0.01963
cg2105276	NAV2	HNF-1B [T	579	587	8.357851	GGTTAA	0.11444	0.11669
cg2264768	NAV2	POU2F2 (	1091	1101	8.346865	TGTCTTA	0.0515	0.05239
cg0273928	NAV2	HNF-3alph	458	465	8.343064	CATTTTA	0.27466	0.28528
cg0273928	NAV2	HNF-3alph	1336	1343	8.343064	TTGAAAT	0.27466	0.28528
cg2264768	NAV2	HNF-3alph	1343	1350	8.343064	TTAAAAT	0.27466	0.28528
cg2105276	NAV2	HNF-3alph	1768	1775	8.343064	ATAAAAT	0.27466	0.28528
cg2264768	NAV2	c-Ets-2 [T0	130	138	8.339336	TTCCTG	0.13733	0.13681
cg2264768	NAV2	c-Ets-2 [T0	1415	1423	8.339336	GGGCAG	0.13733	0.13681
cg0273928	NAV2	PR B [T00	59	65	8.338824	TTCTGTT	1.09863	1.10009
cg0273928	NAV2	PR B [T00	282	288	8.338824	GCCTGTT	1.09863	1.10009
cg0273928	NAV2	PR B [T00	1331	1337	8.338824	CCCTGTT	1.09863	1.10009

cg0273928	NAV2	PR B [T00	1704	1710	8.338824	TGCTGTT	1.09863	1.10009
cg0273928	NAV2	PR B [T00	1716	1722	8.338824	GGCTGT	1.09863	1.10009
cg0273928	NAV2	PR A [T01	59	65	8.338824	TTCTGTT	1.09863	1.10009
cg0273928	NAV2	PR A [T01	282	288	8.338824	GCCTGTT	1.09863	1.10009
cg0273928	NAV2	PR A [T01	1331	1337	8.338824	CCCTGTT	1.09863	1.10009
cg0273928	NAV2	PR A [T01	1704	1710	8.338824	TGCTGTT	1.09863	1.10009
cg0273928	NAV2	PR A [T01	1716	1722	8.338824	GGCTGT	1.09863	1.10009
cg2264768	NAV2	PR B [T00	783	789	8.338824	TCCTGTT	1.09863	1.10009
cg2264768	NAV2	PR B [T00	1003	1009	8.338824	AACAGG	1.09863	1.10009
cg2264768	NAV2	PR B [T00	1059	1065	8.338824	GGCTGT	1.09863	1.10009
cg2264768	NAV2	PR B [T00	1474	1480	8.338824	TGCTGTT	1.09863	1.10009
cg2264768	NAV2	PR A [T01	783	789	8.338824	TCCTGTT	1.09863	1.10009
cg2264768	NAV2	PR A [T01	1003	1009	8.338824	AACAGG	1.09863	1.10009
cg2264768	NAV2	PR A [T01	1059	1065	8.338824	GGCTGT	1.09863	1.10009
cg2264768	NAV2	PR A [T01	1474	1480	8.338824	TGCTGTT	1.09863	1.10009
cg2105276	NAV2	PR B [T00	597	603	8.338824	AACAGA	1.09863	1.10009
cg2105276	NAV2	PR B [T00	857	863	8.338824	AACAGC	1.09863	1.10009
cg2105276	NAV2	PR B [T00	1646	1652	8.338824	TTCTGTT	1.09863	1.10009
cg2105276	NAV2	PR B [T00	1882	1888	8.338824	CTCTGTT	1.09863	1.10009
cg2105276	NAV2	PR B [T00	1896	1902	8.338824	TGCTGTT	1.09863	1.10009
cg2105276	NAV2	PR A [T01	597	603	8.338824	AACAGA	1.09863	1.10009
cg2105276	NAV2	PR A [T01	857	863	8.338824	AACAGC	1.09863	1.10009
cg2105276	NAV2	PR A [T01	1646	1652	8.338824	TTCTGTT	1.09863	1.10009
cg2105276	NAV2	PR A [T01	1882	1888	8.338824	CTCTGTT	1.09863	1.10009
cg2105276	NAV2	PR A [T01	1896	1902	8.338824	TGCTGTT	1.09863	1.10009
cg0273928	NAV2	IRF-1 [T0	1580	1588	8.316022	CTGAGG	0.20599	0.20664
cg2105276	NAV2	AR [T000	227	235	8.295755	AGCATG	0.10681	0.10625
cg2105276	NAV2	AR [T000	1352	1360	8.295755	AGCATG	0.10681	0.10625
cg0273928	NAV2	GR-alpha [	204	208	8.281568	CCTTG	7.8125	7.72956
cg0273928	NAV2	GR-alpha [	321	325	8.281568	CCTCC	7.8125	7.72956
cg0273928	NAV2	GR-alpha [	418	422	8.281568	CCTTC	7.8125	7.72956
cg0273928	NAV2	GR-alpha [	493	497	8.281568	GAAGG	7.8125	7.72956
cg0273928	NAV2	GR-alpha [	647	651	8.281568	CCTTG	7.8125	7.72956
cg0273928	NAV2	GR-alpha [	1011	1015	8.281568	CCTTG	7.8125	7.72956
cg0273928	NAV2	GR-alpha [	1183	1187	8.281568	CCTTC	7.8125	7.72956
cg0273928	NAV2	GR-alpha [	1900	1904	8.281568	CAAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	136	140	8.281568	CCTTG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	231	235	8.281568	CCTTC	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	504	508	8.281568	GAAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	538	542	8.281568	CGAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	555	559	8.281568	GAAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	665	669	8.281568	CCTCC	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1391	1395	8.281568	CCTTG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1435	1439	8.281568	CAAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1581	1585	8.281568	GAAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1603	1607	8.281568	CCTCC	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1752	1756	8.281568	CAAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1802	1806	8.281568	GAAGG	7.8125	7.72956

cg2264768	NAV2	GR-alpha [	1835	1839	8.281568	CCTTG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1852	1856	8.281568	CAAGG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1908	1912	8.281568	CCTTG	7.8125	7.72956
cg2264768	NAV2	GR-alpha [	1927	1931	8.281568	CCTTG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	23	27	8.281568	CCTTG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	413	417	8.281568	CCTTC	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	505	509	8.281568	CCTTC	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	623	627	8.281568	GGAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	643	647	8.281568	GAAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	660	664	8.281568	GGAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	724	728	8.281568	GAAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	927	931	8.281568	CAAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	944	948	8.281568	GGAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1045	1049	8.281568	CCTTG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1097	1101	8.281568	CCTTC	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1103	1107	8.281568	CCTTG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1159	1163	8.281568	CCTTG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1196	1200	8.281568	GGAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1436	1440	8.281568	CCTCC	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1510	1514	8.281568	CAAGG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1623	1627	8.281568	CCTCG	7.8125	7.72956
cg2105276	NAV2	GR-alpha [	1745	1749	8.281568	GGAGG	7.8125	7.72956
cg2264768	NAV2	c-Ets-1 [T	764	770	8.244941	GTGGAA	0.24414	0.2425
cg2264768	NAV2	HNF-1B [	1670	1678	8.241969	AAATTA	0.06866	0.07026
cg0273928	NAV2	NFI/CTF [	1023	1030	8.241664	CTGGTT	0.18311	0.1823
cg0273928	NAV2	NFI/CTF [	1913	1920	8.241664	CTGGTT	0.18311	0.1823
cg2264768	NAV2	NFI/CTF [	212	219	8.241664	CTGGTT	0.18311	0.1823
cg2105276	NAV2	HOXD9 [T	1586	1595	8.224939	AATATA	0.08774	0.09025
cg2105276	NAV2	HOXD10 [	1586	1595	8.224939	AATATA	0.08774	0.09025
cg0273928	NAV2	NF-AT2 [T	1904	1913	8.21356	GTGTAT	0.08965	0.09068
cg2264768	NAV2	ENKTF-1	1749	1756	8.19852	TGGCAA	0.73242	0.71737
cg2105276	NAV2	ENKTF-1	811	818	8.19852	TGGCAG	0.73242	0.71737
cg2105276	NAV2	ENKTF-1	1231	1238	8.19852	CGTGGC	0.73242	0.71737
cg2264768	NAV2	HNF-1C [	1097	1105	8.193285	ATACCT	0.19836	0.20224
cg2105276	NAV2	NF-1 [T00	19	26	8.191058	TTGGCC	0.24414	0.24409
cg2105276	NAV2	NF-1 [T00	54	61	8.191058	TTGGAC	0.24414	0.24409
cg2105276	NAV2	NF-1 [T00	92	99	8.191058	AAGCCC	0.24414	0.24409
cg0273928	NAV2	PXR-1:RX	636	643	8.180749	AACGTT	0.12207	0.12407
cg0273928	NAV2	SRY [T00	1567	1575	8.174786	CCCACA	0.15259	0.15383
cg2105276	NAV2	SRY [T00	1652	1660	8.174786	TCTTCA	0.15259	0.15383
cg2105276	NAV2	IRF-1 [T0	1103	1111	8.151819	CCTTGG	0.25177	0.25263
cg2264768	NAV2	c-Jun [T00	1149	1155	8.128539	TGACGT	0.48828	0.49076
cg0273928	NAV2	NF-AT1 [T	537	545	8.12076	GAATTT	0.1297	0.12988
cg2264768	NAV2	NF-AT1 [T	1983	1991	8.12076	GACTTT	0.1297	0.12988
cg0273928	NAV2	LEF-1 [T0	421	428	8.117221	TCTCAA	0.12207	0.1241
cg2264768	NAV2	LEF-1 [T0	1969	1976	8.117221	CTTTGA	0.12207	0.1241
cg0273928	NAV2	AR [T000	1651	1659	8.11332	GGACAG	0.19836	0.19634
cg2264768	NAV2	VDR [T00	185	193	8.079962	GATTTG	0.24414	0.24712

cg2105276	NAV2	VDR [T00	992	1000	8.079962	GTTCAA	0.24414	0.24712
cg2105276	NAV2	VDR [T00	1127	1135	8.079962	GTTCAG	0.24414	0.24712
cg0273928	NAV2	IRF-1 [T0	541	549	8.078284	TTTCCAC	0.25177	0.25263
cg0273928	NAV2	IRF-1 [T0	887	895	8.078284	TTTCCAC	0.25177	0.25263
cg0273928	NAV2	GR-alpha [	35	39	8.073878	CCAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	90	94	8.073878	CCTGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	161	165	8.073878	CCTAG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	162	166	8.073878	CTAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	324	328	8.073878	CCTAG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	603	607	8.073878	CCTAG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	821	825	8.073878	CCAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	890	894	8.073878	CCAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	927	931	8.073878	CTAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1436	1440	8.073878	GTAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1520	1524	8.073878	CCTAG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1537	1541	8.073878	CCAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1562	1566	8.073878	CCAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1702	1706	8.073878	CCTGC	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1817	1821	8.073878	CTAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1912	1916	8.073878	CCTGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1956	1960	8.073878	GCAGG	7.8125	7.72238
cg0273928	NAV2	GR-alpha [	1978	1982	8.073878	GCAGG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	76	80	8.073878	CCTAG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	106	110	8.073878	CCAGG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	132	136	8.073878	CCTGC	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	407	411	8.073878	CCTGG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	457	461	8.073878	CCTGC	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	669	673	8.073878	CCTGC	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	704	708	8.073878	CCTAG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	774	778	8.073878	GCAGG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	1030	1034	8.073878	GTAGG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	1125	1129	8.073878	CCTGC	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	1137	1141	8.073878	CCTGC	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	1417	1421	8.073878	GCAGG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	1430	1434	8.073878	CCAGG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	1879	1883	8.073878	CCTAG	7.8125	7.72238
cg2264768	NAV2	GR-alpha [	1892	1896	8.073878	CCTGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	192	196	8.073878	CCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	240	244	8.073878	CCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	509	513	8.073878	CCTGC	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	551	555	8.073878	CCTAG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	552	556	8.073878	CTAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	570	574	8.073878	CCTGC	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	576	580	8.073878	CCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	615	619	8.073878	GCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	730	734	8.073878	GCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	813	817	8.073878	GCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	831	835	8.073878	GCAGG	7.8125	7.72238

cg2105276	NAV2	GR-alpha [	862	866	8.073878	CCTGC	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	877	881	8.073878	CCTGC	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	966	970	8.073878	CCTGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	988	992	8.073878	CTAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1081	1085	8.073878	CTAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1184	1188	8.073878	GCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1201	1205	8.073878	GCAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1240	1244	8.073878	CCTAG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1303	1307	8.073878	CCTGC	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1342	1346	8.073878	CCTGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1359	1363	8.073878	CCTGC	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1440	1444	8.073878	CCTGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1540	1544	8.073878	CCTGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1601	1605	8.073878	CCTAG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1640	1644	8.073878	CTAGG	7.8125	7.72238
cg2105276	NAV2	GR-alpha [	1976	1980	8.073878	CCAGG	7.8125	7.72238
cg0273928	NAV2	HNF-1C [	1274	1282	8.067744	TTATCTA	0.19836	0.20224
cg2264768	NAV2	HNF-1C [	948	956	8.067744	GTTAGA	0.19836	0.20224
cg0273928	NAV2	Pax-5 [T0	226	232	8.014558	GGGCTG	2.19727	2.14502
cg0273928	NAV2	Pax-5 [T0	841	847	8.014558	GGGCAG	2.19727	2.14502
cg0273928	NAV2	Pax-5 [T0	930	936	8.014558	GGGCTG	2.19727	2.14502
cg0273928	NAV2	Pax-5 [T0	1169	1175	8.014558	GGGCTG	2.19727	2.14502
cg0273928	NAV2	Pax-5 [T0	1477	1483	8.014558	TGTGCC	2.19727	2.14502
cg0273928	NAV2	Pax-5 [T0	1531	1537	8.014558	TAAGCC	2.19727	2.14502
cg0273928	NAV2	TFIID [T0	19	25	8.014558	TTTCTA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	395	401	8.014558	TTTCCA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	421	427	8.014558	TCTCAA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	591	597	8.014558	TAGGAA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	734	740	8.014558	TTAGAA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	1114	1120	8.014558	TTTGTG	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	1240	1246	8.014558	TAGGAA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	1279	1285	8.014558	TAACAA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	1767	1773	8.014558	TTTCCTA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	1801	1807	8.014558	TTTCATA	2.19727	2.24348
cg0273928	NAV2	TFIID [T0	1844	1850	8.014558	TTTCTTA	2.19727	2.24348
cg2264768	NAV2	Pax-5 [T0	321	327	8.014558	GGGCTT	2.19727	2.14502
cg2264768	NAV2	Pax-5 [T0	645	651	8.014558	GGGCCT	2.19727	2.14502
cg2264768	NAV2	Pax-5 [T0	1036	1042	8.014558	GCTGCC	2.19727	2.14502
cg2264768	NAV2	Pax-5 [T0	1508	1514	8.014558	GGGCTT	2.19727	2.14502
cg2264768	NAV2	Pax-5 [T0	1855	1861	8.014558	GGAGCC	2.19727	2.14502
cg2264768	NAV2	TFIID [T0	93	99	8.014558	TTTGCA	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	151	157	8.014558	TTTCTTA	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	222	228	8.014558	TTTGAG	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	519	525	8.014558	TAGCAA	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	830	836	8.014558	TTGGAA	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	1118	1124	8.014558	TTTGTTA	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	1307	1313	8.014558	TAAGAA	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	1617	1623	8.014558	TCTGAA	2.19727	2.24348

cg2264768	NAV2	TFIID [T0	1722	1728	8.014558	TTTCATA	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	1970	1976	8.014558	TTTGAG	2.19727	2.24348
cg2264768	NAV2	TFIID [T0	1987	1993	8.014558	TTTCCTA	2.19727	2.24348
cg2105276	NAV2	Pax-5 [T0	91	97	8.014558	GAAGCC	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	218	224	8.014558	GCAGCC	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	335	341	8.014558	GCAGCC	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	451	457	8.014558	TCTGCC	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	711	717	8.014558	TGGGCC	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	712	718	8.014558	GGGCCC	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	737	743	8.014558	GGGCAG	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	823	829	8.014558	TGAGCC	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	1443	1449	8.014558	GGGCCT	2.19727	2.14502
cg2105276	NAV2	Pax-5 [T0	1849	1855	8.014558	GAAGCC	2.19727	2.14502
cg2105276	NAV2	TFIID [T0	147	153	8.014558	TTTGAA	2.19727	2.24348
cg2105276	NAV2	TFIID [T0	377	383	8.014558	TCTCAA	2.19727	2.24348
cg2105276	NAV2	TFIID [T0	530	536	8.014558	TTTCAA	2.19727	2.24348
cg2105276	NAV2	TFIID [T0	1105	1111	8.014558	TTGGAA	2.19727	2.24348
cg2105276	NAV2	TFIID [T0	1416	1422	8.014558	TTTCCA	2.19727	2.24348
cg2105276	NAV2	TFIID [T0	1730	1736	8.014558	TAAGAA	2.19727	2.24348
cg2105276	NAV2	TFIID [T0	1826	1832	8.014558	TTTGAG	2.19727	2.24348
cg2105276	NAV2	TFIID [T0	1902	1908	8.014558	TTTGAA	2.19727	2.24348
cg0273928	NAV2	C/EBPalph	962	968	8.006685	CATTGG	0.24414	0.24674
cg2264768	NAV2	HNF-1C [	261	269	8.002145	CTCTGTA	0.19836	0.20224
cg2264768	NAV2	CTF [T001	1011	1022	7.899258	AAAAAT	0.02003	0.0203
cg0273928	NAV2	IRF-1 [T0	589	597	7.896985	CTTAGG	0.25177	0.25263
cg0273928	NAV2	IRF-1 [T0	1238	1246	7.896985	CTTAGG	0.25177	0.25263
cg2105276	NAV2	ETF [T002	1071	1081	7.870358	GGGGGT	0.07153	0.06862
cg2105276	NAV2	ATF-1 [T0	895	905	7.870358	GAGTCA	0.07153	0.07147
cg0273928	NAV2	EBF [T05	818	828	7.860096	CACCCA	0.04196	0.04106
cg0273928	NAV2	c-Ets-2 [T	888	896	7.84116	TTCCAG	0.32043	0.32298
cg0273928	NAV2	c-Ets-2 [T	1092	1100	7.84116	TTTCAG	0.32043	0.32298
cg0273928	NAV2	c-Ets-2 [T	1910	1918	7.84116	TTCCTG	0.32043	0.32298
cg2264768	NAV2	p53 [T006	1855	1861	7.833758	GGAGCC	0.48828	0.47377
cg2264768	NAV2	IRF-1 [T0	1416	1424	7.82345	GGCAGG	0.25177	0.25263
cg2105276	NAV2	RXR-alpha	1235	1241	7.815913	GCCACC	0.24414	0.24104
cg2105276	NAV2	EBF [T05	220	230	7.780217	AGCCCT	0.04196	0.04106
cg0273928	NAV2	NF-AT2 [	825	834	7.779688	GGAAAA	0.08965	0.09068
cg2264768	NAV2	NF-AT2 [	778	787	7.779688	GGAAAT	0.08965	0.09068
cg0273928	NAV2	T3R-beta1	817	825	7.774776	TCACCC	0.27466	0.27236
cg0273928	NAV2	c-Ets-2 [T	1768	1776	7.76635	TTCCTAT	0.32043	0.32298
cg0273928	NAV2	c-Myb [T0	1191	1198	7.739476	CACAGT	0.42725	0.43114
cg2264768	NAV2	c-Myb [T0	190	197	7.739476	GAACTG	0.42725	0.43114
cg0273928	NAV2	HNF-1B [	1707	1715	7.737819	TGTTAA	0.09155	0.09368
cg0273928	NAV2	NF-AT1 [	1242	1250	7.72101	GGAAAC	0.19836	0.19941
cg2264768	NAV2	NF-AT1 [	559	567	7.72101	GGAAAC	0.19836	0.19941
cg0273928	NAV2	HNF-1C [	18	26	7.717465	CTTTCTA	0.08392	0.08549
cg0273928	NAV2	c-Jun [T00	1051	1057	7.686747	TGACTG	0.48828	0.48775
cg2105276	NAV2	c-Jun [T00	786	792	7.686747	ACAGTC	0.48828	0.48775

cg2105276	NAV2	p53 [T006	1296	1302	7.641867	AAGGCC	0.73242	0.7186
cg2105276	NAV2	p53 [T006	1391	1397	7.641867	GGGCCG	0.73242	0.7186
cg0273928	NAV2	AR [T0004	198	206	7.588908	GGACAT	0.25177	0.25079
cg0273928	NAV2	NFI/CTF [	1737	1744	7.587343	CCAAAT	0.36621	0.36674
cg2105276	NAV2	NFI/CTF [	96	103	7.587343	CCAAAA	0.36621	0.36674
cg0273928	NAV2	NF-AT1 [	593	601	7.574801	GGAAAA	0.19836	0.19941
cg0273928	NAV2	NF-AT1 [	1411	1419	7.574801	GGAAAA	0.19836	0.19941
cg0273928	NAV2	NF-AT1 [	1905	1913	7.551065	TGTATT	0.19836	0.19941
cg2105276	NAV2	PU.1 [T02	1478	1490	7.546536	GTACTT	0.01001	0.01007
cg0273928	NAV2	c-Myb [T0	1463	1470	7.545286	AAACTG	0.42725	0.43114
cg0273928	NAV2	c-Myb [T0	1877	1884	7.545286	TGCAGT	0.42725	0.43114
cg2264768	NAV2	PPAR-alpl	641	651	7.529496	ATCTGG	0.04482	0.04393
cg2105276	NAV2	PPAR-alpl	1439	1449	7.529496	CCCTGG	0.04482	0.04393
cg0273928	NAV2	GR [T050	365	371	7.527031	CCTTTTC	1.83105	1.86007
cg0273928	NAV2	GR [T050	488	494	7.527031	CAAAAG	1.83105	1.86007
cg0273928	NAV2	GR [T050	520	526	7.527031	CAAAAT	1.83105	1.86007
cg0273928	NAV2	GR [T050	685	691	7.527031	CAAATA	1.83105	1.86007
cg0273928	NAV2	GR [T050	1149	1155	7.527031	TTGTTTC	1.83105	1.86007
cg0273928	NAV2	GR [T050	1218	1224	7.527031	TCTTTTG	1.83105	1.86007
cg0273928	NAV2	GR [T050	1282	1288	7.527031	CAAAAG	1.83105	1.86007
cg0273928	NAV2	GR [T050	1381	1387	7.527031	AGCTTTC	1.83105	1.86007
cg0273928	NAV2	GR [T050	1827	1833	7.527031	TCTTTTG	1.83105	1.86007
cg0273928	NAV2	GR [T050	1890	1896	7.527031	TTGTTTC	1.83105	1.86007
cg2264768	NAV2	GR [T050	116	122	7.527031	CAAAAG	1.83105	1.86007
cg2264768	NAV2	GR [T050	785	791	7.527031	CTGTTTC	1.83105	1.86007
cg2264768	NAV2	GR [T050	1061	1067	7.527031	CTGTTTC	1.83105	1.86007
cg2264768	NAV2	GR [T050	1465	1471	7.527031	CAAAGC	1.83105	1.86007
cg2264768	NAV2	GR [T050	1476	1482	7.527031	CTGTTTC	1.83105	1.86007
cg2264768	NAV2	GR [T050	1497	1503	7.527031	ATGTTTC	1.83105	1.86007
cg2105276	NAV2	GR [T050	97	103	7.527031	CAAAAG	1.83105	1.86007
cg2105276	NAV2	GR [T050	144	150	7.527031	ATGTTTC	1.83105	1.86007
cg2105276	NAV2	GR [T050	380	386	7.527031	CAAAAT	1.83105	1.86007
cg2105276	NAV2	GR [T050	426	432	7.527031	CAAATA	1.83105	1.86007
cg2105276	NAV2	GR [T050	436	442	7.527031	ACTTTTC	1.83105	1.86007
cg2105276	NAV2	GR [T050	1823	1829	7.527031	AATTTTC	1.83105	1.86007
cg2105276	NAV2	RAR-beta	1962	1971	7.496706	GGGGTT	0.24414	0.24343
cg2264768	NAV2	c-Jun [T00	534	540	7.491008	TGACCG	0.48828	0.48775
cg2264768	NAV2	IRF-1 [T0	1187	1195	7.477948	TTTCCTC	0.14496	0.14449
cg2264768	NAV2	C/EBPalpl	95	101	7.465744	TGCAAT	0.48828	0.49653
cg0273928	NAV2	NF-1 [T00	1122	1129	7.445595	TTGGCA	0.24414	0.24565
cg0273928	NAV2	PEA3 [T0	84	92	7.421728	CCCCAT	0.34332	0.34161
cg0273928	NAV2	PEA3 [T0	1450	1458	7.421728	GAGCAT	0.34332	0.34161
cg2105276	NAV2	PEA3 [T0	234	242	7.421728	CCTCATC	0.34332	0.34161
cg2264768	NAV2	AR [T0004	376	384	7.406474	CATCTGT	0.25177	0.25079
cg2105276	NAV2	LEF-1 [T0	1544	1551	7.396545	GCACAA	0.21362	0.21302
cg2264768	NAV2	C/EBPalpl	592	598	7.396431	AATTGG	0.48828	0.49653
cg2105276	NAV2	C/EBPalpl	1418	1424	7.396431	TCCAATT	0.48828	0.49653
cg2105276	NAV2	PXR-1:RX	181	188	7.362674	CATGTTC	0.24414	0.24395

cg2105276	NAV2	NF-AT1 [	353	361	7.278086	GGAAAG	0.19836	0.19941
cg2264768	NAV2	HOXD9 [	1248	1257	7.270719	TGTTTAT	0.06866	0.07152
cg2264768	NAV2	HOXD10	1248	1257	7.270719	TGTTTAT	0.06866	0.07152
cg0273928	NAV2	c-Ets-2 [T	1954	1962	7.268173	CAGCAG	0.09155	0.09191
cg2105276	NAV2	c-Ets-2 [T	507	515	7.268173	TTCCTG	0.09155	0.09191
cg0273928	NAV2	p53 [T006	721	727	7.266844	GGGCTT	0.73242	0.7186
cg0273928	NAV2	p53 [T006	1344	1350	7.266844	GGGCTT	0.73242	0.7186
cg2264768	NAV2	p53 [T006	1058	1064	7.266844	GGGCTG	0.73242	0.7186
cg2105276	NAV2	p53 [T006	1930	1936	7.266844	GGGCTG	0.73242	0.7186
cg2105276	NAV2	EBF [T05	453	463	7.262068	TGCCCT	0.01144	0.01125
cg2264768	NAV2	HNF-1C [	1669	1677	7.229698	AAAATT	0.08392	0.08606
cg0273928	NAV2	c-Ets-1 [T	1409	1415	7.199436	TGGGAA	0.73242	0.73099
cg0273928	NAV2	c-Ets-1 [T	1615	1621	7.199436	TGGGAA	0.73242	0.73099
cg2105276	NAV2	c-Ets-1 [T	327	333	7.199436	TGGGAA	0.73242	0.73099
cg0273928	NAV2	GCF [T00	977	985	7.186486	GCGCAG	0.45776	0.44706
cg0273928	NAV2	XBP-1 [T	43	48	7.172312	CCTCAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	131	136	7.172312	ATGAAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	248	253	7.172312	CATCAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	756	761	7.172312	CCTCAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	832	837	7.172312	ATGAGT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	899	904	7.172312	CATCAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	903	908	7.172312	ATTCAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	1250	1255	7.172312	AATCAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	1313	1318	7.172312	ATGATG	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	1361	1366	7.172312	ATGAAT	2.92969	2.97018
cg0273928	NAV2	XBP-1 [T	1488	1493	7.172312	ATGATG	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	4	9	7.172312	CATCAT	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	183	188	7.172312	ATGATT	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	437	442	7.172312	ATGAAG	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	648	653	7.172312	CCTCAT	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	680	685	7.172312	CTTCAT	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	1113	1118	7.172312	ACTCAT	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	1168	1173	7.172312	ATGATG	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	1511	1516	7.172312	CTTCAT	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	1960	1965	7.172312	ATGATG	2.92969	2.97018
cg2264768	NAV2	XBP-1 [T	1976	1981	7.172312	ATGAGT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	89	94	7.172312	ATGAAG	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	133	138	7.172312	ATGAAG	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	234	239	7.172312	CCTCAT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	308	313	7.172312	CCTCAT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	484	489	7.172312	ACTCAT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	650	655	7.172312	ATGAGT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	756	761	7.172312	AATCAT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	1067	1072	7.172312	ATGAGG	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	1453	1458	7.172312	CCTCAT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	1701	1706	7.172312	AATCAT	2.92969	2.97018
cg2105276	NAV2	XBP-1 [T	1854	1859	7.172312	CCTCAT	2.92969	2.97018
cg2105276	NAV2	p53 [T006	711	717	7.153797	TGGGCC	1.09863	1.07125

cg2105276	NAV2	p53 [T006	712	718	7.153797	GGGCCC	1.09863	1.07125
cg0273928	NAV2	p53 [T006	1137	1143	7.150251	GTGGCC	1.09863	1.07125
cg2264768	NAV2	p53 [T006	71	77	7.150251	GTGGCC	1.09863	1.07125
cg2264768	NAV2	p53 [T006	101	107	7.150251	GTGGCC	1.09863	1.07125
cg2105276	NAV2	p53 [T006	1085	1091	7.150251	GTGGCC	1.09863	1.07125
cg2105276	NAV2	p53 [T006	1263	1269	7.150251	GTGGCC	1.09863	1.07125
cg0273928	NAV2	c-Jun [T00	314	320	7.096776	GCAGTC	0.73242	0.73173
cg0273928	NAV2	c-Jun [T00	1873	1879	7.096776	TGACTG	0.73242	0.73173
cg0273928	NAV2	c-Ets-1 [T	823	829	7.071349	AGGGAA	0.73242	0.73099
cg2264768	NAV2	c-Ets-1 [T	557	563	7.071349	AGGGAA	0.73242	0.73099
cg2264768	NAV2	c-Ets-1 [T	776	782	7.071349	AGGGAA	0.73242	0.73099
cg2264768	NAV2	c-Ets-1 [T	1821	1827	7.071349	AGGGAA	0.73242	0.73099
cg2105276	NAV2	c-Ets-1 [T	351	357	7.071349	AGGGAA	0.73242	0.73099
cg2264768	NAV2	AR [T000	332	340	7.049779	CCTGTG	0.23651	0.23551
cg2105276	NAV2	IRF-1 [T0	953	961	7.044985	GAGAGG	0.1297	0.13036
cg0273928	NAV2	HNF-1C [	350	358	7.028835	TTTACTA	0.08392	0.08606
cg2264768	NAV2	NFI/CTF [	539	546	7.014249	GAGGTT	0.73242	0.73214
cg0273928	NAV2	C/EBPalph	242	248	7.00174	CATTGG	0.73242	0.74337
cg2105276	NAV2	C/EBPalph	818	824	7.00174	GACAAT	0.73242	0.74337
cg0273928	NAV2	RelA [T00	1408	1418	7.000813	ATGGGA	0.01192	0.01181
cg0273928	NAV2	HNF-3alph	53	60	7.000129	AGAAAA	0.82397	0.84946
cg2264768	NAV2	HNF-3alph	954	961	7.000129	TAAAAA	0.82397	0.84946
cg2264768	NAV2	HNF-3alph	1010	1017	7.000129	AAAAAA	0.82397	0.84946
cg2264768	NAV2	HNF-3alph	1733	1740	7.000129	TGCAAA	0.82397	0.84946
cg2105276	NAV2	HNF-3alph	39	46	7.000129	TATAAA	0.82397	0.84946
cg2105276	NAV2	HNF-3alph	424	431	7.000129	TCCAAA	0.82397	0.84946
cg2105276	NAV2	HNF-3alph	1582	1589	7.000129	GAAAAA	0.82397	0.84946
cg2264768	NAV2	AR [T000	1695	1703	6.974607	GGACAG	0.23651	0.23551
cg0273928	NAV2	IRF-1 [T0	1613	1621	6.968314	TCTGGG	0.1297	0.13036
cg2264768	NAV2	TCF-4 [T0	357	366	6.961804	TCTTTGA	0.01144	0.01152
cg2264768	NAV2	IRF-1 [T0	281	289	6.954318	TTTCCAC	0.1297	0.13036
cg0273928	NAV2	NF-1 [T00	619	626	6.948522	TTGGTTC	0.48828	0.4856
cg2264768	NAV2	NF-1 [T00	543	550	6.948522	TTGGGG	0.48828	0.4856
cg2105276	NAV2	NF-1 [T00	299	306	6.948522	TTGGTTC	0.48828	0.4856
cg2105276	NAV2	NF-1 [T00	421	428	6.948522	TGCTCC	0.48828	0.4856
cg2105276	NAV2	NF-1 [T00	1124	1131	6.948522	TTGGTTC	0.48828	0.4856
cg2105276	NAV2	NF-1 [T00	1802	1809	6.948522	AGAGCC	0.48828	0.4856
cg2264768	NAV2	c-Ets-1 [T	1609	1615	6.943262	TTTCCCC	0.73242	0.73099
cg0273928	NAV2	ENKTF-1	1537	1544	6.942764	CCAGGC	1.46484	1.44228
cg0273928	NAV2	ENKTF-1	1599	1606	6.942764	CACTGC	1.46484	1.44228
cg2264768	NAV2	ENKTF-1	1462	1469	6.942764	TGGCAA	1.46484	1.44228
cg2264768	NAV2	ENKTF-1	1848	1855	6.942764	TGGCCA	1.46484	1.44228
cg2105276	NAV2	ENKTF-1	322	329	6.942764	TGGCTTC	1.46484	1.44228
cg2105276	NAV2	ENKTF-1	890	897	6.942764	TGGCTG	1.46484	1.44228
cg2105276	NAV2	ENKTF-1	968	975	6.942764	TGGCAA	1.46484	1.44228
cg2105276	NAV2	ENKTF-1	1344	1351	6.942764	TGGCTG	1.46484	1.44228
cg2264768	NAV2	p53 [T006	645	651	6.938545	GGGCCT	1.09863	1.07125
cg0273928	NAV2	VDR [T00	639	647	6.925682	GTTCAC	0.42725	0.43062

cg2264768	NAV2	VDR [T00	928	936	6.925682	AAACTG	0.42725	0.43062
cg2264768	NAV2	VDR [T00	1541	1549	6.925682	GTTCAA	0.42725	0.43062
cg2105276	NAV2	VDR [T00	184	192	6.925682	GTTCAG	0.42725	0.43062
cg2105276	NAV2	VDR [T00	1399	1407	6.925682	GAATTG	0.42725	0.43062
cg2264768	NAV2	STAT1bet	774	783	6.908963	GCAGGG	0.103	0.10372
cg2264768	NAV2	STAT1bet	1819	1828	6.908963	TTAGGG	0.103	0.10372
cg2105276	NAV2	STAT1bet	349	358	6.908963	ACAGGG	0.103	0.10372
cg0273928	NAV2	C/EBPalp	1099	1105	6.85549	AATTGC	0.73242	0.74337
cg0273928	NAV2	C/EBPalp	1269	1275	6.85549	TGCAAT	0.73242	0.74337
cg0273928	NAV2	C/EBPalp	1607	1613	6.85549	TGCAAT	0.73242	0.74337
cg2105276	NAV2	C/EBPalp	383	389	6.85549	AATTGC	0.73242	0.74337
cg2105276	NAV2	C/EBPalp	1400	1406	6.85549	AATTGA	0.73242	0.74337
cg2264768	NAV2	HOXD9 [	1681	1690	6.852796	AATAAT	0.07629	0.0789
cg2264768	NAV2	HOXD10 [	1681	1690	6.852796	AATAAT	0.07629	0.0789
cg0273928	NAV2	PEA3 [T0	622	630	6.824411	GTTCAT	0.22888	0.22933
cg2105276	NAV2	STAT5A [	1951	1963	6.810722	TTTCAA	0.01341	0.01369
cg0273928	NAV2	c-Jun [T00	1680	1686	6.787369	TCTGTC	0.73242	0.73173
cg2105276	NAV2	c-Jun [T00	749	755	6.787369	TGACAG	0.73242	0.73173
cg0273928	NAV2	NFI/CTF [	220	227	6.786076	CAGTTT	0.73242	0.73214
cg2264768	NAV2	NFI/CTF [	785	792	6.786076	CTGTTT	0.73242	0.73214
cg2264768	NAV2	NFI/CTF [	990	997	6.786076	TGGATT	0.73242	0.73214
cg2264768	NAV2	NFI/CTF [	1476	1483	6.786076	CTGTTT	0.73242	0.73214
cg2105276	NAV2	NFI/CTF [	322	329	6.786076	TGGCTT	0.73242	0.73214
cg2105276	NAV2	NFI/CTF [	1047	1054	6.786076	TTGATT	0.73242	0.73214
cg2105276	NAV2	NFI/CTF [	1381	1388	6.786076	CCAAAC	0.73242	0.73214
cg2105276	NAV2	p53 [T006	823	829	6.778774	TGAGCC	1.09863	1.07125
cg2264768	NAV2	EBF [T05	1857	1867	6.76967	AGCCCT	0.03052	0.02964
cg0273928	NAV2	LEF-1 [T0	480	487	6.75468	CTTTGA	0.06104	0.06131
cg2264768	NAV2	ATF3 [T0	1257	1264	6.744803	TGACTT	0.27466	0.27656
cg2105276	NAV2	ATF3 [T0	670	677	6.744803	TGACTT	0.27466	0.27656
cg0273928	NAV2	TCF-4 [T0	479	488	6.735684	TCTTTGA	0.04959	0.05016
cg2264768	NAV2	HNF-1B [	947	955	6.728796	AGTTAG	0.04578	0.04691
cg0273928	NAV2	AR [T000	1729	1737	6.723093	AGTCTG	0.19836	0.19597
cg2105276	NAV2	NF-1 [T00	851	858	6.722386	CTGGCC	0.24414	0.24147
cg2105276	NAV2	T3R-beta1	682	690	6.702681	AGGGGG	0.21362	0.21147
cg0273928	NAV2	c-Ets-2 [T	513	521	6.695187	TTCCTGT	0.09155	0.09289
cg2264768	NAV2	c-Ets-2 [T	1531	1539	6.695187	TTCCTAT	0.09155	0.09289
cg2264768	NAV2	c-Ets-2 [T	1988	1996	6.695187	TTCCTAT	0.09155	0.09289
cg2264768	NAV2	PXR-1:RX	932	939	6.668182	TGAACA	0.24414	0.24672
cg2264768	NAV2	PXR-1:RX	1538	1545	6.668182	TGTGTT	0.24414	0.24672
cg0273928	NAV2	c-Jun [T00	1118	1124	6.668031	TGACTT	0.61035	0.60769
cg0273928	NAV2	IRF-1 [T0	1767	1775	6.625948	TTTCCTA	0.19073	0.19127
cg2105276	NAV2	IRF-1 [T0	325	333	6.622811	CTTGGG	0.19073	0.19127
cg0273928	NAV2	TFII-I [T0	74	79	6.581441	GGAGAT	0.97656	0.97366
cg0273928	NAV2	TFII-I [T0	1656	1661	6.581441	GGAGTG	0.97656	0.97366
cg0273928	NAV2	FOXP3 [T	360	365	6.581441	TAAAAC	0.97656	0.99397
cg0273928	NAV2	FOXP3 [T	775	780	6.581441	TTCAAC	0.97656	0.99397
cg0273928	NAV2	FOXP3 [T	1209	1214	6.581441	GTTGAA	0.97656	0.99397

cg0273928	NAV2	FOXP3 [T	1229	1234	6.581441	TTCAAC	0.97656	0.99397
cg0273928	NAV2	FOXP3 [T	1335	1340	6.581441	GTTGAA	0.97656	0.99397
cg0273928	NAV2	FOXP3 [T	1754	1759	6.581441	TAAAAC	0.97656	0.99397
cg2264768	NAV2	TFII-I [T0	1073	1078	6.581441	ATCTCC	0.97656	0.97366
cg2264768	NAV2	TFII-I [T0	1934	1939	6.581441	ATCTCC	0.97656	0.97366
cg2264768	NAV2	FOXP3 [T	920	925	6.581441	TAAAAC	0.97656	0.99397
cg2264768	NAV2	FOXP3 [T	1108	1113	6.581441	GTTTTA	0.97656	0.99397
cg2105276	NAV2	TFII-I [T0	566	571	6.581441	CACTCC	0.97656	0.97366
cg2105276	NAV2	TFII-I [T0	626	631	6.581441	GGAGTG	0.97656	0.97366
cg2105276	NAV2	FOXP3 [T	1796	1801	6.581441	GTTTTA	0.97656	0.99397
cg2105276	NAV2	FOXP3 [T	1965	1970	6.581441	GTTTTA	0.97656	0.99397
cg0273928	NAV2	p53 [T006	1169	1175	6.563521	GGGCTG	0.48828	0.47541
cg2264768	NAV2	p53 [T006	1508	1514	6.563521	GGGCTT	0.48828	0.47541
cg2105276	NAV2	p53 [T006	91	97	6.563521	GAAGCC	0.48828	0.47541
cg2105276	NAV2	p53 [T006	218	224	6.563521	GCAGCC	0.48828	0.47541
cg2105276	NAV2	p53 [T006	335	341	6.563521	GCAGCC	0.48828	0.47541
cg2105276	NAV2	p53 [T006	1849	1855	6.563521	GAAGCC	0.48828	0.47541
cg2105276	NAV2	NF-AT1 [	957	965	6.562181	GGAAAA	0.03815	0.03835
cg2105276	NAV2	MEF-2A [	1579	1589	6.559479	GGAGAA	0.02384	0.02461
cg0273928	NAV2	PXR-1:RX	368	375	6.5446	TTTGTTC	0.24414	0.24672
cg2105276	NAV2	PXR-1:RX	1403	1410	6.5446	TGAACA	0.24414	0.24672
cg2105276	NAV2	PPAR-alph	881	891	6.51544	CTCTGG	0.03719	0.03639
cg0273928	NAV2	TCF-4 [T0	420	429	6.509564	TTCTCA	0.04959	0.05016
cg2264768	NAV2	IRF-1 [T0	1886	1894	6.497844	TTTCCA	0.19073	0.19127
cg0273928	NAV2	XBP-1 [T	245	250	6.478682	TGGCAT	0.97656	0.97062
cg0273928	NAV2	XBP-1 [T	1123	1128	6.478682	TGGCAT	0.97656	0.97062
cg2264768	NAV2	XBP-1 [T	125	130	6.478682	GGGCAT	0.97656	0.97062
cg2264768	NAV2	XBP-1 [T	373	378	6.478682	TGGCAT	0.97656	0.97062
cg2264768	NAV2	XBP-1 [T	817	822	6.478682	TGGCAT	0.97656	0.97062
cg2264768	NAV2	XBP-1 [T	939	944	6.478682	ATGCCA	0.97656	0.97062
cg2264768	NAV2	XBP-1 [T	1218	1223	6.478682	TGGCAT	0.97656	0.97062
cg2264768	NAV2	XBP-1 [T	1490	1495	6.478682	ATGCCC	0.97656	0.97062
cg2105276	NAV2	XBP-1 [T	466	471	6.478682	ATGCCC	0.97656	0.97062
cg2105276	NAV2	XBP-1 [T	488	493	6.478682	ATGCCC	0.97656	0.97062
cg2105276	NAV2	XBP-1 [T	536	541	6.478682	ATGCCA	0.97656	0.97062
cg2105276	NAV2	C/EBPalph	646	652	6.460799	GGCAAT	0.48828	0.49071
cg2105276	NAV2	c-Myb [T0	115	122	6.454077	CTCAGT	0.30518	0.3056
cg0273928	NAV2	c-Ets-1 [T	395	401	6.423689	TTTCCA	0.48828	0.48798
cg2264768	NAV2	c-Ets-1 [T	830	836	6.423689	TTGGAA	0.48828	0.48798
cg2105276	NAV2	c-Ets-1 [T	1105	1111	6.423689	TTGGAA	0.48828	0.48798
cg2105276	NAV2	c-Ets-1 [T	1416	1422	6.423689	TTTCCA	0.48828	0.48798
cg0273928	NAV2	c-Myb [T0	1142	1149	6.422836	CCCAGT	0.30518	0.3056
cg2105276	NAV2	c-Myb [T0	339	346	6.422836	CCCAGT	0.30518	0.3056
cg2105276	NAV2	RAR-beta	26	35	6.39673	TGGGTT	0.18311	0.183
cg2264768	NAV2	C/EBPalph	80	86	6.391486	GACAAT	0.48828	0.49071
cg2264768	NAV2	C/EBPalph	1014	1020	6.391486	AATTGG	0.48828	0.49071
cg2105276	NAV2	C/EBPalph	1805	1811	6.391486	GCCAAT	0.48828	0.49071
cg2264768	NAV2	TCF-4E [T	1463	1469	6.302385	GGCAAA	0.61035	0.61344

cg2105276	NAV2	TCF-4E [T	969	975	6.302385	GGCAAA	0.61035	0.61344
cg2105276	NAV2	TCF-4E [T	1654	1660	6.302385	TTCAAA	0.61035	0.61344
cg0273928	NAV2	c-Ets-1 [T	1947	1953	6.295602	TTTCCAT	0.48828	0.48798
cg0273928	NAV2	GR-alpha [	43	47	6.263098	CCTCA	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	260	264	6.263098	TGAGG	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	337	341	6.263098	CCTTA	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	732	736	6.263098	CCTTA	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	756	760	6.263098	CCTCA	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	1237	1241	6.263098	CCTTA	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	1298	1302	6.263098	CCTTA	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	1552	1556	6.263098	CCTTA	3.90625	3.91061
cg0273928	NAV2	GR-alpha [	1581	1585	6.263098	TGAGG	3.90625	3.91061
cg2264768	NAV2	GR-alpha [	361	365	6.263098	TGAGG	3.90625	3.91061
cg2264768	NAV2	GR-alpha [	528	532	6.263098	TGAGG	3.90625	3.91061
cg2264768	NAV2	GR-alpha [	648	652	6.263098	CCTCA	3.90625	3.91061
cg2264768	NAV2	GR-alpha [	799	803	6.263098	TAAGG	3.90625	3.91061
cg2264768	NAV2	GR-alpha [	909	913	6.263098	TGAGG	3.90625	3.91061
cg2264768	NAV2	GR-alpha [	1199	1203	6.263098	CCTCA	3.90625	3.91061
cg2264768	NAV2	GR-alpha [	1641	1645	6.263098	CCTTA	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	121	125	6.263098	TGAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	175	179	6.263098	TGAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	234	238	6.263098	CCTCA	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	292	296	6.263098	TGAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	308	312	6.263098	CCTCA	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	315	319	6.263098	TGAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	360	364	6.263098	CCTCA	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	493	497	6.263098	CCTCA	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	582	586	6.263098	TAAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	981	985	6.263098	TGAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	1068	1072	6.263098	TGAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	1295	1299	6.263098	TAAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	1453	1457	6.263098	CCTCA	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	1723	1727	6.263098	TGAGG	3.90625	3.91061
cg2105276	NAV2	GR-alpha [	1854	1858	6.263098	CCTCA	3.90625	3.91061
cg2105276	NAV2	NF-AT1 [	1107	1115	6.253078	GGAAAG	0.03815	0.03835
cg0273928	NAV2	C/EBPalph	1425	1431	6.245236	TGCAAT	0.97656	0.99
cg2105276	NAV2	IRF-1 [T0	1450	1458	6.24301	TTTCCTC	0.16785	0.16909
cg2264768	NAV2	POU2F2 (	1257	1267	6.233489	TGACTT	0.01431	0.01481
cg0273928	NAV2	IRF-1 [T0	512	520	6.206911	TTTCCTC	0.16785	0.16909
cg2105276	NAV2	NF-AT1 [	1412	1421	6.201624	TTAGTTT	0.03815	0.03846
cg0273928	NAV2	HNF-4alph	1571	1583	6.184269	CAAAGT	0.00501	0.0051
cg2105276	NAV2	SRY [T00	1543	1551	6.176442	GGCACA	0.15259	0.15366
cg0273928	NAV2	c-Ets-1 [T	1926	1932	6.167515	TTTCCAC	0.36621	0.36731
cg2264768	NAV2	c-Ets-1 [T	281	287	6.167515	TTTCCAC	0.36621	0.36731
cg2264768	NAV2	c-Ets-1 [T	1886	1892	6.167515	TTTCCAC	0.36621	0.36731
cg2105276	NAV2	c-Ets-1 [T	344	350	6.167515	TTTCCAC	0.36621	0.36731
cg2264768	NAV2	c-Jun [T00	1064	1070	6.152811	TTTGTCA	0.36621	0.37082
cg2264768	NAV2	RXR-alpha	1028	1034	6.119461	GGGTAG	0.73242	0.72249

cg2264768	NAV2	GCF [T00	1707	1715	6.116216	GCGCAG	0.64087	0.6219
cg0273928	NAV2	c-Fos [T00	1440	1449	6.103724	GAGTCA	0.09155	0.09126
cg2105276	NAV2	p53 [T006	1051	1057	6.095267	TTGGCC	0.61035	0.594
cg2105276	NAV2	p53 [T006	1378	1384	6.095267	GGGCCA	0.61035	0.594
cg0273928	NAV2	IRF-1 [T0	395	403	6.078807	TTTCCA	0.16785	0.16909
cg2264768	NAV2	PU.1 [T02	1527	1539	6.056941	ACACTT	0.00432	0.00433
cg0273928	NAV2	GR-alpha [	301	305	6.055408	CCTAA	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	358	362	6.055408	CCTAA	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	562	566	6.055408	CCTGA	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	590	594	6.055408	TTAGG	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	652	656	6.055408	TTAGG	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	1094	1098	6.055408	TCAGG	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	1239	1243	6.055408	TTAGG	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	1456	1460	6.055408	CCTGA	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	1646	1650	6.055408	TTAGG	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	1695	1699	6.055408	CCTAA	3.90625	3.9065
cg0273928	NAV2	GR-alpha [	1855	1859	6.055408	CCTGA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	311	315	6.055408	TTAGG	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	500	504	6.055408	TCAGG	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	841	845	6.055408	TCAGG	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1100	1104	6.055408	CCTAA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1163	1167	6.055408	CCTAA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1190	1194	6.055408	CCTGA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1201	1205	6.055408	TCAGG	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1209	1213	6.055408	CCTAA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1277	1281	6.055408	CCTGA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1292	1296	6.055408	CCTAA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1305	1309	6.055408	CCTAA	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1577	1581	6.055408	TTAGG	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1717	1721	6.055408	TCAGG	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1819	1823	6.055408	TTAGG	3.90625	3.9065
cg2264768	NAV2	GR-alpha [	1860	1864	6.055408	CCTGA	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	75	79	6.055408	TCAGG	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	223	227	6.055408	CCTGA	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	456	460	6.055408	CCTGA	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	557	561	6.055408	CCTGA	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	747	751	6.055408	CCTGA	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	941	945	6.055408	TCAGG	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	1009	1013	6.055408	CCTGA	3.90625	3.9065
cg2105276	NAV2	GR-alpha [	1040	1044	6.055408	TCAGG	3.90625	3.9065
cg0273928	NAV2	c-Myb [T0	741	748	6.04018	GTCAGT	0.21362	0.21535
cg0273928	NAV2	c-Ets-1 [T	541	547	6.039428	TTTCCAC	0.36621	0.36731
cg0273928	NAV2	c-Ets-1 [T	887	893	6.039428	TTTCCAC	0.36621	0.36731
cg0273928	NAV2	HNF-1B [	351	359	6.006024	TTACTA	0.09918	0.10196
cg0273928	NAV2	HNF-1B [	1324	1332	6.006024	TTAATA	0.09918	0.10196
cg2264768	NAV2	NF-AT2 [	1881	1890	6.002309	TAGACT	0.04196	0.04255
cg0273928	NAV2	HOXD9 [	1522	1531	5.898575	TAGTGA	0.05722	0.0598
cg0273928	NAV2	HOXD10 [	1522	1531	5.898575	TAGTGA	0.05722	0.0598

cg2105276	NAV2	p53 [T006	1443	1449	5.883561	GGGCCT	0.61035	0.594
cg2264768	NAV2	STAT4 [T	503	508	5.882353	GGAAGG	0.48828	0.48408
cg2264768	NAV2	STAT4 [T	554	559	5.882353	GGAAGG	0.48828	0.48408
cg2264768	NAV2	STAT4 [T	1580	1585	5.882353	GGAAGG	0.48828	0.48408
cg2105276	NAV2	STAT4 [T	505	510	5.882353	CCTTCC	0.48828	0.48408
cg2105276	NAV2	STAT4 [T	642	647	5.882353	GGAAGG	0.48828	0.48408
cg2105276	NAV2	STAT4 [T	1097	1102	5.882353	CCTTCC	0.48828	0.48408
cg2105276	NAV2	C/EBPalph	43	49	5.850545	AATTGA	0.97656	0.99
cg2105276	NAV2	c-Ets-1 [T	640	646	5.814485	TGGGAA	0.36621	0.36731
cg2264768	NAV2	TCF-4 [T0	1968	1977	5.810677	ACTTTG	0.04578	0.04635
cg0273928	NAV2	STAT1bet	886	895	5.796867	TTTTCCA	0.1545	0.1557
cg0273928	NAV2	STAT1bet	1613	1622	5.796867	TCTGGG	0.1545	0.1557
cg0273928	NAV2	STAT1bet	1766	1775	5.796867	ATTTCCT	0.1545	0.1557
cg0273928	NAV2	STAT1bet	1925	1934	5.796867	ATTTCCA	0.1545	0.1557
cg0273928	NAV2	c-Jun [T00	738	744	5.783074	AAAGTC	0.36621	0.37082
cg2264768	NAV2	c-Jun [T00	27	33	5.783074	TGACTTT	0.36621	0.37082
cg2264768	NAV2	c-Jun [T00	1982	1988	5.783074	TGACTTT	0.36621	0.37082
cg2105276	NAV2	c-Jun [T00	1548	1554	5.783074	AAAGTC	0.36621	0.37082
cg2264768	NAV2	C/EBPalph	1088	1094	5.781231	TATTGT	0.97656	0.99
cg0273928	NAV2	HNF-1C [	1323	1331	5.777116	CTTAAT	0.14496	0.14811
cg2105276	NAV2	VDR [T00	924	932	5.771401	GTTCAA	0.42725	0.42999
cg2264768	NAV2	POU2F2 (	624	634	5.731804	TGGTTT	0.06437	0.06564
cg2264768	NAV2	HNF-1C [	508	516	5.695506	GTTAAA	0.07629	0.07817
cg0273928	NAV2	ENKTF-1	136	143	5.687009	TGGCTT	0.73242	0.7249
cg0273928	NAV2	ENKTF-1	162	169	5.687009	CTAGGC	0.73242	0.7249
cg0273928	NAV2	ENKTF-1	1123	1130	5.687009	TGGCAT	0.73242	0.7249
cg2264768	NAV2	ENKTF-1	102	109	5.687009	TGGCCC	0.73242	0.7249
cg2105276	NAV2	ENKTF-1	20	27	5.687009	TGGCCTT	0.73242	0.7249
cg2105276	NAV2	ENKTF-1	603	610	5.687009	CTGGGC	0.73242	0.7249
cg2105276	NAV2	ENKTF-1	778	785	5.687009	TGGCAC	0.73242	0.7249
cg0273928	NAV2	c-Ets-1 [T	1851	1857	5.686398	CTTCCCT	0.36621	0.3623
cg2264768	NAV2	c-Ets-1 [T	108	114	5.686398	AGGGAA	0.36621	0.3623
cg2264768	NAV2	c-Ets-1 [T	1301	1307	5.686398	CTTCCCT	0.36621	0.3623
cg2105276	NAV2	c-Ets-1 [T	743	749	5.686398	CTTCCCT	0.36621	0.3623
cg2105276	NAV2	c-Fos [T00	895	904	5.679695	GAGTCA	0.04578	0.04537
cg0273928	NAV2	NF-1 [T00	79	86	5.626299	TTGGTC	0.24414	0.24258
cg2264768	NAV2	HNF-1A [	253	260	5.610392	CACTTA	0.24414	0.2469
cg2105276	NAV2	c-Jun [T00	1333	1339	5.590308	TGACAC	0.48828	0.48665
cg0273928	NAV2	AP-2alpha	102	107	5.568965	GCCTAT	0.48828	0.4878
cg0273928	NAV2	AP-2alpha	1127	1132	5.568965	ATAGGC	0.48828	0.4878
cg0273928	NAV2	AP-2alpha	1429	1434	5.568965	ATAGGC	0.48828	0.4878
cg2264768	NAV2	AP-2alpha	812	817	5.568965	GCCTAT	0.48828	0.4878
cg2264768	NAV2	AP-2alpha	1128	1133	5.568965	GCCTAT	0.48828	0.4878
cg2264768	NAV2	AP-2alpha	1239	1244	5.568965	GCCTAT	0.48828	0.4878
cg2105276	NAV2	AP-2alpha	1445	1450	5.568965	GCCTAT	0.48828	0.4878
cg2105276	NAV2	AP-2alpha	1594	1599	5.568965	GCCTAT	0.48828	0.4878
cg2105276	NAV2	AP-2alpha	1869	1874	5.568965	GCCTAT	0.48828	0.4878
cg0273928	NAV2	C/EBPalph	1749	1755	5.565669	GATTGT	0.73242	0.74391

cg0273928	NAV2	IRF-1 [T0	610	618	5.564062	TTTCCGT	0.22888	0.23087
cg0273928	NAV2	IRF-1 [T0	1947	1955	5.564062	TTTCCAT	0.22888	0.23087
cg0273928	NAV2	NFI/CTF [	75	82	5.558661	GAGATT	0.54932	0.55038
cg0273928	NAV2	NFI/CTF [	615	622	5.558661	GTGCTT	0.54932	0.55038
cg2264768	NAV2	NFI/CTF [	119	126	5.558661	AAGTTT	0.54932	0.55038
cg2264768	NAV2	NFI/CTF [	652	659	5.558661	ATGCTT	0.54932	0.55038
cg2105276	NAV2	NFI/CTF [	50	57	5.558661	AAGTTT	0.54932	0.55038
cg2105276	NAV2	NFI/CTF [	295	302	5.558661	GGGTTT	0.54932	0.55038
cg2105276	NAV2	NFI/CTF [	1739	1746	5.558661	GAGCTT	0.54932	0.55038
cg2264768	NAV2	c-Ets-1 [T	552	558	5.558311	GGGGAA	0.36621	0.3623
cg2105276	NAV2	c-Ets-1 [T	1098	1104	5.558311	CTTCCC	0.36621	0.3623
cg0273928	NAV2	GATA-2 [	1627	1635	5.555555	TCGTTAT	0.18311	0.1835
cg2264768	NAV2	T3R-beta1	295	303	5.553412	CTGGGG	0.21362	0.21287
cg0273928	NAV2	TFIID [T0	1707	1713	5.544826	TGTTAA	0.73242	0.75085
cg2264768	NAV2	TFIID [T0	310	316	5.544826	TTTAGG	0.73242	0.75085
cg2264768	NAV2	TFIID [T0	1285	1291	5.544826	TTTAGA	0.73242	0.75085
cg2105276	NAV2	TFIID [T0	1061	1067	5.544826	TGGTAA	0.73242	0.75085
cg2105276	NAV2	TFIID [T0	1572	1578	5.544826	TGTTAA	0.73242	0.75085
cg2105276	NAV2	TFIID [T0	1707	1713	5.544826	TTTACC	0.73242	0.75085
cg0273928	NAV2	p53 [T006	226	232	5.508538	GGGCTG	0.61035	0.59991
cg0273928	NAV2	p53 [T006	930	936	5.508538	GGGCTG	0.61035	0.59991
cg0273928	NAV2	p53 [T006	1531	1537	5.508538	TAAGCC	0.61035	0.59991
cg2264768	NAV2	p53 [T006	321	327	5.508538	GGGCTT	0.61035	0.59991
cg2264768	NAV2	ATF-2 [T0	1148	1157	5.504497	TTGACG	0.03433	0.03426
cg0273928	NAV2	AP-1 [T00	1303	1311	5.496182	TGACTC	0.09155	0.09214
cg2105276	NAV2	AP-1 [T00	1936	1944	5.496182	TAAGAG	0.09155	0.09214
cg0273928	NAV2	NF-AT2 [	390	399	5.474728	AACACT	0.01144	0.01156
cg0273928	NAV2	IRF-1 [T0	1909	1917	5.404935	TTTCCTC	0.22888	0.23087
cg0273928	NAV2	NF-1 [T00	163	170	5.377909	TAGGCC	0.24414	0.24258
cg0273928	NAV2	NF-1 [T00	224	231	5.377909	TTGGGC	0.24414	0.24258
cg0273928	NAV2	RAR-beta	655	664	5.370617	GGGGTT	0.15259	0.15189
cg0273928	NAV2	IRF-1 [T0	1407	1415	5.351774	GATGGG	0.22888	0.23087
cg0273928	NAV2	HNF-1C [	1708	1716	5.345227	GTTAAA	0.07629	0.07817
cg2264768	NAV2	IRF-1 [T0	1801	1809	5.309227	TGAAGG	0.22888	0.23087
cg0273928	NAV2	PPAR-alp	910	920	5.285833	TCGACC	0.03529	0.03451
cg0273928	NAV2	PPAR-alp	1138	1148	5.285833	TGGCCC	0.03529	0.03451
cg2105276	NAV2	HOXD9 [	1963	1972	5.275652	GGGTTT	0.04578	0.04743
cg2105276	NAV2	HOXD10 [	1963	1972	5.275652	GGGTTT	0.04578	0.04743
cg2264768	NAV2	RXR-alph	236	242	5.271235	TCTACC	0.61035	0.6044
cg2264768	NAV2	RXR-alph	1048	1054	5.271235	GGGTGG	0.61035	0.6044
cg2264768	NAV2	RXR-alph	1922	1928	5.271235	TCTACC	0.61035	0.6044
cg2105276	NAV2	RXR-alph	733	739	5.271235	GGGTGG	0.61035	0.6044
cg2105276	NAV2	RXR-alph	1073	1079	5.271235	GGGTGG	0.61035	0.6044
cg2264768	NAV2	C/EBPalp	1254	1260	5.240291	TATTGA	0.97656	0.99332
cg2264768	NAV2	C/EBPalp	1386	1392	5.240291	TATTGC	0.97656	0.99332
cg0273928	NAV2	NF-AT2 [	1921	1930	5.231211	TAGAAT	0.03815	0.03879
cg2264768	NAV2	HNF-1C [	604	612	5.214027	ATTTAT	0.04578	0.04693
cg2105276	NAV2	GR [T050	1117	1123	5.207533	GGTTTT	0.24414	0.24606

cg2264768	NAV2	c-Jun [T00	111	117	5.193102	GAAGTC.	0.61035	0.61057
cg2105276	NAV2	c-Ets-2 [T(	580	588	5.162974	GTTAAG(	0.13733	0.13828
cg2264768	NAV2	c-Myb [T0	1023	1030	5.137438	TAACTG(	0.30518	0.30568
cg0273928	NAV2	NF-AT1 [T	1584	1592	5.125037	GGAAAA	0.05341	0.05402
cg2264768	NAV2	NF-AT1 [T	277	285	5.125037	TTTTTTT	0.05341	0.05402
cg2264768	NAV2	NF-AT1 [T	1420	1428	5.125037	GGAAAA	0.05341	0.05402
cg2264768	NAV2	POU2F2 ((	916	926	5.123481	CTTTTAA	0.02432	0.02504
cg2105276	NAV2	HNF-1A [	1504	1511	5.116518	GTTAAG(	0.36621	0.37179
cg0273928	NAV2	AP-2alpha	1674	1679	5.100982	AAAGGC	0.97656	0.97567
cg0273928	NAV2	AP-2alpha	1713	1718	5.100982	AAAGGC	0.97656	0.97567
cg0273928	NAV2	AP-2alpha	1859	1864	5.100982	AAAGGC	0.97656	0.97567
cg2105276	NAV2	AP-2alpha	961	966	5.100982	AAAGGC	0.97656	0.97567
cg2105276	NAV2	AP-2alpha	1016	1021	5.100982	GCCTTT	0.97656	0.97567
cg0273928	NAV2	RXR-alpha	816	822	5.089356	ATCACC(	0.48828	0.484
cg0273928	NAV2	RXR-alpha	1934	1940	5.089356	AGCACC(	0.48828	0.484
cg2264768	NAV2	RXR-alpha	298	304	5.089356	GGGTGA'	0.48828	0.484
cg2105276	NAV2	RXR-alpha	685	691	5.089356	GGGTGA'	0.48828	0.484
cg0273928	NAV2	SRY [T00(	469	477	5.086565	CTTTGTA	0.06104	0.06209
cg0273928	NAV2	SRY [T00(	860	868	5.086565	CTTTGAT	0.06104	0.06209
cg2264768	NAV2	ELF-1 [T0	1527	1539	5.085535	ACACTT(	0.00143	0.00145
cg2264768	NAV2	HNF-1B [	507	515	5.055806	GGTTAA.	0.04578	0.04699
cg0273928	NAV2	USF2 [T0(	1979	1988	5.052423	CAGGTG(	0.103	0.10178
cg0273928	NAV2	GR-beta [T	208	212	5.042296	GGATT	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	293	297	5.042296	GGATT	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	696	700	5.042296	GTATT	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	895	899	5.042296	AATAC	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	1161	1165	5.042296	GTATT	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	1354	1358	5.042296	AATAC	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	1547	1551	5.042296	GGATT	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	1724	1728	5.042296	AATCC	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	1743	1747	5.042296	GTATT	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	1808	1812	5.042296	AATAC	3.90625	3.95351
cg0273928	NAV2	GR-beta [T	1906	1910	5.042296	GTATT	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	60	64	5.042296	GTATT	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	618	622	5.042296	GGATT	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	781	785	5.042296	AATCC	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	991	995	5.042296	GGATT	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	1206	1210	5.042296	AATCC	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	1655	1659	5.042296	GGATT	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	1737	1741	5.042296	AATAC	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	1867	1871	5.042296	AATCC	3.90625	3.95351
cg2264768	NAV2	GR-beta [T	1905	1909	5.042296	AATCC	3.90625	3.95351
cg2105276	NAV2	GR-beta [T	699	703	5.042296	AATAC	3.90625	3.95351
cg2105276	NAV2	GR-beta [T	1187	1191	5.042296	GGATT	3.90625	3.95351
cg2105276	NAV2	GR-beta [T	1514	1518	5.042296	GTATT	3.90625	3.95351
cg2105276	NAV2	GR-beta [T	1668	1672	5.042296	GTATT	3.90625	3.95351
cg2105276	NAV2	GR-beta [T	1833	1837	5.042296	AATAC	3.90625	3.95351
cg2105276	NAV2	E2F-1 [T0	1193	1200	5.042045	GCGGGA	0.18311	0.17901

cg0273928	NAV2	PXR-1:RX	1211	1218	5.032032	TGAACC	0.12207	0.12266
cg2264768	NAV2	Elk-1 [T00	1576	1584	5.027151	CTTAGG	0.03052	0.03091
cg2264768	NAV2	NFI/CTF [	1042	1049	5.021086	CCCTTTC	0.24414	0.24103
cg2105276	NAV2	NFI/CTF [	1101	1108	5.021086	CCCCTTC	0.24414	0.24103
cg2105276	NAV2	c-Jun [T00	933	939	5.000337	GGTGTC	0.61035	0.61057
cg0273928	NAV2	AP-1 [T00	1437	1445	4.990183	TAGGAG	0.12207	0.12162
cg0273928	NAV2	c-Myb [T0	1885	1892	4.974489	TGCAGT	0.30518	0.30568
cg2105276	NAV2	HNF-1A [	580	587	4.972635	GTTAAG	0.36621	0.37179
cg2264768	NAV2	IRF-1 [T0	1609	1617	4.968836	TTTCCCC	0.1297	0.1302
cg0273928	NAV2	c-Ets-1 [T	500	506	4.910652	ATGGAA	0.48828	0.49031
cg2264768	NAV2	XBP-1 [T	228	233	4.894955	ATGCCT	0.97656	0.96979
cg2264768	NAV2	XBP-1 [T	329	334	4.894955	ATGCCT	0.97656	0.96979
cg2264768	NAV2	XBP-1 [T	801	806	4.894955	AGGCAT	0.97656	0.96979
cg2105276	NAV2	XBP-1 [T	1747	1752	4.894955	AGGCAT	0.97656	0.96979
cg2264768	NAV2	PPAR-alph	101	111	4.88658	GTGGCC	0.01717	0.01681
cg2264768	NAV2	NF-1 [T00	169	176	4.880836	TGTTCC	0.24414	0.24398
cg2264768	NAV2	NF-1 [T00	463	470	4.880836	TTGGGA	0.24414	0.24398
cg2264768	NAV2	NF-Y [T0	462	469	4.867193	ATTGGG	0.36621	0.36847
cg2264768	NAV2	C/EBPalph	176	182	4.845599	AATTGA	0.97656	0.99332
cg2264768	NAV2	C/EBPalph	977	983	4.845599	AATTGA	0.97656	0.99332
cg2105276	NAV2	C/EBPalph	523	529	4.845599	AATTGC	0.97656	0.99332
cg2105276	NAV2	C/EBPalph	1679	1685	4.845599	AATTGC	0.97656	0.99332
cg2105276	NAV2	C/EBPalph	1889	1895	4.845599	AGCAAT	0.97656	0.99332
cg2264768	NAV2	HNF-3alph	973	980	4.842999	TTAAAA	0.09155	0.09582
cg2264768	NAV2	NF-AT1 [	277	286	4.823485	TTTTTTT	0.07629	0.07704
cg2105276	NAV2	p53 [T006	802	808	4.786849	GGGCAC	0.48828	0.47747
cg0273928	NAV2	c-Ets-1 [T	671	677	4.782565	CTTCCA	0.48828	0.49031
cg2264768	NAV2	C/EBPalph	50	56	4.776286	TATTGTT	0.97656	0.99332
cg0273928	NAV2	TFII-I [T0	198	203	4.756447	GGACAT	2.92969	2.93695
cg0273928	NAV2	TFII-I [T0	263	268	4.756447	GGAAAT	2.92969	2.93695
cg0273928	NAV2	TFII-I [T0	511	516	4.756447	ATTTCC	2.92969	2.93695
cg0273928	NAV2	TFII-I [T0	1392	1397	4.756447	CAGTCC	2.92969	2.93695
cg0273928	NAV2	TFII-I [T0	1766	1771	4.756447	ATTTCC	2.92969	2.93695
cg0273928	NAV2	TFII-I [T0	1908	1913	4.756447	ATTTCC	2.92969	2.93695
cg0273928	NAV2	TFII-I [T0	1925	1930	4.756447	ATTTCC	2.92969	2.93695
cg0273928	NAV2	FOXP3 [T	63	68	4.756447	GTTTTT	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	169	174	4.756447	AAAAAC	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	376	381	4.756447	CTCAAC	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	413	418	4.756447	GTTTTC	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	662	667	4.756447	GTTTTT	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	745	750	4.756447	GTTTTT	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	826	831	4.756447	GAAAAC	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	1112	1117	4.756447	GTTTTG	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	1146	1151	4.756447	GTTTTG	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	1412	1417	4.756447	GAAAAC	2.92969	2.96063
cg0273928	NAV2	FOXP3 [T	1881	1886	4.756447	GTTTTG	2.92969	2.96063
cg2264768	NAV2	TFII-I [T0	128	133	4.756447	CATTCC	2.92969	2.93695
cg2264768	NAV2	TFII-I [T0	466	471	4.756447	GGACTG	2.92969	2.93695

cg2264768	NAV2	TFII-I [T0	618	623	4.756447	GGATTG	2.92969	2.93695
cg2264768	NAV2	TFII-I [T0	778	783	4.756447	GGAAAT	2.92969	2.93695
cg2264768	NAV2	TFII-I [T0	991	996	4.756447	GGATTG	2.92969	2.93695
cg2264768	NAV2	TFII-I [T0	1081	1086	4.756447	CATTCC	2.92969	2.93695
cg2264768	NAV2	TFII-I [T0	1374	1379	4.756447	GGACTG	2.92969	2.93695
cg2264768	NAV2	TFII-I [T0	1608	1613	4.756447	ATTTCC	2.92969	2.93695
cg2264768	NAV2	TFII-I [T0	1823	1828	4.756447	GGAAAT	2.92969	2.93695
cg2264768	NAV2	FOXP3 [T	721	726	4.756447	GTTTTT	2.92969	2.96063
cg2264768	NAV2	FOXP3 [T	740	745	4.756447	GTTTTT	2.92969	2.96063
cg2264768	NAV2	FOXP3 [T	907	912	4.756447	GTTGAG	2.92969	2.96063
cg2264768	NAV2	FOXP3 [T	926	931	4.756447	AAAAAC	2.92969	2.96063
cg2264768	NAV2	FOXP3 [T	1153	1158	4.756447	GTTTTT	2.92969	2.96063
cg2264768	NAV2	FOXP3 [T	1807	1812	4.756447	AAAAAC	2.92969	2.96063
cg2264768	NAV2	FOXP3 [T	1980	1985	4.756447	GTTGAC	2.92969	2.96063
cg2105276	NAV2	TFII-I [T0	178	183	4.756447	GGACAT	2.92969	2.93695
cg2105276	NAV2	TFII-I [T0	230	235	4.756447	ATGTCC	2.92969	2.93695
cg2105276	NAV2	TFII-I [T0	329	334	4.756447	GGAAAT	2.92969	2.93695
cg2105276	NAV2	TFII-I [T0	429	434	4.756447	ATATCC	2.92969	2.93695
cg2105276	NAV2	TFII-I [T0	1355	1360	4.756447	ATGTCC	2.92969	2.93695
cg2105276	NAV2	TFII-I [T0	1449	1454	4.756447	ATTTCC	2.92969	2.93695
cg2105276	NAV2	TFII-I [T0	1470	1475	4.756447	GGATAT	2.92969	2.93695
cg2105276	NAV2	FOXP3 [T	69	74	4.756447	GTTTTT	2.92969	2.96063
cg2105276	NAV2	FOXP3 [T	119	124	4.756447	GTTGAG	2.92969	2.96063
cg2105276	NAV2	FOXP3 [T	150	155	4.756447	GAAAAC	2.92969	2.96063
cg2105276	NAV2	FOXP3 [T	1118	1123	4.756447	GTTTTG	2.92969	2.96063
cg2105276	NAV2	FOXP3 [T	1756	1761	4.756447	GTTGAT	2.92969	2.96063
cg2105276	NAV2	FOXP3 [T	1900	1905	4.756447	GTTTTG	2.92969	2.96063
cg0273928	NAV2	c-Ets-1 [T	610	616	4.74411	TTTCCG	0.85449	0.85764
cg0273928	NAV2	c-Ets-1 [T	1503	1509	4.654478	CTTCCA	0.85449	0.85764
cg2264768	NAV2	c-Ets-1 [T	244	250	4.654478	CTTCCA	0.85449	0.85764
cg2105276	NAV2	c-Ets-1 [T	1556	1562	4.654478	CTGGAA	0.85449	0.85764
cg0273928	NAV2	VDR [T00	622	630	4.617121	GTTCAT	0.37384	0.37445
cg0273928	NAV2	VDR [T00	1207	1215	4.617121	AAGTTG	0.37384	0.37445
cg0273928	NAV2	VDR [T00	1575	1583	4.617121	GTTCAC	0.37384	0.37445
cg2264768	NAV2	VDR [T00	284	292	4.617121	CCACTG	0.37384	0.37445
cg2264768	NAV2	c-Ets-2 [T	1800	1808	4.589988	CTGAAG	0.06866	0.06881
cg2105276	NAV2	c-Ets-2 [T	503	511	4.589988	TTCCTTC	0.06866	0.06881
cg2264768	NAV2	C/EBPalph	992	998	4.560723	GATTGG	0.24414	0.24411
cg2105276	NAV2	C/EBPalph	1049	1055	4.560723	GATTGG	0.24414	0.24411
cg2264768	NAV2	T3R-beta1	596	604	4.481316	GGATGG	0.27466	0.27551
cg2105276	NAV2	USF1 [T0	895	904	4.464121	GAGTCA	0.06866	0.06835
cg2105276	NAV2	IRF-1 [T0	1416	1424	4.462268	TTTCCA	0.05341	0.05405
cg2105276	NAV2	c-Jun [T00	937	943	4.441904	TCAGTC	0.12207	0.12266
cg0273928	NAV2	AP-2alpha	162	167	4.438035	CTAGGC	0.97656	0.96979
cg0273928	NAV2	AP-2alpha	602	607	4.438035	GCCTAG	0.97656	0.96979
cg0273928	NAV2	AP-2alpha	1817	1822	4.438035	CTAGGC	0.97656	0.96979
cg2264768	NAV2	AP-2alpha	703	708	4.438035	GCCTAG	0.97656	0.96979
cg2105276	NAV2	AP-2alpha	552	557	4.438035	CTAGGC	0.97656	0.96979

cg2105276	NAV2	RXR-alph	948	954	4.423008	GGGTGG	0.24414	0.24292
cg0273928	NAV2	AP-2alpha	1297	1302	4.422424	GCCTTA	0.97656	0.96979
cg2264768	NAV2	AP-2alpha	799	804	4.422424	TAAGGC	0.97656	0.96979
cg2105276	NAV2	AP-2alpha	1295	1300	4.422424	TAAGGC	0.97656	0.96979
cg0273928	NAV2	STAT4 [T	502	507	4.411765	GGAAGA	1.95312	1.94235
cg0273928	NAV2	STAT4 [T	670	675	4.411765	TCTTCC	1.95312	1.94235
cg0273928	NAV2	STAT4 [T	1007	1012	4.411765	GCTTCC	1.95312	1.94235
cg0273928	NAV2	STAT4 [T	1502	1507	4.411765	GCTTCC	1.95312	1.94235
cg2264768	NAV2	STAT4 [T	128	133	4.411765	CATTCC	1.95312	1.94235
cg2264768	NAV2	STAT4 [T	243	248	4.411765	TCTTCC	1.95312	1.94235
cg2264768	NAV2	STAT4 [T	1081	1086	4.411765	CATTCC	1.95312	1.94235
cg2264768	NAV2	STAT4 [T	1195	1200	4.411765	GCTTCC	1.95312	1.94235
cg2264768	NAV2	STAT4 [T	1300	1305	4.411765	TCTTCC	1.95312	1.94235
cg2264768	NAV2	STAT4 [T	1320	1325	4.411765	TCTTCC	1.95312	1.94235
cg2105276	NAV2	STAT4 [T	585	590	4.411765	GGAAGA	1.95312	1.94235
cg2105276	NAV2	STAT4 [T	742	747	4.411765	GCTTCC	1.95312	1.94235
cg2105276	NAV2	STAT4 [T	975	980	4.411765	GGAAGC	1.95312	1.94235
cg2105276	NAV2	STAT4 [T	1558	1563	4.411765	GGAAGA	1.95312	1.94235
cg0273928	NAV2	c-Ets-1 [T	1549	1555	4.411026	ATTCCT	0.85449	0.85764
cg2264768	NAV2	c-Ets-1 [T	1777	1783	4.411026	AAGGAA	0.85449	0.85764
cg2105276	NAV2	c-Ets-1 [T	502	508	4.411026	ATTCCT	0.85449	0.85764
cg0273928	NAV2	NF-AT1 [	1922	1930	4.396744	AGAATT	0.06866	0.06925
cg2264768	NAV2	NF-AT1 [	778	786	4.396744	GGAAAT	0.06866	0.06925
cg2105276	NAV2	c-Fos [T00	652	661	4.351106	GAGTCA	0.04578	0.04591
cg2105276	NAV2	p53 [T006	605	611	4.33696	GGGCCA	0.24414	0.23584
cg2105276	NAV2	p53 [T006	1632	1638	4.33696	GGGCCA	0.24414	0.23584
cg0273928	NAV2	HOXD9 [	876	885	4.321431	ATTTTTT	0.03433	0.03596
cg0273928	NAV2	HOXD10 [	876	885	4.321431	ATTTTTT	0.03433	0.03596
cg0273928	NAV2	RAR-beta	1753	1762	4.252176	GTAAAA	0.14496	0.1447
cg0273928	NAV2	C/EBPalp	1263	1269	4.235345	TATTGC	0.48828	0.49358
cg2264768	NAV2	C/EBPalp	959	965	4.235345	ATCAAT	0.48828	0.49358
cg2264768	NAV2	IRF-1 [T0	1987	1995	4.207433	TTTCCTA	0.1297	0.13087
cg2105276	NAV2	Elk-1 [T00	581	589	4.204473	TTAAGG	0.09155	0.09227
cg0273928	NAV2	GR-beta [	0	4	4.201913	AATAG	7.8125	7.94607
cg0273928	NAV2	GR-beta [	150	154	4.201913	CGATT	7.8125	7.94607
cg0273928	NAV2	GR-beta [	215	219	4.201913	AATAA	7.8125	7.94607
cg0273928	NAV2	GR-beta [	438	442	4.201913	TGATT	7.8125	7.94607
cg0273928	NAV2	GR-beta [	687	691	4.201913	AATAA	7.8125	7.94607
cg0273928	NAV2	GR-beta [	815	819	4.201913	AATCA	7.8125	7.94607
cg0273928	NAV2	GR-beta [	874	878	4.201913	TTATT	7.8125	7.94607
cg0273928	NAV2	GR-beta [	881	885	4.201913	TTATT	7.8125	7.94607
cg0273928	NAV2	GR-beta [	971	975	4.201913	AATCA	7.8125	7.94607
cg0273928	NAV2	GR-beta [	1250	1254	4.201913	AATCA	7.8125	7.94607
cg0273928	NAV2	GR-beta [	1262	1266	4.201913	TTATT	7.8125	7.94607
cg0273928	NAV2	GR-beta [	1326	1330	4.201913	AATAA	7.8125	7.94607
cg0273928	NAV2	GR-beta [	1340	1344	4.201913	AATAG	7.8125	7.94607
cg0273928	NAV2	GR-beta [	1428	1432	4.201913	AATAG	7.8125	7.94607
cg0273928	NAV2	GR-beta [	1748	1752	4.201913	TGATT	7.8125	7.94607

cg2264768	NAV2	GR-beta [T	49	53	4.201913	CTATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	161	165	4.201913	CTATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	184	188	4.201913	TGATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	602	606	4.201913	TGATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	958	962	4.201913	AATCA	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1087	1091	4.201913	CTATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1266	1270	4.201913	TTATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1378	1382	4.201913	TGATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1385	1389	4.201913	TTATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1408	1412	4.201913	AATCA	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1534	1538	4.201913	CTATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1565	1569	4.201913	AATAG	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1630	1634	4.201913	AATAA	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1665	1669	4.201913	AATAA	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1681	1685	4.201913	AATAA	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1684	1688	4.201913	AATAA	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1781	1785	4.201913	AATAA	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1911	1915	4.201913	TGATT	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1947	1951	4.201913	AATAG	7.8125	7.94607
cg2264768	NAV2	GR-beta [T	1991	1995	4.201913	CTATT	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	211	215	4.201913	TGATT	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	500	504	4.201913	CGATT	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	520	524	4.201913	AATAA	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	756	760	4.201913	AATCA	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	997	1001	4.201913	AATCG	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	1048	1052	4.201913	TGATT	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	1447	1451	4.201913	CTATT	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	1464	1468	4.201913	AATCA	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	1701	1705	4.201913	AATCA	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	1814	1818	4.201913	CTATT	7.8125	7.94607
cg2105276	NAV2	GR-beta [T	1968	1972	4.201913	TTATT	7.8125	7.94607
cg0273928	NAV2	NF-Y [T0	963	970	4.186615	ATTGGA	0.18311	0.1853
cg2105276	NAV2	NF-Y [T0	1416	1423	4.186615	TTTCCA	0.18311	0.1853
cg0273928	NAV2	c-Ets-1 [T	891	897	4.154851	CAGGAA	0.24414	0.24526
cg0273928	NAV2	c-Ets-1 [T	1095	1101	4.154851	CAGGAA	0.24414	0.24526
cg0273928	NAV2	c-Ets-1 [T	1957	1963	4.154851	CAGGAA	0.24414	0.24526
cg2264768	NAV2	c-Ets-1 [T	129	135	4.154851	ATTCCT	0.24414	0.24526
cg2264768	NAV2	c-Ets-1 [T	1202	1208	4.154851	CAGGAA	0.24414	0.24526
cg0273928	NAV2	c-Fos [T00	834	843	4.139091	GAGTCA	0.03815	0.03825
cg2105276	NAV2	c-Fos [T00	908	917	4.139091	CACATG	0.03815	0.03825
cg0273928	NAV2	NF-1 [T00	483	490	4.135372	TGAGCC	0.24414	0.24154
cg0273928	NAV2	NF-AT1 [T	883	892	4.134416	ATTTTTT	0.08392	0.08485
cg2264768	NAV2	NF-AT1 [T	1882	1891	4.134416	AGACTT	0.08392	0.08485
cg2105276	NAV2	NF-AT1 [T	1106	1115	4.134416	TGGAAA	0.08392	0.08485
cg0273928	NAV2	p53 [T006	557	563	4.125254	CAGGCC	0.73242	0.71379
cg0273928	NAV2	p53 [T006	1563	1569	4.125254	CAGGCC	0.73242	0.71379
cg0273928	NAV2	c-Ets-2 [T	1009	1017	4.091811	TTCCTT	0.16022	0.16243
cg0273928	NAV2	c-Ets-2 [T	1550	1558	4.091811	TTCCTT	0.16022	0.16243

cg0273928	NAV2	SRY [T00	1669	1677	4.087393	ACATCA	0.12207	0.12407
cg2264768	NAV2	SRY [T00	708	716	4.087393	GCATCA	0.12207	0.12407
cg0273928	NAV2	HOXD9 [T	215	224	4.080895	AATAAC	0.03052	0.03168
cg0273928	NAV2	HOXD10 [	215	224	4.080895	AATAAC	0.03052	0.03168
cg0273928	NAV2	NF-AT1 [	391	399	4.056854	ACACTT	0.07629	0.07734
cg2264768	NAV2	IRF-1 [T0	774	782	4.035054	GCAGGG	0.1297	0.13087
cg2264768	NAV2	IRF-1 [T0	1819	1827	4.035054	TTAGGG	0.1297	0.13087
cg0273928	NAV2	RXR-alph	868	874	4.019014	GGGTCT	0.97656	0.9671
cg2264768	NAV2	RXR-alph	1052	1058	4.019014	GGGTGT	0.97656	0.9671
cg2264768	NAV2	c-Ets-2 [T	1774	1782	4.017001	AGAAAG	0.16022	0.16243
cg2105276	NAV2	c-Ets-2 [T	970	978	4.017001	GCAAAG	0.16022	0.16243
cg0273928	NAV2	Pax-5 [T0	721	727	4.007279	GGGCTT	1.09863	1.07975
cg0273928	NAV2	Pax-5 [T0	1344	1350	4.007279	GGGCTT	1.09863	1.07975
cg0273928	NAV2	TFIID [T0	350	356	4.007279	TTTACT	1.09863	1.13456
cg0273928	NAV2	TFIID [T0	700	706	4.007279	TTTAAG	1.09863	1.13456
cg0273928	NAV2	TFIID [T0	810	816	4.007279	TCATAA	1.09863	1.13456
cg0273928	NAV2	TFIID [T0	1348	1354	4.007279	TTTACT	1.09863	1.13456
cg0273928	NAV2	TFIID [T0	1751	1757	4.007279	TTGTAA	1.09863	1.13456
cg0273928	NAV2	TFIID [T0	1803	1809	4.007279	TCATAA	1.09863	1.13456
cg2264768	NAV2	Pax-5 [T0	125	131	4.007279	GGGCAT	1.09863	1.07975
cg2264768	NAV2	Pax-5 [T0	1058	1064	4.007279	GGGCTG	1.09863	1.07975
cg2264768	NAV2	Pax-5 [T0	1489	1495	4.007279	AATGCC	1.09863	1.07975
cg2264768	NAV2	TFIID [T0	33	39	4.007279	TTTTAA	1.09863	1.13456
cg2264768	NAV2	TFIID [T0	605	611	4.007279	TTTATA	1.09863	1.13456
cg2264768	NAV2	TFIID [T0	744	750	4.007279	TTTTAA	1.09863	1.13456
cg2264768	NAV2	TFIID [T0	917	923	4.007279	TTTTAA	1.09863	1.13456
cg2264768	NAV2	TFIID [T0	1341	1347	4.007279	TTTTAA	1.09863	1.13456
cg2264768	NAV2	TFIID [T0	1562	1568	4.007279	TTTAAT	1.09863	1.13456
cg2264768	NAV2	TFIID [T0	1587	1593	4.007279	TCTTAA	1.09863	1.13456
cg2105276	NAV2	Pax-5 [T0	802	808	4.007279	GGGCAC	1.09863	1.07975
cg2105276	NAV2	Pax-5 [T0	1001	1007	4.007279	GGGCTC	1.09863	1.07975
cg2105276	NAV2	Pax-5 [T0	1028	1034	4.007279	GGGCTC	1.09863	1.07975
cg2105276	NAV2	Pax-5 [T0	1296	1302	4.007279	AAGGCC	1.09863	1.07975
cg2105276	NAV2	Pax-5 [T0	1337	1343	4.007279	ACTGCC	1.09863	1.07975
cg2105276	NAV2	Pax-5 [T0	1391	1397	4.007279	GGGCCG	1.09863	1.07975
cg2105276	NAV2	Pax-5 [T0	1930	1936	4.007279	GGGCTG	1.09863	1.07975
cg2105276	NAV2	TFIID [T0	1518	1524	4.007279	TCGTAA	1.09863	1.13456
cg2105276	NAV2	TFIID [T0	1798	1804	4.007279	TTTAAG	1.09863	1.13456
cg2264768	NAV2	AP-2alpha	135	140	3.970052	GCCTTG	0.97656	0.96469
cg2264768	NAV2	AP-2alpha	1390	1395	3.970052	GCCTTG	0.97656	0.96469
cg2105276	NAV2	AP-2alpha	22	27	3.970052	GCCTTG	0.97656	0.96469
cg2105276	NAV2	AP-2alpha	1044	1049	3.970052	GCCTTG	0.97656	0.96469
cg2105276	NAV2	p53 [T006	1078	1084	3.961937	GGGCTA	0.73242	0.71379
cg2264768	NAV2	NF-Y [T0	593	600	3.95898	ATTGGA	0.18311	0.1853
cg2264768	NAV2	Elk-1 [T00	1530	1538	3.944668	CTTCCT	0.09155	0.09227
cg0273928	NAV2	NF-AT1 [	1763	1771	3.917696	ATCATT	0.07629	0.07734
cg2105276	NAV2	PPAR-alp	571	581	3.872523	CTGCCC	0.02575	0.02522
cg0273928	NAV2	GR [T050	424	430	3.763516	CAAAGA	0.73242	0.74251

cg0273928	NAV2	GR [T050	467	473	3.763516	CTCTTTC	0.73242	0.74251
cg0273928	NAV2	GR [T050	478	484	3.763516	ATCTTTC	0.73242	0.74251
cg0273928	NAV2	GR [T050	858	864	3.763516	ATCTTTC	0.73242	0.74251
cg0273928	NAV2	GR [T050	1111	1117	3.763516	TGTTTTC	0.73242	0.74251
cg0273928	NAV2	GR [T050	1145	1151	3.763516	AGTTTTC	0.73242	0.74251
cg0273928	NAV2	GR [T050	1880	1886	3.763516	AGTTTTC	0.73242	0.74251
cg2264768	NAV2	GR [T050	356	362	3.763516	TTCTTTG	0.73242	0.74251
cg2264768	NAV2	GR [T050	712	718	3.763516	CAAAGA	0.73242	0.74251
cg2105276	NAV2	GR [T050	1656	1662	3.763516	CAAAGA	0.73242	0.74251
cg2105276	NAV2	GR [T050	1899	1905	3.763516	TGTTTTC	0.73242	0.74251
cg2264768	NAV2	p53 [T006	546	552	3.750231	GGGCTG	0.73242	0.71379
cg2105276	NAV2	p53 [T006	1982	1988	3.750231	CCAGCC	0.73242	0.71379
cg2264768	NAV2	AP-2alpha	230	235	3.743866	GCCTTC	0.48828	0.48238
cg2264768	NAV2	AP-2alpha	1581	1586	3.743866	GAAGGC	0.48828	0.48238
cg2105276	NAV2	AP-2alpha	412	417	3.743866	GCCTTC	0.48828	0.48238
cg2105276	NAV2	AP-2alpha	643	648	3.743866	GAAGGC	0.48828	0.48238
cg0273928	NAV2	IRF-1 [T0	821	829	3.689552	CCAGGG	0.06866	0.06927
cg0273928	NAV2	NF-AT2 [	882	891	3.571424	TATTTTT	0.03433	0.03499
cg0273928	NAV2	C/EBPalp	77	83	3.555778	GATTGG	0.24414	0.24752
cg0273928	NAV2	c-Myb [T0	1205	1212	3.555283	GCAAGT	0.12207	0.12203
cg0273928	NAV2	c-Ets-2 [T	416	424	3.518824	TTCCTTC	0.18311	0.18304
cg2264768	NAV2	p53 [T006	125	131	3.516613	GGGCAT	0.73242	0.7189
cg2264768	NAV2	p53 [T006	1489	1495	3.516613	AATGCC	0.73242	0.7189
cg2105276	NAV2	p53 [T006	1337	1343	3.516613	ACTGCC	0.73242	0.7189
cg0273928	NAV2	HNF-3alp	519	526	3.500065	TCAAAA	0.27466	0.28532
cg0273928	NAV2	HNF-3alp	875	882	3.500065	TATTTTT	0.27466	0.28532
cg0273928	NAV2	HNF-3alp	882	889	3.500065	TATTTTT	0.27466	0.28532
cg2264768	NAV2	HNF-3alp	61	68	3.500065	TATTTTT	0.27466	0.28532
cg2264768	NAV2	HNF-3alp	747	754	3.500065	TAAAAA	0.27466	0.28532
cg2264768	NAV2	HNF-3alp	1661	1668	3.500065	AAAAAA	0.27466	0.28532
cg2264768	NAV2	HNF-3alp	1667	1674	3.500065	TAAAAA	0.27466	0.28532
cg2105276	NAV2	HNF-3alp	379	386	3.500065	TCAAAA	0.27466	0.28532
cg2105276	NAV2	HNF-3alp	1823	1830	3.500065	AATTTC	0.27466	0.28532
cg0273928	NAV2	c-Ets-1 [T	988	994	3.487246	CTTCCG	0.61035	0.60765
cg0273928	NAV2	c-Myb [T0	190	197	3.469384	GACAGT	0.12207	0.12203
cg0273928	NAV2	VDR [T00	371	379	3.462841	GTTCAC	0.21362	0.21341
cg2105276	NAV2	VDR [T00	302	310	3.462841	GTTCAG	0.21362	0.21341
cg2264768	NAV2	RelA [T00	442	452	3.45524	GAAATT	0.0062	0.00622
cg0273928	NAV2	NF-AT1 [	391	400	3.445347	ACACTT	0.07629	0.07722
cg0273928	NAV2	NF-AT1 [	1922	1931	3.445347	AGAATT	0.07629	0.07722
cg2264768	NAV2	NF-AT1 [	831	840	3.445347	TGGAAA	0.07629	0.07722
cg2105276	NAV2	NF-AT1 [	340	349	3.445347	CCAGTT	0.07629	0.07722
cg0273928	NAV2	NF-AT1 [	411	419	3.407861	ACGTTT	0.03052	0.03089
cg2105276	NAV2	RXR-alph	1169	1175	3.392904	TGTACC	1.09863	1.08572
cg2264768	NAV2	Elk-1 [T00	499	507	3.381796	CTCAGG	0.04578	0.04588
cg2264768	NAV2	Elk-1 [T00	1196	1204	3.381796	CTTCCTC	0.04578	0.04588
cg2105276	NAV2	c-Fos [T00	1939	1948	3.366997	GAGTCA	0.05341	0.05347
cg0273928	NAV2	GR-beta [	76	80	3.361531	AGATT	3.90625	3.99611

cg0273928	NAV2	GR-beta [T	464	468	3.361531	AATCT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	509	513	3.361531	AGATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	691	695	3.361531	AATCT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	803	807	3.361531	AATAT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	845	849	3.361531	AGATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	1320	1324	3.361531	AATCT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	1527	1531	3.361531	ATATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	1792	1796	3.361531	AATAT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	962	966	3.361531	AATAT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	965	969	3.361531	ATATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1072	1076	3.361531	AATCT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1174	1178	3.361531	ATATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1253	1257	3.361531	ATATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1282	1286	3.361531	AGATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1296	1300	3.361531	AATAT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1359	1363	3.361531	AGATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1633	1637	3.361531	AATAT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1933	1937	3.361531	AATCT	3.90625	3.99611
cg2105276	NAV2	GR-beta [T	169	173	3.361531	AATCT	3.90625	3.99611
cg2105276	NAV2	GR-beta [T	428	432	3.361531	AATAT	3.90625	3.99611
cg2105276	NAV2	GR-beta [T	1472	1476	3.361531	ATATT	3.90625	3.99611
cg2105276	NAV2	GR-beta [T	1586	1590	3.361531	AATAT	3.90625	3.99611
cg2105276	NAV2	GR-beta [T	1612	1616	3.361531	AATAT	3.90625	3.99611
cg2105276	NAV2	GR-beta [T	1783	1787	3.361531	AATAT	3.90625	3.99611
cg2105276	NAV2	T3R-beta1	1327	1335	3.351341	TACAGG	0.27466	0.2755
cg0273928	NAV2	GATA-2 [T	723	731	3.333333	GCTTTAT	0.30518	0.30786
cg2264768	NAV2	PR B [T00	1245	1251	3.29756	AAATGT	0.24414	0.25122
cg2264768	NAV2	PR A [T01	1245	1251	3.29756	AAATGT	0.24414	0.25122
cg2105276	NAV2	PR B [T00	142	148	3.29756	AAATGT	0.24414	0.25122
cg2105276	NAV2	PR A [T01	142	148	3.29756	AAATGT	0.24414	0.25122
cg0273928	NAV2	c-Ets-2 [T0	258	266	3.2883	AGTGAG	0.18311	0.18304
cg0273928	NAV2	c-Ets-2 [T0	1579	1587	3.2883	ACTGAG	0.18311	0.18304
cg2264768	NAV2	c-Ets-2 [T0	1197	1205	3.2883	TTCCTCA	0.18311	0.18304
cg0273928	NAV2	PXR-1:RX	619	626	3.2723	TTGGTTC	0.12207	0.12271
cg2105276	NAV2	PXR-1:RX	299	306	3.2723	TTGGTTC	0.12207	0.12271
cg2105276	NAV2	PXR-1:RX	989	996	3.2723	TAGGTTC	0.12207	0.12271
cg2105276	NAV2	PXR-1:RX	1124	1131	3.2723	TTGGTTC	0.12207	0.12271
cg0273928	NAV2	NF-Y [T0	243	250	3.263282	ATTGGCA	0.48828	0.48904
cg2264768	NAV2	NF-Y [T0	993	1000	3.263282	ATTGGCA	0.48828	0.48904
cg0273928	NAV2	c-Jun [T00	1303	1309	3.244843	TGACTCT	0.24414	0.24403
cg2105276	NAV2	c-Jun [T00	1938	1944	3.244843	AGAGTCA	0.24414	0.24403
cg0273928	NAV2	AP-2alpha	704	709	3.229049	AGAGGC	0.48828	0.48238
cg2264768	NAV2	AP-2alpha	1235	1240	3.229049	AGAGGC	0.48828	0.48238
cg2105276	NAV2	AP-2alpha	204	209	3.229049	GCCTCT	0.48828	0.48238
cg0273928	NAV2	RXR-alpha	1755	1761	3.170788	AAAACC	0.24414	0.24522
cg2105276	NAV2	RXR-alpha	1963	1969	3.170788	GGGTTTT	0.24414	0.24522
cg0273928	NAV2	AR [T0004	189	197	3.165392	GGACAG	0.06104	0.06058
cg2264768	NAV2	AR [T0004	364	372	3.165392	GGACAG	0.06104	0.06058

cg2264768	NAV2	CREB [T0	1149	1157	3.15839	TGACGT	0.06104	0.06133
cg0273928	NAV2	c-Fos [T00	920	929	3.154982	GAGTCA	0.06104	0.06065
cg0273928	NAV2	TCF-4E [T	276	282	3.151193	TGCAAA	0.24414	0.24672
cg0273928	NAV2	TCF-4E [T	860	866	3.151193	CTTTGA	0.24414	0.24672
cg0273928	NAV2	TCF-4E [T	1671	1677	3.151193	ATCAAA	0.24414	0.24672
cg2264768	NAV2	TCF-4E [T	710	716	3.151193	ATCAAA	0.24414	0.24672
cg0273928	NAV2	Elk-1 [T00	1008	1016	3.121991	CTTCCTT	0.07629	0.07656
cg2105276	NAV2	Elk-1 [T00	971	979	3.121991	CAAAGG	0.07629	0.07656
cg2264768	NAV2	NF-AT1 [T	1882	1890	3.098758	AGACTT	0.03052	0.03049
cg2264768	NAV2	TCF-4 [T0	708	717	3.085213	GCATCA	0.03433	0.0351
cg2105276	NAV2	TCF-4 [T0	1652	1661	3.085213	TCTTCA	0.03433	0.0351
cg0273928	NAV2	TFIID [T0	1882	1888	3.075094	TTTTGC	0.12207	0.12409
cg2264768	NAV2	TFIID [T0	92	98	3.075094	TTTTGC	0.12207	0.12409
cg2105276	NAV2	TFIID [T0	438	444	3.075094	TTTTGC	0.12207	0.12409
cg0273928	NAV2	p53 [T006	1477	1483	3.028543	TGTGCC	0.48828	0.47786
cg2264768	NAV2	C/EBPalph	461	467	2.981957	CATTGG	0.48828	0.4911
cg0273928	NAV2	STAT4 [T	294	299	2.941176	GATTCC	2.92969	2.929
cg0273928	NAV2	STAT4 [T	388	393	2.941176	GGAACA	2.92969	2.929
cg0273928	NAV2	STAT4 [T	394	399	2.941176	CTTTCC	2.92969	2.929
cg0273928	NAV2	STAT4 [T	893	898	2.941176	GGAATA	2.92969	2.929
cg0273928	NAV2	STAT4 [T	987	992	2.941176	ACTTCC	2.92969	2.929
cg0273928	NAV2	STAT4 [T	1318	1323	2.941176	GGAATC	2.92969	2.929
cg0273928	NAV2	STAT4 [T	1548	1553	2.941176	GATTCC	2.92969	2.929
cg0273928	NAV2	STAT4 [T	1850	1855	2.941176	ACTTCC	2.92969	2.929
cg2264768	NAV2	STAT4 [T	110	115	2.941176	GGAAGT	2.92969	2.929
cg2264768	NAV2	STAT4 [T	169	174	2.941176	TGTTCC	2.92969	2.929
cg2264768	NAV2	STAT4 [T	1204	1209	2.941176	GGAATC	2.92969	2.929
cg2264768	NAV2	STAT4 [T	1529	1534	2.941176	ACTTCC	2.92969	2.929
cg2264768	NAV2	STAT4 [T	1779	1784	2.941176	GGAATA	2.92969	2.929
cg2264768	NAV2	STAT4 [T	1885	1890	2.941176	CTTTCC	2.92969	2.929
cg2264768	NAV2	STAT4 [T	1912	1917	2.941176	GATTCC	2.92969	2.929
cg2105276	NAV2	STAT4 [T	353	358	2.941176	GGAAAG	2.92969	2.929
cg2105276	NAV2	STAT4 [T	501	506	2.941176	GATTCC	2.92969	2.929
cg2105276	NAV2	STAT4 [T	1107	1112	2.941176	GGAAAG	2.92969	2.929
cg2105276	NAV2	STAT4 [T	1480	1485	2.941176	ACTTCC	2.92969	2.929
cg0273928	NAV2	STAT1bet	1908	1917	2.898434	ATTTCCT	0.0515	0.05191
cg0273928	NAV2	IRF-1 [T0	415	423	2.890712	TTTCCTT	0.07629	0.07756
cg2264768	NAV2	p53 [T006	1036	1042	2.813291	GCTGCC	0.48828	0.47786
cg2105276	NAV2	p53 [T006	737	743	2.813291	GGGCAG	0.48828	0.47786
cg2105276	NAV2	NF-1 [T00	1368	1375	2.813149	TGGACC	0.24414	0.24101
cg2264768	NAV2	PR B [T00	50	56	2.80933	TATTGTT	0.73242	0.74818
cg2264768	NAV2	PR B [T00	428	434	2.80933	GAATGT	0.73242	0.74818
cg2264768	NAV2	PR A [T01	50	56	2.80933	TATTGTT	0.73242	0.74818
cg2264768	NAV2	PR A [T01	428	434	2.80933	GAATGT	0.73242	0.74818
cg2264768	NAV2	AR [T000	314	322	2.808697	GGACAC	0.06104	0.06058
cg2264768	NAV2	TBP [T00	1250	1259	2.807313	TTTATAT	0.12207	0.12635
cg2264768	NAV2	NF-AT2 [T	1805	1814	2.800326	GGAAAA	0.03433	0.03494
cg0273928	NAV2	RXR-alph	910	916	2.726556	TCGACC	0.85449	0.84796

cg0273928	NAV2	c-Jun [T00	1439	1445	2.654872	GGAGTC	0.48828	0.48929
cg0273928	NAV2	AP-2alpha	42	47	2.550491	GCCTCA	0.48828	0.48266
cg2264768	NAV2	AP-2alpha	528	533	2.550491	TGAGGC	0.48828	0.48266
cg2264768	NAV2	AP-2alpha	647	652	2.550491	GCCTCA	0.48828	0.48266
cg2105276	NAV2	AP-2alpha	307	312	2.550491	GCCTCA	0.48828	0.48266
cg2105276	NAV2	AP-2alpha	1723	1728	2.550491	TGAGGC	0.48828	0.48266
cg0273928	NAV2	TCF-4 [T0	859	868	2.548903	TCTTTG	0.03433	0.03506
cg0273928	NAV2	RXR-alph	1327	1333	2.544678	ATAACC	0.85449	0.84796
cg2105276	NAV2	RXR-alph	27	33	2.544678	GGGTTC	0.85449	0.84796
cg0273928	NAV2	c-Jun [T00	303	309	2.538231	TAAGTC	0.48828	0.48929
cg2264768	NAV2	c-Jun [T00	1257	1263	2.538231	TGACTT	0.48828	0.48929
cg2105276	NAV2	c-Jun [T00	670	676	2.538231	TGACTT	0.48828	0.48929
cg0273928	NAV2	NF-AT1 [	606	614	2.449764	AGCTTT	0.09155	0.0926
cg2264768	NAV2	IRF-1 [T0	555	563	2.418514	GAAGGG	0.02289	0.02311
cg2264768	NAV2	C/EBPalph	1871	1877	2.371703	CACAAT	0.48828	0.49114
cg2264768	NAV2	NF-Y [T0	1015	1022	2.355069	ATTGGC	0.21362	0.21485
cg2105276	NAV2	GCF [T00	613	621	2.339499	GCGCAG	0.06104	0.05925
cg2105276	NAV2	RXR-alph	885	891	2.322562	GGGTCT	0.85449	0.84796
cg2105276	NAV2	RXR-alph	1943	1949	2.322562	CAGACC	0.85449	0.84796
cg2264768	NAV2	Elk-1 [T00	1321	1329	2.299314	CTTCCT	0.09155	0.09114
cg2105276	NAV2	Elk-1 [T00	1481	1489	2.299314	CTTCCT	0.09155	0.09114
cg0273928	NAV2	T3R-beta1	318	326	2.259951	TCACCT	0.03052	0.03041
cg0273928	NAV2	GATA-2 [	1758	1766	2.222222	ACCCTA	0.22888	0.23091
cg0273928	NAV2	T3R-beta1	179	187	2.221365	CTCTGG	0.15259	0.15262
cg2105276	NAV2	c-Ets-2 [T	1451	1459	2.217136	TTCCTC	0.16785	0.16856
cg2105276	NAV2	RAR-beta	294	303	2.144554	AGGGTT	0.07629	0.07625
cg2264768	NAV2	c-Ets-2 [T	1322	1330	2.142327	TTCCTC	0.16785	0.16856
cg2105276	NAV2	c-Ets-2 [T	952	960	2.142327	GGAGAG	0.16785	0.16856
cg2105276	NAV2	NF-Y [T0	1803	1810	2.12821	GAGCCA	0.21362	0.21508
cg2105276	NAV2	AP-2alpha	1622	1627	2.098119	GCCTCG	0.97656	0.95407
cg0273928	NAV2	NF-1 [T00	195	202	2.067686	TTGGGA	0.12207	0.12133
cg0273928	NAV2	NF-1 [T00	1733	1740	2.067686	TGTCCC	0.12207	0.12133
cg2264768	NAV2	NF-1 [T00	994	1001	2.067686	TTGGCA	0.12207	0.12133
cg0273928	NAV2	GATA-1 [	727	732	2.001358	TATCCC	3.90625	3.92756
cg0273928	NAV2	GATA-1 [	1631	1636	2.001358	TATCCC	3.90625	3.92756
cg2264768	NAV2	GATA-1 [	1131	1136	2.001358	TATCCC	3.90625	3.92756
cg2264768	NAV2	GATA-1 [	1787	1792	2.001358	TATCCC	3.90625	3.92756
cg2105276	NAV2	GATA-1 [	430	435	2.001358	TATCCC	3.90625	3.92756
cg0273928	NAV2	NF-AT1 [	825	833	1.970716	GGAAAA	0.06866	0.07012
cg2105276	NAV2	USF1 [T0	899	908	1.908112	CACGTG	0.03624	0.03558
cg2105276	NAV2	GATA-1 [	1469	1474	1.896347	CGGATA	3.90625	3.92756
cg0273928	NAV2	PR B [T00	390	396	1.892895	AACACT	0.12207	0.12429
cg0273928	NAV2	PR B [T00	984	990	1.892895	AACACT	0.12207	0.12429
cg0273928	NAV2	PR A [T01	390	396	1.892895	AACACT	0.12207	0.12429
cg0273928	NAV2	PR A [T01	984	990	1.892895	AACACT	0.12207	0.12429
cg2264768	NAV2	PR B [T00	1526	1532	1.892895	AACACT	0.12207	0.12429
cg2264768	NAV2	PR A [T01	1526	1532	1.892895	AACACT	0.12207	0.12429
cg2264768	NAV2	AP-2alpha	1602	1607	1.871933	GCCTCC	0.97656	0.95407

cg2105276	NAV2	AP-2alpha	660	665	1.871933	GGAGGC	0.97656	0.95407
cg2105276	NAV2	AP-2alpha	1745	1750	1.871933	GGAGGC	0.97656	0.95407
cg2264768	NAV2	TBP [T007	605	614	1.871542	TTTATA	0.18311	0.18942
cg2264768	NAV2	TBP [T007	627	636	1.871542	TTTATAT	0.18311	0.18942
cg2264768	NAV2	TBP [T007	1238	1247	1.871542	GGCCTAT	0.18311	0.18942
cg2105276	NAV2	TBP [T007	35	44	1.871542	CATCTAT	0.18311	0.18942
cg2105276	NAV2	PPAR-alph	601	611	1.869153	GACTGG	0.00668	0.00659
cg0273928	NAV2	C/EBPalph	769	775	1.830762	CTCAATT	0.48828	0.49438
cg0273928	NAV2	C/EBPalph	1065	1071	1.830762	AATTGA	0.48828	0.49438
cg2264768	NAV2	C/EBPalph	1826	1832	1.830762	AATTGA	0.48828	0.49438
cg2105276	NAV2	C/EBPalph	1720	1726	1.830762	AATTGA	0.48828	0.49438
cg0273928	NAV2	TFII-I [T0	1029	1034	1.824994	GGAGAG	0.48828	0.48408
cg2264768	NAV2	FOXP3 [T	493	498	1.824994	GTTGTA	0.48828	0.49451
cg2264768	NAV2	FOXP3 [T	795	800	1.824994	GTTGTA	0.48828	0.49451
cg2264768	NAV2	FOXP3 [T	1395	1400	1.824994	GTTGTA	0.48828	0.49451
cg2105276	NAV2	TFII-I [T0	952	957	1.824994	GGAGAG	0.48828	0.48408
cg2105276	NAV2	TFII-I [T0	1175	1180	1.824994	CTCTCC	0.48828	0.48408
cg2105276	NAV2	TFII-I [T0	1205	1210	1.824994	GGAGAG	0.48828	0.48408
cg2105276	NAV2	TFII-I [T0	1432	1437	1.824994	CTCTCC	0.48828	0.48408
cg0273928	NAV2	c-Ets-1 [T	591	597	1.769212	TAGGAA	0.12207	0.12414
cg0273928	NAV2	c-Ets-1 [T	1240	1246	1.769212	TAGGAA	0.12207	0.12414
cg0273928	NAV2	c-Ets-1 [T	1767	1773	1.769212	TTTCCTA	0.12207	0.12414
cg2264768	NAV2	c-Ets-1 [T	1987	1993	1.769212	TTTCCTA	0.12207	0.12414
cg2264768	NAV2	C/EBPalph	1535	1541	1.761449	TATTGT	0.48828	0.49438
cg2105276	NAV2	C/EBPalph	517	523	1.761449	CACAAT	0.48828	0.49438
cg2264768	NAV2	PXR-1:RX	189	196	1.759733	TGAACT	0.06104	0.06168
cg0273928	NAV2	p53 [T006	841	847	1.758307	GGGCAG	0.36621	0.36261
cg2105276	NAV2	p53 [T006	451	457	1.758307	TCTGCC	0.36621	0.36261
cg0273928	NAV2	c-Fos [T00	1299	1308	1.752617	CTTATG	0.01526	0.01542
cg2105276	NAV2	NF-Y [T00	1050	1057	1.749852	ATTGGC	0.18311	0.18459
cg0273928	NAV2	LEF-1 [T0	860	867	1.703176	CTTTGAT	0.09155	0.09326
cg0273928	NAV2	LEF-1 [T0	1670	1677	1.703176	CATCAA	0.09155	0.09326
cg2264768	NAV2	LEF-1 [T0	709	716	1.703176	CATCAA	0.09155	0.09326
cg0273928	NAV2	GR-beta [T	57	61	1.680765	AATTC	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	457	461	1.680765	GCATT	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	537	541	1.680765	GAATT	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	935	939	1.680765	GAATT	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	936	940	1.680765	AATTC	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	961	965	1.680765	GCATT	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	1098	1102	1.680765	GAATT	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	1363	1367	1.680765	GAATT	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	1610	1614	1.680765	AATTC	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	1923	1927	1.680765	GAATT	3.90625	3.94936
cg0273928	NAV2	GR-beta [T	1960	1964	1.680765	GAATT	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	83	87	1.680765	AATTC	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	127	131	1.680765	GCATT	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	305	309	1.680765	AATTC	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	328	332	1.680765	AATGC	3.90625	3.94936

cg2264768	NAV2	GR-beta [T	444	448	1.680765	AATTC	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	460	464	1.680765	GCATT	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	1489	1493	1.680765	AATGC	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	1546	1550	1.680765	AATTC	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	1700	1704	1.680765	GAATT	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	1731	1735	1.680765	AATGC	3.90625	3.94936
cg2264768	NAV2	GR-beta [T	1874	1878	1.680765	AATTC	3.90625	3.94936
cg2105276	NAV2	GR-beta [T	332	336	1.680765	AATGC	3.90625	3.94936
cg2105276	NAV2	GR-beta [T	442	446	1.680765	GCATT	3.90625	3.94936
cg2105276	NAV2	GR-beta [T	535	539	1.680765	AATGC	3.90625	3.94936
cg2105276	NAV2	GR-beta [T	1399	1403	1.680765	GAATT	3.90625	3.94936
cg2105276	NAV2	GR-beta [T	1421	1425	1.680765	AATTC	3.90625	3.94936
cg2105276	NAV2	GR-beta [T	1525	1529	1.680765	GCATT	3.90625	3.94936
cg2105276	NAV2	GR-beta [T	1822	1826	1.680765	GAATT	3.90625	3.94936
cg2264768	NAV2	AR [T000	1331	1339	1.655418	GAAGTG	0.09155	0.09119
cg0273928	NAV2	c-Ets-1 [T	415	421	1.641124	TTTCCTT	0.36621	0.36952
cg2264768	NAV2	c-Ets-1 [T	1803	1809	1.641124	AAGGAA	0.36621	0.36952
cg0273928	NAV2	C/EBPbeta	79	82	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	167	170	1.639871	CCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	195	198	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	206	209	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	224	227	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	244	247	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	398	401	1.639871	CCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	487	490	1.639871	CCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	619	622	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	684	687	1.639871	CCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	952	955	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	964	967	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1027	1030	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1122	1125	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1385	1388	1.639871	TTGG	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1737	1740	1.639871	CCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1917	1920	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	123	126	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	173	176	1.639871	CCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	216	219	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	449	452	1.639871	CCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	463	466	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	543	546	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	594	597	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	656	659	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	789	792	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	830	833	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	895	898	1.639871	CCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	942	945	1.639871	CCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	994	997	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1016	1019	1.639871	TTGG	15.625	15.72563

cg2264768	NAV2	C/EBPbeta	1046	1049	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1363	1366	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1480	1483	1.639871	TTGG	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1851	1854	1.639871	CCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	19	22	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	25	28	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	54	57	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	96	99	1.639871	CCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	299	302	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	326	329	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	425	428	1.639871	CCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	855	858	1.639871	CCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1051	1054	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1105	1108	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1124	1127	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1372	1375	1.639871	CCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1381	1384	1.639871	CCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1419	1422	1.639871	CCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1488	1491	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1630	1633	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1743	1746	1.639871	TTGG	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1806	1809	1.639871	CCAA	15.625	15.72563
cg0273928	NAV2	PXR-1:RX	1572	1579	1.63615	AAAGTT	0.06104	0.06239
cg2105276	NAV2	IRF-1 [T0	349	357	1.616539	ACAGGG	0.04578	0.04655
cg0273928	NAV2	XBP-1 [T	1682	1687	1.583727	TGTCAT	0.97656	0.98146
cg2264768	NAV2	XBP-1 [T	203	208	1.583727	GGTCAT	0.97656	0.98146
cg2264768	NAV2	XBP-1 [T	1426	1431	1.583727	ATGACC	0.97656	0.98146
cg2264768	NAV2	XBP-1 [T	1441	1446	1.583727	GGTCAT	0.97656	0.98146
cg2264768	NAV2	XBP-1 [T	1895	1900	1.583727	GGTCAT	0.97656	0.98146
cg2105276	NAV2	XBP-1 [T	1838	1843	1.583727	ATGACA	0.97656	0.98146
cg0273928	NAV2	TFIID [T0	540	546	1.537547	TTTTCCA	0.73242	0.75096
cg0273928	NAV2	TFIID [T0	886	892	1.537547	TTTTCCA	0.73242	0.75096
cg0273928	NAV2	TFIID [T0	1226	1232	1.537547	TTTTTCA	0.73242	0.75096
cg0273928	NAV2	TFIID [T0	1752	1758	1.537547	TGTAAA	0.73242	0.75096
cg0273928	NAV2	TFIID [T0	1946	1952	1.537547	TTTTCCA	0.73242	0.75096
cg2264768	NAV2	Pax-5 [T0	1836	1842	1.537547	CTTGCC	0.73242	0.71311
cg2264768	NAV2	TFIID [T0	280	286	1.537547	TTTTCCA	0.73242	0.75096
cg2264768	NAV2	TFIID [T0	725	731	1.537547	TTTTGTA	0.73242	0.75096
cg2264768	NAV2	TFIID [T0	1619	1625	1.537547	TGAAAA	0.73242	0.75096
cg2105276	NAV2	Pax-5 [T0	605	611	1.537547	GGGCCA	0.73242	0.71311
cg2105276	NAV2	Pax-5 [T0	1078	1084	1.537547	GGGCTA	0.73242	0.71311
cg2105276	NAV2	Pax-5 [T0	1632	1638	1.537547	GGGCCA	0.73242	0.71311
cg2105276	NAV2	TFIID [T0	71	77	1.537547	TTTTTCA	0.73242	0.75096
cg2105276	NAV2	TFIID [T0	1901	1907	1.537547	TTTTGA	0.73242	0.75096
cg0273928	NAV2	AR [T000	1688	1696	1.513096	TCAGTG	0.09155	0.09119
cg2105276	NAV2	AR [T000	817	825	1.513096	GGACAA	0.09155	0.09119
cg0273928	NAV2	c-Ets-1 [T	261	267	1.513038	GAGGAA	0.36621	0.36952
cg0273928	NAV2	c-Ets-1 [T	1582	1588	1.513038	GAGGAA	0.36621	0.36952

cg2105276	NAV2	c-Ets-1 [T(	955	961	1.513038	GAGGAA	0.36621	0.36952
cg2105276	NAV2	c-Ets-1 [T(	1450	1456	1.513038	TTTCCTC	0.36621	0.36952
cg2105276	NAV2	CTF [T001	1803	1814	1.511443	GAGCCA.	0.00095	0.00096
cg2264768	NAV2	POU2F2 ((	602	612	1.505053	TGATTTA	0.00858	0.0089
cg0273928	NAV2	RXR-alpha	656	662	1.474336	GGGTTT(	0.48828	0.48222
cg2105276	NAV2	RXR-alpha	295	301	1.474336	GGGTTT(	0.48828	0.48222
cg0273928	NAV2	STAT4 [T(	414	419	1.470588	TTTTCC	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	540	545	1.470588	TTTTCC	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	593	598	1.470588	GGAAAA	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	609	614	1.470588	TTTTCC	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	825	830	1.470588	GGAAAA	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	886	891	1.470588	TTTTCC	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	1097	1102	1.470588	GGAATT	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	1242	1247	1.470588	GGAAAC	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	1411	1416	1.470588	GGAAAA	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	1584	1589	1.470588	GGAAAA	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	1617	1622	1.470588	GGAAAC	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	1946	1951	1.470588	TTTTCC	1.95312	1.96333
cg0273928	NAV2	STAT4 [T(	1959	1964	1.470588	GGAATT	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	280	285	1.470588	TTTTCC	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	444	449	1.470588	AATTCC	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	559	564	1.470588	GGAAAC	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	766	771	1.470588	GGAACT	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	832	837	1.470588	GGAAAC	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	1186	1191	1.470588	GTTTCC	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	1420	1425	1.470588	GGAAAA	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	1805	1810	1.470588	GGAAAA	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	1874	1879	1.470588	AATTCC	1.95312	1.96333
cg2264768	NAV2	STAT4 [T(	1986	1991	1.470588	TTTTCC	1.95312	1.96333
cg2105276	NAV2	STAT4 [T(	101	106	1.470588	AGTTCC	1.95312	1.96333
cg2105276	NAV2	STAT4 [T(	343	348	1.470588	GTTTCC	1.95312	1.96333
cg2105276	NAV2	STAT4 [T(	957	962	1.470588	GGAAAA	1.95312	1.96333
cg2105276	NAV2	STAT4 [T(	1398	1403	1.470588	GGAATT	1.95312	1.96333
cg2105276	NAV2	STAT4 [T(	1415	1420	1.470588	GTTTCC	1.95312	1.96333
cg2105276	NAV2	STAT4 [T(	1821	1826	1.470588	GGAATT	1.95312	1.96333
cg0273928	NAV2	GR [T050	168	174	1.444018	CAAAAA	0.12207	0.1245
cg2264768	NAV2	GR [T050	925	931	1.444018	CAAAAA	0.12207	0.1245
cg2264768	NAV2	GR [T050	1153	1159	1.444018	GTTTTTC	0.12207	0.1245
cg0273928	NAV2	PR B [T00	1104	1110	1.404665	CAGTGT	0.36621	0.37023
cg0273928	NAV2	PR A [T01	1104	1110	1.404665	CAGTGT	0.36621	0.37023
cg2264768	NAV2	PR B [T00	1592	1598	1.404665	AACACT(	0.36621	0.37023
cg2264768	NAV2	PR A [T01	1592	1598	1.404665	AACACT(	0.36621	0.37023
cg2105276	NAV2	PR B [T00	65	71	1.404665	GAGTGT	0.36621	0.37023
cg2105276	NAV2	PR A [T01	65	71	1.404665	GAGTGT	0.36621	0.37023
cg0273928	NAV2	c-Ets-1 [T(	512	518	1.384951	TTTCCTC	0.36621	0.36952
cg0273928	NAV2	c-Ets-1 [T(	1909	1915	1.384951	TTTCCTC	0.36621	0.36952
cg2264768	NAV2	c-Ets-1 [T(	1187	1193	1.384951	TTTCCTC	0.36621	0.36952
cg2264768	NAV2	c-Ets-1 [T(	1418	1424	1.384951	CAGGAA	0.36621	0.36952

cg0273928	NAV2	NF-AT1 [	1943	1952	1.378139	CCATTT	0.01907	0.0194
cg0273928	NAV2	C/EBPbeta	68	71	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	377	380	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	423	426	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	482	485	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	519	522	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	572	575	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	770	773	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	776	779	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	862	865	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	973	976	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1067	1070	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1210	1213	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1230	1233	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1336	1339	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1672	1675	1.366559	TCAA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1747	1750	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1789	1792	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1872	1875	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	C/EBPbeta	1894	1897	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	115	118	1.366559	TCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	178	181	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	188	191	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	223	226	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	360	363	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	711	714	1.366559	TCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	908	911	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	960	963	1.366559	TCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	979	982	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1148	1151	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1157	1160	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1232	1235	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1256	1259	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1543	1546	1.366559	TCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1771	1774	1.366559	TCAA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1828	1831	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1910	1913	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1929	1932	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1971	1974	1.366559	TTGA	15.625	15.72563
cg2264768	NAV2	C/EBPbeta	1981	1984	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	45	48	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	120	123	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	148	151	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	379	382	1.366559	TCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	532	535	1.366559	TCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	926	929	1.366559	TCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	994	997	1.366559	TCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1047	1050	1.366559	TTGA	15.625	15.72563

cg2105276	NAV2	C/EBPbeta	1402	1405	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1655	1658	1.366559	TCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1675	1678	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1722	1725	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1757	1760	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1827	1830	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1903	1906	1.366559	TTGA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1953	1956	1.366559	TCAA	15.625	15.72563
cg2105276	NAV2	C/EBPbeta	1971	1974	1.366559	TTGA	15.625	15.72563
cg0273928	NAV2	AP-2alpha	282	287	1.357116	GCCTGT	0.48828	0.48203
cg0273928	NAV2	AP-2alpha	556	561	1.357116	ACAGGC	0.48828	0.48203
cg0273928	NAV2	AP-2alpha	708	713	1.357116	GCCTGT	0.48828	0.48203
cg2264768	NAV2	AP-2alpha	331	336	1.357116	GCCTGT	0.48828	0.48203
cg2264768	NAV2	AP-2alpha	1004	1009	1.357116	ACAGGC	0.48828	0.48203
cg0273928	NAV2	HNF-3alph	697	704	1.342935	TATTTTA	0.03052	0.03194
cg2105276	NAV2	C/EBPalph	1969	1975	1.220508	TATTGA	0.24414	0.247
cg0273928	NAV2	PEA3 [T0	198	206	1.194633	GGACAT	0.06866	0.06895
cg2264768	NAV2	GATA-2 [	1640	1648	1.111111	ACCTTA	0.09155	0.09208
cg2105276	NAV2	c-Ets-2 [T	1482	1490	1.071163	TTCCTCT	0.06104	0.06166
cg2264768	NAV2	HNF-1A [	1486	1493	1.069403	GTTAAT	0.48828	0.49664
cg2105276	NAV2	HNF-1A [	1573	1580	1.069403	GTTAAA	0.48828	0.49664
cg2105276	NAV2	USF2 [T0	1329	1338	1.048473	CAGGTG	0.01717	0.01694
cg0273928	NAV2	GATA-1 [	1762	1767	1.038567	TATCAT	1.95312	1.98662
cg2264768	NAV2	GATA-1 [	178	183	1.038567	TTGATA	1.95312	1.98662
cg2264768	NAV2	GATA-1 [	1171	1176	1.038567	ATGATA	1.95312	1.98662
cg2264768	NAV2	GATA-1 [	1625	1630	1.038567	ATGATA	1.95312	1.98662
cg0273928	NAV2	TCF-4 [T0	1669	1678	0.98855	ACATCA	0.05722	0.05784
cg2105276	NAV2	TBP [T00	1584	1593	0.935771	AAAATA	0.12207	0.12628
cg0273928	NAV2	GATA-1 [	1524	1529	0.863549	GTGATA	1.95312	1.98662
cg2264768	NAV2	GATA-1 [	300	305	0.863549	GTGATA	1.95312	1.98662
cg2105276	NAV2	GATA-1 [	687	692	0.863549	GTGATA	1.95312	1.98662
cg2105276	NAV2	GATA-1 [	1778	1783	0.863549	GTGATA	1.95312	1.98662
cg2264768	NAV2	RXR-alph	1101	1107	0.848226	CTAACC	0.48828	0.48333
cg0273928	NAV2	GR-beta [	111	115	0.840383	AATGA	7.8125	7.94706
cg0273928	NAV2	GR-beta [	134	138	0.840383	AATGG	7.8125	7.94706
cg0273928	NAV2	GR-beta [	266	270	0.840383	AATGA	7.8125	7.94706
cg0273928	NAV2	GR-beta [	401	405	0.840383	AATTA	7.8125	7.94706
cg0273928	NAV2	GR-beta [	523	527	0.840383	AATTA	7.8125	7.94706
cg0273928	NAV2	GR-beta [	550	554	0.840383	CCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [	771	775	0.840383	CAATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [	901	905	0.840383	TCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [	1064	1068	0.840383	TAATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [	1065	1069	0.840383	AATTG	7.8125	7.94706
cg0273928	NAV2	GR-beta [	1099	1103	0.840383	AATTG	7.8125	7.94706
cg0273928	NAV2	GR-beta [	1252	1256	0.840383	TCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [	1271	1275	0.840383	CAATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [	1272	1276	0.840383	AATTA	7.8125	7.94706
cg0273928	NAV2	GR-beta [	1291	1295	0.840383	CCATT	7.8125	7.94706

cg0273928	NAV2	GR-beta [T	1364	1368	0.840383	AATTA	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1514	1518	0.840383	TCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1609	1613	0.840383	CAATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1636	1640	0.840383	CCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1684	1688	0.840383	TCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1764	1768	0.840383	TCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1823	1827	0.840383	TCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1841	1845	0.840383	TCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1943	1947	0.840383	CCATT	7.8125	7.94706
cg0273928	NAV2	GR-beta [T	1961	1965	0.840383	AATTA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	82	86	0.840383	CAATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	176	180	0.840383	AATTG	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	304	308	0.840383	TAATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	383	387	0.840383	CCATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	436	440	0.840383	AATGA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	592	596	0.840383	AATTG	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	887	891	0.840383	AATGG	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	970	974	0.840383	TCATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	977	981	0.840383	AATTG	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1014	1018	0.840383	AATTG	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1080	1084	0.840383	CCATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1115	1119	0.840383	TCATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1167	1171	0.840383	AATGA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1264	1268	0.840383	AATTA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1425	1429	0.840383	AATGA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1606	1610	0.840383	CCATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1624	1628	0.840383	AATGA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1671	1675	0.840383	AATTA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1783	1787	0.840383	TAATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1784	1788	0.840383	AATTA	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1792	1796	0.840383	CCATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1826	1830	0.840383	AATTG	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1873	1877	0.840383	CAATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1897	1901	0.840383	TCATT	7.8125	7.94706
cg2264768	NAV2	GR-beta [T	1959	1963	0.840383	AATGA	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	43	47	0.840383	AATTG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	383	387	0.840383	AATTG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	392	396	0.840383	AATGG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	522	526	0.840383	TAATT	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	523	527	0.840383	AATTG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	649	653	0.840383	AATGA	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	821	825	0.840383	AATGA	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1066	1070	0.840383	AATGA	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1400	1404	0.840383	AATTG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1420	1424	0.840383	CAATT	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1679	1683	0.840383	AATTG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1689	1693	0.840383	AATGG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1703	1707	0.840383	TCATT	7.8125	7.94706

cg2105276	NAV2	GR-beta [T	1711	1715	0.840383	CCATT	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1719	1723	0.840383	TAATT	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1720	1724	0.840383	AATTG	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1772	1776	0.840383	AATTA	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1807	1811	0.840383	CAATT	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1808	1812	0.840383	AATTA	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1859	1863	0.840383	TAATT	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1891	1895	0.840383	CAATT	7.8125	7.94706
cg2105276	NAV2	GR-beta [T	1948	1952	0.840383	CCATT	7.8125	7.94706
cg2264768	NAV2	POU2F1 [	1729	1739	0.818935	AGAATG	0.01383	0.01413
cg2105276	NAV2	GATA-1 [	844	849	0.758539	CTGATA	1.95312	1.98662
cg0273928	NAV2	NF-Y [T0	78	85	0.680578	ATTGGT	0.09155	0.09259
cg2105276	NAV2	AP-2alpha	75	80	0.678558	TCAGGC	0.48828	0.48199
cg2105276	NAV2	AP-2alpha	556	561	0.678558	GCCTGA	0.48828	0.48199
cg2105276	NAV2	AP-2alpha	1008	1013	0.678558	GCCTGA	0.48828	0.48199
cg2105276	NAV2	AP-2alpha	1040	1045	0.678558	TCAGGC	0.48828	0.48199
cg2264768	NAV2	C/EBPalph	619	625	0.540941	GATTGT	0.24414	0.24507
cg2264768	NAV2	C/EBPalph	1069	1075	0.540941	CACAAT	0.24414	0.24507
cg2105276	NAV2	POU2F2 (	1458	1468	0.501684	TCTGTA	0.01287	0.01325
cg0273928	NAV2	PR B [T00	218	224	0.48823	AACAGT	0.12207	0.12407
cg0273928	NAV2	PR A [T01	218	224	0.48823	AACAGT	0.12207	0.12407
cg2264768	NAV2	PR B [T00	944	950	0.48823	AACAGT	0.12207	0.12407
cg2264768	NAV2	PR A [T01	944	950	0.48823	AACAGT	0.12207	0.12407
cg2264768	NAV2	NF-AT1 [	1805	1813	0.479048	GGAAAA	0.02289	0.02328
cg2105276	NAV2	AP-1 [T00	912	920	0.436196	TGACTC	0.09155	0.09215
cg0273928	NAV2	AP-1 [T00	917	925	0.401835	AGTGAG	0.09155	0.09215
cg2264768	NAV2	c-Ets-1 [T	1530	1536	0.384261	CTTCCT	0.24414	0.24569
cg2264768	NAV2	c-Ets-1 [T	1578	1584	0.384261	TAGGAA	0.24414	0.24569
cg2105276	NAV2	AP-1 [T00	649	657	0.348957	AATGAG	0.09155	0.09215
cg2264768	NAV2	HNF-1A [	348	355	0.287765	ACATTA	0.24414	0.24974
cg2264768	NAV2	HNF-1A [	508	515	0.287765	GTTAAA	0.24414	0.24974
cg0273928	NAV2	GATA-1 [	1275	1280	0.280028	TATCTA	0.97656	0.99875
cg2264768	NAV2	GATA-1 [	950	955	0.280028	TAGATA	0.97656	0.99875
cg2264768	NAV2	GATA-1 [	1298	1303	0.280028	TATCTT	0.97656	0.99875
cg2264768	NAV2	GATA-1 [	1635	1640	0.280028	TATCTA	0.97656	0.99875
cg2264768	NAV2	GATA-1 [	1644	1649	0.280028	TATCTA	0.97656	0.99875
cg2105276	NAV2	GATA-1 [	1715	1720	0.280028	TAGATA	0.97656	0.99875
cg0273928	NAV2	AP-1 [T00	831	839	0.261718	CATGAG	0.09155	0.09215
cg0273928	NAV2	c-Ets-1 [T	1008	1014	0.256174	CTTCCTT	0.24414	0.24569
cg2105276	NAV2	c-Ets-1 [T	583	589	0.256174	AAGGAA	0.24414	0.24569
cg2105276	NAV2	c-Ets-1 [T	973	979	0.256174	AAGGAA	0.24414	0.24569
cg0273928	NAV2	AP-2alpha	1537	1542	0.226186	CCAGGC	0.97656	0.95305
cg0273928	NAV2	AP-2alpha	1562	1567	0.226186	CCAGGC	0.97656	0.95305
cg2264768	NAV2	AP-2alpha	1430	1435	0.226186	CCAGGC	0.97656	0.95305
cg2105276	NAV2	AP-2alpha	240	245	0.226186	CCAGGC	0.97656	0.95305
cg2105276	NAV2	AP-2alpha	965	970	0.226186	GCCTGG	0.97656	0.95305
cg2264768	NAV2	p53 [T006	1836	1842	0.211706	CTTGCC	0.36621	0.35912
cg0273928	NAV2	GR-alpha [	365	369	0.207689	CCTTT	7.8125	7.81264

cg0273928	NAV2	GR-alpha [	384	388	0.207689	AGAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	704	708	0.207689	AGAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1059	1063	0.207689	AAAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1674	1678	0.207689	AAAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1713	1717	0.207689	AAAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1859	1863	0.207689	AAAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	241	245	0.207689	CCTCT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	260	264	0.207689	CCTCT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	715	719	0.207689	AGAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1043	1047	0.207689	CCTTT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1235	1239	0.207689	AGAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1324	1328	0.207689	CCTCT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1338	1342	0.207689	CCTTT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1352	1356	0.207689	AAAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1412	1416	0.207689	AGAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1776	1780	0.207689	AAAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1843	1847	0.207689	AGAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1938	1942	0.207689	CCTCT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	205	209	0.207689	CCTCT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	364	368	0.207689	AGAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	680	684	0.207689	AGAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	766	770	0.207689	AGAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	954	958	0.207689	AGAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	961	965	0.207689	AAAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	972	976	0.207689	AAAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1017	1021	0.207689	CCTTT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1174	1178	0.207689	CCTCT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1313	1317	0.207689	CCTCT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1484	1488	0.207689	CCTCT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1576	1580	0.207689	AAAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1735	1739	0.207689	AAAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1881	1885	0.207689	CCTCT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1907	1911	0.207689	AAAGG	7.8125	7.81264
cg2264768	NAV2	HNF-1A [	1670	1677	0.143882	AAATTA	0.24414	0.25261
cg2105276	NAV2	Elk-1 [T00	506	514	0.134348	CTTCCTC	0.06104	0.06047
cg2264768	NAV2	c-Ets-1 [T	1196	1202	0.128087	CTTCCTC	0.24414	0.2429
cg2264768	NAV2	c-Ets-1 [T	1321	1327	0.128087	CTTCCTC	0.24414	0.2429
cg2105276	NAV2	c-Ets-1 [T	1481	1487	0.128087	CTTCCTC	0.24414	0.2429
cg0273928	NAV2	GATA-1 [	176	181	0.105011	TATCTC	0.97656	0.98738
cg0273928	NAV2	GR-alpha [	103	107	0	CCTAT	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	283	287	0	CCTGT	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	515	519	0	CCTGT	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	556	560	0	ACAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	709	713	0	CCTGT	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1127	1131	0	ATAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1332	1336	0	CCTGT	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1341	1345	0	ATAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1429	1433	0	ATAGG	7.8125	7.81264

cg0273928	NAV2	GR-alpha [	1653	1657	0	ACAGG	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1760	1764	0	CCTAT	7.8125	7.81264
cg0273928	NAV2	GR-alpha [	1770	1774	0	CCTAT	7.8125	7.81264
cg0273928	NAV2	XBP-1 [T	305	310	0	AGTCAT	0.97656	0.98127
cg0273928	NAV2	XBP-1 [T	835	840	0	AGTCAT	0.97656	0.98127
cg0273928	NAV2	XBP-1 [T	1302	1307	0	ATGACT	0.97656	0.98127
cg0273928	NAV2	Pax-5 [T0	557	563	0	CAGGCC	1.09863	1.06846
cg0273928	NAV2	Pax-5 [T0	1563	1569	0	CAGGCC	1.09863	1.06846
cg0273928	NAV2	TFII-I [T0	189	194	0	GGACAG	1.46484	1.45997
cg0273928	NAV2	TFII-I [T0	394	399	0	CTTTCC	1.46484	1.45997
cg0273928	NAV2	TFII-I [T0	1651	1656	0	GGACAG	1.46484	1.45997
cg0273928	NAV2	TFII-I [T0	1732	1737	0	CTGTCC	1.46484	1.45997
cg0273928	NAV2	STAT4 [T	263	268	0	GGAAAT	0.48828	0.49387
cg0273928	NAV2	STAT4 [T	511	516	0	ATTTCC	0.48828	0.49387
cg0273928	NAV2	STAT4 [T	1766	1771	0	ATTTCC	0.48828	0.49387
cg0273928	NAV2	STAT4 [T	1908	1913	0	ATTTCC	0.48828	0.49387
cg0273928	NAV2	STAT4 [T	1925	1930	0	ATTTCC	0.48828	0.49387
cg0273928	NAV2	YY1 [T00	86	89	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	135	138	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	144	147	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	187	190	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	273	276	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	332	335	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	500	503	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	550	553	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	839	842	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	865	868	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1042	1045	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1291	1294	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1316	1319	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1408	1411	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1604	1607	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1636	1639	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1780	1783	0	ATGG	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1943	1946	0	CCAT	7.8125	7.81711
cg0273928	NAV2	YY1 [T00	1950	1953	0	CCAT	7.8125	7.81711
cg0273928	NAV2	GATA-1 [	1020	1025	0	TATCTG	0.97656	0.98738
cg0273928	NAV2	C/EBPbeta	277	280	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	369	372	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	471	474	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	643	646	0	ACAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	649	652	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	660	663	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	982	985	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1013	1016	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1073	1076	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1076	1079	0	TTGC	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1101	1104	0	TTGC	15.625	15.71349

cg0273928	NAV2	C/EBPbeta	1110	1113	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1115	1118	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1135	1138	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1149	1152	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1153	1156	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1165	1168	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1176	1179	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1205	1208	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1222	1225	0	TTGC	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1246	1249	0	ACAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1265	1268	0	TTGC	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1270	1273	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1281	1284	0	ACAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1372	1375	0	TTGC	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1378	1381	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1424	1427	0	TTGC	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1426	1429	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1476	1479	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1570	1573	0	ACAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1608	1611	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1640	1643	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1751	1754	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1831	1834	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1836	1839	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1884	1887	0	TTGC	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1890	1893	0	TTGT	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1899	1902	0	GCAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1931	1934	0	ACAA	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1971	1974	0	TTGC	15.625	15.71349
cg0273928	NAV2	C/EBPbeta	1985	1988	0	GCAA	15.625	15.71349
cg0273928	NAV2	c-Jun [T00	833	839	0	TGAGTC	0.12207	0.12266
cg0273928	NAV2	c-Jun [T00	919	925	0	TGAGTC	0.12207	0.12266
cg0273928	NAV2	TFIID [T0	65	71	0	TTTTTGA	1.09863	1.13474
cg0273928	NAV2	TFIID [T0	443	449	0	TTTTCTA	1.09863	1.13474
cg0273928	NAV2	TFIID [T0	877	883	0	TTTTTTA	1.09863	1.13474
cg0273928	NAV2	TFIID [T0	1227	1233	0	TTTTCA	1.09863	1.13474
cg0273928	NAV2	TFIID [T0	1709	1715	0	TTAAAA	1.09863	1.13474
cg0273928	NAV2	FOXP3 [T	642	647	0	CACAAC	1.46484	1.47315
cg0273928	NAV2	FOXP3 [T	1835	1840	0	GTTGTC	1.46484	1.47315
cg0273928	NAV2	FOXP3 [T	1889	1894	0	GTTGTT	1.46484	1.47315
cg0273928	NAV2	GR-beta [T	56	60	0	AAATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	241	245	0	ACATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	347	351	0	ACATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	400	404	0	AAATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	522	526	0	AAATT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	538	542	0	AATTT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	772	776	0	AATTT	3.90625	3.99611
cg0273928	NAV2	GR-beta [T	1740	1744	0	AATGT	3.90625	3.99611

cg0273928	NAV2	GR-beta [T	1924	1928	0	AATTT	3.90625	3.99611
cg0273928	NAV2	NF-AT1 [T	537	546	0	GAATTT	0.00191	0.00195
cg0273928	NAV2	NF-AT1 [T	883	891	0	ATTTTTT	0.01526	0.01569
cg0273928	NAV2	GR [T050	64	70	0	TTTTTTG	0.36621	0.37562
cg0273928	NAV2	HNF-1A [	1708	1715	0	GTTAAA	0.24414	0.25261
cg0273928	NAV2	IRF-2 [T01	257	262	0	AAGTGA	0.48828	0.49387
cg2264768	NAV2	GR-alpha [	332	336	0	CCTGT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	784	788	0	CCTGT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	813	817	0	CCTAT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1004	1008	0	ACAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1086	1090	0	CCTAT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1129	1133	0	CCTAT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1240	1244	0	CCTAT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1505	1509	0	ATAGG	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1533	1537	0	CCTAT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1918	1922	0	CCTGT	7.8125	7.81264
cg2264768	NAV2	GR-alpha [	1990	1994	0	CCTAT	7.8125	7.81264
cg2264768	NAV2	Pax-5 [T0	546	552	0	GGGCTG	1.09863	1.06846
cg2264768	NAV2	Pax-5 [T0	1415	1421	0	GGGCAG	1.09863	1.06846
cg2264768	NAV2	p53 [T006	1415	1421	0	GGGCAG	0.36621	0.35912
cg2264768	NAV2	TFII-I [T0	364	369	0	GGACAG	1.46484	1.45997
cg2264768	NAV2	TFII-I [T0	379	384	0	CTGTCC	1.46484	1.45997
cg2264768	NAV2	TFII-I [T0	1130	1135	0	CTATCC	1.46484	1.45997
cg2264768	NAV2	TFII-I [T0	1695	1700	0	GGACAG	1.46484	1.45997
cg2264768	NAV2	TFII-I [T0	1885	1890	0	CTTTCC	1.46484	1.45997
cg2264768	NAV2	STAT4 [T	778	783	0	GGAAAT	0.48828	0.49387
cg2264768	NAV2	STAT4 [T	1608	1613	0	ATTTCC	0.48828	0.49387
cg2264768	NAV2	STAT4 [T	1823	1828	0	GGAAAT	0.48828	0.49387
cg2264768	NAV2	c-Ets-1 [T	501	507	0	CAGGAA	0.24414	0.2429
cg2264768	NAV2	YY1 [T00	383	386	0	CCAT	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	598	601	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	639	642	0	CCAT	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	684	687	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	805	808	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	816	819	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	888	891	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1080	1083	0	CCAT	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1372	1375	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1495	1498	0	CCAT	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1606	1609	0	CCAT	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1614	1617	0	CCAT	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1692	1695	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1764	1767	0	ATGG	7.8125	7.81711
cg2264768	NAV2	YY1 [T00	1792	1795	0	CCAT	7.8125	7.81711
cg2264768	NAV2	ER-alpha [	203	207	0	GGTCA	1.95312	1.9404
cg2264768	NAV2	ER-alpha [	534	538	0	TGACC	1.95312	1.9404
cg2264768	NAV2	ER-alpha [	839	843	0	GGTCA	1.95312	1.9404
cg2264768	NAV2	ER-alpha [	844	848	0	GGTCA	1.95312	1.9404

cg2264768	NAV2	ER-alpha [	1427	1431	0	TGACC	1.95312	1.9404
cg2264768	NAV2	ER-alpha [	1441	1445	0	GGTCA	1.95312	1.9404
cg2264768	NAV2	ER-alpha [	1895	1899	0	GGTCA	1.95312	1.9404
cg2264768	NAV2	C/EBPbeta	22	25	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	52	55	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	67	70	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	81	84	0	ACAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	94	97	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	96	99	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	138	141	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	387	390	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	403	406	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	477	480	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	486	489	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	494	497	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	521	524	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	621	624	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	727	730	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	738	741	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	754	757	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	796	799	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	853	856	0	ACAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	924	927	0	ACAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1001	1004	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1008	1011	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1065	1068	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1070	1073	0	ACAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1090	1093	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1119	1122	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1272	1275	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1368	1371	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1388	1391	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1393	1396	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1396	1399	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1434	1437	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1464	1467	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1473	1476	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1484	1487	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1501	1504	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1537	1540	0	TTGT	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1734	1737	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1751	1754	0	GCAA	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1837	1840	0	TTGC	15.625	15.71349
cg2264768	NAV2	C/EBPbeta	1872	1875	0	ACAA	15.625	15.71349
cg2264768	NAV2	TFIID [T0	31	37	0	TTTTTTA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	32	38	0	TTTTTAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	631	637	0	TATAAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	742	748	0	TTTTTTA	1.09863	1.13474

cg2264768	NAV2	TFIID [T0	743	749	0	TTTTTAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	745	751	0	TTTAAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	746	752	0	TTAAAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	918	924	0	TTTAAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	1154	1160	0	TTTTTGA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	1340	1346	0	TTTTTAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	1342	1348	0	TTTAAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	1658	1664	0	TTAAAA	1.09863	1.13474
cg2264768	NAV2	TFIID [T0	1659	1665	0	TAAAAA	1.09863	1.13474
cg2264768	NAV2	FOXP3 [T	476	481	0	GTTGTG	1.46484	1.47315
cg2264768	NAV2	FOXP3 [T	737	742	0	GTTGTT	1.46484	1.47315
cg2264768	NAV2	FOXP3 [T	1483	1488	0	GTTGTT	1.46484	1.47315
cg2264768	NAV2	GR-beta [T	98	102	0	AATGT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	142	146	0	ACATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	175	179	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	348	352	0	ACATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	429	433	0	AATGT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	443	447	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	515	519	0	AATGT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	524	528	0	AATGT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	591	595	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	750	754	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	751	755	0	AATTT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	976	980	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1013	1017	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1144	1148	0	ACATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1246	1250	0	AATGT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1263	1267	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1347	1351	0	AATGT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1545	1549	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1670	1674	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1687	1691	0	AATGT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1701	1705	0	AATTT	3.90625	3.99611
cg2264768	NAV2	GR-beta [T	1825	1829	0	AAATT	3.90625	3.99611
cg2264768	NAV2	GR [T050	18	24	0	TTTTTTG	0.36621	0.37562
cg2264768	NAV2	GR [T050	63	69	0	TTTTTTG	0.36621	0.37562
cg2264768	NAV2	GR [T050	90	96	0	CTTTTTG	0.36621	0.37562
cg2264768	NAV2	GR [T050	723	729	0	TTTTTTG	0.36621	0.37562
cg2264768	NAV2	GR [T050	896	902	0	CAAAAA	0.36621	0.37562
cg2264768	NAV2	GR [T050	1009	1015	0	CAAAAA	0.36621	0.37562
cg2264768	NAV2	IRF-2 [T0	252	257	0	TCACTT	0.48828	0.49387
cg2264768	NAV2	IRF-2 [T0	869	874	0	TCACTT	0.48828	0.49387
cg2264768	NAV2	HOXD9 [T	1665	1674	0	AATAAA	0.01144	0.01207
cg2264768	NAV2	HOXD10 [	1665	1674	0	AATAAA	0.01144	0.01207
cg2105276	NAV2	GR-alpha [	3	7	0	ACAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	349	353	0	ACAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	657	661	0	ATAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1270	1274	0	ACAGG	7.8125	7.81264

cg2105276	NAV2	GR-alpha [	1328	1332	0	ACAGG	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1446	1450	0	CCTAT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1595	1599	0	CCTAT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1870	1874	0	CCTAT	7.8125	7.81264
cg2105276	NAV2	GR-alpha [	1926	1930	0	ATAGG	7.8125	7.81264
cg2105276	NAV2	AP-2alpha	831	836	0	GCAGGC	0.97656	0.95305
cg2105276	NAV2	AP-2alpha	861	866	0	GCCTGC	0.97656	0.95305
cg2105276	NAV2	XBP-1 [T	653	658	0	AGTCAT	0.97656	0.98127
cg2105276	NAV2	XBP-1 [T	669	674	0	ATGACT	0.97656	0.98127
cg2105276	NAV2	XBP-1 [T	788	793	0	AGTCAT	0.97656	0.98127
cg2105276	NAV2	XBP-1 [T	911	916	0	ATGACT	0.97656	0.98127
cg2105276	NAV2	Pax-5 [T0	465	471	0	CATGCC	1.09863	1.06846
cg2105276	NAV2	Pax-5 [T0	487	493	0	CATGCC	1.09863	1.06846
cg2105276	NAV2	Pax-5 [T0	570	576	0	CCTGCC	1.09863	1.06846
cg2105276	NAV2	Pax-5 [T0	728	734	0	GGGCAG	1.09863	1.06846
cg2105276	NAV2	Pax-5 [T0	1199	1205	0	GGGCAG	1.09863	1.06846
cg2105276	NAV2	Pax-5 [T0	1982	1988	0	CCAGCC	1.09863	1.06846
cg2105276	NAV2	p53 [T006	465	471	0	CATGCC	0.36621	0.35912
cg2105276	NAV2	p53 [T006	487	493	0	CATGCC	0.36621	0.35912
cg2105276	NAV2	p53 [T006	570	576	0	CCTGCC	0.36621	0.35912
cg2105276	NAV2	p53 [T006	728	734	0	GGGCAG	0.36621	0.35912
cg2105276	NAV2	p53 [T006	1199	1205	0	GGGCAG	0.36621	0.35912
cg2105276	NAV2	TFII-I [T0	353	358	0	GGAAAG	1.46484	1.45997
cg2105276	NAV2	TFII-I [T0	1107	1112	0	GGAAAG	1.46484	1.45997
cg2105276	NAV2	STAT4 [T	329	334	0	GGAAAT	0.48828	0.49387
cg2105276	NAV2	STAT4 [T	1449	1454	0	ATTTCC	0.48828	0.49387
cg2105276	NAV2	c-Ets-1 [T	506	512	0	CTTCCTC	0.24414	0.2429
cg2105276	NAV2	YY1 [T00	34	37	0	CCAT	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	155	158	0	CCAT	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	157	160	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	393	396	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	710	713	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	716	719	0	CCAT	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	777	780	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	792	795	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	800	803	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1056	1059	0	CCAT	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1367	1370	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1690	1693	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1711	1714	0	CCAT	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1751	1754	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1766	1769	0	CCAT	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1819	1822	0	ATGG	7.8125	7.81711
cg2105276	NAV2	YY1 [T00	1948	1951	0	CCAT	7.8125	7.81711
cg2105276	NAV2	ER-alpha [	1692	1696	0	GGTCA	1.95312	1.9404
cg2105276	NAV2	GATA-1 [	164	169	0	CAGATA	0.97656	0.98738
cg2105276	NAV2	GATA-1 [	848	853	0	TATCTG	0.97656	0.98738
cg2105276	NAV2	C/EBPbeta	48	51	0	ACAA	15.625	15.71349

cg2105276	NAV2	C/EBPbeta	140	143	0	GCAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	385	388	0	TTGC	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	389	392	0	ACAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	440	443	0	TTGC	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	480	483	0	ACAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	518	521	0	ACAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	525	528	0	TTGC	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	595	598	0	GCAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	647	650	0	GCAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	819	822	0	ACAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	922	925	0	TTGT	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	970	973	0	GCAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1121	1124	0	TTGT	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1150	1153	0	TTGT	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1161	1164	0	TTGC	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1494	1497	0	TTGC	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1509	1512	0	GCAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1546	1549	0	ACAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1681	1684	0	TTGC	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1841	1844	0	ACAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1877	1880	0	GCAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1890	1893	0	GCAA	15.625	15.71349
cg2105276	NAV2	C/EBPbeta	1895	1898	0	TTGC	15.625	15.71349
cg2105276	NAV2	NF-1 [T00	1051	1058	0	TTGGCC	0.12207	0.11983
cg2105276	NAV2	NF-1 [T00	1377	1384	0	TGGGCC	0.12207	0.11983
cg2105276	NAV2	NF-1 [T00	1630	1637	0	TTGGGC	0.12207	0.11983
cg2105276	NAV2	AP-1 [T00	892	900	0	GCTGAG	0.03052	0.03051
cg2105276	NAV2	c-Jun [T00	651	657	0	TGAGTC	0.12207	0.12266
cg2105276	NAV2	c-Jun [T00	894	900	0	TGAGTC	0.12207	0.12266
cg2105276	NAV2	c-Jun [T00	912	918	0	TGACTC	0.12207	0.12266
cg2105276	NAV2	TFIID [T0	148	154	0	TTGAAA	1.09863	1.13474
cg2105276	NAV2	TFIID [T0	529	535	0	TTTTCAA	1.09863	1.13474
cg2105276	NAV2	TFIID [T0	1903	1909	0	TTGAAA	1.09863	1.13474
cg2105276	NAV2	FOXP3 [T	921	926	0	GTTGTT	1.46484	1.47315
cg2105276	NAV2	FOXP3 [T	1149	1154	0	GTTGTC	1.46484	1.47315
cg2105276	NAV2	GR-beta [	42	46	0	AAATT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	143	147	0	AATGT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	382	386	0	AAATT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	401	405	0	AATGT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	1661	1665	0	AATGT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	1678	1682	0	AAATT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	1771	1775	0	AAATT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	1823	1827	0	AATTT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	1860	1864	0	AATTT	3.90625	3.99611
cg2105276	NAV2	GR-beta [	1892	1896	0	AATTT	3.90625	3.99611
cg2105276	NAV2	PR B [T00	1145	1151	0	CACTGT	0.36621	0.36944
cg2105276	NAV2	PR B [T00	1792	1798	0	TACTGT	0.36621	0.36944
cg2105276	NAV2	PR A [T01	1145	1151	0	CACTGT	0.36621	0.36944

cg2105276	NAV2	PR A [T01	1792	1798	0	TACTGT	0.36621	0.36944
cg2105276	NAV2	IRF-2 [T0	1776	1781	0	AAGTGA	0.48828	0.49387
cg2105276	NAV2	c-Myc [T0	899	904	0	CACGTG	0.48828	0.48199
cg2758514	NBAS	NF-AT2 [	1760	1769	9.873347	ATTATT	0.08774	0.08205
cg2758514	NBAS	XBP-1 [T	30	35	9.789909	ATGGCT	1.95312	1.94901
cg2758514	NBAS	PR B [T00	358	364	9.743489	AACACC	1.09863	1.0981
cg2758514	NBAS	PR B [T00	956	962	9.743489	AACACA	1.09863	1.0981
cg2758514	NBAS	PR B [T00	968	974	9.743489	TTGTGT	1.09863	1.0981
cg2758514	NBAS	PR B [T00	1042	1048	9.743489	AACACA	1.09863	1.0981
cg2758514	NBAS	PR B [T00	1646	1652	9.743489	AACACA	1.09863	1.0981
cg2758514	NBAS	PR A [T01	358	364	9.743489	AACACC	1.09863	1.0981
cg2758514	NBAS	PR A [T01	956	962	9.743489	AACACA	1.09863	1.0981
cg2758514	NBAS	PR A [T01	968	974	9.743489	TTGTGT	1.09863	1.0981
cg2758514	NBAS	PR A [T01	1042	1048	9.743489	AACACA	1.09863	1.0981
cg2758514	NBAS	PR A [T01	1646	1652	9.743489	AACACA	1.09863	1.0981
cg2758514	NBAS	c-Myb [T0	1192	1199	9.729271	TAACTG	0.36621	0.34746
cg2758514	NBAS	RAR-alph	317	329	9.727162	ACCAAG	0.00125	0.00132
cg2758514	NBAS	LEF-1 [T0	459	466	9.72404	CTTTGC	0.21362	0.21229
cg2758514	NBAS	RAR-beta	1986	1995	9.622793	GGGGTT	0.21362	0.22369
cg2758514	NBAS	TFIID [T0	208	214	9.552105	TGGGAA	1.46484	1.37777
cg2758514	NBAS	TFIID [T0	590	596	9.552105	TGGGAA	1.46484	1.37777
cg2758514	NBAS	TFIID [T0	925	931	9.552105	TCCCAA	1.46484	1.37777
cg2758514	NBAS	TFIID [T0	1336	1342	9.552105	TTTCCC	1.46484	1.37777
cg2758514	NBAS	TFIID [T0	1573	1579	9.552105	TTTGCC	1.46484	1.37777
cg2758514	NBAS	TFIID [T0	1619	1625	9.552105	TGACAA	1.46484	1.37777
cg2758514	NBAS	TFIID [T0	1765	1771	9.552105	TTTCCC	1.46484	1.37777
cg2758514	NBAS	TFIID [T0	1767	1773	9.552105	TCCCAA	1.46484	1.37777
cg2758514	NBAS	Pax-5 [T0	705	711	9.552105	GTTGCC	1.46484	1.61918
cg2758514	NBAS	Pax-5 [T0	1845	1851	9.552105	GTTGCC	1.46484	1.61918
cg2758514	NBAS	NF-1 [T00	602	609	9.535536	TTGGCC	0.73242	0.74634
cg2758514	NBAS	NF-1 [T00	1506	1513	9.535536	CTGACC	0.73242	0.74634
cg2758514	NBAS	FOXP3 [T	299	304	9.512894	GTTGCT	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	347	352	9.512894	GGCAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	355	360	9.512894	AATAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	705	710	9.512894	GTTGCC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	822	827	9.512894	CTAAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	934	939	9.512894	GTTGGG	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	953	958	9.512894	ACCAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	994	999	9.512894	GCCAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1039	1044	9.512894	GCCAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1127	1132	9.512894	GTTCTG	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1141	1146	9.512894	GTTATT	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1273	1278	9.512894	GAGAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1316	1321	9.512894	CCCAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1321	1326	9.512894	CAGAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1385	1390	9.512894	GTTGGT	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1393	1398	9.512894	ATAAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1420	1425	9.512894	GTTATT	7.32422	7.22156

cg2758514	NBAS	FOXP3 [T	1509	1514	9.512894	ACCAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1551	1556	9.512894	CCCAAC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1610	1615	9.512894	GTTCTT	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1658	1663	9.512894	GTTTAT	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1845	1850	9.512894	GTTGCC	7.32422	7.22156
cg2758514	NBAS	FOXP3 [T	1989	1994	9.512894	GTTGGT	7.32422	7.22156
cg2758514	NBAS	TFII-I [T0	68	73	9.512894	TTGTCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	216	221	9.512894	GGACTT	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	449	454	9.512894	AATTCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	494	499	9.512894	AAATCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1073	1078	9.512894	TTTTCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1186	1191	9.512894	AAATCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1266	1271	9.512894	GTTTCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1366	1371	9.512894	CCATCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1547	1552	9.512894	TTGTCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1559	1564	9.512894	GGACTT	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1595	1600	9.512894	TTTTCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1635	1640	9.512894	GGAAAA	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1764	1769	9.512894	TTTTCC	7.32422	7.44385
cg2758514	NBAS	TFII-I [T0	1915	1920	9.512894	GGACAA	7.32422	7.44385
cg2758514	NBAS	TCF-4E [T	1602	1608	9.453578	CTTTGA	0.48828	0.46934
cg2758514	NBAS	c-Jun [T00	1483	1489	9.397655	ATTGTC	0.73242	0.7366
cg2758514	NBAS	MEF-2A [	1713	1723	9.220261	GTCTAA	0.07343	0.06466
cg2758514	NBAS	AP-1 [T00	132	140	9.168921	CTTTAG	0.24414	0.23028
cg2758514	NBAS	c-Ets-1 [T	266	272	9.020687	GGGGAA	0.85449	0.84987
cg2758514	NBAS	NF-AT2 [	1069	1078	8.984657	CTTTTTT	0.05341	0.05145
cg2758514	NBAS	GR [T050	472	478	8.971049	CAAAAT	0.61035	0.5928
cg2758514	NBAS	GR [T050	1014	1020	8.971049	CAAAAG	0.61035	0.5928
cg2758514	NBAS	GR [T050	1972	1978	8.971049	GCTTTT	0.61035	0.5928
cg2758514	NBAS	NFI/CTF [	143	150	8.814757	CCAAGA	0.48828	0.48845
cg2758514	NBAS	NFI/CTF [	318	325	8.814757	CCAAGT	0.48828	0.48845
cg2758514	NBAS	NF-1 [T00	923	930	8.790071	CCTCCC	0.24414	0.24339
cg2758514	NBAS	NF-1 [T00	1765	1772	8.790071	TTTCCC	0.24414	0.24339
cg2758514	NBAS	AR [T000	65	73	8.762682	CTCTTGT	0.04578	0.04758
cg2758514	NBAS	XBP-1 [T	8	13	8.75604	ATGAGA	2.92969	2.75329
cg2758514	NBAS	XBP-1 [T	169	174	8.75604	TCTCAT	2.92969	2.75329
cg2758514	NBAS	XBP-1 [T	949	954	8.75604	ATGAAC	2.92969	2.75329
cg2758514	NBAS	XBP-1 [T	972	977	8.75604	GTTCAT	2.92969	2.75329
cg2758514	NBAS	XBP-1 [T	1096	1101	8.75604	ATGAAA	2.92969	2.75329
cg2758514	NBAS	XBP-1 [T	1739	1744	8.75604	GCTCAT	2.92969	2.75329
cg2758514	NBAS	XBP-1 [T	1993	1998	8.75604	GTTCAT	2.92969	2.75329
cg2758514	NBAS	c-Myb [T0	1700	1707	8.728118	GTAAGT	0.30518	0.28602
cg2758514	NBAS	STAT1bet	276	285	8.695301	GGCTGG	0.22316	0.2175
cg2758514	NBAS	STAT1bet	1335	1344	8.695301	CTTTCC	0.22316	0.2175
cg2758514	NBAS	c-Jun [T00	586	592	8.571705	TGACTG	0.12207	0.1249
cg2758514	NBAS	RAR-beta	118	127	8.541284	CACTAA	0.26703	0.27434
cg2758514	NBAS	USF2 [T0	956	965	8.532138	AACACA	0.103	0.10815
cg2758514	NBAS	c-Ets-1 [T	1283	1289	8.501115	TTGGAA	0.24414	0.23702

cg2758514	NBAS	HNF-3alph	571	578	8.343064	CTAAAAT	0.27466	0.23078
cg2758514	NBAS	HNF-3alph	1143	1150	8.343064	TATTTCA	0.27466	0.23078
cg2758514	NBAS	HNF-3alph	1230	1237	8.343064	CTAAAAT	0.27466	0.23078
cg2758514	NBAS	HNF-3alph	1798	1805	8.343064	TATTTTA	0.27466	0.23078
cg2758514	NBAS	HNF-3alph	1894	1901	8.343064	TATTTGA	0.27466	0.23078
cg2758514	NBAS	HNF-3alph	1961	1968	8.343064	TTAAAAT	0.27466	0.23078
cg2758514	NBAS	PR B [T00	295	301	8.338824	GCCTGTT	1.09863	1.09384
cg2758514	NBAS	PR B [T00	855	861	8.338824	AACAGG	1.09863	1.09384
cg2758514	NBAS	PR B [T00	1090	1096	8.338824	AACAGA	1.09863	1.09384
cg2758514	NBAS	PR B [T00	1287	1293	8.338824	AACAGA	1.09863	1.09384
cg2758514	NBAS	PR B [T00	1319	1325	8.338824	AACAGA	1.09863	1.09384
cg2758514	NBAS	PR B [T00	1554	1560	8.338824	AACAGG	1.09863	1.09384
cg2758514	NBAS	PR A [T01	295	301	8.338824	GCCTGTT	1.09863	1.09384
cg2758514	NBAS	PR A [T01	855	861	8.338824	AACAGG	1.09863	1.09384
cg2758514	NBAS	PR A [T01	1090	1096	8.338824	AACAGA	1.09863	1.09384
cg2758514	NBAS	PR A [T01	1287	1293	8.338824	AACAGA	1.09863	1.09384
cg2758514	NBAS	PR A [T01	1319	1325	8.338824	AACAGA	1.09863	1.09384
cg2758514	NBAS	PR A [T01	1554	1560	8.338824	AACAGG	1.09863	1.09384
cg2758514	NBAS	E2F-1 [T0	1137	1144	8.336446	GCGGGTT	0.15259	0.16676
cg2758514	NBAS	GR-alpha [	39	43	8.281568	CCTTC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	530	534	8.281568	CCTTG	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	583	587	8.281568	CCTTG	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	750	754	8.281568	CCTCG	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	756	760	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	775	779	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	788	792	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	910	914	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	923	927	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	1077	1081	8.281568	CCTTC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	1115	1119	8.281568	CAAGG	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	1226	1230	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	1252	1256	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	1255	1259	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	1326	1330	8.281568	CCTTC	7.8125	8.20394
cg2758514	NBAS	GR-alpha [	1357	1361	8.281568	CCTCC	7.8125	8.20394
cg2758514	NBAS	HOXD9 [T	355	364	8.224939	AATAACA	0.08774	0.0777
cg2758514	NBAS	HOXD9 [T	1624	1633	8.224939	AATATAA	0.08774	0.0777
cg2758514	NBAS	HOXD10 [	355	364	8.224939	AATAACA	0.08774	0.0777
cg2758514	NBAS	HOXD10 [	1624	1633	8.224939	AATATAA	0.08774	0.0777
cg2758514	NBAS	NF-1 [T00	560	567	8.191058	GAGCCCA	0.24414	0.24485
cg2758514	NBAS	NF-1 [T00	1313	1320	8.191058	AAGCCCA	0.24414	0.24485
cg2758514	NBAS	NF-AT1 [T	1592	1600	8.12076	GTATTTT	0.1297	0.12846
cg2758514	NBAS	LEF-1 [T0	1145	1152	8.117221	TTTCAAA	0.12207	0.11275
cg2758514	NBAS	LEF-1 [T0	1602	1609	8.117221	CTTTGAC	0.12207	0.11275
cg2758514	NBAS	VDR [T00	884	892	8.079962	GTCTTGA	0.24414	0.22992
cg2758514	NBAS	IRF-1 [T0	276	284	8.078284	GGCTGGA	0.25177	0.2462
cg2758514	NBAS	GR-alpha [	125	129	8.073878	CCTGG	7.8125	8.20289
cg2758514	NBAS	GR-alpha [	263	267	8.073878	CCTGG	7.8125	8.20289

cg2758514 NBAS	GR-alpha [	366	370	8.073878	CCTGC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	375	379	8.073878	CCTAC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	395	399	8.073878	CCTAC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	406	410	8.073878	CCTGC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	453	457	8.073878	CCTGC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	499	503	8.073878	CCTAC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	760	764	8.073878	CCAGG	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	805	809	8.073878	CCTAC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	827	831	8.073878	CCTGG	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	876	880	8.073878	CCAGG	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	894	898	8.073878	CCTGG	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	913	917	8.073878	CCTGC	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	962	966	8.073878	CCTGG	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	1350	1354	8.073878	CCTAG	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	1577	1581	8.073878	CCAGG	7.8125	8.20289
cg2758514 NBAS	GR-alpha [	1904	1908	8.073878	GTAGG	7.8125	8.20289
cg2758514 NBAS	TFIID [T0	80	86	8.014558	TCACAA	2.19727	1.99811
cg2758514 NBAS	TFIID [T0	221	227	8.014558	TAAGAA	2.19727	1.99811
cg2758514 NBAS	TFIID [T0	235	241	8.014558	TATCAA	2.19727	1.99811
cg2758514 NBAS	TFIID [T0	1145	1151	8.014558	TTTCAA	2.19727	1.99811
cg2758514 NBAS	TFIID [T0	1377	1383	8.014558	TTTGTTA	2.19727	1.99811
cg2758514 NBAS	TFIID [T0	1517	1523	8.014558	TTTGAA	2.19727	1.99811
cg2758514 NBAS	TFIID [T0	1778	1784	8.014558	TTAGAA	2.19727	1.99811
cg2758514 NBAS	TFIID [T0	1788	1794	8.014558	TTTCTTA	2.19727	1.99811
cg2758514 NBAS	Pax-5 [T0	411	417	8.014558	GCTGCC	2.19727	2.42766
cg2758514 NBAS	Pax-5 [T0	559	565	8.014558	TGAGCC	2.19727	2.42766
cg2758514 NBAS	Pax-5 [T0	657	663	8.014558	TGTGCC	2.19727	2.42766
cg2758514 NBAS	Pax-5 [T0	802	808	8.014558	GGGCCT	2.19727	2.42766
cg2758514 NBAS	Pax-5 [T0	1110	1116	8.014558	GGGCTC	2.19727	2.42766
cg2758514 NBAS	Pax-5 [T0	1345	1351	8.014558	GAAGCC	2.19727	2.42766
cg2758514 NBAS	ETF [T002	1354	1364	7.870358	GCCCCT	0.07153	0.08737
cg2758514 NBAS	c-Ets-2 [T	1268	1276	7.84116	TTCCTG	0.32043	0.30792
cg2758514 NBAS	c-Ets-2 [T	15	23	7.76635	ACATAG	0.32043	0.30792
cg2758514 NBAS	NF-AT1 [	592	600	7.744746	GGAAAG	0.19836	0.19379
cg2758514 NBAS	c-Myb [T0	1123	1130	7.739476	CACAGT	0.42725	0.40917
cg2758514 NBAS	NFI/CTF [	1769	1776	7.587343	CCAAAA	0.36621	0.36269
cg2758514 NBAS	c-Myb [T0	1238	1245	7.545286	AAACTG	0.42725	0.40917
cg2758514 NBAS	PPAR-alph	124	134	7.529496	CCCTGG	0.04482	0.04884
cg2758514 NBAS	GR [T050	54	60	7.527031	TCTTTG	1.83105	1.71535
cg2758514 NBAS	GR [T050	176	182	7.527031	ATGTTT	1.83105	1.71535
cg2758514 NBAS	GR [T050	353	359	7.527031	CAAATA	1.83105	1.71535
cg2758514 NBAS	GR [T050	853	859	7.527031	CAAACA	1.83105	1.71535
cg2758514 NBAS	GR [T050	928	934	7.527031	CAAAAT	1.83105	1.71535
cg2758514 NBAS	GR [T050	1023	1029	7.527031	CAAAAT	1.83105	1.71535
cg2758514 NBAS	GR [T050	1622	1628	7.527031	CAAATA	1.83105	1.71535
cg2758514 NBAS	GR [T050	1650	1656	7.527031	CAAAAT	1.83105	1.71535
cg2758514 NBAS	GR [T050	1770	1776	7.527031	CAAAAG	1.83105	1.71535
cg2758514 NBAS	GR [T050	1893	1899	7.527031	TTATTT	1.83105	1.71535

cg2758514	NBAS	RAR-beta	82	91	7.47824	ACAAAA	0.24414	0.25121
cg2758514	NBAS	IRF-1 [T0	1267	1275	7.477948	TTTCCT	0.14496	0.14723
cg2758514	NBAS	MAZ [T00	1354	1366	7.461929	GCCCCT	0.00641	0.00703
cg2758514	NBAS	HNF-4alp	1148	1160	7.282735	CAAAGT	0.0051	0.00479
cg2758514	NBAS	HOXD9 [	110	119	7.270719	AATATA	0.06866	0.05771
cg2758514	NBAS	HOXD10 [	110	119	7.270719	AATATA	0.06866	0.05771
cg2758514	NBAS	c-Ets-2 [T	451	459	7.268173	TTCCTG	0.09155	0.08977
cg2758514	NBAS	p53 [T006	129	135	7.266844	GGGCTT	0.73242	0.79826
cg2758514	NBAS	p53 [T006	1312	1318	7.266844	AAAGCC	0.73242	0.79826
cg2758514	NBAS	GATA-3 [	1044	1055	7.242732	CACACT	0.01121	0.0108
cg2758514	NBAS	c-Ets-1 [T	208	214	7.199436	TGGGAA	0.73242	0.73732
cg2758514	NBAS	c-Ets-1 [T	590	596	7.199436	TGGGAA	0.73242	0.73732
cg2758514	NBAS	c-Ets-1 [T	1336	1342	7.199436	TTTCCC	0.73242	0.73732
cg2758514	NBAS	c-Ets-1 [T	1765	1771	7.199436	TTTCCC	0.73242	0.73732
cg2758514	NBAS	XBP-1 [T	173	178	7.172312	ATGATG	2.92969	2.7512
cg2758514	NBAS	XBP-1 [T	1532	1537	7.172312	ATGAAG	2.92969	2.7512
cg2758514	NBAS	AR [T000	1981	1989	7.107265	GGACAG	0.23651	0.23986
cg2758514	NBAS	NF-AT1 [	1761	1769	7.095752	TTATTT	0.15259	0.14325
cg2758514	NBAS	NFI/CTF [	1510	1517	7.014249	CCAACC	0.73242	0.74795
cg2758514	NBAS	NFI/CTF [	1986	1993	7.014249	GGGGTT	0.73242	0.74795
cg2758514	NBAS	NF-AT2 [	1635	1644	7.008591	GGAAAA	0.04578	0.04306
cg2758514	NBAS	HNF-3alp	673	680	7.000129	TATTTA	0.82397	0.71909
cg2758514	NBAS	HNF-3alp	677	684	7.000129	TATTTA	0.82397	0.71909
cg2758514	NBAS	HNF-3alp	975	982	7.000129	CATTTT	0.82397	0.71909
cg2758514	NBAS	HNF-3alp	1022	1029	7.000129	ACAAAA	0.82397	0.71909
cg2758514	NBAS	HNF-3alp	1593	1600	7.000129	TATTTC	0.82397	0.71909
cg2758514	NBAS	HNF-3alp	1762	1769	7.000129	TATTTC	0.82397	0.71909
cg2758514	NBAS	HNF-3alp	1921	1928	7.000129	AAAAAA	0.82397	0.71909
cg2758514	NBAS	IRF-1 [T0	206	214	6.968314	TCTGGG	0.1297	0.12685
cg2758514	NBAS	IRF-1 [T0	1765	1773	6.968314	TTTCCC	0.1297	0.12685
cg2758514	NBAS	NF-1 [T00	950	957	6.948522	TGAACC	0.48828	0.50205
cg2758514	NBAS	NF-1 [T00	991	998	6.948522	GGAGCC	0.48828	0.50205
cg2758514	NBAS	NF-1 [T00	1107	1114	6.948522	TTGGGG	0.48828	0.50205
cg2758514	NBAS	NF-1 [T00	1990	1997	6.948522	TTGGTT	0.48828	0.50205
cg2758514	NBAS	GATA-3 [	93	104	6.948196	ACCACT	0.01121	0.0108
cg2758514	NBAS	c-Ets-1 [T	1596	1602	6.943262	TTTCCC	0.73242	0.73732
cg2758514	NBAS	c-Ets-1 [T	1633	1639	6.943262	GGGGAA	0.73242	0.73732
cg2758514	NBAS	ENKTF-1	603	610	6.942764	TGGCCG	1.46484	1.56616
cg2758514	NBAS	ENKTF-1	876	883	6.942764	CCAGGC	1.46484	1.56616
cg2758514	NBAS	VDR [T00	946	954	6.925682	GGCATG	0.42725	0.41
cg2758514	NBAS	VDR [T00	972	980	6.925682	GTTCAT	0.42725	0.41
cg2758514	NBAS	c-Jun [T00	1507	1513	6.856451	TGACCA	0.73242	0.73062
cg2758514	NBAS	C/EBPalp	1242	1248	6.85549	TGCAAT	0.73242	0.68282
cg2758514	NBAS	c-Jun [T00	1977	1983	6.787369	TGACGG	0.73242	0.73062
cg2758514	NBAS	NFI/CTF [	598	605	6.786076	CTGCTT	0.73242	0.74795
cg2758514	NBAS	NFI/CTF [	710	717	6.786076	CCAAGC	0.73242	0.74795
cg2758514	NBAS	p53 [T006	559	565	6.778774	TGAGCC	1.09863	1.22478
cg2758514	NBAS	p53 [T006	1110	1116	6.778774	GGGCTC	1.09863	1.22478

cg2758514	NBAS	AR [T000	1544	1552	6.760234	TTTTTGT	0.23651	0.23986
cg2758514	NBAS	AR [T000	1915	1923	6.760234	GGACAA	0.23651	0.23986
cg2758514	NBAS	NF-1 [T00	706	713	6.722386	TTGCCC	0.24414	0.2565
cg2758514	NBAS	PXR-1:RX	969	976	6.668182	TGTGTT	0.24414	0.23169
cg2758514	NBAS	GATA-2 [	26	34	6.666667	GGATAT	0.24414	0.2357
cg2758514	NBAS	FOXP3 [T	1236	1241	6.581441	TAAAAC	0.97656	0.904
cg2758514	NBAS	FOXP3 [T	1775	1780	6.581441	GTTTTA	0.97656	0.904
cg2758514	NBAS	FOXP3 [T	1853	1858	6.581441	TTCAAC	0.97656	0.904
cg2758514	NBAS	FOXP3 [T	1884	1889	6.581441	TAAAAC	0.97656	0.904
cg2758514	NBAS	TFII-I [T0	252	257	6.581441	GGAGTG	0.97656	0.9991
cg2758514	NBAS	TFII-I [T0	717	722	6.581441	GGAGTG	0.97656	0.9991
cg2758514	NBAS	p53 [T006	1345	1351	6.563521	GAAGCC	0.48828	0.54643
cg2758514	NBAS	XBP-1 [T0	1131	1136	6.478682	TGGCAT	0.97656	0.99906
cg2758514	NBAS	c-Myb [T0	1278	1285	6.454077	CTCAGT	0.30518	0.30272
cg2758514	NBAS	HOXD9 [	575	584	6.40726	AATAAA	0.01144	0.01024
cg2758514	NBAS	HOXD10 [	575	584	6.40726	AATAAA	0.01144	0.01024
cg2758514	NBAS	RelA [T00	1632	1642	6.340573	GGGGGA	0.01001	0.01051
cg2758514	NBAS	TCF-4E [	270	276	6.302385	AACAAA	0.61035	0.59686
cg2758514	NBAS	TCF-4E [	459	465	6.302385	CTTTGC	0.61035	0.59686
cg2758514	NBAS	TCF-4E [	1146	1152	6.302385	TTCAAA	0.61035	0.59686
cg2758514	NBAS	TCF-4E [	1522	1528	6.302385	AACAAA	0.61035	0.59686
cg2758514	NBAS	GR-alpha [	243	247	6.263098	TAAGG	3.90625	3.89624
cg2758514	NBAS	GR-alpha [	335	339	6.263098	TAAGG	3.90625	3.89624
cg2758514	NBAS	GR-alpha [	917	921	6.263098	CCTCA	3.90625	3.89624
cg2758514	NBAS	GR-alpha [	988	992	6.263098	TGAGG	3.90625	3.89624
cg2758514	NBAS	GR-alpha [	1398	1402	6.263098	CCTTA	3.90625	3.89624
cg2758514	NBAS	GR-alpha [	1641	1645	6.263098	CCTTA	3.90625	3.89624
cg2758514	NBAS	SRY [T00	1144	1152	6.176442	ATTTCA	0.15259	0.14742
cg2758514	NBAS	c-Jun [T00	1619	1625	6.152811	TGACAA	0.36621	0.34478
cg2758514	NBAS	c-Fos [T00	794	803	6.103724	GAGTCA	0.09155	0.09198
cg2758514	NBAS	GR-alpha [	464	468	6.055408	CCTAA	3.90625	3.89835
cg2758514	NBAS	GR-alpha [	512	516	6.055408	TCAGG	3.90625	3.89835
cg2758514	NBAS	GR-alpha [	570	574	6.055408	CCTAA	3.90625	3.89835
cg2758514	NBAS	GR-alpha [	983	987	6.055408	TTAGG	3.90625	3.89835
cg2758514	NBAS	GR-alpha [	1190	1194	6.055408	CCTAA	3.90625	3.89835
cg2758514	NBAS	GR-alpha [	1229	1233	6.055408	CCTAA	3.90625	3.89835
cg2758514	NBAS	GR-alpha [	1270	1274	6.055408	CCTGA	3.90625	3.89835
cg2758514	NBAS	GR-alpha [	1505	1509	6.055408	CCTGA	3.90625	3.89835
cg2758514	NBAS	c-Ets-1 [T	278	284	6.039428	CTGGAA	0.36621	0.36174
cg2758514	NBAS	NF-AT2 [	1331	1340	6.002309	TATACT	0.04196	0.03934
cg2758514	NBAS	p53 [T006	802	808	5.883561	GGGCCT	0.61035	0.68483
cg2758514	NBAS	AR [T000	812	820	5.86144	GGACAT	0.24414	0.25115
cg2758514	NBAS	C/EBPalph	1486	1492	5.850545	GTCAAT	0.97656	0.91422
cg2758514	NBAS	STAT1bet	588	597	5.796867	ACTGGG	0.1545	0.14881
cg2758514	NBAS	c-Jun [T00	1066	1072	5.783074	TGACTT	0.36621	0.34478
cg2758514	NBAS	C/EBPalph	1482	1488	5.781231	TATTGT	0.97656	0.91422
cg2758514	NBAS	VDR [T00	764	772	5.771401	GTTCAA	0.42725	0.41266
cg2758514	NBAS	PPAR-alph	871	881	5.741676	ATGACC	0.03529	0.03856

cg2758514	NBAS	NFI/CTF [	564	571	5.558661	CCAAAC	0.54932	0.55504
cg2758514	NBAS	TFIID [T0	434	440	5.544826	TTTACC	0.73242	0.65314
cg2758514	NBAS	TFIID [T0	1079	1085	5.544826	TTCTAA	0.73242	0.65314
cg2758514	NBAS	TFIID [T0	1228	1234	5.544826	TCCTAA	0.73242	0.65314
cg2758514	NBAS	TFIID [T0	1691	1697	5.544826	TTTATC	0.73242	0.65314
cg2758514	NBAS	TFIID [T0	1744	1750	5.544826	TGTTAA	0.73242	0.65314
cg2758514	NBAS	TFIID [T0	1777	1783	5.544826	TTTAGA	0.73242	0.65314
cg2758514	NBAS	NF-AT1 [	279	288	5.512555	TGGAAA	0.05913	0.05666
cg2758514	NBAS	HOXD9 [	1683	1692	5.453039	ATCTTTT	0.04578	0.03952
cg2758514	NBAS	HOXD10 [	1683	1692	5.453039	ATCTTTT	0.04578	0.03952
cg2758514	NBAS	C/EBPalph	1887	1893	5.38654	AACAAT	0.73242	0.68229
cg2758514	NBAS	AP-1 [T00	791	799	5.321703	CCAGAG	0.09155	0.08822
cg2758514	NBAS	MEF-2A [	568	578	5.321562	ACCCTA	0.02003	0.01733
cg2758514	NBAS	EBF [T05	122	132	5.295103	AACCCT	0.01907	0.0226
cg2758514	NBAS	HOXD9 [	836	845	5.275652	CTTTTTT	0.04578	0.03952
cg2758514	NBAS	HOXD10 [	836	845	5.275652	CTTTTTT	0.04578	0.03952
cg2758514	NBAS	RXR-alph	1360	1366	5.271235	CCCACC	0.61035	0.65415
cg2758514	NBAS	C/EBPalph	107	113	5.240291	GGCAAT	0.97656	0.90302
cg2758514	NBAS	GR [T050	83	89	5.207533	CAAAAC	0.24414	0.24013
cg2758514	NBAS	c-Jun [T00	1436	1442	5.193102	TGACTT	0.61035	0.60573
cg2758514	NBAS	NF-AT1 [	1070	1078	5.125037	TTTTTTT	0.05341	0.05073
cg2758514	NBAS	AP-2alpha	188	193	5.100982	GCCTTT	0.97656	0.97517
cg2758514	NBAS	AP-2alpha	273	278	5.100982	AAAGGC	0.97656	0.97517
cg2758514	NBAS	AP-2alpha	1083	1088	5.100982	AAAGGC	0.97656	0.97517
cg2758514	NBAS	HNF-1B [	1419	1427	5.077773	AGTTAT	0.04578	0.0409
cg2758514	NBAS	USF2 [T0	400	409	5.052423	CACTCA	0.103	0.10797
cg2758514	NBAS	USF2 [T0	1499	1508	5.052423	CAGGCA	0.103	0.10797
cg2758514	NBAS	GR-beta [	495	499	5.042296	AATCC	3.90625	3.7093
cg2758514	NBAS	GR-beta [	672	676	5.042296	GTATT	3.90625	3.7093
cg2758514	NBAS	GR-beta [	772	776	5.042296	AATCC	3.90625	3.7093
cg2758514	NBAS	GR-beta [	907	911	5.042296	AATCC	3.90625	3.7093
cg2758514	NBAS	GR-beta [	938	942	5.042296	GGATT	3.90625	3.7093
cg2758514	NBAS	GR-beta [	1187	1191	5.042296	AATCC	3.90625	3.7093
cg2758514	NBAS	GR-beta [	1592	1596	5.042296	GTATT	3.90625	3.7093
cg2758514	NBAS	RAR-beta:	1110	1121	4.98533	GGGCTC	0.00966	0.01077
cg2758514	NBAS	IRF-1 [T0	1631	1639	4.968836	AGGGGG	0.1297	0.12724
cg2758514	NBAS	XBP-1 [T	186	191	4.894955	ATGCCT	0.97656	0.99839
cg2758514	NBAS	XBP-1 [T	426	431	4.894955	CGGCAT	0.97656	0.99839
cg2758514	NBAS	XBP-1 [T	945	950	4.894955	AGGCAT	0.97656	0.99839
cg2758514	NBAS	AP-2alpha	463	468	4.890408	GCCTAA	0.97656	0.97517
cg2758514	NBAS	NF-1 [T00	1283	1290	4.880836	TTGGAA	0.24414	0.24345
cg2758514	NBAS	RXR-alph	370	376	4.86724	CATACC	0.48828	0.51407
cg2758514	NBAS	GCF [T00	409	417	4.846987	GCGCTG	0.27466	0.31905
cg2758514	NBAS	C/EBPalph	446	452	4.845599	ATCAAT	0.97656	0.90302
cg2758514	NBAS	HNF-3alph	1806	1813	4.842999	ATAAAA	0.09155	0.07438
cg2758514	NBAS	HNF-3alph	1812	1819	4.842999	TATTTA	0.09155	0.07438
cg2758514	NBAS	HNF-3alph	1828	1835	4.842999	ATAAAA	0.09155	0.07438
cg2758514	NBAS	HNF-1A [	1380	1387	4.828753	GTTAAG	0.36621	0.34064

cg2758514	NBAS	FOXP3 [T	83	88	4.756447	CAAAAC	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	467	472	4.756447	AAAAAC	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	479	484	4.756447	AAAAAC	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	505	510	4.756447	GTTTTT	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	1154	1159	4.756447	GAAAAC	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	1468	1473	4.756447	GTTTTT	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	1543	1548	4.756447	GTTTTT	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	1636	1641	4.756447	GAAAAC	2.92969	2.82
cg2758514	NBAS	FOXP3 [T	1839	1844	4.756447	GTTTTC	2.92969	2.82
cg2758514	NBAS	TFII-I [T0	20	25	4.756447	GGAATG	2.92969	2.89715
cg2758514	NBAS	TFII-I [T0	26	31	4.756447	GGATAT	2.92969	2.89715
cg2758514	NBAS	TFII-I [T0	210	215	4.756447	GGAAAT	2.92969	2.89715
cg2758514	NBAS	TFII-I [T0	280	285	4.756447	GGAAAT	2.92969	2.89715
cg2758514	NBAS	TFII-I [T0	771	776	4.756447	CAATCC	2.92969	2.89715
cg2758514	NBAS	TFII-I [T0	812	817	4.756447	GGACAT	2.92969	2.89715
cg2758514	NBAS	TFII-I [T0	897	902	4.756447	GGACTG	2.92969	2.89715
cg2758514	NBAS	TFII-I [T0	906	911	4.756447	CAATCC	2.92969	2.89715
cg2758514	NBAS	c-Myb [T0	1297	1304	4.754782	GTCAGT	0.30518	0.30087
cg2758514	NBAS	IRF-1 [T0	588	596	4.549799	ACTGGG	0.05341	0.05056
cg2758514	NBAS	IRF-1 [T0	1336	1344	4.549799	TTTCCC	0.05341	0.05056
cg2758514	NBAS	c-Ets-1 [T	18	24	4.539113	TAGGAA	0.85449	0.8381
cg2758514	NBAS	T3R-beta1	982	990	4.481316	ATTAGG	0.27466	0.27245
cg2758514	NBAS	STAT4 [T	20	25	4.411765	GGAATG	1.95312	1.99838
cg2758514	NBAS	c-Ets-1 [T	1861	1867	4.411026	ATTCCT	0.85449	0.8381
cg2758514	NBAS	NF-kappa	1633	1643	4.369436	GGGGAA	0.03242	0.03571
cg2758514	NBAS	HOXD9 [	1811	1820	4.321431	ATATTT	0.03433	0.02831
cg2758514	NBAS	HOXD10 [	1811	1820	4.321431	ATATTT	0.03433	0.02831
cg2758514	NBAS	RXR-alpha	322	328	4.24113	GTGACC	0.97656	1.02803
cg2758514	NBAS	AP-2alpha	804	809	4.211849	GCCTAC	0.97656	1.02535
cg2758514	NBAS	AP-2alpha	1904	1909	4.211849	GTAGGC	0.97656	1.02535
cg2758514	NBAS	GR-beta [	330	334	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	355	359	4.201913	AATAA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	475	479	4.201913	AATCA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	575	579	4.201913	AATAA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	676	680	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	680	684	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	841	845	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	980	984	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1101	1105	4.201913	AATAA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1142	1146	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1213	1217	4.201913	AATAA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1234	1238	4.201913	AATAA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1410	1414	4.201913	CTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1421	1425	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1426	1430	4.201913	AATCA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1481	1485	4.201913	CTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1653	1657	4.201913	AATAA	7.8125	7.23274
cg2758514	NBAS	GR-beta [	1688	1692	4.201913	TTATT	7.8125	7.23274

cg2758514	NBAS	GR-beta [T	1761	1765	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [T	1816	1820	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [T	1893	1897	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [T	1930	1934	4.201913	TGATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [T	1943	1947	4.201913	AATAA	7.8125	7.23274
cg2758514	NBAS	GR-beta [T	1951	1955	4.201913	TTATT	7.8125	7.23274
cg2758514	NBAS	GR-beta [T	1958	1962	4.201913	CTATT	7.8125	7.23274
cg2758514	NBAS	c-Ets-1 [T	450	456	4.154851	ATTCCTC	0.24414	0.23719
cg2758514	NBAS	POU2F2 (	1880	1890	4.120113	TCTTTAA	0.01717	0.01453
cg2758514	NBAS	TCF-4 [T0	1601	1610	4.102712	CCTTTGA	0.01144	0.0116
cg2758514	NBAS	PXR-1:RX	761	768	4.090374	CAGGTT	0.12207	0.12474
cg2758514	NBAS	RXR-alpha	390	396	4.019014	CACACC	0.97656	1.02803
cg2758514	NBAS	RXR-alpha	859	865	4.019014	GGGTCTT	0.97656	1.02803
cg2758514	NBAS	c-Ets-2 [T	1862	1870	4.017001	TTCCTTT	0.16022	0.15061
cg2758514	NBAS	TFIID [T0	979	985	4.007279	TTTATTA	1.09863	0.94722
cg2758514	NBAS	TFIID [T0	1584	1590	4.007279	TTTTAAA	1.09863	0.94722
cg2758514	NBAS	TFIID [T0	1612	1618	4.007279	TCTTAAA	1.09863	0.94722
cg2758514	NBAS	TFIID [T0	1790	1796	4.007279	TCTTAAA	1.09863	0.94722
cg2758514	NBAS	TFIID [T0	1940	1946	4.007279	TTTAATA	1.09863	0.94722
cg2758514	NBAS	TFIID [T0	1950	1956	4.007279	TTTATTA	1.09863	0.94722
cg2758514	NBAS	TFIID [T0	1959	1965	4.007279	TATTAAA	1.09863	0.94722
cg2758514	NBAS	Pax-5 [T0	129	135	4.007279	GGGCTTT	1.09863	1.18533
cg2758514	NBAS	Pax-5 [T0	1312	1318	4.007279	AAAGCC	1.09863	1.18533
cg2758514	NBAS	AP-2alpha	582	587	3.970052	GCCTTG	0.97656	1.02535
cg2758514	NBAS	p53 [T006	1351	1357	3.961937	CTAGCC	0.73242	0.82434
cg2758514	NBAS	c-Jun [T00	134	140	3.807346	TTAGTCA	0.24414	0.23729
cg2758514	NBAS	GR [T050	457	463	3.763516	CTCTTTC	0.73242	0.6946
cg2758514	NBAS	p53 [T006	416	422	3.750231	CCAGCC	0.73242	0.82434
cg2758514	NBAS	PPAR-alph	798	808	3.656974	CACTGG	0.01431	0.015
cg2758514	NBAS	HNF-3alph	229	236	3.500065	TCTAAAT	0.27466	0.23175
cg2758514	NBAS	HNF-3alph	681	688	3.500065	TATTTAC	0.27466	0.23175
cg2758514	NBAS	HNF-3alph	842	849	3.500065	TATTTTT	0.27466	0.23175
cg2758514	NBAS	HNF-3alph	1649	1656	3.500065	ACAAAA	0.27466	0.23175
cg2758514	NBAS	HNF-3alph	1780	1787	3.500065	AGAAAA	0.27466	0.23175
cg2758514	NBAS	GCF [T00	404	412	3.409768	CACCTG	0.03052	0.03366
cg2758514	NBAS	RXR-alpha	871	877	3.392904	ATGACC	1.09863	1.1653
cg2758514	NBAS	GR-beta [T	110	114	3.361531	AATAT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	227	231	3.361531	AATCT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	233	237	3.361531	AATAT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1462	1466	3.361531	AATCT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1624	1628	3.361531	AATAT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1682	1686	3.361531	AATCT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1720	1724	3.361531	AATAT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1784	1788	3.361531	AATAT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1785	1789	3.361531	ATATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1796	1800	3.361531	AATAT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1797	1801	3.361531	ATATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1810	1814	3.361531	AATAT	3.90625	3.51525

cg2758514	NBAS	GR-beta [T	1811	1815	3.361531	ATATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1832	1836	3.361531	AATAT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1859	1863	3.361531	ATATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1946	1950	3.361531	AATCT	3.90625	3.51525
cg2758514	NBAS	IRF-1 [T0	1596	1604	3.352297	TTTCCC	0.06866	0.0661
cg2758514	NBAS	GATA-2 [	94	102	3.333333	CCACTA	0.30518	0.29349
cg2758514	NBAS	PR B [T00	930	936	3.29756	AAATGT	0.24414	0.21408
cg2758514	NBAS	PR B [T00	1157	1163	3.29756	AACATT	0.24414	0.21408
cg2758514	NBAS	PR B [T00	1567	1573	3.29756	AACATT	0.24414	0.21408
cg2758514	NBAS	PR B [T00	1887	1893	3.29756	AACAAT	0.24414	0.21408
cg2758514	NBAS	PR A [T01	930	936	3.29756	AAATGT	0.24414	0.21408
cg2758514	NBAS	PR A [T01	1157	1163	3.29756	AACATT	0.24414	0.21408
cg2758514	NBAS	PR A [T01	1567	1573	3.29756	AACATT	0.24414	0.21408
cg2758514	NBAS	PR A [T01	1887	1893	3.29756	AACAAT	0.24414	0.21408
cg2758514	NBAS	HNF-1C [	1420	1428	3.273679	GTTATT	0.04578	0.04013
cg2758514	NBAS	PXR-1:RX	950	957	3.2723	TGAACC	0.12207	0.11883
cg2758514	NBAS	PXR-1:RX	1990	1997	3.2723	TTGGTT	0.12207	0.11883
cg2758514	NBAS	c-Jun [T00	793	799	3.244843	AGAGTC	0.24414	0.2435
cg2758514	NBAS	AP-2alpha	536	541	3.229049	GCCTCT	0.48828	0.5124
cg2758514	NBAS	AP-2alpha	943	948	3.229049	AGAGGC	0.48828	0.5124
cg2758514	NBAS	RAR-beta	563	572	3.226064	CCCAAA	0.12207	0.12558
cg2758514	NBAS	RXR-alph	84	90	3.170788	AAAACC	0.24414	0.24551
cg2758514	NBAS	TFIID [T0	1012	1018	3.075094	TGCAAA	0.12207	0.11309
cg2758514	NBAS	c-Jun [T00	323	329	3.049104	TGACCC	0.24414	0.2435
cg2758514	NBAS	c-Jun [T00	872	878	3.049104	TGACCC	0.24414	0.2435
cg2758514	NBAS	p53 [T006	657	663	3.028543	TGTGCC	0.48828	0.53227
cg2758514	NBAS	p53 [T006	705	711	3.024997	GTTGCC	0.48828	0.53227
cg2758514	NBAS	p53 [T006	1845	1851	3.024997	GTTGCC	0.48828	0.53227
cg2758514	NBAS	C/EBPalph	769	775	3.014837	AGCAAT	0.48828	0.47526
cg2758514	NBAS	C/EBPalph	904	910	3.014837	AGCAAT	0.48828	0.47526
cg2758514	NBAS	STAT4 [T	268	273	2.941176	GGAACA	2.92969	2.92382
cg2758514	NBAS	STAT4 [T	592	597	2.941176	GGAAAG	2.92969	2.92382
cg2758514	NBAS	STAT4 [T	1285	1290	2.941176	GGAACA	2.92969	2.92382
cg2758514	NBAS	STAT4 [T	1335	1340	2.941176	CTTTCC	2.92969	2.92382
cg2758514	NBAS	STAT4 [T	1860	1865	2.941176	TATTCC	2.92969	2.92382
cg2758514	NBAS	IRF-1 [T0	1074	1082	2.890712	TTTCCTT	0.07629	0.07093
cg2758514	NBAS	p53 [T006	411	417	2.813291	GCTGCC	0.48828	0.53227
cg2758514	NBAS	RXR-alph	1987	1993	2.726556	GGGTTG	0.85449	0.89683
cg2758514	NBAS	NFI/CTF [	995	1002	2.683003	CCAACC	0.06104	0.06609
cg2758514	NBAS	NF-AT1 [	1332	1340	2.619709	ATACTT	0.09155	0.08666
cg2758514	NBAS	PXR-1:RX	888	895	2.577808	TGAACT	0.12207	0.11843
cg2758514	NBAS	AP-2alpha	916	921	2.550491	GCCTCA	0.48828	0.51216
cg2758514	NBAS	RXR-alph	1139	1145	2.544678	GGGTTA	0.85449	0.89683
cg2758514	NBAS	NF-AT1 [	1635	1643	2.449764	GGAAAA	0.09155	0.08666
cg2758514	NBAS	c-Ets-2 [T	1075	1083	2.447661	TTCCTTC	0.07629	0.07844
cg2758514	NBAS	C/EBPalph	1925	1931	2.371703	AATTGT	0.48828	0.47439
cg2758514	NBAS	GATA-2 [	728	736	2.222222	GCACTA	0.22888	0.21978
cg2758514	NBAS	GATA-2 [	1045	1053	2.222222	ACACTA	0.22888	0.21978

cg2758514	NBAS	NF-1 [T00	1548	1555	2.067686	TGTCCC	0.12207	0.12476
cg2758514	NBAS	LEF-1 [T0	1521	1528	2.004405	AAACAA	0.18311	0.17215
cg2758514	NBAS	GATA-1 [	25	30	2.001358	GGGATA	3.90625	3.79558
cg2758514	NBAS	TCF-4 [T0	1144	1153	1.934085	ATTTCA	0.04196	0.03736
cg2758514	NBAS	GATA-1 [	1910	1915	1.896347	TATCCG	3.90625	3.79558
cg2758514	NBAS	AP-2alpha	787	792	1.871933	GCCTCC	0.97656	1.07805
cg2758514	NBAS	AP-2alpha	922	927	1.871933	GCCTCC	0.97656	1.07805
cg2758514	NBAS	TBP [T00	1622	1631	1.871542	CAAATA	0.18311	0.15671
cg2758514	NBAS	TBP [T00	1659	1668	1.871542	TTTATA	0.18311	0.15671
cg2758514	NBAS	TFII-I [T0	259	264	1.824994	CTCTCC	0.48828	0.51201
cg2758514	NBAS	TFII-I [T0	699	704	1.824994	CTCTCC	0.48828	0.51201
cg2758514	NBAS	GR-beta [	46	50	1.680765	GCATT	3.90625	3.70067
cg2758514	NBAS	GR-beta [	202	206	1.680765	GAATT	3.90625	3.70067
cg2758514	NBAS	GR-beta [	203	207	1.680765	AATTC	3.90625	3.70067
cg2758514	NBAS	GR-beta [	449	453	1.680765	AATTC	3.90625	3.70067
cg2758514	NBAS	GR-beta [	1197	1201	1.680765	GAATT	3.90625	3.70067
cg2758514	NBAS	GR-beta [	1493	1497	1.680765	AATTC	3.90625	3.70067
cg2758514	NBAS	GR-beta [	1733	1737	1.680765	AATTC	3.90625	3.70067
cg2758514	NBAS	c-Ets-1 [T	1074	1080	1.641124	TTTCCTT	0.36621	0.35197
cg2758514	NBAS	C/EBPbeta	143	146	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	318	321	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	352	355	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	564	567	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	602	605	1.639871	TTGG	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	710	713	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	927	930	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	935	938	1.639871	TTGG	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	954	957	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	995	998	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1040	1043	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1107	1110	1.639871	TTGG	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1283	1286	1.639871	TTGG	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1317	1320	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1386	1389	1.639871	TTGG	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1510	1513	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1552	1555	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1769	1772	1.639871	CCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1990	1993	1.639871	TTGG	15.625	15.23827
cg2758514	NBAS	XBP-1 [T	871	876	1.583727	ATGACC	0.97656	0.94995
cg2758514	NBAS	XBP-1 [T	1618	1623	1.583727	ATGACA	0.97656	0.94995
cg2758514	NBAS	TFIID [T0	508	514	1.537547	TTTTTCA	0.73242	0.65627
cg2758514	NBAS	TFIID [T0	846	852	1.537547	TTTTGTA	0.73242	0.65627
cg2758514	NBAS	TFIID [T0	1453	1459	1.537547	TGTAAA	0.73242	0.65627
cg2758514	NBAS	TFIID [T0	1800	1806	1.537547	TTTTACA	0.73242	0.65627
cg2758514	NBAS	Pax-5 [T0	1351	1357	1.537547	CTAGCC	0.73242	0.83087
cg2758514	NBAS	RXR-alpha	565	571	1.474336	CAAACC	0.48828	0.52093
cg2758514	NBAS	STAT4 [T	449	454	1.470588	AATTCC	1.95312	1.90161
cg2758514	NBAS	STAT4 [T	1073	1078	1.470588	TTTTCC	1.95312	1.90161

cg2758514	NBAS	STAT4 [T	1266	1271	1.470588	GTTTCC	1.95312	1.90161
cg2758514	NBAS	STAT4 [T	1595	1600	1.470588	TTTTCC	1.95312	1.90161
cg2758514	NBAS	STAT4 [T	1635	1640	1.470588	GGAAAA	1.95312	1.90161
cg2758514	NBAS	STAT4 [T	1764	1769	1.470588	TTTTCC	1.95312	1.90161
cg2758514	NBAS	GR [T050	478	484	1.444018	CAAAAA	0.12207	0.11476
cg2758514	NBAS	GR [T050	1543	1549	1.444018	GTTTTT	0.12207	0.11476
cg2758514	NBAS	PR B [T00	1606	1612	1.404665	GAGTGT	0.36621	0.35143
cg2758514	NBAS	PR A [T01	1606	1612	1.404665	GAGTGT	0.36621	0.35143
cg2758514	NBAS	c-Ets-1 [T	1267	1273	1.384951	TTTCCT	0.36621	0.35197
cg2758514	NBAS	C/EBPbeta	42	45	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	180	183	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	237	240	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	447	450	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	477	480	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	558	561	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	585	588	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	766	769	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	887	890	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1065	1068	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1114	1117	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1147	1150	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1162	1165	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1308	1311	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1414	1417	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1487	1490	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1518	1521	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1604	1607	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1854	1857	1.366559	TCAA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1897	1900	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	C/EBPbeta	1976	1979	1.366559	TTGA	15.625	15.23827
cg2758514	NBAS	AP-2alpha	295	300	1.357116	GCCTGT	0.48828	0.51319
cg2758514	NBAS	AP-2alpha	1002	1007	1.357116	GCCTGT	0.48828	0.51319
cg2758514	NBAS	AP-2alpha	1498	1503	1.357116	ACAGGC	0.48828	0.51319
cg2758514	NBAS	HNF-3alp	1792	1799	1.342935	TTAAAA	0.03052	0.02477
cg2758514	NBAS	T3R-beta1	403	411	1.110682	TCACCT	0.07629	0.07886
cg2758514	NBAS	GATA-1 [	235	240	1.038567	TATCAA	1.95312	1.80234
cg2758514	NBAS	GATA-1 [	445	450	1.038567	TATCAA	1.95312	1.80234
cg2758514	NBAS	SRY [T00	1520	1528	0.999172	GAAACA	0.06104	0.0571
cg2758514	NBAS	HOXD9 [	975	984	0.954221	CATTTT	0.01526	0.01263
cg2758514	NBAS	HOXD9 [	1234	1243	0.954221	AATAAA	0.01526	0.01263
cg2758514	NBAS	HOXD10 [	975	984	0.954221	CATTTT	0.01526	0.01263
cg2758514	NBAS	HOXD10 [	1234	1243	0.954221	AATAAA	0.01526	0.01263
cg2758514	NBAS	GATA-1 [	732	737	0.863549	TATCAC	1.95312	1.80234
cg2758514	NBAS	RXR-alpha	120	126	0.848226	CTAACC	0.48828	0.51313
cg2758514	NBAS	GR-beta [	22	26	0.840383	AATGG	7.8125	7.2174
cg2758514	NBAS	GR-beta [	150	154	0.840383	AATGG	7.8125	7.2174
cg2758514	NBAS	GR-beta [	155	159	0.840383	CCATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	213	217	0.840383	AATGG	7.8125	7.2174

cg2758514	NBAS	GR-beta [	283	287	0.840383	AATGG	7.8125	7.2174
cg2758514	NBAS	GR-beta [	327	331	0.840383	CCATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	448	452	0.840383	CAATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	974	978	0.840383	TCATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1026	1030	0.840383	AATTA	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1095	1099	0.840383	AATGA	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1103	1107	0.840383	TAATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1244	1248	0.840383	CAATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1245	1249	0.840383	AATTA	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1488	1492	0.840383	CAATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1489	1493	0.840383	AATTA	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1492	1496	0.840383	TAATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1514	1518	0.840383	CCATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1617	1621	0.840383	AATGA	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1759	1763	0.840383	AATTA	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1889	1893	0.840383	CAATT	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1900	1904	0.840383	AATGG	7.8125	7.2174
cg2758514	NBAS	GR-beta [	1925	1929	0.840383	AATTG	7.8125	7.2174
cg2758514	NBAS	HNF-1A [	1745	1752	0.781639	GTTAAA	0.48828	0.45029
cg2758514	NBAS	GATA-1 [	1693	1698	0.758539	TATCAG	1.95312	1.80234
cg2758514	NBAS	LEF-1 [T0	269	276	0.641865	GAACAA	0.06104	0.05974
cg2758514	NBAS	GATA-1 [	98	103	0.280028	TATCTT	0.97656	0.8795
cg2758514	NBAS	GATA-1 [	1049	1054	0.280028	TATCTA	0.97656	0.8795
cg2758514	NBAS	GATA-1 [	1202	1207	0.280028	TATCTT	0.97656	0.8795
cg2758514	NBAS	GATA-1 [	1934	1939	0.280028	TATCTT	0.97656	0.8795
cg2758514	NBAS	GATA-1 [	1955	1960	0.280028	TATCTA	0.97656	0.8795
cg2758514	NBAS	AP-2alpha	876	881	0.226186	CCAGGC	0.97656	1.07867
cg2758514	NBAS	GR-alpha [	189	193	0.207689	CCTTT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	273	277	0.207689	AAAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	537	541	0.207689	CCTCT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	943	947	0.207689	AGAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1083	1087	0.207689	AAAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1373	1377	0.207689	CCTTT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1601	1605	0.207689	CCTTT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1629	1633	0.207689	AAAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1850	1854	0.207689	CCTTT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1864	1868	0.207689	CCTTT	7.8125	7.79817
cg2758514	NBAS	GATA-1 [	10	15	0.105011	GAGATA	0.97656	0.92541
cg2758514	NBAS	GR-beta [	931	935	0	AATGT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1025	1029	0	AAATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1054	1058	0	ACATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1059	1063	0	AAATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1060	1064	0	AATTT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1104	1108	0	AATTT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1158	1162	0	ACATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1198	1202	0	AATTT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1568	1572	0	ACATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [	1732	1736	0	AAATT	3.90625	3.51525

cg2758514	NBAS	GR-beta [T	1758	1762	0	AAATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1890	1894	0	AATTT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1924	1928	0	AAATT	3.90625	3.51525
cg2758514	NBAS	GR-beta [T	1965	1969	0	AATGT	3.90625	3.51525
cg2758514	NBAS	XBP-1 [T0	136	141	0	AGTCAT	0.97656	0.94838
cg2758514	NBAS	TFIID [T0	477	483	0	TCAAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	837	843	0	TTTTTTA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1062	1068	0	TTTTTGA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1308	1314	0	TCAAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1455	1461	0	TAAAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1585	1591	0	TTTAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1714	1720	0	TCTAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1754	1760	0	TCTAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1776	1782	0	TTTTAG	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1779	1785	0	TAGAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1882	1888	0	TTTAAA	1.09863	0.95175
cg2758514	NBAS	TFIID [T0	1938	1944	0	TTTTTAA	1.09863	0.95175
cg2758514	NBAS	GR-alpha [	17	21	0	ATAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	296	300	0	CCTGT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	808	812	0	ACAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	856	860	0	ACAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1003	1007	0	CCTGT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1260	1264	0	ACAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1476	1480	0	CCTGT	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1498	1502	0	ACAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1555	1559	0	ACAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1835	1839	0	ATAGG	7.8125	7.79817
cg2758514	NBAS	GR-alpha [	1983	1987	0	ACAGG	7.8125	7.79817
cg2758514	NBAS	FOXP3 [T	247	252	0	GTTGTG	1.46484	1.44953
cg2758514	NBAS	FOXP3 [T	482	487	0	AACAAC	1.46484	1.44953
cg2758514	NBAS	FOXP3 [T	485	490	0	AACAAC	1.46484	1.44953
cg2758514	NBAS	HNF-3alph	1097	1104	0	TGAAAA	0.09155	0.07727
cg2758514	NBAS	HNF-3alph	1716	1723	0	TAAAAA	0.09155	0.07727
cg2758514	NBAS	C/EBPbeta	58	61	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	68	71	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	82	85	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	102	105	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	108	111	0	GCAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	248	251	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	271	274	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	300	303	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	348	351	0	GCAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	387	390	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	461	464	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	471	474	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	483	486	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	486	489	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	489	492	0	ACAA	15.625	15.26275

cg2758514	NBAS	C/EBPbeta	532	535	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	706	709	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	746	749	0	GCAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	770	773	0	GCAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	848	851	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	852	855	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	864	867	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	905	908	0	GCAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	968	971	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1013	1016	0	GCAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1022	1025	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1243	1246	0	GCAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1378	1381	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1407	1410	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1466	1469	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1484	1487	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1523	1526	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1547	1550	0	TTGT	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1574	1577	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1621	1624	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1649	1652	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1725	1728	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1846	1849	0	TTGC	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1888	1891	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1917	1920	0	ACAA	15.625	15.26275
cg2758514	NBAS	C/EBPbeta	1927	1930	0	TTGT	15.625	15.26275
cg2758514	NBAS	YY1 [T00	23	26	0	ATGG	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	30	33	0	ATGG	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	151	154	0	ATGG	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	155	158	0	CCAT	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	184	187	0	CCAT	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	214	217	0	ATGG	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	284	287	0	ATGG	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	327	330	0	CCAT	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	345	348	0	ATGG	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	550	553	0	CCAT	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	1366	1369	0	CCAT	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	1514	1517	0	CCAT	7.8125	7.79459
cg2758514	NBAS	YY1 [T00	1901	1904	0	ATGG	7.8125	7.79459
cg2758514	NBAS	TFII-I [T0	592	597	0	GGAAAG	1.46484	1.48598
cg2758514	NBAS	TFII-I [T0	1222	1227	0	CTGTCC	1.46484	1.48598
cg2758514	NBAS	TFII-I [T0	1335	1340	0	CTTTCC	1.46484	1.48598
cg2758514	NBAS	TFII-I [T0	1909	1914	0	CTATCC	1.46484	1.48598
cg2758514	NBAS	TFII-I [T0	1981	1986	0	GGACAG	1.46484	1.48598
cg2758514	NBAS	STAT4 [T	210	215	0	GGAAAT	0.48828	0.46235
cg2758514	NBAS	STAT4 [T	280	285	0	GGAAAT	0.48828	0.46235
cg2758514	NBAS	ER-alpha [	181	185	0	TGACC	1.95312	1.99744
cg2758514	NBAS	ER-alpha [	323	327	0	TGACC	1.95312	1.99744

cg2758514	NBAS	ER-alpha [	872	876	0	TGACC	1.95312	1.99744
cg2758514	NBAS	ER-alpha [	1507	1511	0	TGACC	1.95312	1.99744
cg2758514	NBAS	SRY [T00	268	276	0	GGAACA	0.03052	0.02847
cg2758514	NBAS	GR [T050	490	496	0	CAAAAA	0.36621	0.33174
cg2758514	NBAS	GR [T050	844	850	0	TTTTTTG	0.36621	0.33174
cg2758514	NBAS	GR [T050	1061	1067	0	ATTTTTC	0.36621	0.33174
cg2758514	NBAS	GR [T050	1309	1315	0	CAAAAA	0.36621	0.33174
cg2758514	NBAS	GR [T050	1374	1380	0	CTTTTTG	0.36621	0.33174
cg2758514	NBAS	GR [T050	1570	1576	0	ATTTTTC	0.36621	0.33174
cg2758514	NBAS	GR [T050	1918	1924	0	CAAAAA	0.36621	0.33174
cg2758514	NBAS	TBP [T00	1388	1397	0	GGTATA	0.03052	0.02611
cg2758514	NBAS	AR [T000	1219	1227	0	GCACTG	0.00763	0.00819
cg2758514	NBAS	GATA-1 [	441	446	0	CAGATA	0.97656	0.92541
cg2758514	NBAS	GATA-1 [	1207	1212	0	TATCTG	0.97656	0.92541
cg2758514	NBAS	Pax-5 [T0	416	422	0	CCAGCC	1.09863	1.24633
cg2758514	NBAS	STAT1bet	206	215	0	TCTGGG	0.01717	0.01622
cg2758514	NBAS	IRF-2 [T0	320	325	0	AAGTGA	0.48828	0.46235
cg2758514	NBAS	IRF-2 [T0	383	388	0	TCACTT	0.48828	0.46235
cg2758514	NBAS	IRF-2 [T0	1150	1155	0	AAGTGA	0.48828	0.46235
cg2758514	NBAS	IRF-2 [T0	1433	1438	0	AAGTGA	0.48828	0.46235
cg1919774	NOV	STAT1bet	992	1001	9.807397	ATTTCC	0.14877	0.14533
cg1919774	NOV	E2F [T002	875	884	9.790721	GAGCGC	0.06866	0.07289
cg1919774	NOV	XBP-1 [T	617	622	9.789909	AGCCAT	1.95312	1.94901
cg1919774	NOV	NF-1 [T00	1937	1944	9.761671	AGCTCC	0.24414	0.24488
cg1919774	NOV	NF-AT2 [	1729	1738	9.755755	TTGTTTT	0.08774	0.08205
cg1919774	NOV	Elk-1 [T00	1028	1036	9.754368	TGATGG	0.10681	0.11027
cg1919774	NOV	PR B [T00	1721	1727	9.743489	TTGTGT	1.09863	1.0981
cg1919774	NOV	PR B [T00	1798	1804	9.743489	GTGTGT	1.09863	1.0981
cg1919774	NOV	PR A [T01	1721	1727	9.743489	TTGTGT	1.09863	1.0981
cg1919774	NOV	PR A [T01	1798	1804	9.743489	GTGTGT	1.09863	1.0981
cg1919774	NOV	LEF-1 [T0	300	307	9.72404	CTTTGC	0.21362	0.21229
cg1919774	NOV	c-Ets-1 [T	766	772	9.713162	ATTCCC	0.36621	0.37402
cg1919774	NOV	NF-AT1 [	893	901	9.691726	GGAAAC	0.16785	0.16528
cg1919774	NOV	RAR-beta	1160	1169	9.585862	ATGTAA	0.21362	0.22369
cg1919774	NOV	TFIID [T0	224	230	9.552105	TTTGGT	1.46484	1.37777
cg1919774	NOV	TFIID [T0	286	292	9.552105	TCCGAA	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1062	1068	9.552105	TTTCCC	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1064	1070	9.552105	TCCCAA	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1101	1107	9.552105	TTTCAC	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1248	1254	9.552105	TTTCAC	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1487	1493	9.552105	TGGGAA	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1639	1645	9.552105	TGAGAA	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1678	1684	9.552105	TTTGGA	1.46484	1.37777
cg1919774	NOV	TFIID [T0	1971	1977	9.552105	TGTGAA	1.46484	1.37777
cg1919774	NOV	Pax-5 [T0	374	380	9.552105	TTTGCC	1.46484	1.61918
cg1919774	NOV	Pax-5 [T0	387	393	9.552105	GTGGCC	1.46484	1.61918
cg1919774	NOV	Pax-5 [T0	529	535	9.552105	TGCGCC	1.46484	1.61918
cg1919774	NOV	Pax-5 [T0	1014	1020	9.552105	GGGCCA	1.46484	1.61918

cg1919774	NOV	Pax-5 [T0	1987	1993	9.552105	GTGGCC	1.46484	1.61918
cg1919774	NOV	FOXP3 [T	43	48	9.512894	GGCAAC	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	107	112	9.512894	GCCAAC	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	667	672	9.512894	AGCAAC	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	1042	1047	9.512894	GTTTAC	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	1076	1081	9.512894	GTTGGG	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	1153	1158	9.512894	GATAAC	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	1198	1203	9.512894	GGCAAC	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	1464	1469	9.512894	GTTCTC	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	1725	1730	9.512894	GTTCTT	7.32422	7.22156
cg1919774	NOV	FOXP3 [T	1791	1796	9.512894	GATAAC	7.32422	7.22156
cg1919774	NOV	TFII-I [T0	58	63	9.512894	CGTTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	184	189	9.512894	GGAAGG	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	310	315	9.512894	CCTTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	555	560	9.512894	GGACGG	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	771	776	9.512894	CCTTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	893	898	9.512894	GGAAAC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1001	1006	9.512894	GGACAC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1061	1066	9.512894	GTTTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1081	1086	9.512894	GGAAAA	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1115	1120	9.512894	TTGTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1152	1157	9.512894	GGATAA	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1278	1283	9.512894	TTGTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1283	1288	9.512894	CCTTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1370	1375	9.512894	CCTTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1398	1403	9.512894	GGAAAA	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1449	1454	9.512894	GGAAAC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1489	1494	9.512894	GGAAAA	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1668	1673	9.512894	GGACTT	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1733	1738	9.512894	TTTTCC	7.32422	7.44385
cg1919774	NOV	TFII-I [T0	1852	1857	9.512894	AATTCC	7.32422	7.44385
cg1919774	NOV	c-Jun [T00	1897	1903	9.442241	GCTGTC	0.73242	0.7366
cg1919774	NOV	NFI/CTF [	866	873	9.352332	GGCTTT	0.54932	0.55369
cg1919774	NOV	NFI/CTF [	1482	1489	9.352332	AACATT	0.54932	0.55369
cg1919774	NOV	NFI/CTF [	1505	1512	9.352332	GACCTT	0.54932	0.55369
cg1919774	NOV	LEF-1 [T0	868	875	9.313676	CTTTGG	0.21362	0.21229
cg1919774	NOV	STAT5A [	1939	1951	9.080962	CTCCAA	0.02816	0.02551
cg1919774	NOV	USF2 [T0	1102	1111	9.056375	TTCACA	0.1545	0.16206
cg1919774	NOV	NFI/CTF [	1073	1080	9.042931	GCAGTT	0.48828	0.48845
cg1919774	NOV	c-Myb [T0	1057	1064	9.024874	CACAGT	0.39673	0.37851
cg1919774	NOV	NF-AT2 [	1489	1498	9.016873	GGAAAA	0.05341	0.05145
cg1919774	NOV	c-Jun [T00	813	819	9.013496	TGACAT	0.61035	0.60549
cg1919774	NOV	GR [T050	277	283	8.971049	GCTTTC	0.61035	0.5928
cg1919774	NOV	GR [T050	866	872	8.971049	GGCTTT	0.61035	0.5928
cg1919774	NOV	Elk-1 [T00	180	188	8.931691	AGGGGG	0.24414	0.26271
cg1919774	NOV	c-Ets-2 [T	933	941	8.912323	TTCCTA	0.27466	0.27171
cg1919774	NOV	AP-1 [T00	1476	1484	8.907204	TGACTG	0.24414	0.23028
cg1919774	NOV	HNF-4alph	1750	1762	8.87767	GCTTTC	0.01502	0.01406

cg1919774	NOV	c-Jun [T00	307	313	8.832178	TGACCT	0.61035	0.60549
cg1919774	NOV	PR B [T00	1391	1397	8.827054	ACCTGT	0.36621	0.35051
cg1919774	NOV	PR A [T01	1391	1397	8.827054	ACCTGT	0.36621	0.35051
cg1919774	NOV	NFI/CTF [	394	401	8.814757	CCATTT	0.48828	0.48845
cg1919774	NOV	NFI/CTF [	924	931	8.814757	TCACTT	0.48828	0.48845
cg1919774	NOV	NFI/CTF [	1017	1024	8.814757	CCACTT	0.48828	0.48845
cg1919774	NOV	c-Ets-1 [T	1853	1859	8.809329	ATTCCA	0.85449	0.84987
cg1919774	NOV	HNF-1B [	1159	1167	8.799296	TATGTA	0.08392	0.07596
cg1919774	NOV	NF-1 [T00	1062	1069	8.790071	TTTCCC	0.24414	0.24339
cg1919774	NOV	NF-1 [T00	1371	1378	8.790071	CTTCCC	0.24414	0.24339
cg1919774	NOV	NF-1 [T00	1486	1493	8.790071	TTGGGA	0.24414	0.24339
cg1919774	NOV	XBP-1 [T	563	568	8.75604	GCTCAT	2.92969	2.75329
cg1919774	NOV	XBP-1 [T	1254	1259	8.75604	ATGATA	2.92969	2.75329
cg1919774	NOV	XBP-1 [T	1573	1578	8.75604	ATGATC	2.92969	2.75329
cg1919774	NOV	XBP-1 [T	1638	1643	8.75604	ATGAGA	2.92969	2.75329
cg1919774	NOV	STAT1bet	1394	1403	8.695301	TGTTGG	0.22316	0.2175
cg1919774	NOV	NF-AT1 [	1081	1089	8.599808	GGAAAA	0.10681	0.10494
cg1919774	NOV	RAR-beta	1673	1682	8.55975	TGGGTT	0.26703	0.27434
cg1919774	NOV	NF-AT2 [	242	251	8.550786	GGAAAG	0.04959	0.04758
cg1919774	NOV	NF-AT2 [	1398	1407	8.550786	GGAAAA	0.04959	0.04758
cg1919774	NOV	c-Ets-1 [T	1679	1685	8.501115	TTGGAA	0.24414	0.23702
cg1919774	NOV	IRF-1 [T0	1394	1402	8.497322	TGTTGG	0.20599	0.20245
cg1919774	NOV	AhR:Arnt	587	596	8.431005	GCCAGC	0.07439	0.08553
cg1919774	NOV	LEF-1 [T0	373	380	8.361499	CTTTGC	0.15259	0.154
cg1919774	NOV	HNF-3alph	1183	1190	8.343064	GTAAAA	0.27466	0.23078
cg1919774	NOV	PR B [T00	708	714	8.338824	TGCTGT	1.09863	1.09384
cg1919774	NOV	PR A [T01	708	714	8.338824	TGCTGT	1.09863	1.09384
cg1919774	NOV	GR-alpha [	89	93	8.281568	CCTCC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	92	96	8.281568	CCTCC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	185	189	8.281568	GAAGG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	310	314	8.281568	CCTTC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	382	386	8.281568	CCTTG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	445	449	8.281568	CCTTG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	459	463	8.281568	CCTTC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	487	491	8.281568	CCTCC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	749	753	8.281568	CCTCC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	753	757	8.281568	CCTTC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	771	775	8.281568	CCTTC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	996	1000	8.281568	CCTTC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1283	1287	8.281568	CCTTC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1299	1303	8.281568	GGAGG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1354	1358	8.281568	CAAGG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1370	1374	8.281568	CCTTC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1460	1464	8.281568	GGAGG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1507	1511	8.281568	CCTTG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1581	1585	8.281568	GAAGG	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1606	1610	8.281568	CCTCC	7.8125	8.20394
cg1919774	NOV	GR-alpha [	1690	1694	8.281568	CCTCC	7.8125	8.20394

cg1919774	NOV	c-Ets-1 [T	59	65	8.244941	GTTCCA	0.24414	0.2494
cg1919774	NOV	c-Jun [T00	715	721	8.242207	TGACCT	0.48828	0.47447
cg1919774	NOV	ENKTF-1	583	590	8.19852	GCCCGC	0.73242	0.80254
cg1919774	NOV	ENKTF-1	594	601	8.19852	TGGCGA	0.73242	0.80254
cg1919774	NOV	ENKTF-1	1496	1503	8.19852	TGGCCA	0.73242	0.80254
cg1919774	NOV	PXR-1:RX	1480	1487	8.180749	TGAACA	0.12207	0.11255
cg1919774	NOV	SRY [T00	949	957	8.174786	TAAGCA	0.15259	0.14791
cg1919774	NOV	NF-kappa	958	968	8.148631	GGGGAG	0.0329	0.03642
cg1919774	NOV	AR [T000	1294	1302	8.11332	GGACAG	0.19836	0.20641
cg1919774	NOV	GR-alpha [	96	100	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	128	132	8.073878	CCAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	178	182	8.073878	CCAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	314	318	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	329	333	8.073878	CCTGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	455	459	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	511	515	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	527	531	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	697	701	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	726	730	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	898	902	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	903	907	8.073878	CCTGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	935	939	8.073878	CCTAG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1009	1013	8.073878	CTAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1091	1095	8.073878	GCAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1148	1152	8.073878	CCTGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1195	1199	8.073878	GCAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1212	1216	8.073878	CCAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1446	1450	8.073878	GTAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1499	1503	8.073878	CCAGG	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1864	1868	8.073878	CCTGC	7.8125	8.20289
cg1919774	NOV	GR-alpha [	1959	1963	8.073878	CCTGG	7.8125	8.20289
cg1919774	NOV	TFIID [T0	1396	1402	8.014558	TTGGAA	2.19727	1.99811
cg1919774	NOV	TFIID [T0	1447	1453	8.014558	TAGGAA	2.19727	1.99811
cg1919774	NOV	TFIID [T0	1468	1474	8.014558	TCGCAA	2.19727	1.99811
cg1919774	NOV	Pax-5 [T0	358	364	8.014558	GATGCC	2.19727	2.42766
cg1919774	NOV	Pax-5 [T0	407	413	8.014558	GGGCTC	2.19727	2.42766
cg1919774	NOV	Pax-5 [T0	482	488	8.014558	GCTGCC	2.19727	2.42766
cg1919774	NOV	Pax-5 [T0	506	512	8.014558	GGTGCC	2.19727	2.42766
cg1919774	NOV	Pax-5 [T0	580	586	8.014558	TGTGCC	2.19727	2.42766
cg1919774	NOV	Pax-5 [T0	1024	1030	8.014558	GGGCTG	2.19727	2.42766
cg1919774	NOV	Pax-5 [T0	1875	1881	8.014558	GGGCAG	2.19727	2.42766
cg1919774	NOV	Pax-5 [T0	1889	1895	8.014558	TGTGCC	2.19727	2.42766
cg1919774	NOV	USF2 [T0	1858	1867	8.007902	AGTGCA	0.01717	0.01801
cg1919774	NOV	C/EBPalph	1263	1269	8.006685	CATTGT	0.24414	0.23098
cg1919774	NOV	HNF-1C [	1158	1166	8.002145	CTATGT	0.19836	0.18126
cg1919774	NOV	c-Myb [T0	365	372	7.825375	CCAAGT	0.21362	0.20997
cg1919774	NOV	c-Myb [T0	1793	1800	7.739476	TAACTG	0.42725	0.40917
cg1919774	NOV	NFI/CTF [	32	39	7.587343	CCAATT	0.36621	0.36269

cg1919774	NOV	NFI/CTF [	858	865	7.587343	GCACTT	0.36621	0.36269
cg1919774	NOV	c-Myb [T0	1200	1207	7.587189	CAACTA	0.42725	0.40917
cg1919774	NOV	COUP-TF	712	724	7.555558	GTTTGA	0.01192	0.01223
cg1919774	NOV	c-Myb [T0	1068	1075	7.545286	AAACTG	0.42725	0.40917
cg1919774	NOV	GR [T050	710	716	7.527031	CTGTTT	1.83105	1.71535
cg1919774	NOV	GR [T050	758	764	7.527031	TCTTTTG	1.83105	1.71535
cg1919774	NOV	GR [T050	791	797	7.527031	CAAATA	1.83105	1.71535
cg1919774	NOV	GR [T050	1130	1136	7.527031	CAAAGC	1.83105	1.71535
cg1919774	NOV	GR [T050	1471	1477	7.527031	CAAAAT	1.83105	1.71535
cg1919774	NOV	RAR-beta:	489	500	7.477995	TCCCCA	0.02861	0.03163
cg1919774	NOV	PEA3 [T0	1543	1551	7.421728	CCTCAT	0.34332	0.35389
cg1919774	NOV	AR [T000	420	428	7.406474	CTTCTGT	0.25177	0.2544
cg1919774	NOV	IRF-1 [T0	1077	1085	7.387351	TTGGGG	0.14496	0.14723
cg1919774	NOV	NF-kappa	1079	1090	7.303291	GGGGAA	0.00727	0.00784
cg1919774	NOV	c-Ets-2 [T	312	320	7.268173	TTCCTG	0.09155	0.08977
cg1919774	NOV	c-Ets-2 [T	1444	1452	7.268173	GAGTAG	0.09155	0.08977
cg1919774	NOV	p53 [T006	865	871	7.266844	GGGCTT	0.73242	0.79826
cg1919774	NOV	p53 [T006	1302	1308	7.266844	GGGCTT	0.73242	0.79826
cg1919774	NOV	NF-AT1 [	1536	1544	7.211175	CCTCTTT	0.15259	0.14325
cg1919774	NOV	c-Ets-1 [T	1062	1068	7.199436	TTTCCC	0.73242	0.73732
cg1919774	NOV	c-Ets-1 [T	1487	1493	7.199436	TGGGAA	0.73242	0.73732
cg1919774	NOV	SRY [T00	1126	1134	7.175614	GAACCA	0.30518	0.29547
cg1919774	NOV	SRY [T00	1746	1754	7.175614	CTTTGCT	0.30518	0.29547
cg1919774	NOV	SRY [T00	1758	1766	7.175614	CTTTGCT	0.30518	0.29547
cg1919774	NOV	XBP-1 [T	1331	1336	7.172312	ATGATT	2.92969	2.7512
cg1919774	NOV	XBP-1 [T	1543	1548	7.172312	CCTCAT	2.92969	2.7512
cg1919774	NOV	XBP-1 [T	1556	1561	7.172312	ATGAGT	2.92969	2.7512
cg1919774	NOV	XBP-1 [T	1611	1616	7.172312	ATGAGG	2.92969	2.7512
cg1919774	NOV	p53 [T006	387	393	7.150251	GTGGCC	1.09863	1.22478
cg1919774	NOV	p53 [T006	1014	1020	7.150251	GGGCCA	1.09863	1.22478
cg1919774	NOV	p53 [T006	1987	1993	7.150251	GTGGCC	1.09863	1.22478
cg1919774	NOV	p53 [T006	781	787	7.103527	GGGCGA	1.09863	1.22478
cg1919774	NOV	Pax-5 [T0	781	787	7.082373	GGGCGA	0.12207	0.13135
cg1919774	NOV	NF-AT2 [	1057	1066	7.016923	CACAGT	0.04578	0.04306
cg1919774	NOV	IRF-1 [T0	1062	1070	6.968314	TTTCCC	0.1297	0.12685
cg1919774	NOV	NF-1 [T00	862	869	6.948522	TTGGGG	0.48828	0.50205
cg1919774	NOV	NF-1 [T00	1021	1028	6.948522	TTGGGG	0.48828	0.50205
cg1919774	NOV	NF-1 [T00	1125	1132	6.948522	TGAACC	0.48828	0.50205
cg1919774	NOV	c-Ets-1 [T	240	246	6.943262	GGGGAA	0.73242	0.73732
cg1919774	NOV	c-Ets-1 [T	1079	1085	6.943262	GGGGAA	0.73242	0.73732
cg1919774	NOV	ENKTF-1	27	34	6.942764	CACAGC	1.46484	1.56616
cg1919774	NOV	ENKTF-1	1883	1890	6.942764	TGGCTG	1.46484	1.56616
cg1919774	NOV	RelA [T00	1078	1088	6.869902	TGGGGA	0.01192	0.01233
cg1919774	NOV	c-Jun [T00	398	404	6.856451	TTGGTC	0.73242	0.73062
cg1919774	NOV	HOXD9 [	796	805	6.852796	AATAAT	0.07629	0.06543
cg1919774	NOV	HOXD10 [	796	805	6.852796	AATAAT	0.07629	0.06543
cg1919774	NOV	E2F-1 [T0	375	382	6.846071	TTGCCC	0.30518	0.33862
cg1919774	NOV	AR [T000	333	341	6.817719	GGACAG	0.23651	0.23986

cg1919774	NOV	NFI/CTF [	199	206	6.786076	CCAATC	0.73242	0.74795
cg1919774	NOV	NFI/CTF [	847	854	6.786076	TGGTTT	0.73242	0.74795
cg1919774	NOV	NFI/CTF [	1066	1073	6.786076	CCAAAC	0.73242	0.74795
cg1919774	NOV	NFI/CTF [	1207	1214	6.786076	CCAATC	0.73242	0.74795
cg1919774	NOV	NFI/CTF [	1842	1849	6.786076	CCAAGC	0.73242	0.74795
cg1919774	NOV	NFI/CTF [	1878	1885	6.786076	CAGATT	0.73242	0.74795
cg1919774	NOV	p53 [T006	407	413	6.778774	GGGCTC	1.09863	1.22478
cg1919774	NOV	NF-AT2 [	1449	1458	6.773407	GGAAAC	0.04578	0.04306
cg1919774	NOV	FOXP3 [T	142	147	6.581441	TAAAAC	0.97656	0.904
cg1919774	NOV	FOXP3 [T	1221	1226	6.581441	TAAAAC	0.97656	0.904
cg1919774	NOV	FOXP3 [T	1270	1275	6.581441	GTTGAA	0.97656	0.904
cg1919774	NOV	TFII-I [T0	81	86	6.581441	ATCTCC	0.97656	0.9991
cg1919774	NOV	TFII-I [T0	325	330	6.581441	ATCTCC	0.97656	0.9991
cg1919774	NOV	TFII-I [T0	1788	1793	6.581441	GGAGAT	0.97656	0.9991
cg1919774	NOV	RelA [T00	239	249	6.577871	AGGGGA	0.01001	0.01051
cg1919774	NOV	CTF [T001	1204	1215	6.536593	TAGCCA	0.02003	0.0197
cg1919774	NOV	XBP-1 [T	359	364	6.478682	ATGCCC	0.97656	0.99906
cg1919774	NOV	XBP-1 [T	678	683	6.478682	TGGCAT	0.97656	0.99906
cg1919774	NOV	XBP-1 [T	1366	1371	6.478682	ATGCCC	0.97656	0.99906
cg1919774	NOV	XBP-1 [T	1686	1691	6.478682	ATGCCC	0.97656	0.99906
cg1919774	NOV	E2F-1 [T0	1891	1898	6.47044	TGCCCC	0.12207	0.1297
cg1919774	NOV	c-Myb [T0	1524	1531	6.454077	CACAGT	0.30518	0.30272
cg1919774	NOV	c-Ets-1 [T	1396	1402	6.423689	TTGGAA	0.48828	0.48842
cg1919774	NOV	p53 [T006	529	535	6.403751	TGCGCC	0.48828	0.54643
cg1919774	NOV	RAR-beta	1081	1090	6.39673	GGAAAA	0.18311	0.1857
cg1919774	NOV	C/EBPalph	31	37	6.391486	GCCAAT	0.48828	0.47407
cg1919774	NOV	C/EBPalph	1113	1119	6.391486	AATTGT	0.48828	0.47407
cg1919774	NOV	TCF-4E [	300	306	6.302385	CTTTGC	0.61035	0.59686
cg1919774	NOV	TCF-4E [	373	379	6.302385	CTTTGC	0.61035	0.59686
cg1919774	NOV	TCF-4E [	1128	1134	6.302385	ACCAAA	0.61035	0.59686
cg1919774	NOV	GR-alpha [	11	15	6.263098	TAAGG	3.90625	3.89624
cg1919774	NOV	GR-alpha [	352	356	6.263098	CCTTA	3.90625	3.89624
cg1919774	NOV	GR-alpha [	922	926	6.263098	CCTCA	3.90625	3.89624
cg1919774	NOV	GR-alpha [	975	979	6.263098	TAAGG	3.90625	3.89624
cg1919774	NOV	GR-alpha [	1457	1461	6.263098	TAAGG	3.90625	3.89624
cg1919774	NOV	GR-alpha [	1543	1547	6.263098	CCTCA	3.90625	3.89624
cg1919774	NOV	GR-alpha [	1612	1616	6.263098	TGAGG	3.90625	3.89624
cg1919774	NOV	GR-alpha [	1952	1956	6.263098	TGAGG	3.90625	3.89624
cg1919774	NOV	C/EBPalph	804	810	6.245236	TGCAAT	0.97656	0.91422
cg1919774	NOV	IRF-1 [T0	1540	1548	6.24301	TTTCCTC	0.16785	0.16217
cg1919774	NOV	AR [T000	1513	1521	6.112954	GGACAT	0.24414	0.25115
cg1919774	NOV	AR [T000	1615	1623	6.112954	GGACAT	0.24414	0.25115
cg1919774	NOV	GR-alpha [	9	13	6.055408	CCTAA	3.90625	3.89835
cg1919774	NOV	GR-alpha [	248	252	6.055408	CCTGA	3.90625	3.89835
cg1919774	NOV	GR-alpha [	305	309	6.055408	CCTGA	3.90625	3.89835
cg1919774	NOV	GR-alpha [	462	466	6.055408	TCAGG	3.90625	3.89835
cg1919774	NOV	GR-alpha [	840	844	6.055408	TCAGG	3.90625	3.89835
cg1919774	NOV	GR-alpha [	1654	1658	6.055408	CCTGA	3.90625	3.89835

cg1919774	NOV	GR-alpha [	1920	1924	6.055408	CCTGA	3.90625	3.89835
cg1919774	NOV	GR-alpha [	1926	1930	6.055408	CCTAA	3.90625	3.89835
cg1919774	NOV	NF-AT1 [	1058	1066	6.003834	ACAGTT	0.06866	0.06621
cg1919774	NOV	RXR-alph	690	696	5.937582	GGGTAA	0.73242	0.78318
cg1919774	NOV	GCF [T00	475	483	5.917256	ACTCAG	0.64087	0.72542
cg1919774	NOV	HOXD9 [	793	802	5.898575	AATAAT	0.05722	0.04686
cg1919774	NOV	HOXD10 [	793	802	5.898575	AATAAT	0.05722	0.04686
cg1919774	NOV	STAT4 [T	184	189	5.882353	GGAAGG	0.48828	0.51201
cg1919774	NOV	STAT4 [T	310	315	5.882353	CCTTCC	0.48828	0.51201
cg1919774	NOV	STAT4 [T	771	776	5.882353	CCTTCC	0.48828	0.51201
cg1919774	NOV	STAT4 [T	1283	1288	5.882353	CCTTCC	0.48828	0.51201
cg1919774	NOV	STAT4 [T	1370	1375	5.882353	CCTTCC	0.48828	0.51201
cg1919774	NOV	C/EBPalph	34	40	5.850545	AATTGC	0.97656	0.91422
cg1919774	NOV	IRF-1 [T0	1445	1453	5.823972	AGTAGG	0.16785	0.16217
cg1919774	NOV	c-Ets-1 [T	772	778	5.814485	CTTCCC	0.36621	0.36174
cg1919774	NOV	c-Ets-1 [T	1371	1377	5.814485	CTTCCC	0.36621	0.36174
cg1919774	NOV	VDR [T00	1121	1129	5.771401	CATTTG	0.42725	0.41266
cg1919774	NOV	VDR [T00	1476	1484	5.771401	TGACTG	0.42725	0.41266
cg1919774	NOV	IRF-1 [T0	238	246	5.770812	GAGGGG	0.16785	0.16217
cg1919774	NOV	HNF-1A [	973	980	5.754274	GTTAAG	0.24414	0.24293
cg1919774	NOV	c-Jun [T00	1809	1815	5.703976	GGGGTC	0.48828	0.49294
cg1919774	NOV	ENKTF-1	194	201	5.687009	CAGTGC	0.73242	0.76357
cg1919774	NOV	ENKTF-1	875	882	5.687009	GAGCGC	0.73242	0.76357
cg1919774	NOV	ENKTF-1	881	888	5.687009	CAGAGC	0.73242	0.76357
cg1919774	NOV	ENKTF-1	1988	1995	5.687009	TGGCCC	0.73242	0.76357
cg1919774	NOV	NF-kappa	872	882	5.626734	GGGGAG	0.02384	0.02626
cg1919774	NOV	NF-AT1 [	1730	1738	5.604085	TGTTTTT	0.03815	0.03643
cg1919774	NOV	c-Jun [T00	1349	1355	5.590308	AGTGTC	0.48828	0.49294
cg1919774	NOV	T3R-beta1	905	913	5.572705	TGGGGG	0.21362	0.21789
cg1919774	NOV	c-Ets-1 [T	65	71	5.558311	CTTCCC	0.36621	0.38732
cg1919774	NOV	c-Ets-1 [T	182	188	5.558311	GGGGAA	0.36621	0.38732
cg1919774	NOV	c-Ets-1 [T	1763	1769	5.558311	CTTCCC	0.36621	0.38732
cg1919774	NOV	TFIID [T0	226	232	5.544826	TGGTAA	0.73242	0.65314
cg1919774	NOV	TFIID [T0	1218	1224	5.544826	TTCTAA	0.73242	0.65314
cg1919774	NOV	p53 [T006	1024	1030	5.508538	GGGCTG	0.61035	0.65765
cg1919774	NOV	RAR-beta	52	61	5.370617	GGGGTT	0.15259	0.15813
cg1919774	NOV	HOXD9 [	1187	1196	5.275652	AATAAA	0.04578	0.03952
cg1919774	NOV	HOXD10 [	1187	1196	5.275652	AATAAA	0.04578	0.03952
cg1919774	NOV	RXR-alph	44	50	5.271235	GCAACC	0.61035	0.65415
cg1919774	NOV	RXR-alph	69	75	5.271235	CCCACC	0.61035	0.65415
cg1919774	NOV	GR [T050	1675	1681	5.207533	GGTTTT	0.24414	0.24013
cg1919774	NOV	c-Jun [T00	986	992	5.193102	GAAGTC	0.61035	0.60573
cg1919774	NOV	c-Ets-2 [T	1352	1360	5.162974	GTCAAG	0.13733	0.13279
cg1919774	NOV	NF-AT1 [	1489	1497	5.125037	GGAAAA	0.05341	0.05073
cg1919774	NOV	AP-2alpha	298	303	5.100982	GCCTTT	0.97656	0.97517
cg1919774	NOV	AP-2alpha	913	918	5.100982	AAAGGC	0.97656	0.97517
cg1919774	NOV	RXR-alph	21	27	5.089356	AGCACC	0.48828	0.51407
cg1919774	NOV	NF-AT1 [	1449	1457	5.045738	GGAAAC	0.05341	0.05073

cg1919774	NOV	GR-beta [T	694	698	5.042296	AATCC	3.90625	3.7093
cg1919774	NOV	GR-beta [T	764	768	5.042296	GTATT	3.90625	3.7093
cg1919774	NOV	GR-beta [T	1209	1213	5.042296	AATCC	3.90625	3.7093
cg1919774	NOV	GR-beta [T	1718	1722	5.042296	GTATT	3.90625	3.7093
cg1919774	NOV	c-Myb [T0	1072	1079	4.974489	TGCAGT	0.30518	0.30087
cg1919774	NOV	IRF-1 [T0	993	1001	4.963725	TTTCCTT	0.1297	0.12724
cg1919774	NOV	c-Ets-1 [T	1030	1036	4.910652	ATGGAA	0.48828	0.48026
cg1919774	NOV	XBP-1 [T0	842	847	4.894955	AGGCAT	0.97656	0.99839
cg1919774	NOV	XBP-1 [T0	915	920	4.894955	AGGCAT	0.97656	0.99839
cg1919774	NOV	AP-2alpha	1925	1930	4.890408	GCCTAA	0.97656	0.97517
cg1919774	NOV	PPAR-alph	1987	1997	4.88658	GTGGCC	0.01717	0.01861
cg1919774	NOV	NF-1 [T00	195	202	4.880836	AGTGCC	0.24414	0.24345
cg1919774	NOV	NF-1 [T00	1679	1686	4.880836	TTGGAA	0.24414	0.24345
cg1919774	NOV	GCF [T00	0	8	4.846987	GCGCCG	0.27466	0.31905
cg1919774	NOV	GCF [T00	480	488	4.846987	GCGCTG	0.27466	0.31905
cg1919774	NOV	GCF [T00	545	553	4.846987	GCGCGG	0.27466	0.31905
cg1919774	NOV	GCF [T00	651	659	4.846987	TCGCAG	0.27466	0.31905
cg1919774	NOV	GCF [T00	656	664	4.846987	GCGCGG	0.27466	0.31905
cg1919774	NOV	C/EBPalph	1241	1247	4.845599	ATCAAT	0.97656	0.90302
cg1919774	NOV	NF-AT1 [	1397	1406	4.823485	TGGAAA	0.07629	0.07281
cg1919774	NOV	p53 [T006	494	500	4.786849	AGTGCC	0.48828	0.53921
cg1919774	NOV	MAZ [T00	484	496	4.770629	TGCCCT	0.00611	0.00711
cg1919774	NOV	FOXP3 [T	1082	1087	4.756447	GAAAAC	2.92969	2.82
cg1919774	NOV	FOXP3 [T	1099	1104	4.756447	GTTTTC	2.92969	2.82
cg1919774	NOV	FOXP3 [T	1399	1404	4.756447	GAAAAC	2.92969	2.82
cg1919774	NOV	FOXP3 [T	1676	1681	4.756447	GTTTTG	2.92969	2.82
cg1919774	NOV	FOXP3 [T	1731	1736	4.756447	GTTTTT	2.92969	2.82
cg1919774	NOV	FOXP3 [T	1950	1955	4.756447	GTTGAG	2.92969	2.82
cg1919774	NOV	TFII-I [T0	918	923	4.756447	CATTCC	2.92969	2.89715
cg1919774	NOV	TFII-I [T0	992	997	4.756447	ATTTCC	2.92969	2.89715
cg1919774	NOV	TFII-I [T0	1208	1213	4.756447	CAATCC	2.92969	2.89715
cg1919774	NOV	TFII-I [T0	1513	1518	4.756447	GGACAT	2.92969	2.89715
cg1919774	NOV	TFII-I [T0	1615	1620	4.756447	GGACAT	2.92969	2.89715
cg1919774	NOV	PPAR-alph	328	338	4.727619	TCCTGG	0.03242	0.03494
cg1919774	NOV	CTF [T001	29	40	4.70535	CAGCCA	0.01001	0.00979
cg1919774	NOV	p53 [T006	4	10	4.645444	CGCGCC	0.24414	0.28373
cg1919774	NOV	IRF-1 [T0	1734	1742	4.626471	TTTCCT	0.05341	0.05056
cg1919774	NOV	VDR [T00	1652	1660	4.617121	CGCCTG	0.37384	0.36855
cg1919774	NOV	c-Ets-2 [T	994	1002	4.589988	TTCCTT	0.06866	0.06805
cg1919774	NOV	C/EBPalph	198	204	4.560723	GCCAAT	0.24414	0.24373
cg1919774	NOV	C/EBPalph	1206	1212	4.560723	GCCAAT	0.24414	0.24373
cg1919774	NOV	C/EBPalph	1276	1282	4.560723	GATTGT	0.24414	0.24373
cg1919774	NOV	C/EBPalph	1880	1886	4.560723	GATTGG	0.24414	0.24373
cg1919774	NOV	IRF-1 [T0	1485	1493	4.549799	ATTGGG	0.05341	0.05056
cg1919774	NOV	E2F-1 [T0	1779	1786	4.549709	GCGGTA	0.15259	0.16681
cg1919774	NOV	E2F-1 [T0	1816	1823	4.549709	TCTACC	0.15259	0.16681
cg1919774	NOV	c-Jun [T00	1476	1482	4.441904	TGACTG	0.12207	0.11843
cg1919774	NOV	STAT4 [T	58	63	4.411765	CGTTCC	1.95312	1.99838

cg1919774	NOV	STAT4 [T	745	750	4.411765	GCTTCC	1.95312	1.99838
cg1919774	NOV	STAT4 [T	918	923	4.411765	CATTCC	1.95312	1.99838
cg1919774	NOV	STAT4 [T	931	936	4.411765	GCTTCC	1.95312	1.99838
cg1919774	NOV	STAT4 [T	1032	1037	4.411765	GGAAGC	1.95312	1.99838
cg1919774	NOV	STAT4 [T	1739	1744	4.411765	TCTTCC	1.95312	1.99838
cg1919774	NOV	STAT4 [T	1762	1767	4.411765	GCTTCC	1.95312	1.99838
cg1919774	NOV	c-Ets-1 [T	1355	1361	4.411026	AAGGAA	0.85449	0.8381
cg1919774	NOV	p53 [T006	978	984	4.33696	GGGCCA	0.24414	0.28373
cg1919774	NOV	HOXD9 [T	1332	1341	4.321431	TGATTT	0.03433	0.02831
cg1919774	NOV	HOXD10 [	1332	1341	4.321431	TGATTT	0.03433	0.02831
cg1919774	NOV	PEA3 [T0	1906	1914	4.30818	TGGATG	0.13733	0.13607
cg1919774	NOV	RAR-beta	1039	1048	4.307573	CGGGTT	0.14496	0.14853
cg1919774	NOV	c-Ets-1 [T	919	925	4.282938	ATTCCTC	0.85449	0.8381
cg1919774	NOV	GR-beta [T	793	797	4.201913	AATAA	7.8125	7.23274
cg1919774	NOV	GR-beta [T	796	800	4.201913	AATAA	7.8125	7.23274
cg1919774	NOV	GR-beta [T	799	803	4.201913	AATAA	7.8125	7.23274
cg1919774	NOV	GR-beta [T	807	811	4.201913	AATAA	7.8125	7.23274
cg1919774	NOV	GR-beta [T	1187	1191	4.201913	AATAA	7.8125	7.23274
cg1919774	NOV	GR-beta [T	1229	1233	4.201913	AATCA	7.8125	7.23274
cg1919774	NOV	GR-beta [T	1332	1336	4.201913	TGATT	7.8125	7.23274
cg1919774	NOV	GR-beta [T	1337	1341	4.201913	TTATT	7.8125	7.23274
cg1919774	NOV	NF-Y [T0	1372	1379	4.186615	TTCCCA	0.18311	0.17499
cg1919774	NOV	NF-Y [T0	1485	1492	4.186615	ATTGGG	0.18311	0.17499
cg1919774	NOV	NF-Y [T0	1765	1772	4.186615	TCCCCA	0.18311	0.17499
cg1919774	NOV	p53 [T006	501	507	4.125254	GGGCCG	0.73242	0.82434
cg1919774	NOV	p53 [T006	506	512	4.083527	GGTGCC	0.73242	0.82434
cg1919774	NOV	RXR-alpha	347	353	4.019014	CACACC	0.97656	1.02803
cg1919774	NOV	c-Ets-2 [T	888	896	4.017001	AGAAAG	0.16022	0.15061
cg1919774	NOV	c-Ets-2 [T	1285	1293	4.017001	TTCCTTT	0.16022	0.15061
cg1919774	NOV	TFIID [T0	1336	1342	4.007279	TTTATTA	1.09863	0.94722
cg1919774	NOV	Pax-5 [T0	494	500	4.007279	AGTGCC	1.09863	1.18533
cg1919774	NOV	Pax-5 [T0	865	871	4.007279	GGGCTT	1.09863	1.18533
cg1919774	NOV	Pax-5 [T0	1302	1308	4.007279	GGGCTT	1.09863	1.18533
cg1919774	NOV	Pax-5 [T0	1365	1371	4.007279	AATGCC	1.09863	1.18533
cg1919774	NOV	Pax-5 [T0	1930	1936	4.007279	ACTGCC	1.09863	1.18533
cg1919774	NOV	AP-2alpha	381	386	3.970052	GCCTTG	0.97656	1.02535
cg1919774	NOV	Elk-1 [T00	932	940	3.944668	CTTCCTA	0.09155	0.08816
cg1919774	NOV	PPAR-alph	423	433	3.872523	CTGTCC	0.02575	0.0279
cg1919774	NOV	NF-kappa	240	250	3.854366	GGGGAA	0.01097	0.01194
cg1919774	NOV	GR [T050	1744	1750	3.763516	CTCTTT	0.73242	0.6946
cg1919774	NOV	AP-2alpha	185	190	3.743866	GAAGGC	0.48828	0.5124
cg1919774	NOV	AP-2alpha	458	463	3.743866	GCCTTC	0.48828	0.5124
cg1919774	NOV	IRF-1 [T0	889	897	3.692688	GAAAGG	0.06866	0.0661
cg1919774	NOV	p53 [T006	1365	1371	3.516613	AATGCC	0.73242	0.80362
cg1919774	NOV	p53 [T006	1930	1936	3.516613	ACTGCC	0.73242	0.80362
cg1919774	NOV	RXR-alpha	539	545	3.392904	GGGTGC	1.09863	1.1653
cg1919774	NOV	RXR-alpha	1162	1168	3.392904	GTAACC	1.09863	1.1653
cg1919774	NOV	RXR-alpha	1810	1816	3.392904	GGGTCA	1.09863	1.1653

cg1919774	NOV	p53 [T006	155	161	3.375208	GGGCGT	0.73242	0.80362
cg1919774	NOV	GR-beta [	201	205	3.361531	AATCT	3.90625	3.51525
cg1919774	NOV	GR-beta [	945	949	3.361531	AATCT	3.90625	3.51525
cg1919774	NOV	GR-beta [	1275	1279	3.361531	AGATT	3.90625	3.51525
cg1919774	NOV	GR-beta [	1359	1363	3.361531	AATCT	3.90625	3.51525
cg1919774	NOV	GR-beta [	1696	1700	3.361531	AATCT	3.90625	3.51525
cg1919774	NOV	GR-beta [	1770	1774	3.361531	AATAT	3.90625	3.51525
cg1919774	NOV	GR-beta [	1771	1775	3.361531	ATATT	3.90625	3.51525
cg1919774	NOV	GR-beta [	1879	1883	3.361531	AGATT	3.90625	3.51525
cg1919774	NOV	c-Ets-2 [T	920	928	3.2883	TTCCTC	0.18311	0.18314
cg1919774	NOV	PXR-1:RX	1125	1132	3.2723	TGAACC	0.12207	0.11883
cg1919774	NOV	NF-Y [T0	196	203	3.263282	GTGCCA	0.48828	0.48427
cg1919774	NOV	AP-2alpha	638	643	3.229049	GCCTCT	0.48828	0.5124
cg1919774	NOV	AP-2alpha	1601	1606	3.229049	AGAGGC	0.48828	0.5124
cg1919774	NOV	NF-kappa	1079	1089	3.202683	GGGGAA	0.01669	0.01859
cg1919774	NOV	RXR-alph	1083	1089	3.170788	AAAACC	0.24414	0.24551
cg1919774	NOV	RXR-alph	1674	1680	3.170788	GGGTTT	0.24414	0.24551
cg1919774	NOV	AR [T000	1275	1283	3.131372	AGATTG	0.06104	0.0627
cg1919774	NOV	NF-AT1 [	242	250	3.098758	GGAAAG	0.03052	0.0304
cg1919774	NOV	p53 [T006	580	586	3.028543	TGTGCC	0.48828	0.53227
cg1919774	NOV	p53 [T006	1889	1895	3.028543	TGTGCC	0.48828	0.53227
cg1919774	NOV	Elk-1 [T00	1284	1292	2.987643	CTTCCTT	0.07629	0.07518
cg1919774	NOV	C/EBPalp	1484	1490	2.981957	CATTGG	0.48828	0.47526
cg1919774	NOV	STAT4 [T	64	69	2.941176	ACTTCC	2.92969	2.92382
cg1919774	NOV	STAT4 [T	242	247	2.941176	GGAAAG	2.92969	2.92382
cg1919774	NOV	STAT4 [T	765	770	2.941176	TATTCC	2.92969	2.92382
cg1919774	NOV	STAT4 [T	1357	1362	2.941176	GGAATC	2.92969	2.92382
cg1919774	NOV	STAT4 [T	1539	1544	2.941176	CTTTCC	2.92969	2.92382
cg1919774	NOV	STAT4 [T	1681	1686	2.941176	GGAACA	2.92969	2.92382
cg1919774	NOV	p53 [T006	358	364	2.813291	GATGCC	0.48828	0.53227
cg1919774	NOV	p53 [T006	482	488	2.813291	GCTGCC	0.48828	0.53227
cg1919774	NOV	PR B [T00	1261	1267	2.80933	AACATT	0.73242	0.66711
cg1919774	NOV	PR B [T00	1482	1488	2.80933	AACATT	0.73242	0.66711
cg1919774	NOV	PR A [T01	1261	1267	2.80933	AACATT	0.73242	0.66711
cg1919774	NOV	PR A [T01	1482	1488	2.80933	AACATT	0.73242	0.66711
cg1919774	NOV	CTF [T001	1877	1888	2.746279	GCAGAT	0.0062	0.0062
cg1919774	NOV	c-Ets-2 [T	747	755	2.715313	TTCCTCC	0.07629	0.07844
cg1919774	NOV	NFI/CTF [	108	115	2.683003	CCAACC	0.06104	0.06609
cg1919774	NOV	RXR-alph	908	914	2.544678	GGGTGA	0.85449	0.89683
cg1919774	NOV	AR [T000	1112	1120	2.519152	TAATTG	0.11444	0.11078
cg1919774	NOV	C/EBPalp	1374	1380	2.371703	CCCAAT	0.48828	0.47439
cg1919774	NOV	NF-Y [T0	29	36	2.355069	CAGCCA	0.21362	0.20842
cg1919774	NOV	NF-Y [T0	1881	1888	2.355069	ATTGGC	0.21362	0.20842
cg1919774	NOV	c-Jun [T00	836	842	2.345465	TGTGTC	0.48828	0.48077
cg1919774	NOV	GCF [T00	525	533	2.339499	GACCTG	0.06104	0.06908
cg1919774	NOV	Elk-1 [T00	1740	1748	2.299314	CTTCCTC	0.09155	0.09306
cg1919774	NOV	LEF-1 [T0	1127	1134	2.21836	AACCAA	0.18311	0.17215
cg1919774	NOV	c-Ets-2 [T	1541	1549	2.217136	TTCCTC	0.16785	0.16456

cg1919774	NOV	LEF-1 [T0	950	957	2.004405	AAGCAA	0.18311	0.17215
cg1919774	NOV	LEF-1 [T0	1746	1753	2.004405	CTTTGC	0.18311	0.17215
cg1919774	NOV	LEF-1 [T0	1758	1765	2.004405	CTTTGC	0.18311	0.17215
cg1919774	NOV	GATA-1 [	783	788	2.001358	GCGATA	3.90625	3.79558
cg1919774	NOV	GATA-1 [	1151	1156	2.001358	GGGATA	3.90625	3.79558
cg1919774	NOV	NF-AT1 [	1398	1406	1.970716	GGAAAA	0.06866	0.0623
cg1919774	NOV	p53 [T006	374	380	1.970013	TTTGCC	0.36621	0.38097
cg1919774	NOV	AP-2alpha	1605	1610	1.871933	GCCTCC	0.97656	1.07805
cg1919774	NOV	TBP [T007	136	145	1.871542	GCGCTA	0.18311	0.15671
cg1919774	NOV	FOXP3 [T	1258	1263	1.824994	TACAAC	0.48828	0.46414
cg1919774	NOV	TFII-I [T0	14	19	1.824994	GGAGAG	0.48828	0.51201
cg1919774	NOV	TFII-I [T0	1827	1832	1.824994	GGAGAG	0.48828	0.51201
cg1919774	NOV	TFII-I [T0	1962	1967	1.824994	GGAGAG	0.48828	0.51201
cg1919774	NOV	c-Ets-1 [T	1447	1453	1.769212	TAGGAA	0.12207	0.11281
cg1919774	NOV	C/EBPalph	1719	1725	1.761449	TATTGT	0.48828	0.46352
cg1919774	NOV	C/EBPalph	1767	1773	1.761449	CCCAAT	0.48828	0.46352
cg1919774	NOV	p53 [T006	1875	1881	1.758307	GGGCAG	0.36621	0.38097
cg1919774	NOV	RXR-alpha	659	665	1.696452	CGGACC	0.48828	0.52093
cg1919774	NOV	GR-beta [	802	806	1.680765	AATGC	3.90625	3.70067
cg1919774	NOV	GR-beta [	917	921	1.680765	GCATT	3.90625	3.70067
cg1919774	NOV	GR-beta [	1192	1196	1.680765	AATGC	3.90625	3.70067
cg1919774	NOV	GR-beta [	1365	1369	1.680765	AATGC	3.90625	3.70067
cg1919774	NOV	GR-beta [	1852	1856	1.680765	AATTC	3.90625	3.70067
cg1919774	NOV	AR [T0004	1001	1009	1.655418	GGACAC	0.09155	0.09239
cg1919774	NOV	c-Ets-1 [T	891	897	1.641124	AAGGAA	0.36621	0.35197
cg1919774	NOV	c-Ets-1 [T	993	999	1.641124	TTTCCTT	0.36621	0.35197
cg1919774	NOV	C/EBPbeta	32	35	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	108	111	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	199	202	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	225	228	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	365	368	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	384	387	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	398	401	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	851	854	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	862	865	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	870	873	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	928	931	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1021	1024	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1066	1069	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1077	1080	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1129	1132	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1207	1210	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1375	1378	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1396	1399	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1486	1489	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1509	1512	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1672	1675	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1679	1682	1.639871	TTGG	15.625	15.23827

cg1919774	NOV	C/EBPbeta	1693	1696	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1768	1771	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1842	1845	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1882	1885	1.639871	TTGG	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1941	1944	1.639871	CCAA	15.625	15.23827
cg1919774	NOV	XBP-1 [T	812	817	1.583727	ATGACA	0.97656	0.94995
cg1919774	NOV	XBP-1 [T	1811	1816	1.583727	GGTCAT	0.97656	0.94995
cg1919774	NOV	TFIID [T0	760	766	1.537547	TTTTGTA	0.73242	0.65627
cg1919774	NOV	TFIID [T0	1246	1252	1.537547	TTTTTCA	0.73242	0.65627
cg1919774	NOV	TFIID [T0	1397	1403	1.537547	TGGAAA	0.73242	0.65627
cg1919774	NOV	TFIID [T0	1677	1683	1.537547	TTTTGGA	0.73242	0.65627
cg1919774	NOV	Pax-5 [T0	4	10	1.537547	CGCGCC	0.73242	0.83087
cg1919774	NOV	Pax-5 [T0	155	161	1.537547	GGGCGT	0.73242	0.83087
cg1919774	NOV	Pax-5 [T0	978	984	1.537547	GGGCCA	0.73242	0.83087
cg1919774	NOV	c-Ets-1 [T	1540	1546	1.513038	TTTCCTC	0.36621	0.35197
cg1919774	NOV	c-Ets-1 [T	1734	1740	1.513038	TTTCCTC	0.36621	0.35197
cg1919774	NOV	STAT4 [T	893	898	1.470588	GGAAAC	1.95312	1.90161
cg1919774	NOV	STAT4 [T	1061	1066	1.470588	GTTTCC	1.95312	1.90161
cg1919774	NOV	STAT4 [T	1081	1086	1.470588	GGAAAA	1.95312	1.90161
cg1919774	NOV	STAT4 [T	1398	1403	1.470588	GGAAAA	1.95312	1.90161
cg1919774	NOV	STAT4 [T	1449	1454	1.470588	GGAAAC	1.95312	1.90161
cg1919774	NOV	STAT4 [T	1489	1494	1.470588	GGAAAA	1.95312	1.90161
cg1919774	NOV	STAT4 [T	1733	1738	1.470588	TTTTCC	1.95312	1.90161
cg1919774	NOV	STAT4 [T	1852	1857	1.470588	AATTCC	1.95312	1.90161
cg1919774	NOV	NF-Y [T0	1204	1211	1.447632	TAGCCA	0.18311	0.17671
cg1919774	NOV	C/EBPbeta	714	717	1.366559	TTGA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1124	1127	1.366559	TTGA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1242	1245	1.366559	TCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1271	1274	1.366559	TTGA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1346	1349	1.366559	TTGA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1353	1356	1.366559	TCAA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1380	1383	1.366559	TTGA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1579	1582	1.366559	TTGA	15.625	15.23827
cg1919774	NOV	C/EBPbeta	1951	1954	1.366559	TTGA	15.625	15.23827
cg1919774	NOV	c-Myb [T0	1928	1935	1.285398	TAACTG	0.06104	0.06236
cg1919774	NOV	NFI/CTF [	221	228	1.227415	TCGTTTC	0.18311	0.19134
cg1919774	NOV	c-Ets-2 [T	1735	1743	1.071163	TTCCTCT	0.06104	0.0583
cg1919774	NOV	c-Ets-2 [T	1741	1749	1.071163	TTCCTCT	0.06104	0.0583
cg1919774	NOV	GATA-1 [	1254	1259	1.038567	ATGATA	1.95312	1.80234
cg1919774	NOV	RXR-alpha	53	59	0.848226	GGGTTC	0.48828	0.51313
cg1919774	NOV	GR-beta [	33	37	0.840383	CAATT	7.8125	7.2174
cg1919774	NOV	GR-beta [	34	38	0.840383	AATTG	7.8125	7.2174
cg1919774	NOV	GR-beta [	394	398	0.840383	CCATT	7.8125	7.2174
cg1919774	NOV	GR-beta [	811	815	0.840383	AATGA	7.8125	7.2174
cg1919774	NOV	GR-beta [	990	994	0.840383	TCATT	7.8125	7.2174
cg1919774	NOV	GR-beta [	1112	1116	0.840383	TAATT	7.8125	7.2174
cg1919774	NOV	GR-beta [	1113	1117	0.840383	AATTG	7.8125	7.2174
cg1919774	NOV	GR-beta [	1120	1124	0.840383	CCATT	7.8125	7.2174

cg1919774	NOV	GR-beta [T	1243	1247	0.840383	CAATT	7.8125	7.2174
cg1919774	NOV	GR-beta [T	1376	1380	0.840383	CAATT	7.8125	7.2174
cg1919774	NOV	GR-beta [T	1474	1478	0.840383	AATGA	7.8125	7.2174
cg1919774	NOV	GR-beta [T	1494	1498	0.840383	AATGG	7.8125	7.2174
cg1919774	NOV	GR-beta [T	1555	1559	0.840383	AATGA	7.8125	7.2174
cg1919774	NOV	PXR-1:RX	1656	1663	0.818075	TGAACT	0.12207	0.11843
cg1919774	NOV	AP-2alpha	247	252	0.678558	GCCTGA	0.48828	0.51196
cg1919774	NOV	AP-2alpha	304	309	0.678558	GCCTGA	0.48828	0.51196
cg1919774	NOV	AP-2alpha	840	845	0.678558	TCAGGC	0.48828	0.51196
cg1919774	NOV	AP-2alpha	1653	1658	0.678558	GCCTGA	0.48828	0.51196
cg1919774	NOV	AP-2alpha	1919	1924	0.678558	GCCTGA	0.48828	0.51196
cg1919774	NOV	RXR-alph	1040	1046	0.62611	GGGTTT	0.12207	0.11915
cg1919774	NOV	c-Ets-1 [T	932	938	0.384261	CTTCCT	0.24414	0.23743
cg1919774	NOV	GATA-1 [	1631	1636	0.280028	TAGATA	0.97656	0.8795
cg1919774	NOV	c-Ets-1 [T	1284	1290	0.256174	CTTCCT	0.24414	0.23743
cg1919774	NOV	AP-2alpha	1212	1217	0.226186	CCAGGC	0.97656	1.07867
cg1919774	NOV	AP-2alpha	1958	1963	0.226186	GCCTGG	0.97656	1.07867
cg1919774	NOV	GR-alpha [	237	241	0.207689	AGAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	299	303	0.207689	CCTTT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	639	643	0.207689	CCTCT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	704	708	0.207689	CCTCT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	718	722	0.207689	CCTCT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	778	782	0.207689	AGAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	890	894	0.207689	AAAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	913	917	0.207689	AAAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	954	958	0.207689	AAAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1167	1171	0.207689	CCTTT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1287	1291	0.207689	CCTTT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1536	1540	0.207689	CCTCT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1601	1605	0.207689	AGAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1665	1669	0.207689	AAAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1737	1741	0.207689	CCTCT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1743	1747	0.207689	CCTCT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1784	1788	0.207689	AGAGG	7.8125	7.79817
cg1919774	NOV	Elk-1 [T00	311	319	0.134348	CTTCCT	0.06104	0.06399
cg1919774	NOV	c-Ets-1 [T	746	752	0.128087	CTTCCT	0.24414	0.24982
cg1919774	NOV	c-Ets-1 [T	1740	1746	0.128087	CTTCCT	0.24414	0.24982
cg1919774	NOV	GATA-1 [	1789	1794	0.105011	GAGATA	0.97656	0.92541
cg1919774	NOV	GR-beta [T	1244	1248	0	AATTT	3.90625	3.51525
cg1919774	NOV	GR-beta [T	1262	1266	0	ACATT	3.90625	3.51525
cg1919774	NOV	GR-beta [T	1377	1381	0	AATTT	3.90625	3.51525
cg1919774	NOV	GR-beta [T	1483	1487	0	ACATT	3.90625	3.51525
cg1919774	NOV	GR-beta [T	1833	1837	0	AAATT	3.90625	3.51525
cg1919774	NOV	GR-beta [T	1834	1838	0	AATTT	3.90625	3.51525
cg1919774	NOV	GR-beta [T	1851	1855	0	AAATT	3.90625	3.51525
cg1919774	NOV	XBP-1 [T	988	993	0	AGTCAT	0.97656	0.94838
cg1919774	NOV	XBP-1 [T	1475	1480	0	ATGACT	0.97656	0.94838
cg1919774	NOV	TFIID [T	140	146	0	TATAAA	1.09863	0.95175

cg1919774	NOV	TFIID [T0	1219	1225	0	TCTAAA	1.09863	0.95175
cg1919774	NOV	TFIID [T0	1424	1430	0	TTTTTAA	1.09863	0.95175
cg1919774	NOV	TFIID [T0	1661	1667	0	TAGAAA	1.09863	0.95175
cg1919774	NOV	GR-alpha [	147	151	0	CCTGT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	335	339	0	ACAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1108	1112	0	CCTGT	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1296	1300	0	ACAGG	7.8125	7.79817
cg1919774	NOV	GR-alpha [	1392	1396	0	CCTGT	7.8125	7.79817
cg1919774	NOV	C/EBPbeta	36	39	0	TTGC	15.625	15.26275
cg1919774	NOV	C/EBPbeta	44	47	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	117	120	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	166	169	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	281	284	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	302	305	0	TTGC	15.625	15.26275
cg1919774	NOV	C/EBPbeta	375	378	0	TTGC	15.625	15.26275
cg1919774	NOV	C/EBPbeta	447	450	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	668	671	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	762	765	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	790	793	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	805	808	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	940	943	0	ACAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	952	955	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1097	1100	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1115	1118	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1179	1182	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1199	1202	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1259	1262	0	ACAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1265	1268	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1278	1281	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1470	1473	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1529	1532	0	TTGC	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1563	1566	0	GCAA	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1593	1596	0	TTGC	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1721	1724	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1729	1732	0	TTGT	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1748	1751	0	TTGC	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1760	1763	0	TTGC	15.625	15.26275
cg1919774	NOV	C/EBPbeta	1849	1852	0	GCAA	15.625	15.26275
cg1919774	NOV	YY1 [T00	39	42	0	CCAT	7.8125	7.79459
cg1919774	NOV	YY1 [T00	41	44	0	ATGG	7.8125	7.79459
cg1919774	NOV	YY1 [T00	323	326	0	CCAT	7.8125	7.79459
cg1919774	NOV	YY1 [T00	394	397	0	CCAT	7.8125	7.79459
cg1919774	NOV	YY1 [T00	619	622	0	CCAT	7.8125	7.79459
cg1919774	NOV	YY1 [T00	846	849	0	ATGG	7.8125	7.79459
cg1919774	NOV	YY1 [T00	1030	1033	0	ATGG	7.8125	7.79459
cg1919774	NOV	YY1 [T00	1120	1123	0	CCAT	7.8125	7.79459
cg1919774	NOV	YY1 [T00	1495	1498	0	ATGG	7.8125	7.79459
cg1919774	NOV	YY1 [T00	1549	1552	0	CCAT	7.8125	7.79459

cg1919774	NOV	YY1 [T00	1609	1612	0	CCAT	7.8125	7.79459
cg1919774	NOV	YY1 [T00	1807	1810	0	ATGG	7.8125	7.79459
cg1919774	NOV	YY1 [T00	1873	1876	0	ATGG	7.8125	7.79459
cg1919774	NOV	TFII-I [T0	242	247	0	GGAAAG	1.46484	1.48598
cg1919774	NOV	TFII-I [T0	333	338	0	GGACAG	1.46484	1.48598
cg1919774	NOV	TFII-I [T0	423	428	0	CTGTCC	1.46484	1.48598
cg1919774	NOV	TFII-I [T0	1294	1299	0	GGACAG	1.46484	1.48598
cg1919774	NOV	TFII-I [T0	1539	1544	0	CTTTCC	1.46484	1.48598
cg1919774	NOV	STAT4 [T	992	997	0	ATTTCC	0.48828	0.46235
cg1919774	NOV	c-Ets-1 [T	311	317	0	CTTCCTC	0.24414	0.24982
cg1919774	NOV	ER-alpha [	307	311	0	TGACC	1.95312	1.99744
cg1919774	NOV	ER-alpha [	400	404	0	GGTCA	1.95312	1.99744
cg1919774	NOV	ER-alpha [	715	719	0	TGACC	1.95312	1.99744
cg1919774	NOV	ER-alpha [	1811	1815	0	GGTCA	1.95312	1.99744
cg1919774	NOV	TCF-4E [T	951	957	0	AGCAAA	0.12207	0.11933
cg1919774	NOV	TCF-4E [T	1746	1752	0	CTTTGCT	0.12207	0.11933
cg1919774	NOV	TCF-4E [T	1758	1764	0	CTTTGCT	0.12207	0.11933
cg1919774	NOV	Pax-5 [T0	501	507	0	GGGCCG	1.09863	1.24633
cg1919774	NOV	Pax-5 [T0	898	904	0	CCTGCC	1.09863	1.24633
cg1919774	NOV	Pax-5 [T0	1685	1691	0	CATGCC	1.09863	1.24633
cg1919774	NOV	p53 [T006	898	904	0	CCTGCC	0.36621	0.40082
cg1919774	NOV	p53 [T006	1685	1691	0	CATGCC	0.36621	0.40082
cg1919774	NOV	AP-2alpha	454	459	0	GCCTGC	0.97656	1.07867
cg1919774	NOV	AP-2alpha	1195	1200	0	GCAGGC	0.97656	1.07867
cg1919774	NOV	Elk-1 [T00	746	754	0	CTTCCTC	0.06104	0.06399
cg1919774	NOV	IRF-2 [T01	735	740	0	AAGTGA	0.48828	0.46235
cg1919774	NOV	IRF-2 [T01	924	929	0	TCACTT	0.48828	0.46235
cg1919774	NOV	IRF-2 [T01	1518	1523	0	TCACTT	0.48828	0.46235
cg1919774	NOV	IRF-2 [T01	1755	1760	0	TCACTT	0.48828	0.46235
cg1919774	NOV	EBF [T05	900	910	0	TGCCCTC	0.00381	0.00466
cg1029199	NR0B1	Egr-3 [T0	1547	1559	9.828903	AGCGCC	0.02503	0.02648
cg1029199	NR0B1	XBP-1 [T	860	865	9.789909	CGCCAT	1.95312	1.94901
cg1029199	NR0B1	NF-AT2 [	1247	1256	9.787971	GGAAAC	0.08774	0.08205
cg1029199	NR0B1	NF-1 [T00	1410	1417	9.761671	GGCTCC	0.24414	0.24488
cg1029199	NR0B1	PR B [T00	1017	1023	9.743489	GTGTGT	1.09863	1.0981
cg1029199	NR0B1	PR B [T00	1569	1575	9.743489	CTGTGT	1.09863	1.0981
cg1029199	NR0B1	PR A [T01	1017	1023	9.743489	GTGTGT	1.09863	1.0981
cg1029199	NR0B1	PR A [T01	1569	1575	9.743489	CTGTGT	1.09863	1.0981
cg1029199	NR0B1	TFIID [T0	1816	1822	9.552105	TTTCTCA	1.46484	1.37777
cg1029199	NR0B1	Pax-5 [T0	288	294	9.552105	GTGGCC	1.46484	1.61918
cg1029199	NR0B1	Pax-5 [T0	493	499	9.552105	GCCGCC	1.46484	1.61918
cg1029199	NR0B1	Pax-5 [T0	575	581	9.552105	GGGCGC	1.46484	1.61918
cg1029199	NR0B1	Pax-5 [T0	691	697	9.552105	TCCGCC	1.46484	1.61918
cg1029199	NR0B1	Pax-5 [T0	873	879	9.552105	GGCGCC	1.46484	1.61918
cg1029199	NR0B1	Pax-5 [T0	880	886	9.552105	GTAGCC	1.46484	1.61918
cg1029199	NR0B1	NF-1 [T00	1397	1404	9.535536	ATGCCC	0.73242	0.74634
cg1029199	NR0B1	HNF-1B [	1733	1741	9.513548	TGTTATA	0.09155	0.08192
cg1029199	NR0B1	FOXP3 [T	851	856	9.512894	GTTCTC	7.32422	7.22156

cg1029199	NR0B1	FOXP3 [T	888	893	9.512894	GTTCTG	7.32422	7.22156
cg1029199	NR0B1	FOXP3 [T	1079	1084	9.512894	AAGAAC	7.32422	7.22156
cg1029199	NR0B1	FOXP3 [T	1272	1277	9.512894	GTAAAC	7.32422	7.22156
cg1029199	NR0B1	FOXP3 [T	1359	1364	9.512894	CAGAAC	7.32422	7.22156
cg1029199	NR0B1	FOXP3 [T	1925	1930	9.512894	GAGAAC	7.32422	7.22156
cg1029199	NR0B1	TFII-I [T0	153	158	9.512894	GTGTCC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	345	350	9.512894	CGGTCC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	688	693	9.512894	CGTTCC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1103	1108	9.512894	GGACAC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1115	1120	9.512894	CCTTCC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1239	1244	9.512894	GGAAAA	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1247	1252	9.512894	GGAAAC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1452	1457	9.512894	GTGTCC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1643	1648	9.512894	GGATAA	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1799	1804	9.512894	GTATCC	7.32422	7.44385
cg1029199	NR0B1	TFII-I [T0	1885	1890	9.512894	GTGTCC	7.32422	7.44385
cg1029199	NR0B1	TCF-4E [T	404	410	9.453578	CTTTGAC	0.48828	0.46934
cg1029199	NR0B1	TCF-4E [T	1268	1274	9.453578	CTTTGTA	0.48828	0.46934
cg1029199	NR0B1	c-Ets-1 [T0	1381	1387	9.276861	TGGGAA	0.36621	0.37402
cg1029199	NR0B1	SRY [T00	404	412	9.264664	CTTTGAC	0.12207	0.11857
cg1029199	NR0B1	NF-AT1 [T	1129	1137	9.18189	CCCCTTT	0.22888	0.22581
cg1029199	NR0B1	PPAR-alph	557	567	9.158357	CGGACC	0.0515	0.05878
cg1029199	NR0B1	c-Ets-1 [T0	1216	1222	9.148774	GTTCCCT	0.85449	0.84987
cg1029199	NR0B1	STAT5A [	1335	1347	9.080962	CATTTC	0.02816	0.02551
cg1029199	NR0B1	USF2 [T00	31	40	9.056375	GCAGCA	0.1545	0.16206
cg1029199	NR0B1	c-Myb [T0	1292	1299	9.024874	CACAGT	0.39673	0.37851
cg1029199	NR0B1	c-Myb [T0	1520	1527	9.024874	CTCAGTT	0.39673	0.37851
cg1029199	NR0B1	c-Ets-1 [T0	1873	1879	9.020687	GTTCCCC	0.85449	0.84987
cg1029199	NR0B1	MEF-2A [	1685	1695	9.003254	TATTTTT	0.07343	0.06466
cg1029199	NR0B1	GR [T050	261	267	8.971049	CAAAAG	0.61035	0.5928
cg1029199	NR0B1	GR [T050	462	468	8.971049	CAAAAG	0.61035	0.5928
cg1029199	NR0B1	GR [T050	660	666	8.971049	CAAAAG	0.61035	0.5928
cg1029199	NR0B1	AP-1 [T00	1303	1311	8.94997	TGACTTA	0.24414	0.23028
cg1029199	NR0B1	c-Ets-2 [T0	1618	1626	8.912323	ACTTAGC	0.27466	0.27171
cg1029199	NR0B1	p53 [T006	166	172	8.912104	GGGCCC	0.12207	0.13824
cg1029199	NR0B1	Elk-1 [T00	500	508	8.897321	ACCCGG	0.24414	0.26271
cg1029199	NR0B1	NF-kappaB	1869	1879	8.816146	TGTTGTT	0.03576	0.03905
cg1029199	NR0B1	NFI/CTF [	1803	1810	8.814757	CCAATA	0.48828	0.48845
cg1029199	NR0B1	NF-1 [T00	1226	1233	8.790071	TTGGGA	0.24414	0.24339
cg1029199	NR0B1	LEF-1 [T0	1268	1275	8.759086	CTTTGTA	0.54932	0.53171
cg1029199	NR0B1	XBP-1 [T0	727	732	8.75604	GCTCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T0	809	814	8.75604	GCTCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T0	1121	1126	8.75604	TCTCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T0	1278	1283	8.75604	TTTCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T0	1332	1337	8.75604	TCTCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T0	1509	1514	8.75604	TATCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T0	1670	1675	8.75604	TTTCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T0	1780	1785	8.75604	TTTCAT	2.92969	2.75329

cg1029199	NR0B1	XBP-1 [T	1818	1823	8.75604	TCTCAT	2.92969	2.75329
cg1029199	NR0B1	XBP-1 [T	1988	1993	8.75604	TCTCAT	2.92969	2.75329
cg1029199	NR0B1	NF-AT1 [	1247	1255	8.746017	GGAAAC	0.10681	0.10494
cg1029199	NR0B1	c-Myb [T0	1274	1281	8.728118	AAACTT	0.30518	0.28602
cg1029199	NR0B1	STAT1bet	1108	1117	8.695301	CTTTCCT	0.22316	0.2175
cg1029199	NR0B1	STAT1bet	1389	1398	8.695301	CGGTGG	0.22316	0.2175
cg1029199	NR0B1	EBF [T05	158	168	8.694128	CCACCA	0.03052	0.03497
cg1029199	NR0B1	IRF-1 [T0	1389	1397	8.570857	CGGTGG	0.20599	0.20245
cg1029199	NR0B1	E2F-1 [T0	254	261	8.536191	TTCACC	0.15259	0.16676
cg1029199	NR0B1	AhR:Arnt	353	362	8.431005	CCACGC	0.07439	0.08553
cg1029199	NR0B1	HNF-1B [	1424	1432	8.379818	TTTCTA	0.11444	0.10456
cg1029199	NR0B1	HNF-3alph	1442	1449	8.343064	CATTTT	0.27466	0.23078
cg1029199	NR0B1	c-Ets-2 [T	1951	1959	8.339336	TTCCTG	0.13733	0.13927
cg1029199	NR0B1	PR B [T00	78	84	8.338824	AACAGG	1.09863	1.09384
cg1029199	NR0B1	PR B [T00	544	550	8.338824	AACAGC	1.09863	1.09384
cg1029199	NR0B1	PR B [T00	742	748	8.338824	AACAGC	1.09863	1.09384
cg1029199	NR0B1	PR B [T00	1082	1088	8.338824	AACAGC	1.09863	1.09384
cg1029199	NR0B1	PR B [T00	1175	1181	8.338824	TGCTGT	1.09863	1.09384
cg1029199	NR0B1	PR B [T00	1866	1872	8.338824	GTCTGT	1.09863	1.09384
cg1029199	NR0B1	PR B [T00	1946	1952	8.338824	TTCTGTT	1.09863	1.09384
cg1029199	NR0B1	PR A [T01	78	84	8.338824	AACAGG	1.09863	1.09384
cg1029199	NR0B1	PR A [T01	544	550	8.338824	AACAGC	1.09863	1.09384
cg1029199	NR0B1	PR A [T01	742	748	8.338824	AACAGC	1.09863	1.09384
cg1029199	NR0B1	PR A [T01	1082	1088	8.338824	AACAGC	1.09863	1.09384
cg1029199	NR0B1	PR A [T01	1175	1181	8.338824	TGCTGT	1.09863	1.09384
cg1029199	NR0B1	PR A [T01	1866	1872	8.338824	GTCTGT	1.09863	1.09384
cg1029199	NR0B1	PR A [T01	1946	1952	8.338824	TTCTGTT	1.09863	1.09384
cg1029199	NR0B1	E2F-1 [T0	855	862	8.336446	TCGCCC	0.15259	0.16676
cg1029199	NR0B1	GR-alpha [	97	101	8.281568	CCTCG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	149	153	8.281568	GGAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	170	174	8.281568	CCTCG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	181	185	8.281568	CCTCC	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	373	377	8.281568	CCTCG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	571	575	8.281568	CCTCG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	580	584	8.281568	CCTTC	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	905	909	8.281568	CCTCC	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	953	957	8.281568	CCTCG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	965	969	8.281568	CAAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	974	978	8.281568	GGAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1033	1037	8.281568	CCTCG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1045	1049	8.281568	GAAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1112	1116	8.281568	CCTCC	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1115	1119	8.281568	CCTTC	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1154	1158	8.281568	GGAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1201	1205	8.281568	CCTCG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1229	1233	8.281568	GGAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1327	1331	8.281568	GGAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1347	1351	8.281568	CCTTG	7.8125	8.20394

cg1029199	NR0B1	GR-alpha [	1638	1642	8.281568	CGAGG	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1841	1845	8.281568	CCTCC	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1847	1851	8.281568	CCTTC	7.8125	8.20394
cg1029199	NR0B1	GR-alpha [	1878	1882	8.281568	CCTCC	7.8125	8.20394
cg1029199	NR0B1	c-Jun [T00	1030	1036	8.242207	TGACCT	0.48828	0.47447
cg1029199	NR0B1	NFI/CTF [	1414	1421	8.241664	CCAACC	0.18311	0.1922
cg1029199	NR0B1	p53 [T006	165	171	8.208781	GGGGCC	0.48828	0.55336
cg1029199	NR0B1	ENKTF-1	837	844	8.19852	CCCTGC	0.73242	0.80254
cg1029199	NR0B1	ENKTF-1	857	864	8.19852	GCCCGC	0.73242	0.80254
cg1029199	NR0B1	ENKTF-1	1978	1985	8.19852	GGCCGC	0.73242	0.80254
cg1029199	NR0B1	p53 [T006	377	383	8.162057	GGGCGC	0.48828	0.55336
cg1029199	NR0B1	p53 [T006	1547	1553	8.162057	AGCGCC	0.48828	0.55336
cg1029199	NR0B1	c-Ets-1 [T	1858	1864	8.116854	GTTCCA	0.24414	0.2494
cg1029199	NR0B1	GR-alpha [	25	29	8.073878	CCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	37	41	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	44	48	8.073878	GCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	161	165	8.073878	CCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	193	197	8.073878	CCTGC	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	238	242	8.073878	CCTGC	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	300	304	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	321	325	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	338	342	8.073878	GTAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	363	367	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	439	443	8.073878	CCTGC	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	637	641	8.073878	CCTGC	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	838	842	8.073878	CCTGC	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	908	912	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	925	929	8.073878	CCTAG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	937	941	8.073878	GCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1100	1104	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1169	1173	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1234	1238	8.073878	GCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1458	1462	8.073878	CCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1475	1479	8.073878	CCTAG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1561	1565	8.073878	CCTGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1596	1600	8.073878	GCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1789	1793	8.073878	CCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1854	1858	8.073878	GTAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1881	1885	8.073878	CCTAG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1889	1893	8.073878	CCAGG	7.8125	8.20289
cg1029199	NR0B1	GR-alpha [	1953	1957	8.073878	CCTGC	7.8125	8.20289
cg1029199	NR0B1	HNF-1C [	1734	1742	8.067744	GTTATA	0.19836	0.18126
cg1029199	NR0B1	TFIID [T0	1269	1275	8.014558	TTTGTA	2.19727	1.99811
cg1029199	NR0B1	TFIID [T0	1338	1344	8.014558	TTTCTG	2.19727	1.99811
cg1029199	NR0B1	TFIID [T0	1424	1430	8.014558	TTTCTA	2.19727	1.99811
cg1029199	NR0B1	TFIID [T0	1483	1489	8.014558	TTTGAA	2.19727	1.99811
cg1029199	NR0B1	TFIID [T0	1731	1737	8.014558	TTTGTTA	2.19727	1.99811
cg1029199	NR0B1	TFIID [T0	1963	1969	8.014558	TTTGCT	2.19727	1.99811

cg1029199	NR0B1	Pax-5 [T0	29	35	8.014558	GGGCAG	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	165	171	8.014558	GGGGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	233	239	8.014558	GCTGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	434	440	8.014558	GCTGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	491	497	8.014558	GGGCCG	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	505	511	8.014558	GAAGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	515	521	8.014558	TCTGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	632	638	8.014558	GCTGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	703	709	8.014558	GCAGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	713	719	8.014558	TCTGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	725	731	8.014558	GGGCTC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	833	839	8.014558	GCTGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	890	896	8.014558	TCTGCC	2.19727	2.42766
cg1029199	NR0B1	Pax-5 [T0	1587	1593	8.014558	GGGCAG	2.19727	2.42766
cg1029199	NR0B1	USF2 [T0	103	112	8.007902	AGACCA	0.01717	0.01801
cg1029199	NR0B1	MEF-2A [	917	927	7.982343	TATTTAT	0.04005	0.03447
cg1029199	NR0B1	ETF [T002	867	877	7.870358	GCCCGC	0.07153	0.08737
cg1029199	NR0B1	p53 [T006	864	870	7.853573	ATGGCC	0.48828	0.55336
cg1029199	NR0B1	c-Ets-2 [T	1141	1149	7.84116	TCTCAG	0.32043	0.30792
cg1029199	NR0B1	E2F-1 [T0	289	296	7.839654	TGGCCC	0.30518	0.32869
cg1029199	NR0B1	E2F-1 [T0	865	872	7.839654	TGGCCC	0.30518	0.32869
cg1029199	NR0B1	T3R-beta1	1785	1793	7.774776	TCACCC	0.27466	0.28753
cg1029199	NR0B1	HNF-1C [	1423	1431	7.717465	CTTTCTA	0.08392	0.07663
cg1029199	NR0B1	GR [T050	402	408	7.527031	TGCTTT	1.83105	1.71535
cg1029199	NR0B1	GR [T050	600	606	7.527031	TGCTTT	1.83105	1.71535
cg1029199	NR0B1	GR [T050	1309	1315	7.527031	ATATTT	1.83105	1.71535
cg1029199	NR0B1	GR [T050	1936	1942	7.527031	ATATTT	1.83105	1.71535
cg1029199	NR0B1	RAR-beta:	1191	1202	7.477995	TCCATT	0.02861	0.03163
cg1029199	NR0B1	C/EBPalph	1193	1199	7.465744	CATTGA	0.48828	0.45033
cg1029199	NR0B1	p53 [T006	575	581	7.458735	GGGCGC	0.73242	0.79826
cg1029199	NR0B1	p53 [T006	873	879	7.458735	GGCGCC	0.73242	0.79826
cg1029199	NR0B1	PEA3 [T0	429	437	7.421728	AGGATG	0.34332	0.35389
cg1029199	NR0B1	PEA3 [T0	627	635	7.421728	AGGATG	0.34332	0.35389
cg1029199	NR0B1	PEA3 [T0	828	836	7.421728	AGGATG	0.34332	0.35389
cg1029199	NR0B1	LEF-1 [T0	602	609	7.396545	CTTTGC	0.21362	0.21504
cg1029199	NR0B1	PPAR-alph	546	556	7.370536	CAGCCC	0.04482	0.04884
cg1029199	NR0B1	PPAR-alph	744	754	7.370536	CAGCCC	0.04482	0.04884
cg1029199	NR0B1	E2F-1 [T0	439	446	7.336545	CCTGCC	0.45776	0.49661
cg1029199	NR0B1	HOXD9 [T	1625	1634	7.270719	AATATA	0.06866	0.05771
cg1029199	NR0B1	HOXD10 [	1625	1634	7.270719	AATATA	0.06866	0.05771
cg1029199	NR0B1	p53 [T006	545	551	7.266844	ACAGCC	0.73242	0.79826
cg1029199	NR0B1	p53 [T006	743	749	7.266844	ACAGCC	0.73242	0.79826
cg1029199	NR0B1	GCF [T00	65	73	7.186486	GCGCAG	0.45776	0.50397
cg1029199	NR0B1	GCF [T00	326	334	7.186486	CCTCTG	0.45776	0.50397
cg1029199	NR0B1	GCF [T00	1004	1012	7.186486	GTGCTG	0.45776	0.50397
cg1029199	NR0B1	SRY [T00	1962	1970	7.175614	CTTTGCT	0.30518	0.29547
cg1029199	NR0B1	XBP-1 [T	1374	1379	7.172312	CATCAT	2.92969	2.7512
cg1029199	NR0B1	XBP-1 [T	1973	1978	7.172312	ATGATG	2.92969	2.7512

cg1029199	NR0B1	p53 [T006	288	294	7.150251	GTGGCC	1.09863	1.22478
cg1029199	NR0B1	NF-AT1 [T	1239	1247	7.095752	GGAAAA	0.15259	0.14325
cg1029199	NR0B1	c-Ets-1 [T	1133	1139	7.071349	TTTCCCT	0.73242	0.73732
cg1029199	NR0B1	HNF-3alph	1310	1317	7.000129	TATTTGT	0.82397	0.71909
cg1029199	NR0B1	HNF-3alph	1351	1358	7.000129	GAAAAA	0.82397	0.71909
cg1029199	NR0B1	RXR-alpha	246	252	6.967687	GGGTGG	0.36621	0.38841
cg1029199	NR0B1	RXR-alpha	447	453	6.967687	GGGTGG	0.36621	0.38841
cg1029199	NR0B1	RXR-alpha	645	651	6.967687	GGGTGG	0.36621	0.38841
cg1029199	NR0B1	c-Ets-1 [T	1237	1243	6.943262	GGGGAA	0.73242	0.73732
cg1029199	NR0B1	ENKTF-1	365	372	6.942764	TGGCCG	1.46484	1.56616
cg1029199	NR0B1	ENKTF-1	386	393	6.942764	CGGAGC	1.46484	1.56616
cg1029199	NR0B1	p53 [T006	491	497	6.938545	GGGCCG	1.09863	1.22478
cg1029199	NR0B1	VDR [T00	1710	1718	6.925682	GTTCAG	0.42725	0.41
cg1029199	NR0B1	STAT1beta	1132	1141	6.908963	CTTTCCC	0.103	0.09938
cg1029199	NR0B1	p53 [T006	980	986	6.891821	GGGCGG	1.09863	1.22478
cg1029199	NR0B1	E2F-1 [T0	585	592	6.839754	GGTGCC	0.30518	0.33862
cg1029199	NR0B1	E2F-1 [T0	688	695	6.839754	CGTTCC	0.30518	0.33862
cg1029199	NR0B1	AR [T000	1554	1562	6.834366	ACTATG	0.23651	0.23986
cg1029199	NR0B1	C/EBPalph	1802	1808	6.786177	TCCAAT	0.73242	0.68282
cg1029199	NR0B1	p53 [T006	725	731	6.778774	GGGCTC	1.09863	1.22478
cg1029199	NR0B1	p53 [T006	880	886	6.775228	GTAGCC	1.09863	1.22478
cg1029199	NR0B1	LEF-1 [T0	404	411	6.75468	CTTTGA	0.06104	0.05927
cg1029199	NR0B1	c-Ets-1 [T	689	695	6.693449	GTTCCG	0.48828	0.48842
cg1029199	NR0B1	T3R-beta1	255	263	6.683388	TCACCG	0.21362	0.2251
cg1029199	NR0B1	AR [T000	1449	1457	6.617912	ACGGTG	0.19836	0.20813
cg1029199	NR0B1	FOXP3 [T	75	80	6.581441	TTCAAC	0.97656	0.904
cg1029199	NR0B1	FOXP3 [T	1614	1619	6.581441	TAAAAC	0.97656	0.904
cg1029199	NR0B1	TFII-I [T0	481	486	6.581441	GGAGTG	0.97656	0.9991
cg1029199	NR0B1	p53 [T006	505	511	6.563521	GAAGCC	0.48828	0.54643
cg1029199	NR0B1	p53 [T006	703	709	6.563521	GCAGCC	0.48828	0.54643
cg1029199	NR0B1	XBP-1 [T	1397	1402	6.478682	ATGCCC	0.97656	0.99906
cg1029199	NR0B1	XBP-1 [T	1529	1534	6.478682	ATGCCA	0.97656	0.99906
cg1029199	NR0B1	TCF-4E [T	602	608	6.302385	CTTTGC	0.61035	0.59686
cg1029199	NR0B1	c-Ets-1 [T	1189	1195	6.295602	TTTCCAT	0.48828	0.48842
cg1029199	NR0B1	GR-alpha [	89	93	6.263098	TGAGG	3.90625	3.89624
cg1029199	NR0B1	GR-alpha [	781	785	6.263098	CCTCA	3.90625	3.89624
cg1029199	NR0B1	ETF [T002	1580	1590	6.253495	GAGCTG	0.00954	0.01147
cg1029199	NR0B1	IRF-1 [T0	1109	1117	6.24301	TTTCCTC	0.16785	0.16217
cg1029199	NR0B1	p53 [T006	493	499	6.188498	GCCGCC	0.61035	0.68483
cg1029199	NR0B1	c-Ets-1 [T	1391	1397	6.167515	GTGGAA	0.36621	0.36174
cg1029199	NR0B1	c-Jun [T00	58	64	6.152811	TGACGA	0.36621	0.34478
cg1029199	NR0B1	GR-alpha [	783	787	6.055408	TCAGG	3.90625	3.89835
cg1029199	NR0B1	GR-alpha [	1143	1147	6.055408	TCAGG	3.90625	3.89835
cg1029199	NR0B1	GR-alpha [	1407	1411	6.055408	TCAGG	3.90625	3.89835
cg1029199	NR0B1	GR-alpha [	1612	1616	6.055408	CCTAA	3.90625	3.89835
cg1029199	NR0B1	GR-alpha [	1620	1624	6.055408	TTAGG	3.90625	3.89835
cg1029199	NR0B1	GR-alpha [	1706	1710	6.055408	TTAGG	3.90625	3.89835
cg1029199	NR0B1	GR-alpha [	1712	1716	6.055408	TCAGG	3.90625	3.89835

cg1029199	NR0B1	c-Ets-1 [T	1069	1075	6.039428	CTGGAA	0.36621	0.36174
cg1029199	NR0B1	RXR-alph	1125	1131	5.937582	ATTACC	0.73242	0.78318
cg1029199	NR0B1	GCF [T00	134	142	5.917256	CCGCAG	0.64087	0.72542
cg1029199	NR0B1	GCF [T00	283	291	5.917256	GCGCCG	0.64087	0.72542
cg1029199	NR0B1	GCF [T00	379	387	5.917256	GCGCTG	0.64087	0.72542
cg1029199	NR0B1	GCF [T00	787	795	5.917256	GAGCCG	0.64087	0.72542
cg1029199	NR0B1	GCF [T00	869	877	5.917256	CCGCGG	0.64087	0.72542
cg1029199	NR0B1	GCF [T00	970	978	5.917256	GCGCGG	0.64087	0.72542
cg1029199	NR0B1	AR [T000	150	158	5.8965	GAGGTG	0.24414	0.25115
cg1029199	NR0B1	STAT4 [T	1115	1120	5.882353	CCTTCC	0.48828	0.51201
cg1029199	NR0B1	c-Ets-1 [T	1833	1839	5.814485	CTTCCC	0.36621	0.36174
cg1029199	NR0B1	STAT1bet	1067	1076	5.796867	AGCTGG	0.1545	0.14881
cg1029199	NR0B1	ENKTF-1	122	129	5.687009	GAGCGC	0.73242	0.76357
cg1029199	NR0B1	ENKTF-1	680	687	5.687009	GAGCGC	0.73242	0.76357
cg1029199	NR0B1	IRF-1 [T0	1067	1075	5.65977	AGCTGG	0.22888	0.21959
cg1029199	NR0B1	AhR:Arnt	933	942	5.620669	GCACGC	0.0515	0.05997
cg1029199	NR0B1	NFI/CTF [	1401	1408	5.558661	CCAATC	0.54932	0.55504
cg1029199	NR0B1	NFI/CTF [	1761	1768	5.558661	GGGTTT	0.54932	0.55504
cg1029199	NR0B1	TFIID [T0	1676	1682	5.544826	TTTAGT	0.73242	0.65314
cg1029199	NR0B1	Pax-5 [T0	377	383	5.544826	GGGCGC	0.73242	0.79
cg1029199	NR0B1	Pax-5 [T0	864	870	5.544826	ATGGCC	0.73242	0.79
cg1029199	NR0B1	Pax-5 [T0	980	986	5.544826	GGGCGG	0.73242	0.79
cg1029199	NR0B1	Pax-5 [T0	1547	1553	5.544826	AGCGCC	0.73242	0.79
cg1029199	NR0B1	NF-AT1 [	1070	1079	5.512555	TGGAAA	0.05913	0.05666
cg1029199	NR0B1	NF-AT2 [	1104	1113	5.474728	GACACT	0.01144	0.011
cg1029199	NR0B1	HNF-1A [	1573	1580	5.466509	GTTAAG	0.24414	0.23087
cg1029199	NR0B1	IRF-1 [T0	1235	1243	5.42531	CAGGGG	0.22888	0.21959
cg1029199	NR0B1	C/EBPalp	1664	1670	5.38654	AATTGT	0.73242	0.68229
cg1029199	NR0B1	RAR-beta	1727	1736	5.370617	CGGGTT	0.15259	0.15813
cg1029199	NR0B1	p53 [T006	1022	1028	5.345221	TTCGCC	0.61035	0.65765
cg1029199	NR0B1	TCF-4 [T0	403	412	5.337909	GCTTTG	0.04959	0.04908
cg1029199	NR0B1	RXR-alph	497	503	5.271235	CCCACC	0.61035	0.65415
cg1029199	NR0B1	RXR-alph	519	525	5.271235	CCCACC	0.61035	0.65415
cg1029199	NR0B1	RXR-alph	717	723	5.271235	CCCACC	0.61035	0.65415
cg1029199	NR0B1	RXR-alph	1836	1842	5.271235	CCCACC	0.61035	0.65415
cg1029199	NR0B1	POU2F2 (	1303	1313	5.23012	TGACTT	0.02432	0.02134
cg1029199	NR0B1	c-Myb [T0	884	891	5.137438	CCCAGT	0.30518	0.30087
cg1029199	NR0B1	p53 [T006	691	697	5.133514	TCCGCC	0.48828	0.53921
cg1029199	NR0B1	NF-Y [T0	1225	1232	5.094053	ATTGGG	0.36621	0.35921
cg1029199	NR0B1	RXR-alph	229	235	5.089356	GGGTGC	0.48828	0.51407
cg1029199	NR0B1	RXR-alph	1053	1059	5.089356	GGGTGC	0.48828	0.51407
cg1029199	NR0B1	RXR-alph	1784	1790	5.089356	ATCACC	0.48828	0.51407
cg1029199	NR0B1	GR-beta [	1355	1359	5.042296	AATAC	3.90625	3.7093
cg1029199	NR0B1	GR-beta [	1462	1466	5.042296	GGATT	3.90625	3.7093
cg1029199	NR0B1	GR-beta [	1538	1542	5.042296	GTATT	3.90625	3.7093
cg1029199	NR0B1	GR-beta [	1810	1814	5.042296	GTATT	3.90625	3.7093
cg1029199	NR0B1	HOXD9 [	1304	1313	5.035116	GACTTA	0.00763	0.00669
cg1029199	NR0B1	HOXD10 [	1304	1313	5.035116	GACTTA	0.00763	0.00669

cg1029199	NR0B1	PXR-1:RX	1196	1203	5.032032	TGAACC	0.12207	0.11843
cg1029199	NR0B1	c-Ets-1 [T	1075	1081	4.910652	ATGGAA	0.48828	0.48026
cg1029199	NR0B1	AP-2alpha	1611	1616	4.890408	GCCTAA	0.97656	0.97517
cg1029199	NR0B1	GCF [T00	999	1007	4.846987	GCGCGG	0.27466	0.31905
cg1029199	NR0B1	C/EBPalp	1746	1752	4.845599	AATTGC	0.97656	0.90302
cg1029199	NR0B1	EBF [T05	1455	1465	4.802704	TCCCCA	0.02289	0.02569
cg1029199	NR0B1	C/EBPalp	1649	1655	4.776286	TATTGT	0.97656	0.90302
cg1029199	NR0B1	FOXP3 [T	1668	1673	4.756447	GTTTTC	2.92969	2.82
cg1029199	NR0B1	FOXP3 [T	1943	1948	4.756447	GTTTTC	2.92969	2.82
cg1029199	NR0B1	TFII-I [T0	1071	1076	4.756447	GGAAAT	2.92969	2.89715
cg1029199	NR0B1	TFII-I [T0	1393	1398	4.756447	GGAAAT	2.92969	2.89715
cg1029199	NR0B1	TFII-I [T0	1557	1562	4.756447	ATGTCC	2.92969	2.89715
cg1029199	NR0B1	c-Ets-1 [T	38	44	4.654478	CTGGAA	0.85449	0.8381
cg1029199	NR0B1	p53 [T006	356	362	4.645444	CGCGCC	0.24414	0.28373
cg1029199	NR0B1	p53 [T006	968	974	4.645444	GGGCGC	0.24414	0.28373
cg1029199	NR0B1	p53 [T006	997	1003	4.645444	GGGCGC	0.24414	0.28373
cg1029199	NR0B1	IRF-1 [T0	1243	1251	4.626471	AAGAGG	0.05341	0.05056
cg1029199	NR0B1	c-Ets-1 [T	1621	1627	4.539113	TAGGAA	0.85449	0.8381
cg1029199	NR0B1	T3R-beta1	1888	1896	4.462023	TCCAGG	0.27466	0.27245
cg1029199	NR0B1	STAT4 [T	40	45	4.411765	GGAAGC	1.95312	1.99838
cg1029199	NR0B1	STAT4 [T	504	509	4.411765	GGAAGC	1.95312	1.99838
cg1029199	NR0B1	STAT4 [T	688	693	4.411765	CGTTCC	1.95312	1.99838
cg1029199	NR0B1	STAT4 [T	1077	1082	4.411765	GGAAGA	1.95312	1.99838
cg1029199	NR0B1	STAT4 [T	1146	1151	4.411765	GGAAGA	1.95312	1.99838
cg1029199	NR0B1	STAT4 [T	1832	1837	4.411765	TCTTCC	1.95312	1.99838
cg1029199	NR0B1	RAR-beta	1760	1769	4.307573	GGGGTT	0.14496	0.14853
cg1029199	NR0B1	Sp1 [T007	689	698	4.236199	GTTCCG	0.08965	0.10391
cg1029199	NR0B1	GR-beta [	201	205	4.201913	TGATT	7.8125	7.23274
cg1029199	NR0B1	GR-beta [	916	920	4.201913	CTATT	7.8125	7.23274
cg1029199	NR0B1	GR-beta [	1223	1227	4.201913	TTATT	7.8125	7.23274
cg1029199	NR0B1	GR-beta [	1630	1634	4.201913	AATAA	7.8125	7.23274
cg1029199	NR0B1	GR-beta [	1777	1781	4.201913	TTATT	7.8125	7.23274
cg1029199	NR0B1	GR-beta [	1795	1799	4.201913	AATAG	7.8125	7.23274
cg1029199	NR0B1	GR-beta [	1805	1809	4.201913	AATAG	7.8125	7.23274
cg1029199	NR0B1	GR-beta [	1902	1906	4.201913	TTATT	7.8125	7.23274
cg1029199	NR0B1	NF-AT1 [	1185	1194	4.134416	ACTCTT	0.08392	0.07965
cg1029199	NR0B1	NF-AT1 [	1392	1401	4.134416	TGGAAA	0.08392	0.07965
cg1029199	NR0B1	p53 [T006	80	86	4.125254	CAGGCC	0.73242	0.82434
cg1029199	NR0B1	SRY [T00	1268	1276	4.087393	CTTTGTA	0.12207	0.11312
cg1029199	NR0B1	NF-AT1 [	1105	1113	4.056854	ACACTT	0.07629	0.07182
cg1029199	NR0B1	E2F-1 [T0	272	279	4.052917	GCGGTA	0.15259	0.15999
cg1029199	NR0B1	E2F-1 [T0	473	480	4.052917	GCGGTA	0.15259	0.15999
cg1029199	NR0B1	E2F-1 [T0	671	678	4.052917	GCGGTA	0.15259	0.15999
cg1029199	NR0B1	Sp1 [T007	979	988	4.029243	CGGGCG	0.08965	0.10391
cg1029199	NR0B1	TFIID [T0	1270	1276	4.007279	TTGTAA	1.09863	0.94722
cg1029199	NR0B1	TFIID [T0	1541	1547	4.007279	TTTATA	1.09863	0.94722
cg1029199	NR0B1	Pax-5 [T0	166	172	4.007279	GGGCCC	1.09863	1.18533
cg1029199	NR0B1	Pax-5 [T0	545	551	4.007279	ACAGCC	1.09863	1.18533

cg1029199	NR0B1	Pax-5 [T0	743	749	4.007279	ACAGCC	1.09863	1.18533
cg1029199	NR0B1	Pax-5 [T0	1396	1402	4.007279	AATGCC	1.09863	1.18533
cg1029199	NR0B1	USF2 [T0	1890	1899	4.003951	CAGGTG	0.01144	0.01199
cg1029199	NR0B1	NF-AT2 [	1184	1193	3.814941	AACTCT	0.01144	0.01081
cg1029199	NR0B1	AR [T000	1882	1890	3.814754	CTAGTG	0.06866	0.06981
cg1029199	NR0B1	Sp1 [T007	491	500	3.783309	GGGCCG	0.08965	0.10391
cg1029199	NR0B1	GR [T050	1266	1272	3.763516	CTCTTT	0.73242	0.6946
cg1029199	NR0B1	AP-2alpha	579	584	3.743866	GCCTTC	0.48828	0.5124
cg1029199	NR0B1	IRF-1 [T0	1189	1197	3.602021	TTTCCA	0.06866	0.0661
cg1029199	NR0B1	p53 [T006	854	860	3.586914	CTCGCC	0.73242	0.80362
cg1029199	NR0B1	p53 [T006	1396	1402	3.516613	AATGCC	0.73242	0.80362
cg1029199	NR0B1	HNF-3alpl	917	924	3.500065	TATTTA	0.27466	0.23175
cg1029199	NR0B1	HNF-3alpl	1498	1505	3.500065	TCTAAA	0.27466	0.23175
cg1029199	NR0B1	HNF-3alpl	1539	1546	3.500065	TATTTA	0.27466	0.23175
cg1029199	NR0B1	HNF-3alpl	1685	1692	3.500065	TATTTT	0.27466	0.23175
cg1029199	NR0B1	HNF-3alpl	1811	1818	3.500065	TATTTT	0.27466	0.23175
cg1029199	NR0B1	VDR [T00	1192	1200	3.462841	CCATTG	0.21362	0.21283
cg1029199	NR0B1	c-Ets-1 [T	1950	1956	3.462376	GTTCCT	0.61035	0.61936
cg1029199	NR0B1	RXR-alpha	314	320	3.392904	TTTACC	1.09863	1.1653
cg1029199	NR0B1	AR [T000	1103	1111	3.382886	GGACAC	0.06866	0.06629
cg1029199	NR0B1	Elk-1 [T00	1142	1150	3.381796	CTCAGG	0.04578	0.04517
cg1029199	NR0B1	p53 [T006	292	298	3.375208	CCCGCC	0.73242	0.80362
cg1029199	NR0B1	p53 [T006	695	701	3.375208	CCCGCC	0.73242	0.80362
cg1029199	NR0B1	p53 [T006	1049	1055	3.375208	GGGCGG	0.73242	0.80362
cg1029199	NR0B1	GR-beta [	1309	1313	3.361531	ATATT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1403	1407	3.361531	AATCT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1436	1440	3.361531	AATCT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1502	1506	3.361531	AATAT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1625	1629	3.361531	AATAT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1647	1651	3.361531	AATAT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1648	1652	3.361531	ATATT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1684	1688	3.361531	ATATT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1774	1778	3.361531	AGATT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [	1936	1940	3.361531	ATATT	3.90625	3.51525
cg1029199	NR0B1	GATA-2 [	1321	1329	3.333333	GGATAG	0.30518	0.29349
cg1029199	NR0B1	PR B [T00	1664	1670	3.29756	AATTGT	0.24414	0.21408
cg1029199	NR0B1	PR A [T01	1664	1670	3.29756	AATTGT	0.24414	0.21408
cg1029199	NR0B1	PXR-1:RX	1707	1714	3.2723	TAGGTT	0.12207	0.11883
cg1029199	NR0B1	AP-2alpha	309	314	3.229049	GCCTCT	0.48828	0.5124
cg1029199	NR0B1	AP-2alpha	325	330	3.229049	GCCTCT	0.48828	0.5124
cg1029199	NR0B1	c-Ets-1 [T	502	508	3.102985	CCGGAA	0.24414	0.26272
cg1029199	NR0B1	Pax-5 [T0	854	860	3.075094	CTCGCC	0.12207	0.13819
cg1029199	NR0B1	E2F-1 [T0	653	660	3.059334	TTTACC	0.03052	0.03038
cg1029199	NR0B1	NF-Y [T0	1800	1807	3.051543	TATCCA	0.06104	0.05632
cg1029199	NR0B1	STAT4 [T	1108	1113	2.941176	CTTTCC	2.92969	2.92382
cg1029199	NR0B1	STAT4 [T	1132	1137	2.941176	CTTTCC	2.92969	2.92382
cg1029199	NR0B1	STAT4 [T	1188	1193	2.941176	CTTTCC	2.92969	2.92382
cg1029199	NR0B1	STAT4 [T	1215	1220	2.941176	TGTTCC	2.92969	2.92382

cg1029199	NR0B1	STAT4 [T	1623	1628	2.941176	GGAATA	2.92969	2.92382
cg1029199	NR0B1	STAT4 [T	1857	1862	2.941176	GGTTCC	2.92969	2.92382
cg1029199	NR0B1	STAT4 [T	1872	1877	2.941176	TGTTCC	2.92969	2.92382
cg1029199	NR0B1	STAT4 [T	1949	1954	2.941176	TGTTCC	2.92969	2.92382
cg1029199	NR0B1	p53 [T006	29	35	2.813291	GGGCAG	0.48828	0.53227
cg1029199	NR0B1	p53 [T006	233	239	2.813291	GCTGCC	0.48828	0.53227
cg1029199	NR0B1	p53 [T006	434	440	2.813291	GCTGCC	0.48828	0.53227
cg1029199	NR0B1	p53 [T006	632	638	2.813291	GCTGCC	0.48828	0.53227
cg1029199	NR0B1	p53 [T006	833	839	2.813291	GCTGCC	0.48828	0.53227
cg1029199	NR0B1	p53 [T006	1587	1593	2.813291	GGGCAG	0.48828	0.53227
cg1029199	NR0B1	PR B [T00	1649	1655	2.80933	TATTGT	0.73242	0.66711
cg1029199	NR0B1	PR A [T01	1649	1655	2.80933	TATTGT	0.73242	0.66711
cg1029199	NR0B1	TBP [T007	1541	1550	2.807313	TTTATA	0.12207	0.10444
cg1029199	NR0B1	NF-Y [T0	1398	1405	2.673185	TGCCCA	0.21362	0.20842
cg1029199	NR0B1	AP-2alpha	89	94	2.550491	TGAGGC	0.48828	0.51216
cg1029199	NR0B1	AP-2alpha	780	785	2.550491	GCCTCA	0.48828	0.51216
cg1029199	NR0B1	c-Jun [T00	1303	1309	2.538231	TGACTT	0.48828	0.48077
cg1029199	NR0B1	USF1 [T0	392	401	2.394035	CACGTG	0.02861	0.03048
cg1029199	NR0B1	GCF [T00	191	199	2.339499	CGCCTG	0.06104	0.06908
cg1029199	NR0B1	T3R-beta1	456	464	2.240658	TCACCA	0.15259	0.15303
cg1029199	NR0B1	GATA-1 [	1320	1325	2.176375	TGGATA	3.90625	3.79558
cg1029199	NR0B1	GATA-1 [	1800	1805	2.176375	TATCCA	3.90625	3.79558
cg1029199	NR0B1	Elk-1 [T00	1116	1124	2.164966	CTTCCT	0.05341	0.05461
cg1029199	NR0B1	AP-2alpha	96	101	2.098119	GCCTCG	0.97656	1.07805
cg1029199	NR0B1	AP-2alpha	372	377	2.098119	GCCTCG	0.97656	1.07805
cg1029199	NR0B1	AP-2alpha	570	575	2.098119	GCCTCG	0.97656	1.07805
cg1029199	NR0B1	AP-2alpha	952	957	2.098119	GCCTCG	0.97656	1.07805
cg1029199	NR0B1	NF-AT1 [	1185	1193	2.086138	ACTCTT	0.06866	0.0623
cg1029199	NR0B1	LEF-1 [T0	1962	1969	2.004405	CTTTGC	0.18311	0.17215
cg1029199	NR0B1	GATA-1 [	1642	1647	2.001358	GGGATA	3.90625	3.79558
cg1029199	NR0B1	Sp1 [T007	693	702	1.965514	CGCCCG	0.03624	0.04341
cg1029199	NR0B1	USF1 [T0	388	397	1.908112	GAGCCA	0.03624	0.03891
cg1029199	NR0B1	AP-2alpha	904	909	1.871933	GCCTCC	0.97656	1.07805
cg1029199	NR0B1	AP-2alpha	974	979	1.871933	GGAGGC	0.97656	1.07805
cg1029199	NR0B1	FOXP3 [T	821	826	1.824994	GTTGTA	0.48828	0.46414
cg1029199	NR0B1	TFII-I [T0	1157	1162	1.824994	GGAGAG	0.48828	0.51201
cg1029199	NR0B1	TFII-I [T0	1825	1830	1.824994	CTCTCC	0.48828	0.51201
cg1029199	NR0B1	C/EBPalph	1224	1230	1.761449	TATTGG	0.48828	0.46352
cg1029199	NR0B1	p53 [T006	515	521	1.758307	TCTGCC	0.36621	0.38097
cg1029199	NR0B1	p53 [T006	713	719	1.758307	TCTGCC	0.36621	0.38097
cg1029199	NR0B1	p53 [T006	890	896	1.758307	TCTGCC	0.36621	0.38097
cg1029199	NR0B1	RXR-alph	557	563	1.696452	CGGACC	0.48828	0.52093
cg1029199	NR0B1	GR-beta [	1396	1400	1.680765	AATGC	3.90625	3.70067
cg1029199	NR0B1	GR-beta [	1441	1445	1.680765	GCATT	3.90625	3.70067
cg1029199	NR0B1	GR-beta [	1528	1532	1.680765	AATGC	3.90625	3.70067
cg1029199	NR0B1	GR-beta [	1663	1667	1.680765	GAATT	3.90625	3.70067
cg1029199	NR0B1	GR-beta [	1745	1749	1.680765	GAATT	3.90625	3.70067
cg1029199	NR0B1	GR-beta [	1956	1960	1.680765	GCATT	3.90625	3.70067

cg1029199	NR0B1	c-Ets-2 [T	1110	1118	1.64415	TTCCTCC	0.04578	0.04602
cg1029199	NR0B1	C/EBPbeta	1226	1229	1.639871	TTGG	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1401	1404	1.639871	CCAA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1414	1417	1.639871	CCAA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1765	1768	1.639871	TTGG	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1803	1806	1.639871	CCAA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1940	1943	1.639871	TTGG	15.625	15.23827
cg1029199	NR0B1	Sp1 [T007	290	299	1.628725	GGCCCG	0.03242	0.03924
cg1029199	NR0B1	IRF-1 [T0	1133	1141	1.616539	TTTCCCT	0.04578	0.04268
cg1029199	NR0B1	XBP-1 [T	1029	1034	1.583727	ATGACC	0.97656	0.94995
cg1029199	NR0B1	Sp1 [T007	1048	1057	1.566059	GGGGCG	0.03242	0.03924
cg1029199	NR0B1	TFIID [T0	1350	1356	1.537547	TGAAAA	0.73242	0.65627
cg1029199	NR0B1	TFIID [T0	1602	1608	1.537547	TGTAAA	0.73242	0.65627
cg1029199	NR0B1	Pax-5 [T0	47	53	1.537547	GGGCAA	0.73242	0.83087
cg1029199	NR0B1	Pax-5 [T0	292	298	1.537547	CCCGCC	0.73242	0.83087
cg1029199	NR0B1	Pax-5 [T0	356	362	1.537547	CGCGCC	0.73242	0.83087
cg1029199	NR0B1	Pax-5 [T0	695	701	1.537547	CCCGCC	0.73242	0.83087
cg1029199	NR0B1	Pax-5 [T0	962	968	1.537547	GGGCAA	0.73242	0.83087
cg1029199	NR0B1	Pax-5 [T0	968	974	1.537547	GGGCGC	0.73242	0.83087
cg1029199	NR0B1	Pax-5 [T0	997	1003	1.537547	GGGCGC	0.73242	0.83087
cg1029199	NR0B1	Pax-5 [T0	1049	1055	1.537547	GGGCGG	0.73242	0.83087
cg1029199	NR0B1	c-Ets-1 [T	1109	1115	1.513038	TTTCCTC	0.36621	0.35197
cg1029199	NR0B1	c-Ets-1 [T	1245	1251	1.513038	GAGGAA	0.36621	0.35197
cg1029199	NR0B1	RXR-alph	1728	1734	1.474336	GGGTTT	0.48828	0.52093
cg1029199	NR0B1	RXR-alph	1761	1767	1.474336	GGGTTT	0.48828	0.52093
cg1029199	NR0B1	STAT4 [T	1239	1244	1.470588	GGAAAA	1.95312	1.90161
cg1029199	NR0B1	STAT4 [T	1247	1252	1.470588	GGAAAC	1.95312	1.90161
cg1029199	NR0B1	STAT4 [T	1383	1388	1.470588	GGAACT	1.95312	1.90161
cg1029199	NR0B1	C/EBPbeta	57	60	1.366559	TTGA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	76	79	1.366559	TCAA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	120	123	1.366559	TTGA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	200	203	1.366559	TTGA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	406	409	1.366559	TTGA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1195	1198	1.366559	TTGA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1349	1352	1.366559	TTGA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1484	1487	1.366559	TTGA	15.625	15.23827
cg1029199	NR0B1	C/EBPbeta	1850	1853	1.366559	TCAA	15.625	15.23827
cg1029199	NR0B1	AP-2alpha	79	84	1.357116	ACAGGC	0.48828	0.51319
cg1029199	NR0B1	p53 [T006	215	221	1.270236	GGGCAC	0.12207	0.13816
cg1029199	NR0B1	HIF-1 [T0	393	401	1.102279	ACGTGC	0.09918	0.10583
cg1029199	NR0B1	RAR-beta	1194	1203	1.08151	ATTGAA	0.03052	0.03086
cg1029199	NR0B1	c-Ets-2 [T	1117	1125	1.071163	TTCCTCT	0.06104	0.0583
cg1029199	NR0B1	c-Ets-2 [T	1242	1250	1.071163	AAAGAG	0.06104	0.0583
cg1029199	NR0B1	GATA-1 [	1509	1514	1.038567	TATCAT	1.95312	1.80234
cg1029199	NR0B1	TBP [T007	919	928	0.935771	TTTATAC	0.12207	0.10448
cg1029199	NR0B1	GATA-1 [	1289	1294	0.863549	TATCAC	1.95312	1.80234
cg1029199	NR0B1	GATA-1 [	1933	1938	0.863549	GTGATA	1.95312	1.80234
cg1029199	NR0B1	GR-beta [	1074	1078	0.840383	AATGG	7.8125	7.2174

cg1029199	NR0B1	GR-beta [T	1123	1127	0.840383	TCATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1192	1196	0.840383	CCATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1210	1214	0.840383	TAATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1280	1284	0.840383	TCATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1286	1290	0.840383	AATTA	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1334	1338	0.840383	TCATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1632	1636	0.840383	TAATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1633	1637	0.840383	AATTA	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1664	1668	0.840383	AATTG	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1672	1676	0.840383	TCATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1746	1750	0.840383	AATTG	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1820	1824	0.840383	TCATT	7.8125	7.2174
cg1029199	NR0B1	GR-beta [T	1990	1994	0.840383	TCATT	7.8125	7.2174
cg1029199	NR0B1	HNF-1A [	1696	1703	0.781639	CTTTTAA	0.48828	0.45029
cg1029199	NR0B1	AP-2alpha	1407	1412	0.678558	TCAGGC	0.48828	0.51196
cg1029199	NR0B1	C/EBPalph	1400	1406	0.540941	CCCAAT	0.24414	0.24432
cg1029199	NR0B1	AP-2alpha	299	304	0.226186	GCCTGG	0.97656	1.07867
cg1029199	NR0B1	AP-2alpha	1168	1173	0.226186	GCCTGG	0.97656	1.07867
cg1029199	NR0B1	p53 [T006	47	53	0.211706	GGGCAA	0.36621	0.40082
cg1029199	NR0B1	p53 [T006	962	968	0.211706	GGGCAA	0.36621	0.40082
cg1029199	NR0B1	GR-alpha [	146	150	0.207689	AGAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	226	230	0.207689	AGAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	310	314	0.207689	CCTCT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	326	330	0.207689	CCTCT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	427	431	0.207689	AGAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	625	629	0.207689	AGAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	709	713	0.207689	CCTCT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	826	830	0.207689	AGAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1119	1123	0.207689	CCTCT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1131	1135	0.207689	CCTTT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1220	1224	0.207689	CCTTT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1244	1248	0.207689	AGAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1830	1834	0.207689	CCTCT	7.8125	7.79817
cg1029199	NR0B1	c-Ets-1 [T	1116	1122	0.128087	CTTCCTC	0.24414	0.24982
cg1029199	NR0B1	GR-beta [T	1211	1215	0	AATTT	3.90625	3.51525
cg1029199	NR0B1	GR-beta [T	1285	1289	0	AAATT	3.90625	3.51525
cg1029199	NR0B1	TFIID [T0	1061	1067	0	TTTAAA	1.09863	0.95175
cg1029199	NR0B1	TFIID [T0	1349	1355	0	TTGAAA	1.09863	0.95175
cg1029199	NR0B1	TFIID [T0	1484	1490	0	TTGAAA	1.09863	0.95175
cg1029199	NR0B1	GR-alpha [	79	83	0	ACAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	109	113	0	CCTGT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	478	482	0	ACAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	676	680	0	ACAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	915	919	0	CCTAT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1137	1141	0	CCTGT	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1323	1327	0	ATAGG	7.8125	7.79817
cg1029199	NR0B1	GR-alpha [	1806	1810	0	ATAGG	7.8125	7.79817
cg1029199	NR0B1	FOXP3 [T	1870	1875	0	GTTGTT	1.46484	1.44953

cg1029199	NR0B1	C/EBPbeta	0	3	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	49	52	0	GCAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	205	208	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	260	263	0	GCAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	401	404	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	418	421	0	GCAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	461	464	0	ACAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	599	602	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	604	607	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	659	662	0	GCAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	800	803	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	822	825	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	964	967	0	GCAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1180	1183	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1182	1185	0	GCAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1214	1217	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1270	1273	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1298	1301	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1313	1316	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1369	1372	0	ACAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1651	1654	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1666	1669	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1732	1735	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1748	1751	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1752	1755	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1871	1874	0	TTGT	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1917	1920	0	TTGC	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1919	1922	0	GCAA	15.625	15.26275
cg1029199	NR0B1	C/EBPbeta	1964	1967	0	TTGC	15.625	15.26275
cg1029199	NR0B1	YY1 [T00	862	865	0	CCAT	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	864	867	0	ATGG	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	1027	1030	0	CCAT	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	1075	1078	0	ATGG	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	1192	1195	0	CCAT	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	1319	1322	0	ATGG	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	1380	1383	0	ATGG	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	1532	1535	0	CCAT	7.8125	7.79459
cg1029199	NR0B1	YY1 [T00	1976	1979	0	ATGG	7.8125	7.79459
cg1029199	NR0B1	TFII-I [T0	1108	1113	0	CTTTCC	1.46484	1.48598
cg1029199	NR0B1	TFII-I [T0	1132	1137	0	CTTTCC	1.46484	1.48598
cg1029199	NR0B1	TFII-I [T0	1188	1193	0	CTTTCC	1.46484	1.48598
cg1029199	NR0B1	TFII-I [T0	1321	1326	0	GGATAG	1.46484	1.48598
cg1029199	NR0B1	STAT4 [T	1071	1076	0	GGAAAT	0.48828	0.46235
cg1029199	NR0B1	STAT4 [T	1393	1398	0	GGAAAT	0.48828	0.46235
cg1029199	NR0B1	c-Ets-1 [T	1144	1150	0	CAGGAA	0.24414	0.24982
cg1029199	NR0B1	ER-alpha [	1030	1034	0	TGACC	1.95312	1.99744
cg1029199	NR0B1	RXR-alpha	1196	1202	0	TGAACC	0.24414	0.24342
cg1029199	NR0B1	PEA3 [T0	1598	1606	0	AGGATG	0.00763	0.00702

cg1029199	NR0B1	TCF-4E [T	1962	1968	0	CTTTGCT	0.12207	0.11933
cg1029199	NR0B1	c-Myc [T0	392	397	0	CACGTG	0.48828	0.51196
cg1029199	NR0B1	Pax-5 [T0	80	86	0	CAGGCC	1.09863	1.24633
cg1029199	NR0B1	Pax-5 [T0	215	221	0	GGGCAC	1.09863	1.24633
cg1029199	NR0B1	Pax-5 [T0	1232	1238	0	GGGCAG	1.09863	1.24633
cg1029199	NR0B1	p53 [T006	1232	1238	0	GGGCAG	0.36621	0.40082
cg1029199	NR0B1	AP-2alpha	192	197	0	GCCTGC	0.97656	1.07867
cg1029199	NR0B1	AP-2alpha	937	942	0	GCAGGC	0.97656	1.07867
cg1029199	NR0B1	IRF-2 [T0	1741	1746	0	AAGTGA	0.48828	0.46235
cg1029199	NR0B1	IRF-2 [T0	1921	1926	0	AAGTGA	0.48828	0.46235
cg1029199	NR0B1	HNF-1A [	1443	1450	0	ATTTTA	0.24414	0.20853
cg0767413	NRK	c-Ets-1 [T	486	492	9.969337	ATTCCC	0.24414	0.2459
cg0767413	NRK	PEA3 [T0	1240	1248	9.937959	CTTCATC	0.18311	0.18304
cg0767413	NRK	XBP-1 [T	45	50	9.789909	AGCCAT	1.95312	1.95208
cg0767413	NRK	XBP-1 [T	404	409	9.789909	ATGGCT	1.95312	1.95208
cg0767413	NRK	XBP-1 [T	1309	1314	9.789909	AGCCAT	1.95312	1.95208
cg0767413	NRK	XBP-1 [T	1313	1318	9.789909	ATGGCG	1.95312	1.95208
cg0767413	NRK	AhR:Arnt	1170	1179	9.738501	CCACGC	0.17929	0.17456
cg0767413	NRK	LEF-1 [T0	1567	1574	9.72404	AGGCAA	0.21362	0.2139
cg0767413	NRK	Elk-1 [T00	78	86	9.719998	AAACGG	0.07629	0.07577
cg0767413	NRK	NF-AT1 [	1148	1156	9.691726	CACGTT	0.16785	0.1682
cg0767413	NRK	GATA-3 [	1159	1170	9.652214	TCCTCTA	0.01597	0.01612
cg0767413	NRK	MAZ [T00	777	789	9.576901	ACGTGG	0.01425	0.014
cg0767413	NRK	NF-AT1 [	1520	1528	9.557905	GGAAAA	0.16785	0.1682
cg0767413	NRK	Pax-5 [T0	436	442	9.552105	GGGCGT	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	756	762	9.552105	GGGCGG	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	862	868	9.552105	GTGGCC	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	889	895	9.552105	GGGCGG	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	1083	1089	9.552105	TTAGCC	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	1357	1363	9.552105	GGGCCA	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	1380	1386	9.552105	GACGCC	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	1443	1449	9.552105	GACGCC	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	1526	1532	9.552105	GGCGCC	1.46484	1.43083
cg0767413	NRK	Pax-5 [T0	1775	1781	9.552105	GCCGCC	1.46484	1.43083
cg0767413	NRK	TFIID [T0	8	14	9.552105	TTTCTCA	1.46484	1.48472
cg0767413	NRK	TFIID [T0	1799	1805	9.552105	TTTGCC	1.46484	1.48472
cg0767413	NRK	NF-1 [T00	95	102	9.535536	TTGGGC	0.73242	0.73053
cg0767413	NRK	E2F-1 [T0	959	966	9.529774	TGCACC	0.15259	0.14917
cg0767413	NRK	TFII-I [T0	75	80	9.512894	GGAAAA	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	105	110	9.512894	GGAAAA	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	148	153	9.512894	GGAACG	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	163	168	9.512894	GGAAGG	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	175	180	9.512894	GGAATT	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	450	455	9.512894	CCTTCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	688	693	9.512894	TTTTCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	711	716	9.512894	GGAAAA	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	718	723	9.512894	GTTTCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1118	1123	9.512894	GTTTCC	7.32422	7.29728

cg0767413	NRK	TFII-I [T0	1151	1156	9.512894	GTTTCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1185	1190	9.512894	CGATCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1216	1221	9.512894	CCTTCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1468	1473	9.512894	GGACTT	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1493	1498	9.512894	GGAAGG	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1520	1525	9.512894	GGAAAA	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1544	1549	9.512894	GGACCG	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1588	1593	9.512894	GGAAGG	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1705	1710	9.512894	CGTTCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1760	1765	9.512894	CCTTCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1768	1773	9.512894	TTATCC	7.32422	7.29728
cg0767413	NRK	TFII-I [T0	1979	1984	9.512894	GGAAGG	7.32422	7.29728
cg0767413	NRK	FOXP3 [T	277	282	9.512894	GAGAAC	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	290	295	9.512894	GTTCTG	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	489	494	9.512894	CCCAAC	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	580	585	9.512894	GCCAAC	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	1087	1092	9.512894	CCCAAC	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	1131	1136	9.512894	CCCAAC	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	1417	1422	9.512894	GTTCTG	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	1633	1638	9.512894	CTAAAC	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	1767	1772	9.512894	GTTATC	7.32422	7.35678
cg0767413	NRK	FOXP3 [T	1959	1964	9.512894	AAGAAC	7.32422	7.35678
cg0767413	NRK	TCF-4E [T	11	17	9.453578	CTCAAA	0.48828	0.49215
cg0767413	NRK	TCF-4E [T	238	244	9.453578	CTTTGG	0.48828	0.49215
cg0767413	NRK	c-Jun [T00	425	431	9.442241	TGACAG	0.73242	0.73031
cg0767413	NRK	c-Jun [T00	1844	1850	9.442241	TGACAG	0.73242	0.73031
cg0767413	NRK	NFI/CTF [	236	243	9.352332	GGCTTT	0.54932	0.54821
cg0767413	NRK	LEF-1 [T0	238	245	9.313676	CTTTGG	0.21362	0.2139
cg0767413	NRK	c-Ets-1 [T	363	369	9.276861	GTTCCC	0.36621	0.36441
cg0767413	NRK	HNF-1C [	513	521	9.253863	TTCTGT	0.19836	0.20229
cg0767413	NRK	E2F-1 [T0	880	887	9.028527	CTCCCC	0.27466	0.26875
cg0767413	NRK	PXR-1:RX	298	305	8.998824	TGAACG	0.24414	0.2439
cg0767413	NRK	GR [T050	236	242	8.971049	GGCTTT	0.61035	0.61632
cg0767413	NRK	GR [T050	406	412	8.971049	GGCTTT	0.61035	0.61632
cg0767413	NRK	Elk-1 [T00	1249	1257	8.931691	CTTCCA	0.24414	0.24034
cg0767413	NRK	T3R-beta1	1822	1830	8.924046	GCGGGG	0.2594	0.25766
cg0767413	NRK	c-Myb [T0	319	326	8.872587	GAACTA	0.39673	0.40028
cg0767413	NRK	c-Jun [T00	1828	1834	8.832178	TGACCT	0.61035	0.61059
cg0767413	NRK	PR B [T00	280	286	8.827054	AACAGG	0.36621	0.36944
cg0767413	NRK	PR A [T01	280	286	8.827054	AACAGG	0.36621	0.36944
cg0767413	NRK	NFI/CTF [	1406	1413	8.814757	TCTTTTG	0.48828	0.48804
cg0767413	NRK	NFI/CTF [	1971	1978	8.814757	CCTTTT	0.48828	0.48804
cg0767413	NRK	Elk-1 [T00	159	167	8.797343	GGCTGG	0.24414	0.24034
cg0767413	NRK	NF-1 [T00	607	614	8.790071	TTGGGA	0.24414	0.24467
cg0767413	NRK	Elk-1 [T00	1489	1497	8.762973	GCGCGG	0.24414	0.24034
cg0767413	NRK	LEF-1 [T0	531	538	8.759086	CTTTGC	0.54932	0.55326
cg0767413	NRK	XBP-1 [T	123	128	8.75604	ATGAGC	2.92969	2.9674
cg0767413	NRK	XBP-1 [T	135	140	8.75604	ATGAAA	2.92969	2.9674

cg0767413	NRK	HNF-1B [	514	522	8.696557	TCTGTA	0.11444	0.11669
cg0767413	NRK	STAT1bet	101	110	8.695301	ACTTGG	0.22316	0.22446
cg0767413	NRK	RAR-beta	488	497	8.55975	TCCCAA	0.26703	0.26657
cg0767413	NRK	p53 [T006	2	8	8.537081	GGGCTC	0.12207	0.11986
cg0767413	NRK	NF-AT1 [	75	83	8.532897	GGAAAA	0.10681	0.10725
cg0767413	NRK	USF2 [T0	268	277	8.532138	TGCGCA	0.103	0.10183
cg0767413	NRK	USF2 [T0	282	291	8.532138	CAGGTG	0.103	0.10183
cg0767413	NRK	USF2 [T0	896	905	8.532138	TGCCCA	0.103	0.10183
cg0767413	NRK	c-Ets-1 [T	1706	1712	8.501115	GTTCCA	0.24414	0.24529
cg0767413	NRK	LEF-1 [T0	408	415	8.457856	CTTTGA	0.15259	0.15214
cg0767413	NRK	HNF-3alp	460	467	8.343064	TTCAAA	0.27466	0.28528
cg0767413	NRK	HNF-3alp	1646	1653	8.343064	CATTTA	0.27466	0.28528
cg0767413	NRK	c-Ets-2 [T	170	178	8.339336	ATGCAG	0.13733	0.13681
cg0767413	NRK	PR B [T00	286	292	8.338824	TGCTGT	1.09863	1.10009
cg0767413	NRK	PR B [T00	455	461	8.338824	CTCTGT	1.09863	1.10009
cg0767413	NRK	PR B [T00	576	582	8.338824	AACAGC	1.09863	1.10009
cg0767413	NRK	PR B [T00	1636	1642	8.338824	AACAGC	1.09863	1.10009
cg0767413	NRK	PR B [T00	1711	1717	8.338824	AACAGA	1.09863	1.10009
cg0767413	NRK	PR B [T00	1763	1769	8.338824	TCCTGT	1.09863	1.10009
cg0767413	NRK	PR A [T01	286	292	8.338824	TGCTGT	1.09863	1.10009
cg0767413	NRK	PR A [T01	455	461	8.338824	CTCTGT	1.09863	1.10009
cg0767413	NRK	PR A [T01	576	582	8.338824	AACAGC	1.09863	1.10009
cg0767413	NRK	PR A [T01	1636	1642	8.338824	AACAGC	1.09863	1.10009
cg0767413	NRK	PR A [T01	1711	1717	8.338824	AACAGA	1.09863	1.10009
cg0767413	NRK	PR A [T01	1763	1769	8.338824	TCCTGT	1.09863	1.10009
cg0767413	NRK	E2F-1 [T0	1283	1290	8.336446	TCGCCC	0.15259	0.14963
cg0767413	NRK	E2F-1 [T0	1696	1703	8.336446	TAGCCC	0.15259	0.14963
cg0767413	NRK	ATF3 [T0	49	56	8.313799	ATATGT	0.27466	0.27431
cg0767413	NRK	GR-alpha [	156	160	8.281568	GGAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	164	168	8.281568	GAAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	395	399	8.281568	CCTCG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	412	416	8.281568	GAAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	450	454	8.281568	CCTTC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	511	515	8.281568	CCTTC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	782	786	8.281568	GGAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	792	796	8.281568	GGAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	803	807	8.281568	GGAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	812	816	8.281568	GAAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	840	844	8.281568	CCTTC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	849	853	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	853	857	8.281568	CCTCG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	867	871	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	879	883	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	956	960	8.281568	CCTTG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	970	974	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1033	1037	8.281568	CCTTC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1104	1108	8.281568	CCTCG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1123	1127	8.281568	CCTCC	7.8125	7.72956

cg0767413	NRK	GR-alpha [	1157	1161	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1210	1214	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1213	1217	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1216	1220	8.281568	CCTTC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1227	1231	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1231	1235	8.281568	CCTTC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1303	1307	8.281568	CCTCG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1332	1336	8.281568	GGAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1342	1346	8.281568	GGAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1433	1437	8.281568	GGAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1494	1498	8.281568	GAAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1589	1593	8.281568	GAAGG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1666	1670	8.281568	CCTTG	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1757	1761	8.281568	CCTCC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1760	1764	8.281568	CCTTC	7.8125	7.72956
cg0767413	NRK	GR-alpha [	1980	1984	8.281568	GAAGG	7.8125	7.72956
cg0767413	NRK	GCF [T00	765	773	8.256755	GCGCAG	0.09155	0.09002
cg0767413	NRK	c-Ets-1 [T	725	731	8.244941	GTGGAA	0.24414	0.2425
cg0767413	NRK	c-Jun [T00	1343	1349	8.242207	GAGGTC	0.48828	0.49076
cg0767413	NRK	c-Jun [T00	1715	1721	8.242207	GAGGTC	0.48828	0.49076
cg0767413	NRK	NFI/CTF [	490	497	8.241664	CCAACC	0.18311	0.1823
cg0767413	NRK	p53 [T006	652	658	8.208781	GGGGCC	0.48828	0.47377
cg0767413	NRK	ENKTF-1	640	647	8.19852	TGGCAG	0.73242	0.71737
cg0767413	NRK	ENKTF-1	732	739	8.19852	ACTCGC	0.73242	0.71737
cg0767413	NRK	ENKTF-1	1314	1321	8.19852	TGGCGG	0.73242	0.71737
cg0767413	NRK	ENKTF-1	1411	1418	8.19852	TGGCGG	0.73242	0.71737
cg0767413	NRK	NF-1 [T00	413	420	8.191058	AAGGCC	0.24414	0.24409
cg0767413	NRK	NF-1 [T00	632	639	8.191058	TTGGAC	0.24414	0.24409
cg0767413	NRK	SRY [T00	408	416	8.174786	CTTTGA	0.15259	0.15383
cg0767413	NRK	LEF-1 [T0	10	17	8.117221	TCTCAA	0.12207	0.1241
cg0767413	NRK	VDR [T00	459	467	8.079962	GTTCAA	0.24414	0.24712
cg0767413	NRK	IRF-1 [T0	707	715	8.078284	GCCTGG	0.25177	0.25263
cg0767413	NRK	GR-alpha [	172	176	8.073878	GCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	223	227	8.073878	CCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	228	232	8.073878	GCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	266	270	8.073878	CCTGC	7.8125	7.72238
cg0767413	NRK	GR-alpha [	311	315	8.073878	CCTGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	326	330	8.073878	CCTGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	348	352	8.073878	CCTGC	7.8125	7.72238
cg0767413	NRK	GR-alpha [	476	480	8.073878	CCTAG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	477	481	8.073878	CTAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	525	529	8.073878	GTAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	616	620	8.073878	CTAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	642	646	8.073878	GCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	708	712	8.073878	CCTGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	752	756	8.073878	GCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	789	793	8.073878	GCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	818	822	8.073878	CCTGC	7.8125	7.72238

cg0767413	NRK	GR-alpha [	870	874	8.073878	CCTAG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	875	879	8.073878	CCTGC	7.8125	7.72238
cg0767413	NRK	GR-alpha [	902	906	8.073878	CCTGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1052	1056	8.073878	CCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1322	1326	8.073878	CCTGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1363	1367	8.073878	CCTGC	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1465	1469	8.073878	CCAGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1503	1507	8.073878	CCTGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1533	1537	8.073878	CCTGG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1694	1698	8.073878	CCTAG	7.8125	7.72238
cg0767413	NRK	GR-alpha [	1922	1926	8.073878	CCAGG	7.8125	7.72238
cg0767413	NRK	Pax-5 [T0	652	658	8.014558	GGGGCC	2.19727	2.14502
cg0767413	NRK	Pax-5 [T0	653	659	8.014558	GGGCCC	2.19727	2.14502
cg0767413	NRK	Pax-5 [T0	894	900	8.014558	GCTGCC	2.19727	2.14502
cg0767413	NRK	Pax-5 [T0	1002	1008	8.014558	GGGCAG	2.19727	2.14502
cg0767413	NRK	Pax-5 [T0	1536	1542	8.014558	GGGCAC	2.19727	2.14502
cg0767413	NRK	TFIID [T0	10	16	8.014558	TCTCAA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	28	34	8.014558	TTTGTG	2.19727	2.24348
cg0767413	NRK	TFIID [T0	103	109	8.014558	TTGGAA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	113	119	8.014558	TTTGCA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	532	538	8.014558	TTTGCA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	823	829	8.014558	TCGCAA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	1106	1112	8.014558	TCGCAA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	1882	1888	8.014558	TTTCTTA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	1890	1896	8.014558	TTTCTAA	2.19727	2.24348
cg0767413	NRK	TFIID [T0	1902	1908	8.014558	TTTCTAA	2.19727	2.24348
cg0767413	NRK	c-Ets-2 [T	1743	1751	7.84116	TTCCTGA	0.32043	0.32298
cg0767413	NRK	c-Ets-2 [T	1933	1941	7.84116	TTCCTGA	0.32043	0.32298
cg0767413	NRK	E2F-1 [T0	1659	1666	7.839654	TGACCC	0.30518	0.3
cg0767413	NRK	RXR-alph	1736	1742	7.815913	GGGTGG	0.24414	0.24104
cg0767413	NRK	E2F-1 [T0	181	188	7.771357	TTCTCC	0.30518	0.3
cg0767413	NRK	c-Ets-2 [T	720	728	7.76635	TTCCTGT	0.32043	0.32298
cg0767413	NRK	NF-AT1 [	1093	1101	7.744746	TTGCTTT	0.19836	0.19941
cg0767413	NRK	IRF-1 [T0	689	697	7.732782	TTTCCGC	0.14496	0.14449
cg0767413	NRK	NFI/CTF [	99	106	7.587343	GCACTT	0.36621	0.36674
cg0767413	NRK	NF-AT1 [	685	693	7.574801	CGGTTTT	0.19836	0.19941
cg0767413	NRK	COUP-TF	1712	1724	7.555558	ACAGAG	0.01192	0.01183
cg0767413	NRK	GR [T050	13	19	7.527031	CAAAGC	1.83105	1.86007
cg0767413	NRK	GR [T050	87	93	7.527031	CAAACA	1.83105	1.86007
cg0767413	NRK	GR [T050	462	468	7.527031	CAAATA	1.83105	1.86007
cg0767413	NRK	GR [T050	628	634	7.527031	TTGTTTG	1.83105	1.86007
cg0767413	NRK	GR [T050	1406	1412	7.527031	TCTTTTG	1.83105	1.86007
cg0767413	NRK	GR [T050	1796	1802	7.527031	TCTTTTG	1.83105	1.86007
cg0767413	NRK	GR [T050	1971	1977	7.527031	CCTTTTG	1.83105	1.86007
cg0767413	NRK	RAR-beta	135	144	7.496706	ATGAAA	0.24414	0.24343
cg0767413	NRK	RAR-beta	1414	1423	7.47824	CGGGTT	0.24414	0.24343
cg0767413	NRK	C/EBPalp	115	121	7.465744	TGCAAT	0.48828	0.49653
cg0767413	NRK	p53 [T006	1526	1532	7.458735	GGCGCC	0.73242	0.7186

cg0767413	NRK	E2F-1 [T0	1491	1498	7.336545	GCGGAA	0.45776	0.44878
cg0767413	NRK	p53 [T006	235	241	7.266844	GGGCTT	0.73242	0.7186
cg0767413	NRK	p53 [T006	427	433	7.266844	ACAGCC	0.73242	0.7186
cg0767413	NRK	p53 [T006	645	651	7.266844	GGGCTG	0.73242	0.7186
cg0767413	NRK	GCF [T00	1261	1269	7.186486	ACTCTG	0.45776	0.44706
cg0767413	NRK	c-Jun [T00	1659	1665	7.178905	TGACCC	0.73242	0.73173
cg0767413	NRK	XBP-1 [T	119	124	7.172312	ATGAAT	2.92969	2.97018
cg0767413	NRK	XBP-1 [T	131	136	7.172312	ATGAAT	2.92969	2.97018
cg0767413	NRK	XBP-1 [T	1240	1245	7.172312	CTTCAT	2.92969	2.97018
cg0767413	NRK	PPAR-alpl	303	313	7.154987	GACTGG	0.01431	0.01397
cg0767413	NRK	p53 [T006	653	659	7.153797	GGGCCC	1.09863	1.07125
cg0767413	NRK	p53 [T006	862	868	7.150251	GTGGCC	1.09863	1.07125
cg0767413	NRK	p53 [T006	1357	1363	7.150251	GGGCCA	1.09863	1.07125
cg0767413	NRK	c-Ets-1 [T	1119	1125	7.071349	TTTCCCT	0.73242	0.73099
cg0767413	NRK	HNF-3alpl	177	184	7.000129	AATTTC	0.82397	0.84946
cg0767413	NRK	HNF-3alpl	1855	1862	7.000129	AGAAAA	0.82397	0.84946
cg0767413	NRK	GCF [T00	1489	1497	6.987525	GCGCGG	0.45776	0.44706
cg0767413	NRK	NF-1 [T00	918	925	6.948522	TGCACC	0.48828	0.4856
cg0767413	NRK	NF-1 [T00	1548	1555	6.948522	CGCACC	0.48828	0.4856
cg0767413	NRK	c-Ets-1 [T	1152	1158	6.943262	TTTCCCC	0.73242	0.73099
cg0767413	NRK	ENKTF-1	1306	1313	6.942764	CGAAGC	1.46484	1.44228
cg0767413	NRK	ENKTF-1	1611	1618	6.942764	TGGCAG	1.46484	1.44228
cg0767413	NRK	MAZ [T00	1428	1440	6.916183	CAGAGG	0.00918	0.00907
cg0767413	NRK	STAT1bet	507	516	6.908963	ATTTCCT	0.103	0.10372
cg0767413	NRK	p53 [T006	962	968	6.891821	ACCGCC	1.09863	1.07125
cg0767413	NRK	p53 [T006	1580	1586	6.891821	GGGCGG	1.09863	1.07125
cg0767413	NRK	AR [T000	1687	1695	6.817719	TACCTG	0.23651	0.23551
cg0767413	NRK	c-Ets-1 [T	1097	1103	6.815175	TTTCCCC	0.73242	0.73099
cg0767413	NRK	STAT5A [	533	545	6.810722	TTGCAA	0.01341	0.01369
cg0767413	NRK	NFI/CTF [	417	424	6.786076	CCAAGC	0.73242	0.73214
cg0767413	NRK	NFI/CTF [	628	635	6.786076	TTGTTTC	0.73242	0.73214
cg0767413	NRK	POU2F2 (	1890	1900	6.735173	TTTCTA	0.04292	0.04408
cg0767413	NRK	T3R-beta1	1365	1373	6.683388	TGCCGG	0.21362	0.21147
cg0767413	NRK	PXR-1:RX	456	463	6.668182	TCTGTTC	0.24414	0.24672
cg0767413	NRK	c-Jun [T00	501	507	6.668031	CAAGTC	0.61035	0.60769
cg0767413	NRK	RBP-Jkap	604	615	6.651996	TTCTTGC	0.01311	0.01319
cg0767413	NRK	TFII-I [T0	338	343	6.581441	GGAGAT	0.97656	0.97366
cg0767413	NRK	TFII-I [T0	1127	1132	6.581441	CACTCC	0.97656	0.97366
cg0767413	NRK	TFII-I [T0	1165	1170	6.581441	ATCTCC	0.97656	0.97366
cg0767413	NRK	TFII-I [T0	1808	1813	6.581441	GGAGAT	0.97656	0.97366
cg0767413	NRK	TFII-I [T0	1983	1988	6.581441	GGAGTG	0.97656	0.97366
cg0767413	NRK	FOXP3 [T	1233	1238	6.581441	TTCAAC	0.97656	0.99397
cg0767413	NRK	FOXP3 [T	1906	1911	6.581441	TAAAAC	0.97656	0.99397
cg0767413	NRK	c-Ets-1 [T	146	152	6.565361	CCGGAA	0.48828	0.48798
cg0767413	NRK	IRF-1 [T0	1097	1105	6.549276	TTTCCCC	0.19073	0.19127
cg0767413	NRK	c-Myb [T0	91	98	6.539977	CAACTT	0.30518	0.3056
cg0767413	NRK	IRF-1 [T0	1516	1524	6.497844	ATGCGG	0.19073	0.19127
cg0767413	NRK	XBP-1 [T	1643	1648	6.478682	GGGCAT	0.97656	0.97062

cg0767413	NRK	E2F-1 [T0	1640	1647	6.47044	GCGGGG	0.12207	0.12031
cg0767413	NRK	C/EBPalph	1926	1932	6.460799	GGCAAT	0.48828	0.49071
cg0767413	NRK	RAR-beta	1176	1185	6.452127	CACGAA	0.18311	0.183
cg0767413	NRK	c-Ets-1 [T	103	109	6.423689	TTGGAA	0.48828	0.48798
cg0767413	NRK	p53 [T006	1282	1288	6.400205	GTCGCC	0.48828	0.47541
cg0767413	NRK	p53 [T006	1387	1393	6.400205	GTCGCC	0.48828	0.47541
cg0767413	NRK	RAR-beta	259	268	6.39673	ACTCAA	0.18311	0.183
cg0767413	NRK	TCF-4E [T	408	414	6.302385	CTTTGA	0.61035	0.61344
cg0767413	NRK	TCF-4E [T	1568	1574	6.302385	GGCAAA	0.61035	0.61344
cg0767413	NRK	GR-alpha [	343	347	6.263098	TAAGG	3.90625	3.91061
cg0767413	NRK	GR-alpha [	1081	1085	6.263098	CCTTA	3.90625	3.91061
cg0767413	NRK	GR-alpha [	1255	1259	6.263098	CCTCA	3.90625	3.91061
cg0767413	NRK	GR-alpha [	1448	1452	6.263098	CCTCA	3.90625	3.91061
cg0767413	NRK	GR-alpha [	1862	1866	6.263098	TAAGG	3.90625	3.91061
cg0767413	NRK	GR-alpha [	1911	1915	6.263098	CCTTA	3.90625	3.91061
cg0767413	NRK	p53 [T006	756	762	6.188498	GGGCGG	0.61035	0.594
cg0767413	NRK	p53 [T006	889	895	6.188498	GGGCGG	0.61035	0.594
cg0767413	NRK	p53 [T006	1380	1386	6.188498	GACGCC	0.61035	0.594
cg0767413	NRK	p53 [T006	1443	1449	6.188498	GACGCC	0.61035	0.594
cg0767413	NRK	p53 [T006	1775	1781	6.188498	GCCGCC	0.61035	0.594
cg0767413	NRK	AR [T000	562	570	6.110872	GGACAG	0.24414	0.24229
cg0767413	NRK	IRF-1 [T0	101	109	6.078807	ACTTGG	0.16785	0.16909
cg0767413	NRK	GR-alpha [	216	220	6.055408	TTAGG	3.90625	3.9065
cg0767413	NRK	GR-alpha [	274	278	6.055408	CCTGA	3.90625	3.9065
cg0767413	NRK	GR-alpha [	979	983	6.055408	CCTGA	3.90625	3.9065
cg0767413	NRK	GR-alpha [	995	999	6.055408	CCTGA	3.90625	3.9065
cg0767413	NRK	GR-alpha [	1065	1069	6.055408	TCAGG	3.90625	3.9065
cg0767413	NRK	GR-alpha [	1632	1636	6.055408	CCTAA	3.90625	3.9065
cg0767413	NRK	GR-alpha [	1745	1749	6.055408	CCTGA	3.90625	3.9065
cg0767413	NRK	GR-alpha [	1839	1843	6.055408	TTAGG	3.90625	3.9065
cg0767413	NRK	GR-alpha [	1935	1939	6.055408	CCTGA	3.90625	3.9065
cg0767413	NRK	c-Ets-1 [T	709	715	6.039428	CTGGAA	0.36621	0.36731
cg0767413	NRK	RXR-alph	1825	1831	5.937582	GGGTGA	0.73242	0.72249
cg0767413	NRK	GCF [T00	666	674	5.917256	GAGCGG	0.64087	0.6219
cg0767413	NRK	GCF [T00	1008	1016	5.917256	ACACAG	0.64087	0.6219
cg0767413	NRK	STAT4 [T	163	168	5.882353	GGAAGG	0.48828	0.48408
cg0767413	NRK	STAT4 [T	450	455	5.882353	CCTTCC	0.48828	0.48408
cg0767413	NRK	STAT4 [T	1216	1221	5.882353	CCTTCC	0.48828	0.48408
cg0767413	NRK	STAT4 [T	1493	1498	5.882353	GGAAGG	0.48828	0.48408
cg0767413	NRK	STAT4 [T	1588	1593	5.882353	GGAAGG	0.48828	0.48408
cg0767413	NRK	STAT4 [T	1760	1765	5.882353	CCTTCC	0.48828	0.48408
cg0767413	NRK	STAT4 [T	1979	1984	5.882353	GGAAGG	0.48828	0.48408
cg0767413	NRK	IRF-1 [T0	719	727	5.861409	TTTCCTC	0.16785	0.16909
cg0767413	NRK	AP-1 [T00	245	253	5.818984	GACGAG	0.09155	0.09072
cg0767413	NRK	c-Ets-1 [T	608	614	5.814485	TGGGAA	0.36621	0.36731
cg0767413	NRK	c-Ets-1 [T	1586	1592	5.814485	TGGGAA	0.36621	0.36731
cg0767413	NRK	AR [T000	1336	1344	5.811663	GGACAG	0.24414	0.24229
cg0767413	NRK	c-Jun [T00	590	596	5.783074	AAAGTC	0.36621	0.37082

cg0767413	NRK	IRF-1 [T0	1152	1160	5.770812	TTTCCCC	0.16785	0.16909
cg0767413	NRK	p53 [T006	1083	1089	5.720243	TTAGCC	0.61035	0.59991
cg0767413	NRK	ENKTF-1	405	412	5.687009	TGGCTTT	0.73242	0.7249
cg0767413	NRK	ENKTF-1	1355	1362	5.687009	CTGGGC	0.73242	0.7249
cg0767413	NRK	c-Ets-2 [T	1762	1770	5.624023	TTCCTGT	0.01526	0.0156
cg0767413	NRK	c-Jun [T00	912	918	5.590308	TGACGC	0.48828	0.48665
cg0767413	NRK	c-Jun [T00	1059	1065	5.590308	TGACGC	0.48828	0.48665
cg0767413	NRK	NFI/CTF [	922	929	5.558661	CCAATC	0.54932	0.55038
cg0767413	NRK	NFI/CTF [	1552	1559	5.558661	CCAAAC	0.54932	0.55038
cg0767413	NRK	c-Ets-1 [T	1977	1983	5.558311	GGGGAA	0.36621	0.3623
cg0767413	NRK	Pax-5 [T0	962	968	5.544826	ACCGCC	0.73242	0.72046
cg0767413	NRK	Pax-5 [T0	1580	1586	5.544826	GGGCGG	0.73242	0.72046
cg0767413	NRK	Pax-5 [T0	1925	1931	5.544826	GGGCAA	0.73242	0.72046
cg0767413	NRK	TFIID [T0	1903	1909	5.544826	TTCTAA	0.73242	0.75085
cg0767413	NRK	EBF [T05	220	230	5.519385	GACCCA	0.01907	0.0183
cg0767413	NRK	NF-1 [T00	1084	1091	5.377909	TAGCCC	0.24414	0.24258
cg0767413	NRK	RXR-alpha	974	980	5.271235	CCCACC	0.61035	0.6044
cg0767413	NRK	ETF [T002	743	753	5.246906	GGGGCG	0.02861	0.02737
cg0767413	NRK	ETF [T002	965	975	5.246906	GCCCCC	0.02861	0.02737
cg0767413	NRK	GR [T050	529	535	5.207533	GTCTTTC	0.24414	0.24606
cg0767413	NRK	p53 [T006	436	442	5.133514	GGGCGT	0.48828	0.47747
cg0767413	NRK	EBF [T05	1530	1540	5.130966	CCCCCT	0.02289	0.02224
cg0767413	NRK	TCF-4 [T0	9	18	5.111789	TTCTCA	0.03433	0.03427
cg0767413	NRK	AP-2alpha	1523	1528	5.100982	AAAGGC	0.97656	0.97567
cg0767413	NRK	AP-2alpha	1565	1570	5.100982	AAAGGC	0.97656	0.97567
cg0767413	NRK	AP-2alpha	1571	1576	5.100982	AAAGGC	0.97656	0.97567
cg0767413	NRK	AP-2alpha	1970	1975	5.100982	GCCTTT	0.97656	0.97567
cg0767413	NRK	RXR-alpha	1028	1034	5.089356	AGCACC	0.48828	0.484
cg0767413	NRK	RXR-alpha	1619	1625	5.089356	GGGTGC	0.48828	0.484
cg0767413	NRK	GR-beta [	197	201	5.042296	AATAC	3.90625	3.95351
cg0767413	NRK	GR-beta [	924	928	5.042296	AATCC	3.90625	3.95351
cg0767413	NRK	GR-beta [	1895	1899	5.042296	AATAC	3.90625	3.95351
cg0767413	NRK	NF-AT2 [	105	114	4.979362	GGAAAA	0.03815	0.03879
cg0767413	NRK	XBP-1 [T	201	206	4.894955	CGGCAT	0.97656	0.96979
cg0767413	NRK	XBP-1 [T	1512	1517	4.894955	CGGCAT	0.97656	0.96979
cg0767413	NRK	PPAR-alph	1353	1363	4.88658	ATCTGG	0.01717	0.01681
cg0767413	NRK	c-Jun [T00	50	56	4.883696	TATGTC	0.61035	0.61057
cg0767413	NRK	NF-1 [T00	1705	1712	4.880836	CGTTCC	0.24414	0.24398
cg0767413	NRK	GCF [T00	182	190	4.846987	TCTCCG	0.27466	0.26486
cg0767413	NRK	GCF [T00	189	197	4.846987	GCGCTG	0.27466	0.26486
cg0767413	NRK	GCF [T00	671	679	4.846987	GCGCGG	0.27466	0.26486
cg0767413	NRK	HNF-3alph	1649	1656	4.842999	TTTAAA	0.09155	0.09582
cg0767413	NRK	p53 [T006	97	103	4.786849	GGGCAC	0.48828	0.47747
cg0767413	NRK	c-Ets-1 [T	1249	1255	4.782565	CTTCCA	0.48828	0.49031
cg0767413	NRK	TFII-I [T0	55	60	4.756447	CAGTCC	2.92969	2.93695
cg0767413	NRK	TFII-I [T0	480	485	4.756447	GGACTG	2.92969	2.93695
cg0767413	NRK	TFII-I [T0	507	512	4.756447	ATTTCC	2.92969	2.93695
cg0767413	NRK	TFII-I [T0	634	639	4.756447	GGACTG	2.92969	2.93695

cg0767413	NRK	TFII-I [T0	923	928	4.756447	CAATCC	2.92969	2.93695
cg0767413	NRK	TFII-I [T0	1055	1060	4.756447	GGACTG	2.92969	2.93695
cg0767413	NRK	FOXP3 [T	76	81	4.756447	GAAAAC	2.92969	2.96063
cg0767413	NRK	FOXP3 [T	111	116	4.756447	GTTTTG	2.92969	2.96063
cg0767413	NRK	FOXP3 [T	210	215	4.756447	CAAAAC	2.92969	2.96063
cg0767413	NRK	FOXP3 [T	260	265	4.756447	CTCAAC	2.92969	2.96063
cg0767413	NRK	FOXP3 [T	573	578	4.756447	GAAAAC	2.92969	2.96063
cg0767413	NRK	FOXP3 [T	687	692	4.756447	GTTTTC	2.92969	2.96063
cg0767413	NRK	FOXP3 [T	1451	1456	4.756447	CAAAAC	2.92969	2.96063
cg0767413	NRK	Sp1 [T007	888	897	4.670035	CGGGCG	0.08583	0.08339
cg0767413	NRK	c-Ets-1 [T	161	167	4.654478	CTGGAA	0.85449	0.85764
cg0767413	NRK	p53 [T006	619	625	4.645444	GGGCGC	0.24414	0.23584
cg0767413	NRK	p53 [T006	1487	1493	4.645444	GGGCGC	0.24414	0.23584
cg0767413	NRK	c-Ets-1 [T	1518	1524	4.616023	GCGGAA	0.85449	0.85764
cg0767413	NRK	NF-AT1 [	715	723	4.566689	AAAGTT	0.06866	0.06925
cg0767413	NRK	E2F-1 [T0	1316	1323	4.545253	GCGGGA	0.15259	0.14941
cg0767413	NRK	USF2 [T0	1357	1366	4.528187	GGGCCA	0.06866	0.06782
cg0767413	NRK	c-Ets-1 [T	689	695	4.487936	TTTCCG	0.85449	0.85764
cg0767413	NRK	AP-2alpha	475	480	4.438035	GCCTAG	0.97656	0.96979
cg0767413	NRK	RXR-alph	625	631	4.423008	GGGTTG	0.24414	0.24292
cg0767413	NRK	AP-2alpha	343	348	4.422424	TAAGGC	0.97656	0.96979
cg0767413	NRK	AP-2alpha	1080	1085	4.422424	GCCTTA	0.97656	0.96979
cg0767413	NRK	AP-2alpha	1862	1867	4.422424	TAAGGC	0.97656	0.96979
cg0767413	NRK	STAT4 [T	82	87	4.411765	GGAAGC	1.95312	1.94235
cg0767413	NRK	STAT4 [T	148	153	4.411765	GGAACG	1.95312	1.94235
cg0767413	NRK	STAT4 [T	1248	1253	4.411765	GCTTCC	1.95312	1.94235
cg0767413	NRK	STAT4 [T	1705	1710	4.411765	CGTTCC	1.95312	1.94235
cg0767413	NRK	STAT4 [T	1741	1746	4.411765	GCTTCC	1.95312	1.94235
cg0767413	NRK	p53 [T006	330	336	4.33696	GGGCCA	0.24414	0.23584
cg0767413	NRK	RXR-alph	945	951	4.24113	GGGTCC	0.97656	0.9671
cg0767413	NRK	RXR-alph	1478	1484	4.24113	GGGTCC	0.97656	0.9671
cg0767413	NRK	RXR-alph	1658	1664	4.24113	GTGACC	0.97656	0.9671
cg0767413	NRK	AR [T000	373	381	4.241082	GCTCTG	0.06866	0.06828
cg0767413	NRK	GR-beta [	21	25	4.201913	AATCA	7.8125	7.94607
cg0767413	NRK	GR-beta [	464	468	4.201913	AATAG	7.8125	7.94607
cg0767413	NRK	GR-beta [	484	488	4.201913	TGATT	7.8125	7.94607
cg0767413	NRK	GR-beta [	554	558	4.201913	AATCA	7.8125	7.94607
cg0767413	NRK	GR-beta [	1886	1890	4.201913	TTATT	7.8125	7.94607
cg0767413	NRK	GR-beta [	1913	1917	4.201913	TTATT	7.8125	7.94607
cg0767413	NRK	GR-beta [	1937	1941	4.201913	TGATT	7.8125	7.94607
cg0767413	NRK	c-Ets-1 [T	173	179	4.154851	CAGGAA	0.24414	0.24526
cg0767413	NRK	c-Jun [T00	247	253	4.1298	CGAGTC	0.24414	0.24526
cg0767413	NRK	p53 [T006	795	801	4.125254	GGGCCG	0.73242	0.71379
cg0767413	NRK	p53 [T006	815	821	4.125254	GGGCCT	0.73242	0.71379
cg0767413	NRK	p53 [T006	1536	1542	4.083527	GGGCAC	0.73242	0.71379
cg0767413	NRK	IRF-1 [T0	1119	1127	4.035054	TTTCCCT	0.1297	0.13087
cg0767413	NRK	RXR-alph	137	143	4.019014	GAAACC	0.97656	0.9671
cg0767413	NRK	Pax-5 [T0	2	8	4.007279	GGGCTC	1.09863	1.07975

cg0767413	NRK	Pax-5 [T0	97	103	4.007279	GGGCAC	1.09863	1.07975
cg0767413	NRK	Pax-5 [T0	235	241	4.007279	GGGCTT	1.09863	1.07975
cg0767413	NRK	Pax-5 [T0	427	433	4.007279	ACAGCC	1.09863	1.07975
cg0767413	NRK	Pax-5 [T0	645	651	4.007279	GGGCTG	1.09863	1.07975
cg0767413	NRK	Pax-5 [T0	1643	1649	4.007279	GGGCAT	1.09863	1.07975
cg0767413	NRK	TFIID [T0	1648	1654	4.007279	TTTTAA	1.09863	1.13456
cg0767413	NRK	AP-2alpha	1665	1670	3.970052	GCCTTG	0.97656	0.96469
cg0767413	NRK	p53 [T006	1457	1463	3.961937	GGGCTA	0.73242	0.71379
cg0767413	NRK	p53 [T006	1695	1701	3.961937	CTAGCC	0.73242	0.71379
cg0767413	NRK	NF-Y [T0	1271	1278	3.95898	CACCCA	0.18311	0.1853
cg0767413	NRK	GR [T050	110	116	3.763516	AGTTTC	0.73242	0.74251
cg0767413	NRK	GR [T050	210	216	3.763516	CAAAC	0.73242	0.74251
cg0767413	NRK	GR [T050	1451	1457	3.763516	CAAAC	0.73242	0.74251
cg0767413	NRK	p53 [T006	695	701	3.750231	GGGCTG	0.73242	0.71379
cg0767413	NRK	p53 [T006	1327	1333	3.750231	GGGCTG	0.73242	0.71379
cg0767413	NRK	AP-2alpha	412	417	3.743866	GAAGGC	0.48828	0.48238
cg0767413	NRK	AP-2alpha	449	454	3.743866	GCCTTC	0.48828	0.48238
cg0767413	NRK	p53 [T006	1925	1931	3.728319	GGGCAA	0.73242	0.7189
cg0767413	NRK	Sp1 [T007	755	764	3.720644	GGGGCG	0.07439	0.07186
cg0767413	NRK	IRF-1 [T0	71	79	3.692688	TAAAGG	0.06866	0.06927
cg0767413	NRK	C/EBPalph	921	927	3.555778	ACCAAT	0.24414	0.24752
cg0767413	NRK	c-Myb [T0	1089	1096	3.555283	CAACTT	0.12207	0.12203
cg0767413	NRK	c-Ets-2 [T	509	517	3.518824	TTCCTTC	0.18311	0.18304
cg0767413	NRK	p53 [T006	1643	1649	3.516613	GGGCAT	0.73242	0.7189
cg0767413	NRK	HNF-3alph	1887	1894	3.500065	TATTTC	0.27466	0.28532
cg0767413	NRK	VDR [T00	294	302	3.462841	TGAGTG	0.21362	0.21341
cg0767413	NRK	c-Ets-1 [T	1932	1938	3.462376	GTTCCTC	0.61035	0.60765
cg0767413	NRK	NF-AT1 [	104	113	3.445347	TGGAAA	0.07629	0.07722
cg0767413	NRK	RXR-alpha	218	224	3.392904	AGGACC	1.09863	1.08572
cg0767413	NRK	RXR-alpha	990	996	3.392904	CGCACC	1.09863	1.08572
cg0767413	NRK	RXR-alpha	1269	1275	3.392904	CGCACC	1.09863	1.08572
cg0767413	NRK	Elk-1 [T00	1742	1750	3.381796	CTTCCTC	0.04578	0.04588
cg0767413	NRK	p53 [T006	744	750	3.375208	GGGCGG	0.73242	0.7189
cg0767413	NRK	p53 [T006	1205	1211	3.375208	CCCGCC	0.73242	0.7189
cg0767413	NRK	GR-beta [	34	38	3.361531	AGATT	3.90625	3.99611
cg0767413	NRK	GR-beta [	1653	1657	3.361531	AATAT	3.90625	3.99611
cg0767413	NRK	c-Ets-1 [T	80	86	3.359159	ACGGAA	0.61035	0.60765
cg0767413	NRK	T3R-beta1	1838	1846	3.351341	TTTAGG	0.27466	0.2755
cg0767413	NRK	GATA-2 [	1160	1168	3.333333	CCTCTA	0.30518	0.30786
cg0767413	NRK	c-Ets-1 [T	1491	1497	3.231072	GCGGAA	0.24414	0.23981
cg0767413	NRK	AP-2alpha	985	990	3.229049	AGAGGC	0.48828	0.48238
cg0767413	NRK	NF-AT2 [	714	723	3.201983	AAAAGT	0.03433	0.03494
cg0767413	NRK	TCF-4E [T	531	537	3.151193	CTTTGC	0.24414	0.24672
cg0767413	NRK	TFIID [T0	112	118	3.075094	TTTTGC	0.12207	0.12409
cg0767413	NRK	TFIID [T0	208	214	3.075094	TGCAAA	0.12207	0.12409
cg0767413	NRK	NF-AT2 [	711	720	3.043843	GGAAAA	0.03433	0.03494
cg0767413	NRK	c-Fos [T00	248	257	3.022518	GAGTCA	0.06104	0.06065
cg0767413	NRK	c-Ets-2 [T	70	78	2.945838	TTAAAG	0.06104	0.06231

cg0767413	NRK	STAT4 [T	485	490	2.941176	GATTCC	2.92969	2.929
cg0767413	NRK	STAT4 [T	610	615	2.941176	GGAAGT	2.92969	2.929
cg0767413	NRK	STAT4 [T	727	732	2.941176	GGAACA	2.92969	2.929
cg0767413	NRK	STAT4 [T	1096	1101	2.941176	CTTTCC	2.92969	2.929
cg0767413	NRK	STAT4 [T	1931	1936	2.941176	TGTTCC	2.92969	2.929
cg0767413	NRK	IRF-1 [T0	508	516	2.890712	TTTCCTT	0.07629	0.07756
cg0767413	NRK	Sp1 [T007	1579	1588	2.842119	GGGGCG	0.03433	0.03306
cg0767413	NRK	p53 [T006	894	900	2.813291	GCTGCC	0.48828	0.47786
cg0767413	NRK	PR B [T00	1928	1934	2.80933	CAATGT	0.73242	0.74818
cg0767413	NRK	PR A [T01	1928	1934	2.80933	CAATGT	0.73242	0.74818
cg0767413	NRK	NF-AT1 [	710	719	2.756277	TGGAAA	0.05913	0.05995
cg0767413	NRK	RXR-alpha	490	496	2.726556	CCAACC	0.85449	0.84796
cg0767413	NRK	RXR-alpha	1415	1421	2.544678	GGGTTC	0.85449	0.84796
cg0767413	NRK	ENKTF-1	904	911	2.511511	TGGCGA	0.12207	0.11894
cg0767413	NRK	Sp1 [T007	960	969	2.505331	GCACCG	0.04005	0.03892
cg0767413	NRK	Sp1 [T007	1773	1782	2.491373	CCGCCG	0.04005	0.03892
cg0767413	NRK	MAZ [T00	967	979	2.378507	CCCCCT	0.00405	0.00399
cg0767413	NRK	C/EBPalph	1273	1279	2.371703	CCCAAT	0.48828	0.49114
cg0767413	NRK	GCF [T00	264	272	2.339499	ACCCTG	0.06104	0.05925
cg0767413	NRK	Elk-1 [T00	451	459	2.299314	CTTCCT	0.09155	0.09114
cg0767413	NRK	Elk-1 [T00	1761	1769	2.299314	CTTCCT	0.09155	0.09114
cg0767413	NRK	E2F-1 [T0	1518	1525	2.294501	GCGGAA	0.06104	0.06059
cg0767413	NRK	Sp1 [T007	1203	1212	2.282776	CTCCCG	0.04005	0.03892
cg0767413	NRK	NF-Y [T0	919	926	2.194008	GCACCA	0.21362	0.21508
cg0767413	NRK	Elk-1 [T00	1217	1225	2.164966	CTTCCT	0.05341	0.05317
cg0767413	NRK	c-Ets-2 [T	452	460	2.142327	TTCCTCT	0.16785	0.16856
cg0767413	NRK	c-Ets-2 [T	1218	1226	2.142327	TTCCTCT	0.16785	0.16856
cg0767413	NRK	GCF [T00	621	629	2.140539	GCGCGG	0.09155	0.08882
cg0767413	NRK	AP-2alpha	1103	1108	2.098119	GCCTCG	0.97656	0.95407
cg0767413	NRK	GATA-1 [	547	552	2.001358	GCGATA	3.90625	3.92756
cg0767413	NRK	GATA-1 [	1769	1774	2.001358	TATCCC	3.90625	3.92756
cg0767413	NRK	NF-AT1 [	105	113	1.970716	GGAAAA	0.06866	0.07012
cg0767413	NRK	PR B [T00	598	604	1.892895	AAGTGT	0.12207	0.12429
cg0767413	NRK	PR A [T01	598	604	1.892895	AAGTGT	0.12207	0.12429
cg0767413	NRK	RXR-alpha	261	267	1.87833	TCAACC	0.12207	0.12194
cg0767413	NRK	AP-2alpha	156	161	1.871933	GGAGGC	0.97656	0.95407
cg0767413	NRK	AP-2alpha	803	808	1.871933	GGAGGC	0.97656	0.95407
cg0767413	NRK	AP-2alpha	878	883	1.871933	GCCTCC	0.97656	0.95407
cg0767413	NRK	TFII-I [T0	952	957	1.824994	CTCTCC	0.48828	0.48408
cg0767413	NRK	TFII-I [T0	1201	1206	1.824994	CTCTCC	0.48828	0.48408
cg0767413	NRK	TFII-I [T0	1223	1228	1.824994	CTCTCC	0.48828	0.48408
cg0767413	NRK	TFII-I [T0	1592	1597	1.824994	GGAGAG	0.48828	0.48408
cg0767413	NRK	p53 [T006	1002	1008	1.758307	GGGCAG	0.36621	0.36261
cg0767413	NRK	RXR-alpha	1627	1633	1.696452	CGGACC	0.48828	0.48222
cg0767413	NRK	GR-beta [	176	180	1.680765	GAATT	3.90625	3.94936
cg0767413	NRK	GR-beta [	1276	1280	1.680765	AATTC	3.90625	3.94936
cg0767413	NRK	GR-beta [	1399	1403	1.680765	AATGC	3.90625	3.94936
cg0767413	NRK	GR-beta [	1645	1649	1.680765	GCATT	3.90625	3.94936

cg0767413	NRK	GR-beta [T	1988	1992	1.680765	GAATT	3.90625	3.94936
cg0767413	NRK	GR-beta [T	1989	1993	1.680765	AATTC	3.90625	3.94936
cg0767413	NRK	c-Ets-1 [T	73	79	1.641124	AAGGAA	0.36621	0.36952
cg0767413	NRK	c-Ets-1 [T	508	514	1.641124	TTTCCTT	0.36621	0.36952
cg0767413	NRK	C/EBPbeta	95	98	1.639871	TTGG	15.625	15.72563
cg0767413	NRK	C/EBPbeta	103	106	1.639871	TTGG	15.625	15.72563
cg0767413	NRK	C/EBPbeta	240	243	1.639871	TTGG	15.625	15.72563
cg0767413	NRK	C/EBPbeta	417	420	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	490	493	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	581	584	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	607	610	1.639871	TTGG	15.625	15.72563
cg0767413	NRK	C/EBPbeta	632	635	1.639871	TTGG	15.625	15.72563
cg0767413	NRK	C/EBPbeta	922	925	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1088	1091	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1132	1135	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1274	1277	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1410	1413	1.639871	TTGG	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1552	1555	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1559	1562	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1709	1712	1.639871	CCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1975	1978	1.639871	TTGG	15.625	15.72563
cg0767413	NRK	Pax-5 [T0	330	336	1.537547	GGGCCA	0.73242	0.71311
cg0767413	NRK	Pax-5 [T0	390	396	1.537547	CTTGCC	0.73242	0.71311
cg0767413	NRK	Pax-5 [T0	619	625	1.537547	GGGCGC	0.73242	0.71311
cg0767413	NRK	Pax-5 [T0	744	750	1.537547	GGGCGG	0.73242	0.71311
cg0767413	NRK	Pax-5 [T0	1205	1211	1.537547	CCCGCC	0.73242	0.71311
cg0767413	NRK	Pax-5 [T0	1457	1463	1.537547	GGGCTA	0.73242	0.71311
cg0767413	NRK	Pax-5 [T0	1487	1493	1.537547	GGGCGC	0.73242	0.71311
cg0767413	NRK	Pax-5 [T0	1695	1701	1.537547	CTAGCC	0.73242	0.71311
cg0767413	NRK	TFIID [T	104	110	1.537547	TGGAAA	0.73242	0.75096
cg0767413	NRK	TFIID [T	710	716	1.537547	TGGAAA	0.73242	0.75096
cg0767413	NRK	E2F-1 [T0	1202	1209	1.490375	TCTCCC	0.06104	0.06008
cg0767413	NRK	E2F-1 [T0	1769	1776	1.490375	TATCCC	0.06104	0.06008
cg0767413	NRK	STAT4 [T	75	80	1.470588	GGAAAA	1.95312	1.96333
cg0767413	NRK	STAT4 [T	105	110	1.470588	GGAAAA	1.95312	1.96333
cg0767413	NRK	STAT4 [T	175	180	1.470588	GGAATT	1.95312	1.96333
cg0767413	NRK	STAT4 [T	362	367	1.470588	AGTTCC	1.95312	1.96333
cg0767413	NRK	STAT4 [T	688	693	1.470588	TTTTCC	1.95312	1.96333
cg0767413	NRK	STAT4 [T	711	716	1.470588	GGAAAA	1.95312	1.96333
cg0767413	NRK	STAT4 [T	718	723	1.470588	GTTTCC	1.95312	1.96333
cg0767413	NRK	STAT4 [T	1118	1123	1.470588	GTTTCC	1.95312	1.96333
cg0767413	NRK	STAT4 [T	1151	1156	1.470588	GTTTCC	1.95312	1.96333
cg0767413	NRK	STAT4 [T	1520	1525	1.470588	GGAAAA	1.95312	1.96333
cg0767413	NRK	NF-AT1 [	711	719	1.437145	GGAAAA	0.00763	0.00776
cg0767413	NRK	PR B [T00	729	735	1.404665	AACACT	0.36621	0.37023
cg0767413	NRK	PR B [T00	1942	1948	1.404665	TAGTGT	0.36621	0.37023
cg0767413	NRK	PR A [T01	729	735	1.404665	AACACT	0.36621	0.37023
cg0767413	NRK	PR A [T01	1942	1948	1.404665	TAGTGT	0.36621	0.37023

cg0767413	NRK	c-Ets-1 [T(	719	725	1.384951	TTTCCTC	0.36621	0.36952
cg0767413	NRK	C/EBPbeta	12	15	1.366559	TCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	261	264	1.366559	TCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	410	413	1.366559	TTGA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	461	464	1.366559	TCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1234	1237	1.366559	TCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1450	1453	1.366559	TCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1719	1722	1.366559	TCAA	15.625	15.72563
cg0767413	NRK	C/EBPbeta	1870	1873	1.366559	TTGA	15.625	15.72563
cg0767413	NRK	E2F [T002	1409	1418	1.31691	TTTGGC(	0.00763	0.00754
cg0767413	NRK	ENKTF-1	1170	1177	1.255756	CCACGC(	0.24414	0.23904
cg0767413	NRK	TCF-4 [T0	407	416	1.151128	GCTTTG/	0.05722	0.05784
cg0767413	NRK	GCF [T00	60	68	1.070269	CCCCAG(	0.18311	0.17647
cg0767413	NRK	RXR-alpha	1178	1184	0.848226	CGAACC(	0.48828	0.48333
cg0767413	NRK	GR-beta [T	118	122	0.840383	AATGA	7.8125	7.94706
cg0767413	NRK	GR-beta [T	122	126	0.840383	AATGA	7.8125	7.94706
cg0767413	NRK	GR-beta [T	130	134	0.840383	AATGA	7.8125	7.94706
cg0767413	NRK	GR-beta [T	134	138	0.840383	AATGA	7.8125	7.94706
cg0767413	NRK	GR-beta [T	380	384	0.840383	CCATT	7.8125	7.94706
cg0767413	NRK	GR-beta [T	403	407	0.840383	AATGG	7.8125	7.94706
cg0767413	NRK	GR-beta [T	505	509	0.840383	TCATT	7.8125	7.94706
cg0767413	NRK	GR-beta [T	541	545	0.840383	AATGG	7.8125	7.94706
cg0767413	NRK	GR-beta [T	1275	1279	0.840383	CAATT	7.8125	7.94706
cg0767413	NRK	GR-beta [T	1859	1863	0.840383	AATTA	7.8125	7.94706
cg0767413	NRK	AP-2alpha	1065	1070	0.678558	TCAGGC	0.48828	0.48199
cg0767413	NRK	Sp1 [T007	743	752	0.336788	GGGGCG	0.00763	0.00733
cg0767413	NRK	AP-2alpha	325	330	0.226186	GCCTGG	0.97656	0.95305
cg0767413	NRK	AP-2alpha	707	712	0.226186	GCCTGG	0.97656	0.95305
cg0767413	NRK	p53 [T006	390	396	0.211706	CTTGCC(	0.36621	0.35912
cg0767413	NRK	GR-alpha [	72	76	0.207689	AAAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	335	339	0.207689	AGAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	454	458	0.207689	CCTCT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	558	562	0.207689	AGAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	928	932	0.207689	CCTTT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	951	955	0.207689	CCTCT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	985	989	0.207689	AGAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1072	1076	0.207689	CCTCT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1160	1164	0.207689	CCTCT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1198	1202	0.207689	CCTCT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1220	1224	0.207689	CCTCT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1376	1380	0.207689	AGAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1429	1433	0.207689	AGAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1523	1527	0.207689	AAAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1565	1569	0.207689	AAAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1571	1575	0.207689	AAAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1714	1718	0.207689	AGAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1831	1835	0.207689	CCTTT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1971	1975	0.207689	CCTTT	7.8125	7.81264

cg0767413	NRK	c-Ets-1 [T	451	457	0.128087	CTTCCTC	0.24414	0.2429
cg0767413	NRK	c-Ets-1 [T	1217	1223	0.128087	CTTCCTC	0.24414	0.2429
cg0767413	NRK	GATA-1 [	339	344	0.105011	GAGATA	0.97656	0.98738
cg0767413	NRK	GATA-1 [	1164	1169	0.105011	TATCTC	0.97656	0.98738
cg0767413	NRK	GR-alpha [	281	285	0	ACAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	465	469	0	ATAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	722	726	0	CCTGT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1338	1342	0	ACAGG	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1689	1693	0	CCTGT	7.8125	7.81264
cg0767413	NRK	GR-alpha [	1764	1768	0	CCTGT	7.8125	7.81264
cg0767413	NRK	AP-2alpha	228	233	0	GCAGGC	0.97656	0.95305
cg0767413	NRK	AP-2alpha	347	352	0	GCCTGC	0.97656	0.95305
cg0767413	NRK	AP-2alpha	817	822	0	GCCTGC	0.97656	0.95305
cg0767413	NRK	AP-2alpha	874	879	0	GCCTGC	0.97656	0.95305
cg0767413	NRK	XBP-1 [T	503	508	0	AGTCAT	0.97656	0.98127
cg0767413	NRK	Pax-5 [T0	226	232	0	GGGCAG	1.09863	1.06846
cg0767413	NRK	Pax-5 [T0	695	701	0	GGGCTG	1.09863	1.06846
cg0767413	NRK	Pax-5 [T0	750	756	0	GGGCAG	1.09863	1.06846
cg0767413	NRK	Pax-5 [T0	787	793	0	GGGCAG	1.09863	1.06846
cg0767413	NRK	Pax-5 [T0	795	801	0	GGGCCG	1.09863	1.06846
cg0767413	NRK	Pax-5 [T0	815	821	0	GGGCCT	1.09863	1.06846
cg0767413	NRK	Pax-5 [T0	1327	1333	0	GGGCTG	1.09863	1.06846
cg0767413	NRK	p53 [T006	226	232	0	GGGCAG	0.36621	0.35912
cg0767413	NRK	p53 [T006	750	756	0	GGGCAG	0.36621	0.35912
cg0767413	NRK	p53 [T006	787	793	0	GGGCAG	0.36621	0.35912
cg0767413	NRK	ENKTF-1	763	770	0	TGGCGC	0.12207	0.1201
cg0767413	NRK	E2F-1 [T0	1097	1104	0	TTTCCCC	0.03052	0.03017
cg0767413	NRK	TFII-I [T0	376	381	0	CTGTCC	1.46484	1.45997
cg0767413	NRK	TFII-I [T0	562	567	0	GGACAG	1.46484	1.45997
cg0767413	NRK	TFII-I [T0	1096	1101	0	CTTTCC	1.46484	1.45997
cg0767413	NRK	TFII-I [T0	1336	1341	0	GGACAG	1.46484	1.45997
cg0767413	NRK	TFII-I [T0	1690	1695	0	CTGTCC	1.46484	1.45997
cg0767413	NRK	STAT4 [T	507	512	0	ATTTCC	0.48828	0.49387
cg0767413	NRK	c-Ets-1 [T	1742	1748	0	CTTCCTC	0.24414	0.2429
cg0767413	NRK	c-Ets-1 [T	1761	1767	0	CTTCCTC	0.24414	0.2429
cg0767413	NRK	YY1 [T00	47	50	0	CCAT	7.8125	7.81711
cg0767413	NRK	YY1 [T00	380	383	0	CCAT	7.8125	7.81711
cg0767413	NRK	YY1 [T00	404	407	0	ATGG	7.8125	7.81711
cg0767413	NRK	YY1 [T00	495	498	0	CCAT	7.8125	7.81711
cg0767413	NRK	YY1 [T00	497	500	0	ATGG	7.8125	7.81711
cg0767413	NRK	YY1 [T00	542	545	0	ATGG	7.8125	7.81711
cg0767413	NRK	YY1 [T00	1311	1314	0	CCAT	7.8125	7.81711
cg0767413	NRK	YY1 [T00	1313	1316	0	ATGG	7.8125	7.81711
cg0767413	NRK	YY1 [T00	1610	1613	0	ATGG	7.8125	7.81711
cg0767413	NRK	YY1 [T00	1781	1784	0	CCAT	7.8125	7.81711
cg0767413	NRK	YY1 [T00	1803	1806	0	CCAT	7.8125	7.81711
cg0767413	NRK	YY1 [T00	1805	1808	0	ATGG	7.8125	7.81711
cg0767413	NRK	ER-alpha [	1345	1349	0	GGTCA	1.95312	1.9404

cg0767413	NRK	ER-alpha [	1659	1663	0	TGACC	1.95312	1.9404
cg0767413	NRK	ER-alpha [	1717	1721	0	GGTCA	1.95312	1.9404
cg0767413	NRK	ER-alpha [	1828	1832	0	TGACC	1.95312	1.9404
cg0767413	NRK	C/EBPbeta	29	32	0	TTGT	15.625	15.71349
cg0767413	NRK	C/EBPbeta	86	89	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	90	93	0	ACAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	114	117	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	116	119	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	209	212	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	391	394	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	500	503	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	533	536	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	535	538	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	628	631	0	TTGT	15.625	15.71349
cg0767413	NRK	C/EBPbeta	825	828	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	958	961	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1093	1096	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1108	1111	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1569	1572	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1668	1671	0	TTGT	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1728	1731	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1788	1791	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1800	1803	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1820	1823	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1919	1922	0	TTGC	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1927	1930	0	GCAA	15.625	15.71349
cg0767413	NRK	C/EBPbeta	1947	1950	0	TTGT	15.625	15.71349
cg0767413	NRK	TFIID [T0	586	592	0	TAGAAA	1.09863	1.13474
cg0767413	NRK	TFIID [T0	1719	1725	0	TCAAAA	1.09863	1.13474
cg0767413	NRK	TFIID [T0	1854	1860	0	TAGAAA	1.09863	1.13474
cg0767413	NRK	TFIID [T0	1889	1895	0	TTTTCTA	1.09863	1.13474
cg0767413	NRK	TFIID [T0	1904	1910	0	TCTAAA	1.09863	1.13474
cg0767413	NRK	FOXP3 [T	89	94	0	AACAAC	1.46484	1.47315
cg0767413	NRK	FOXP3 [T	627	632	0	GTTGTT	1.46484	1.47315
cg0767413	NRK	FOXP3 [T	1946	1951	0	GTTGTG	1.46484	1.47315
cg0767413	NRK	GR-beta [	177	181	0	AATTT	3.90625	3.99611
cg0767413	NRK	GR-beta [	1858	1862	0	AAATT	3.90625	3.99611
cg0767413	NRK	GR-beta [	1929	1933	0	AATGT	3.90625	3.99611
cg0767413	NRK	GR [T050	1720	1726	0	CAAAAA	0.36621	0.37562
cg0767413	NRK	WT1 [T00	740	748	0	GCGGGG	0.00763	0.00729
cg0767413	NRK	GATA-2 [	340	348	0	AGATAA	0.01526	0.01525
cg2316742	ODZ2	STAT5A [	1050	1062	9.952027	GTAAAA	0.01878	0.01918
cg2316742	ODZ2	NF-AT2 [	168	177	9.873347	GTGAAT	0.08774	0.08903
cg2316742	ODZ2	NF-AT2 [	328	337	9.873347	ATTATT	0.08774	0.08903
cg2316742	ODZ2	c-Ets-1 [T	1849	1855	9.841249	AGGGAA	0.24414	0.2459
cg2316742	ODZ2	c-Myb [T0	24	31	9.815171	TCAAGT	0.36621	0.3712
cg2316742	ODZ2	STAT1bet	269	278	9.807397	AAAGGG	0.14877	0.1495
cg2316742	ODZ2	XBP-1 [T	45	50	9.789909	ATGTCT	1.95312	1.95208

cg2316742	ODZ2	XBP-1 [T	128	133	9.789909	ATGTCT	1.95312	1.95208
cg2316742	ODZ2	XBP-1 [T	1000	1005	9.789909	CGACAT	1.95312	1.95208
cg2316742	ODZ2	NF-AT2 [	440	449	9.755755	GGAAAG	0.08774	0.08903
cg2316742	ODZ2	NF-AT2 [	484	493	9.755755	GGAAAG	0.08774	0.08903
cg2316742	ODZ2	PR B [T00	657	663	9.743489	AACACA	1.09863	1.10292
cg2316742	ODZ2	PR B [T00	819	825	9.743489	AACACC	1.09863	1.10292
cg2316742	ODZ2	PR B [T00	1175	1181	9.743489	AACACA	1.09863	1.10292
cg2316742	ODZ2	PR A [T01	657	663	9.743489	AACACA	1.09863	1.10292
cg2316742	ODZ2	PR A [T01	819	825	9.743489	AACACC	1.09863	1.10292
cg2316742	ODZ2	PR A [T01	1175	1181	9.743489	AACACA	1.09863	1.10292
cg2316742	ODZ2	c-Myb [T0	339	346	9.729271	GAACTG	0.36621	0.37054
cg2316742	ODZ2	HNF-1C [	949	957	9.576203	GTCCTT	0.19836	0.20229
cg2316742	ODZ2	TFIID [T0	90	96	9.552105	TTTGCC	1.46484	1.48472
cg2316742	ODZ2	TFIID [T0	318	324	9.552105	TTTCTCA	1.46484	1.48472
cg2316742	ODZ2	TFIID [T0	652	658	9.552105	TTCCAA	1.46484	1.48472
cg2316742	ODZ2	TFIID [T0	681	687	9.552105	TTTGTC	1.46484	1.48472
cg2316742	ODZ2	TFIID [T0	1038	1044	9.552105	TGGGAA	1.46484	1.48472
cg2316742	ODZ2	TFIID [T0	1299	1305	9.552105	TTTGTC	1.46484	1.48472
cg2316742	ODZ2	NF-AT1 [	169	177	9.521781	TGAATT	0.16785	0.1682
cg2316742	ODZ2	TFII-I [T0	115	120	9.512894	TTTTCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	332	337	9.512894	TTTTCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	406	411	9.512894	GGAAGG	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	410	415	9.512894	GGAAGG	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	414	419	9.512894	GGAAAA	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	428	433	9.512894	GGAAGG	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	432	437	9.512894	GGAAGG	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	436	441	9.512894	GGAAGG	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	650	655	9.512894	GTTTCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	762	767	9.512894	GGATTT	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	770	775	9.512894	GGAAGG	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	808	813	9.512894	AATTCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	823	828	9.512894	CCATCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	846	851	9.512894	TTATCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	860	865	9.512894	TTATCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	908	913	9.512894	GGAATT	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	1009	1014	9.512894	TTGTCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	1132	1137	9.512894	GGAAGG	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	1267	1272	9.512894	AATTCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	1394	1399	9.512894	GTTTCC	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	1421	1426	9.512894	GGACAA	7.32422	7.29728
cg2316742	ODZ2	TFII-I [T0	1774	1779	9.512894	GGATTT	7.32422	7.29728
cg2316742	ODZ2	FOXP3 [T	252	257	9.512894	AAGAAC	7.32422	7.35678
cg2316742	ODZ2	FOXP3 [T	514	519	9.512894	GTTTAG	7.32422	7.35678
cg2316742	ODZ2	FOXP3 [T	1179	1184	9.512894	CAGAAC	7.32422	7.35678
cg2316742	ODZ2	FOXP3 [T	1209	1214	9.512894	GCCAAC	7.32422	7.35678
cg2316742	ODZ2	FOXP3 [T	1501	1506	9.512894	AAGAAC	7.32422	7.35678
cg2316742	ODZ2	FOXP3 [T	1764	1769	9.512894	CAGAAC	7.32422	7.35678
cg2316742	ODZ2	c-Jun [T00	1745	1751	9.397655	ATTGTC	0.73242	0.73031

cg2316742	ODZ2	AP-1 [T00	1605	1613	9.256161	ATTTAGT	0.09155	0.09305
cg2316742	ODZ2	HNF-1C [	813	821	9.225924	CTTCTTA	0.12207	0.12495
cg2316742	ODZ2	MEF-2A [	1555	1565	9.220261	GCATAA	0.07343	0.07563
cg2316742	ODZ2	c-Myb [T0	1516	1523	9.142015	CTAAGTT	0.39673	0.40028
cg2316742	ODZ2	NF-AT1 [	1040	1048	9.042733	GGAAAT	0.22888	0.22959
cg2316742	ODZ2	c-Myb [T0	1390	1397	9.024874	CTCAGTT	0.39673	0.40028
cg2316742	ODZ2	c-Ets-1 [T	549	555	9.020687	GGGGAA	0.85449	0.85523
cg2316742	ODZ2	MEF-2A [	733	743	9.003254	AAAAAA	0.07343	0.07563
cg2316742	ODZ2	AP-1 [T00	1316	1324	9.002849	TGACTTA	0.24414	0.24693
cg2316742	ODZ2	NF-AT2 [	1666	1675	8.984657	CTTTATT	0.05341	0.05386
cg2316742	ODZ2	GR [T050	629	635	8.971049	CAAAAT	0.61035	0.61632
cg2316742	ODZ2	GR [T050	655	661	8.971049	CAAACA	0.61035	0.61632
cg2316742	ODZ2	c-Ets-2 [T	1127	1135	8.912323	CTTTAGC	0.27466	0.27495
cg2316742	ODZ2	p53 [T006	1335	1341	8.912104	AGGGCC	0.12207	0.11837
cg2316742	ODZ2	p53 [T006	1336	1342	8.912104	GGGCCC	0.12207	0.11837
cg2316742	ODZ2	T3R-beta1	1242	1250	8.904753	TCACCCT	0.2594	0.25766
cg2316742	ODZ2	NFI/CTF [	1676	1683	8.814757	CCAAGA	0.48828	0.48804
cg2316742	ODZ2	XBP-1 [T	472	477	8.75604	ATGAAA	2.92969	2.9674
cg2316742	ODZ2	XBP-1 [T	695	700	8.75604	ATGAGA	2.92969	2.9674
cg2316742	ODZ2	XBP-1 [T	1080	1085	8.75604	GCTCAT	2.92969	2.9674
cg2316742	ODZ2	XBP-1 [T	1410	1415	8.75604	ATGAGA	2.92969	2.9674
cg2316742	ODZ2	XBP-1 [T	1685	1690	8.75604	ATGAAA	2.92969	2.9674
cg2316742	ODZ2	XBP-1 [T	1993	1998	8.75604	ATGAAA	2.92969	2.9674
cg2316742	ODZ2	c-Jun [T00	1445	1451	8.571705	CCAGTCA	0.12207	0.12139
cg2316742	ODZ2	NF-AT2 [	646	655	8.497624	CTATGTT	0.04959	0.05001
cg2316742	ODZ2	IRF-1 [T0	651	659	8.497322	TTTCCAA	0.20599	0.20664
cg2316742	ODZ2	HNF-3alph	1775	1782	8.343064	GATTTTA	0.27466	0.28528
cg2316742	ODZ2	c-Ets-2 [T	1269	1277	8.339336	TTCCTAC	0.13733	0.13681
cg2316742	ODZ2	PR B [T00	788	794	8.338824	TCCTGTT	1.09863	1.10009
cg2316742	ODZ2	PR A [T01	788	794	8.338824	TCCTGTT	1.09863	1.10009
cg2316742	ODZ2	ATF3 [T01	1544	1551	8.313799	GTATGTC	0.27466	0.27431
cg2316742	ODZ2	GR-alpha [	285	289	8.281568	GGAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	403	407	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	407	411	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	411	415	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	429	433	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	433	437	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	437	441	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	771	775	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	812	816	8.281568	CCTTC	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	881	885	8.281568	CCTTC	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1013	1017	8.281568	CCTCC	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1017	1021	8.281568	CAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1020	1024	8.281568	GGAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1109	1113	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1133	1137	8.281568	GAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1188	1192	8.281568	CCTCC	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1191	1195	8.281568	CCTCC	7.8125	7.72956

cg2316742	ODZ2	GR-alpha [	1194	1198	8.281568	CCTCC	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1398	1402	8.281568	CCTTC	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1550	1554	8.281568	CAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1656	1660	8.281568	CAAGG	7.8125	7.72956
cg2316742	ODZ2	GR-alpha [	1937	1941	8.281568	CCTTG	7.8125	7.72956
cg2316742	ODZ2	HNF-1B [	1	9	8.241969	AGTTAA	0.06866	0.07026
cg2316742	ODZ2	NF-1 [T00	542	549	8.191058	TTGGAC	0.24414	0.24409
cg2316742	ODZ2	c-Jun [T00	499	505	8.128539	TGACAT	0.48828	0.49076
cg2316742	ODZ2	c-Jun [T00	1853	1859	8.128539	AATGTC	0.48828	0.49076
cg2316742	ODZ2	NF-AT1 [	112	120	8.12076	GAATTT	0.1297	0.12988
cg2316742	ODZ2	LEF-1 [T0	228	235	8.117221	CTTTGA	0.12207	0.1241
cg2316742	ODZ2	LEF-1 [T0	921	928	8.117221	ATTCAA	0.12207	0.1241
cg2316742	ODZ2	GR-alpha [	1170	1174	8.073878	CCAGG	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1198	1202	8.073878	CCTAG	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1199	1203	8.073878	CTAGG	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1271	1275	8.073878	CCTAC	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1340	1344	8.073878	CCTGC	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1351	1355	8.073878	CTAGG	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1474	1478	8.073878	CCTGG	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1959	1963	8.073878	CCTAG	7.8125	7.72238
cg2316742	ODZ2	GR-alpha [	1960	1964	8.073878	CTAGG	7.8125	7.72238
cg2316742	ODZ2	Pax-5 [T0	1553	1559	8.014558	GGGCAT	2.19727	2.14502
cg2316742	ODZ2	TFIID [T0	153	159	8.014558	TTTGTGA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	173	179	8.014558	TTTCCA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	229	235	8.014558	TTTGAA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	651	657	8.014558	TTTCCA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	689	695	8.014558	TTTGTGA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	1090	1096	8.014558	TAAGAA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	1155	1161	8.014558	TCTGAA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	1258	1264	8.014558	TTTGCTA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	1703	1709	8.014558	TTTCTTA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	1735	1741	8.014558	TTAGAA	2.19727	2.24348
cg2316742	ODZ2	TFIID [T0	1883	1889	8.014558	TTTGAA	2.19727	2.24348
cg2316742	ODZ2	ATF-1 [T0	573	583	7.870358	CTACGT	0.07153	0.07147
cg2316742	ODZ2	c-Ets-2 [T	117	125	7.84116	TTCCTGA	0.32043	0.32298
cg2316742	ODZ2	c-Ets-2 [T	1168	1176	7.84116	TGCCAG	0.32043	0.32298
cg2316742	ODZ2	c-Myb [T0	176	183	7.825375	CCAAGT	0.21362	0.21454
cg2316742	ODZ2	IRF-1 [T0	116	124	7.82345	TTTCCTC	0.25177	0.25263
cg2316742	ODZ2	NF-AT1 [	455	463	7.744746	GGAAAG	0.19836	0.19941
cg2316742	ODZ2	NF-AT1 [	647	655	7.72101	TATGTT	0.19836	0.19941
cg2316742	ODZ2	NFI/CTF [	244	251	7.587343	GCTCTT	0.36621	0.36674
cg2316742	ODZ2	c-Myb [T0	293	300	7.545286	AGCAGT	0.42725	0.43114
cg2316742	ODZ2	GR [T050	139	145	7.527031	CATTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	150	156	7.527031	CATTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	226	232	7.527031	CGCTTT	1.83105	1.86007
cg2316742	ODZ2	GR [T050	530	536	7.527031	TTGTTT	1.83105	1.86007
cg2316742	ODZ2	GR [T050	534	540	7.527031	TTGTTT	1.83105	1.86007
cg2316742	ODZ2	GR [T050	538	544	7.527031	TTGTTT	1.83105	1.86007

cg2316742	ODZ2	GR [T050	686	692	7.527031	CATTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	790	796	7.527031	CTGTTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	1068	1074	7.527031	AATTTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	1255	1261	7.527031	TTGTTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	1296	1302	7.527031	TCTTTTG	1.83105	1.86007
cg2316742	ODZ2	GR [T050	1308	1314	7.527031	CAAATA	1.83105	1.86007
cg2316742	ODZ2	GR [T050	1636	1642	7.527031	CATTTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	1717	1723	7.527031	CTATTTC	1.83105	1.86007
cg2316742	ODZ2	GR [T050	1785	1791	7.527031	CAAAGC	1.83105	1.86007
cg2316742	ODZ2	AR [T000	1421	1429	7.467081	GGACAA	0.25177	0.25079
cg2316742	ODZ2	C/EBPalph	1495	1501	7.465744	CATTGC	0.48828	0.49653
cg2316742	ODZ2	HNF-1B [	950	958	7.4296	TCCTTA	0.09155	0.09368
cg2316742	ODZ2	LEF-1 [T0	991	998	7.396545	GCACAA	0.21362	0.21302
cg2316742	ODZ2	C/EBPalph	1861	1867	7.396431	AATTGG	0.48828	0.49653
cg2316742	ODZ2	IRF-1 [T0	1671	1679	7.387351	TTTCCCC	0.14496	0.14449
cg2316742	ODZ2	PXR-1:RX	795	802	7.362674	TGAACA	0.24414	0.24395
cg2316742	ODZ2	POU2F2 (	1776	1786	7.236857	ATTTTA	0.00238	0.00249
cg2316742	ODZ2	c-Ets-1 [T	1038	1044	7.199436	TGGGAA	0.73242	0.73099
cg2316742	ODZ2	SRY [T00	228	236	7.175614	CTTTGA	0.30518	0.30739
cg2316742	ODZ2	SRY [T00	920	928	7.175614	AATTCA	0.30518	0.30739
cg2316742	ODZ2	SRY [T00	990	998	7.175614	TGCACA	0.30518	0.30739
cg2316742	ODZ2	SRY [T00	1781	1789	7.175614	AAAGCA	0.30518	0.30739
cg2316742	ODZ2	XBP-1 [T	110	115	7.172312	ATGAAT	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	563	568	7.172312	ATGATT	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	621	626	7.172312	ATGATG	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	670	675	7.172312	AATCAT	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	956	961	7.172312	ACTCAT	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	1214	1219	7.172312	CCTCAT	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	1406	1411	7.172312	ATGAAT	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	1633	1638	7.172312	CCTCAT	2.92969	2.97018
cg2316742	ODZ2	XBP-1 [T	1943	1948	7.172312	ATTCAT	2.92969	2.97018
cg2316742	ODZ2	c-Jun [T00	1459	1465	7.096776	TGACTG	0.73242	0.73173
cg2316742	ODZ2	NF-AT1 [	329	337	7.095752	TTATTTT	0.15259	0.1548
cg2316742	ODZ2	NF-AT1 [	414	422	7.095752	GGAAAA	0.15259	0.1548
cg2316742	ODZ2	NF-AT1 [	273	281	7.072017	GGAAAT	0.15259	0.1548
cg2316742	ODZ2	NF-AT1 [	1667	1675	7.072017	TTTATTT	0.15259	0.1548
cg2316742	ODZ2	c-Ets-1 [T	271	277	7.071349	AGGGAA	0.73242	0.73099
cg2316742	ODZ2	c-Jun [T00	1912	1918	7.052189	TGACTA	0.73242	0.73173
cg2316742	ODZ2	IRF-1 [T0	480	488	7.044985	GAGAGG	0.1297	0.13036
cg2316742	ODZ2	NFI/CTF [	1210	1217	7.014249	CCAACC	0.73242	0.73214
cg2316742	ODZ2	C/EBPalph	1744	1750	7.00174	CATTGTC	0.73242	0.74337
cg2316742	ODZ2	HNF-3alph	231	238	7.000129	TGAAAA	0.82397	0.84946
cg2316742	ODZ2	HNF-3alph	330	337	7.000129	TATTTC	0.82397	0.84946
cg2316742	ODZ2	HNF-3alph	1094	1101	7.000129	AAAAAA	0.82397	0.84946
cg2316742	ODZ2	HNF-3alph	1306	1313	7.000129	TACAAA	0.82397	0.84946
cg2316742	ODZ2	NF-1 [T00	1206	1213	6.948522	AGAGCC	0.48828	0.4856
cg2316742	ODZ2	c-Ets-1 [T	1671	1677	6.943262	TTTCCCC	0.73242	0.73099
cg2316742	ODZ2	ENKTF-1	1360	1367	6.942764	TGGCAG	1.46484	1.44228

cg2316742	ODZ2	C/EBPalph	585	591	6.85549	AATTGC	0.73242	0.74337
cg2316742	ODZ2	C/EBPalph	588	594	6.85549	TGCAAT	0.73242	0.74337
cg2316742	ODZ2	C/EBPalph	591	597	6.85549	AATTGC	0.73242	0.74337
cg2316742	ODZ2	C/EBPalph	1342	1348	6.85549	TGCAAT	0.73242	0.74337
cg2316742	ODZ2	c-Ets-1 [T	1820	1826	6.821536	GTTCCG	0.73242	0.73099
cg2316742	ODZ2	c-Ets-1 [T	333	339	6.815175	TTTCCC	0.73242	0.73099
cg2316742	ODZ2	NFI/CTF [	538	545	6.786076	TTGTTT	0.73242	0.73214
cg2316742	ODZ2	ATF3 [T0	1316	1323	6.744803	TGACTT	0.27466	0.27656
cg2316742	ODZ2	ATF3 [T0	1640	1647	6.744803	TTGTGT	0.27466	0.27656
cg2316742	ODZ2	POU2F2 (	1316	1326	6.735173	TGACTT	0.04292	0.04408
cg2316742	ODZ2	AR [T000	944	952	6.677479	TCCATG	0.19836	0.19597
cg2316742	ODZ2	PXR-1:RX	1840	1847	6.668182	TGAACA	0.24414	0.24672
cg2316742	ODZ2	TFII-I [T0	1163	1168	6.581441	GGAGAT	0.97656	0.97366
cg2316742	ODZ2	TFII-I [T0	1567	1572	6.581441	GGAGTG	0.97656	0.97366
cg2316742	ODZ2	FOXP3 [T	301	306	6.581441	GTTTTA	0.97656	0.99397
cg2316742	ODZ2	FOXP3 [T	983	988	6.581441	TAAAAC	0.97656	0.99397
cg2316742	ODZ2	FOXP3 [T	1114	1119	6.581441	TAAAAC	0.97656	0.99397
cg2316742	ODZ2	FOXP3 [T	1520	1525	6.581441	GTTGAA	0.97656	0.99397
cg2316742	ODZ2	FOXP3 [T	1615	1620	6.581441	TTCAAC	0.97656	0.99397
cg2316742	ODZ2	FOXP3 [T	1825	1830	6.581441	GTTTTA	0.97656	0.99397
cg2316742	ODZ2	FOXP3 [T	1893	1898	6.581441	GTTGAA	0.97656	0.99397
cg2316742	ODZ2	IRF-1 [T0	333	341	6.549276	TTTCCC	0.19073	0.19127
cg2316742	ODZ2	XBP-1 [T	147	152	6.478682	TGGCAT	0.97656	0.97062
cg2316742	ODZ2	XBP-1 [T	236	241	6.478682	ATGCCA	0.97656	0.97062
cg2316742	ODZ2	XBP-1 [T	801	806	6.478682	TGGCAT	0.97656	0.97062
cg2316742	ODZ2	XBP-1 [T	853	858	6.478682	ATGCCA	0.97656	0.97062
cg2316742	ODZ2	XBP-1 [T	1167	1172	6.478682	ATGCCA	0.97656	0.97062
cg2316742	ODZ2	XBP-1 [T	1553	1558	6.478682	GGGCAT	0.97656	0.97062
cg2316742	ODZ2	C/EBPalph	1448	1454	6.460799	GTCAAT	0.48828	0.49071
cg2316742	ODZ2	c-Ets-1 [T	173	179	6.423689	TTTCCA	0.48828	0.48798
cg2316742	ODZ2	c-Ets-1 [T	651	657	6.423689	TTTCCA	0.48828	0.48798
cg2316742	ODZ2	C/EBPalph	1058	1064	6.391486	AATTGT	0.48828	0.49071
cg2316742	ODZ2	RelA [T00	1848	1858	6.389531	TAGGGA	0.01001	0.00989
cg2316742	ODZ2	TCF-4E [	228	234	6.302385	CTTTGA	0.61035	0.61344
cg2316742	ODZ2	TCF-4E [	922	928	6.302385	TTCAAA	0.61035	0.61344
cg2316742	ODZ2	GR-alpha [	219	223	6.263098	CCTTA	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	905	909	6.263098	TAAGG	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	951	955	6.263098	CCTTA	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1121	1125	6.263098	TGAGG	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1214	1218	6.263098	CCTCA	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1246	1250	6.263098	CCTTA	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1333	1337	6.263098	TAAGG	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1564	1568	6.263098	TAAGG	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1621	1625	6.263098	TAAGG	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1633	1637	6.263098	CCTCA	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1693	1697	6.263098	TGAGG	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1829	1833	6.263098	TAAGG	3.90625	3.91061
cg2316742	ODZ2	GR-alpha [	1970	1974	6.263098	TAAGG	3.90625	3.91061

cg2316742	ODZ2	C/EBPalp	594	600	6.245236	TGCAAT	0.97656	0.99
cg2316742	ODZ2	C/EBPalp	900	906	6.245236	TGCAAT	0.97656	0.99
cg2316742	ODZ2	C/EBPalp	1382	1388	6.245236	TATTGA	0.97656	0.99
cg2316742	ODZ2	c-Myb [T0	493	500	6.157321	GAAAGT	0.21362	0.21535
cg2316742	ODZ2	c-Jun [T00	681	687	6.152811	TTTGTC	0.36621	0.37082
cg2316742	ODZ2	c-Jun [T00	1299	1305	6.152811	TTTGTC	0.36621	0.37082
cg2316742	ODZ2	HNF-1C [	28	36	6.127396	GTTAGT	0.14496	0.14811
cg2316742	ODZ2	AR [T000	1023	1031	6.110872	GGACAG	0.24414	0.24229
cg2316742	ODZ2	IRF-1 [T0	173	181	6.078807	TTTCCA	0.16785	0.16909
cg2316742	ODZ2	GR-alpha [	119	123	6.055408	CCTGA	3.90625	3.9065
cg2316742	ODZ2	GR-alpha [	1129	1133	6.055408	TTAGG	3.90625	3.9065
cg2316742	ODZ2	GR-alpha [	1465	1469	6.055408	CCTGA	3.90625	3.9065
cg2316742	ODZ2	GR-alpha [	1510	1514	6.055408	CCTAA	3.90625	3.9065
cg2316742	ODZ2	HOXD9 [	932	941	5.898575	AATAAG	0.05722	0.0598
cg2316742	ODZ2	HOXD9 [	1897	1906	5.898575	AATATC	0.05722	0.0598
cg2316742	ODZ2	HOXD9 [	1903	1912	5.898575	AATAAG	0.05722	0.0598
cg2316742	ODZ2	HOXD10 [	932	941	5.898575	AATAAG	0.05722	0.0598
cg2316742	ODZ2	HOXD10 [	1897	1906	5.898575	AATATC	0.05722	0.0598
cg2316742	ODZ2	HOXD10 [	1903	1912	5.898575	AATAAG	0.05722	0.0598
cg2316742	ODZ2	STAT4 [T	406	411	5.882353	GGAAGG	0.48828	0.48408
cg2316742	ODZ2	STAT4 [T	410	415	5.882353	GGAAGG	0.48828	0.48408
cg2316742	ODZ2	STAT4 [T	428	433	5.882353	GGAAGG	0.48828	0.48408
cg2316742	ODZ2	STAT4 [T	432	437	5.882353	GGAAGG	0.48828	0.48408
cg2316742	ODZ2	STAT4 [T	436	441	5.882353	GGAAGG	0.48828	0.48408
cg2316742	ODZ2	STAT4 [T	770	775	5.882353	GGAAGG	0.48828	0.48408
cg2316742	ODZ2	STAT4 [T	1132	1137	5.882353	GGAAGG	0.48828	0.48408
cg2316742	ODZ2	STAT1bet	1670	1679	5.796867	ATTTCC	0.1545	0.1557
cg2316742	ODZ2	c-Jun [T00	33	39	5.783074	TGACTT	0.36621	0.37082
cg2316742	ODZ2	c-Jun [T00	1739	1745	5.783074	AAAGTC	0.36621	0.37082
cg2316742	ODZ2	NF-AT1 [	398	406	5.77403	GGAAAG	0.06866	0.06922
cg2316742	ODZ2	NF-AT1 [	440	448	5.77403	GGAAAG	0.06866	0.06922
cg2316742	ODZ2	NF-AT1 [	484	492	5.77403	GGAAAG	0.06866	0.06922
cg2316742	ODZ2	VDR [T00	791	799	5.771401	TGTTTG	0.42725	0.42999
cg2316742	ODZ2	VDR [T00	1614	1622	5.771401	GTTCAA	0.42725	0.42999
cg2316742	ODZ2	POU2F2 (	78	88	5.731804	TCTCTA	0.06437	0.06564
cg2316742	ODZ2	POU2F2 (	870	880	5.731804	TGTATT	0.06437	0.06564
cg2316742	ODZ2	ENKTF-1	851	858	5.687009	CTATGC	0.73242	0.7249
cg2316742	ODZ2	ENKTF-1	1205	1212	5.687009	CAGAGC	0.73242	0.7249
cg2316742	ODZ2	ENKTF-1	1483	1490	5.687009	CTGTGC	0.73242	0.7249
cg2316742	ODZ2	T3R-beta1	216	224	5.591999	TCACCT	0.21362	0.21287
cg2316742	ODZ2	AP-2alpha	1759	1764	5.568965	ATAGGC	0.48828	0.4878
cg2316742	ODZ2	C/EBPalp	1325	1331	5.565669	TACAAT	0.73242	0.74391
cg2316742	ODZ2	NFI/CTF [	654	661	5.558661	CCAAAC	0.54932	0.55038
cg2316742	ODZ2	NFI/CTF [	1231	1238	5.558661	CCAAGC	0.54932	0.55038
cg2316742	ODZ2	c-Ets-1 [T	768	774	5.558311	GGGGAA	0.36621	0.3623
cg2316742	ODZ2	TFIID [T0	1128	1134	5.544826	TTTAGG	0.73242	0.75085
cg2316742	ODZ2	C/EBPalp	240	246	5.455853	CATTGC	0.73242	0.74391
cg2316742	ODZ2	C/EBPalp	360	366	5.455853	ATCAAT	0.73242	0.74391

cg2316742	ODZ2	C/EBPalph	1003	1009	5.455853	CATTGA	0.73242	0.74391
cg2316742	ODZ2	HOXD9 [	740	749	5.453039	AATAAA	0.04578	0.04743
cg2316742	ODZ2	HOXD10 [	740	749	5.453039	AATAAA	0.04578	0.04743
cg2316742	ODZ2	C/EBPalph	1264	1270	5.38654	ACCAAT	0.73242	0.74391
cg2316742	ODZ2	IRF-1 [T0	410	418	5.309227	GGAAGG	0.22888	0.23087
cg2316742	ODZ2	IRF-1 [T0	436	444	5.309227	GGAAGG	0.22888	0.23087
cg2316742	ODZ2	GR [T050	994	1000	5.207533	CAAAGA	0.24414	0.24606
cg2316742	ODZ2	AP-2alpha	1125	1130	5.100982	GCCTTT	0.97656	0.97567
cg2316742	ODZ2	AP-2alpha	1752	1757	5.100982	GCCTTT	0.97656	0.97567
cg2316742	ODZ2	RXR-alph	198	204	5.089356	AGCACC	0.48828	0.484
cg2316742	ODZ2	RXR-alph	1241	1247	5.089356	ATCACC	0.48828	0.484
cg2316742	ODZ2	GR-beta [	597	601	5.042296	AATAC	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	702	706	5.042296	GGATT	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	762	766	5.042296	GGATT	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	871	875	5.042296	GTATT	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	1323	1327	5.042296	AATAC	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	1661	1665	5.042296	AATAC	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	1774	1778	5.042296	GGATT	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	1794	1798	5.042296	AATAC	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	1865	1869	5.042296	GGATT	3.90625	3.95351
cg2316742	ODZ2	GR-beta [	1953	1957	5.042296	GGATT	3.90625	3.95351
cg2316742	ODZ2	c-Ets-1 [T	248	254	5.038739	TTGGAA	0.48828	0.49031
cg2316742	ODZ2	Elk-1 [T00	1128	1136	5.027151	TTTAGG	0.03052	0.03091
cg2316742	ODZ2	c-Myb [T0	1889	1896	4.974489	AGCAGT	0.30518	0.30568
cg2316742	ODZ2	HNF-1A [	950	957	4.972635	TCCTTA	0.36621	0.37179
cg2316742	ODZ2	ATF3 [T0	573	580	4.941398	CTACGT	0.09155	0.09183
cg2316742	ODZ2	XBP-1 [T	1471	1476	4.894955	ATGCCT	0.97656	0.96979
cg2316742	ODZ2	AP-2alpha	1509	1514	4.890408	GCCTAA	0.97656	0.97567
cg2316742	ODZ2	c-Jun [T00	574	580	4.883696	TACGTC	0.61035	0.61057
cg2316742	ODZ2	c-Jun [T00	1545	1551	4.883696	TATGTC	0.61035	0.61057
cg2316742	ODZ2	C/EBPalph	85	91	4.845599	AGCAAT	0.97656	0.99332
cg2316742	ODZ2	C/EBPalph	805	811	4.845599	ATCAAT	0.97656	0.99332
cg2316742	ODZ2	C/EBPalph	1535	1541	4.845599	ATCAAT	0.97656	0.99332
cg2316742	ODZ2	NF-AT1 [	647	656	4.823485	TATGTT	0.07629	0.07704
cg2316742	ODZ2	c-Ets-1 [T	1723	1729	4.782565	GTGGAA	0.48828	0.49031
cg2316742	ODZ2	TFII-I [T0	172	177	4.756447	ATTTCC	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	273	278	4.756447	GGAAAT	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	544	549	4.756447	GGACTG	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	947	952	4.756447	ATGTCC	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	1040	1045	4.756447	GGAAAT	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	1184	1189	4.756447	CATTCC	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	1670	1675	4.756447	ATTTCC	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	1851	1856	4.756447	GGAATG	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	1865	1870	4.756447	GGATTG	2.92969	2.93695
cg2316742	ODZ2	TFII-I [T0	1953	1958	4.756447	GGATTG	2.92969	2.93695
cg2316742	ODZ2	FOXP3 [T	20	25	4.756447	GTTTTC	2.92969	2.96063
cg2316742	ODZ2	FOXP3 [T	497	502	4.756447	GTTGAC	2.92969	2.96063
cg2316742	ODZ2	FOXP3 [T	509	514	4.756447	GTTGAG	2.92969	2.96063

cg2316742	ODZ2	FOXP3 [T	519	524	4.756447	GTTTTT	2.92969	2.96063
cg2316742	ODZ2	FOXP3 [T	609	614	4.756447	GTTTTG	2.92969	2.96063
cg2316742	ODZ2	FOXP3 [T	1314	1319	4.756447	GTTGAC	2.92969	2.96063
cg2316742	ODZ2	FOXP3 [T	1921	1926	4.756447	AAAAAC	2.92969	2.96063
cg2316742	ODZ2	FOXP3 [T	1930	1935	4.756447	AAAAAC	2.92969	2.96063
cg2316742	ODZ2	c-Myb [T0	1610	1617	4.754782	GTCAGT	0.30518	0.30568
cg2316742	ODZ2	HNF-1A [	814	821	4.684871	TTCTTA	0.12207	0.12485
cg2316742	ODZ2	VDR [T00	1836	1844	4.617121	AGTTTG	0.37384	0.37445
cg2316742	ODZ2	c-Ets-2 [T	405	413	4.589988	AGGAAG	0.06866	0.06881
cg2316742	ODZ2	c-Ets-2 [T	409	417	4.589988	AGGAAG	0.06866	0.06881
cg2316742	ODZ2	c-Ets-2 [T	427	435	4.589988	AGGAAG	0.06866	0.06881
cg2316742	ODZ2	c-Ets-2 [T	431	439	4.589988	AGGAAG	0.06866	0.06881
cg2316742	ODZ2	c-Ets-2 [T	435	443	4.589988	AGGAAG	0.06866	0.06881
cg2316742	ODZ2	C/EBPalph	1007	1013	4.560723	GATTGT	0.24414	0.24411
cg2316742	ODZ2	IRF-1 [T0	1036	1044	4.549799	ACTGGG	0.05341	0.05405
cg2316742	ODZ2	c-Ets-1 [T	1268	1274	4.539113	ATTCCT	0.85449	0.85764
cg2316742	ODZ2	AP-2alpha	1958	1963	4.438035	GCCTAG	0.97656	0.96979
cg2316742	ODZ2	STAT4 [T	250	255	4.411765	GGAAGA	1.95312	1.94235
cg2316742	ODZ2	STAT4 [T	460	465	4.411765	GGAAGA	1.95312	1.94235
cg2316742	ODZ2	STAT4 [T	1184	1189	4.411765	CATTCC	1.95312	1.94235
cg2316742	ODZ2	STAT4 [T	1725	1730	4.411765	GGAAGC	1.95312	1.94235
cg2316742	ODZ2	STAT4 [T	1851	1856	4.411765	GGAATG	1.95312	1.94235
cg2316742	ODZ2	c-Ets-1 [T	809	815	4.411026	ATTCCT	0.85449	0.85764
cg2316742	ODZ2	c-Ets-1 [T	906	912	4.411026	AAGGAA	0.85449	0.85764
cg2316742	ODZ2	c-Ets-1 [T	1657	1663	4.411026	AAGGAA	0.85449	0.85764
cg2316742	ODZ2	c-Ets-1 [T	1971	1977	4.411026	AAGGAA	0.85449	0.85764
cg2316742	ODZ2	HOXD9 [	729	738	4.321431	AATAAA	0.03433	0.03596
cg2316742	ODZ2	HOXD10 [	729	738	4.321431	AATAAA	0.03433	0.03596
cg2316742	ODZ2	CREB [T0	572	580	4.299974	TCTACG	0.04578	0.04561
cg2316742	ODZ2	c-Ets-1 [T	1185	1191	4.282938	ATTCCT	0.85449	0.85764
cg2316742	ODZ2	c-Ets-1 [T	1630	1636	4.282938	ATTCCT	0.85449	0.85764
cg2316742	ODZ2	HNF-1B [	27	35	4.252262	AGTTAG	0.05341	0.0549
cg2316742	ODZ2	RXR-alpha	1087	1093	4.24113	GGGTAA	0.97656	0.9671
cg2316742	ODZ2	AR [T000	1202	1210	4.241082	GGACAG	0.06866	0.06828
cg2316742	ODZ2	C/EBPalph	1900	1906	4.235345	ATCAAT	0.48828	0.49358
cg2316742	ODZ2	GR-beta [	124	128	4.201913	AATAA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	221	225	4.201913	TTATT	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	276	280	4.201913	AATAA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	329	333	4.201913	TTATT	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	359	363	4.201913	AATCA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	564	568	4.201913	TGATT	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	670	674	4.201913	AATCA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	729	733	4.201913	AATAA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	740	744	4.201913	AATAA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	903	907	4.201913	AATAA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	932	936	4.201913	AATAA	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	938	942	4.201913	AATAG	7.8125	7.94607
cg2316742	ODZ2	GR-beta [	1006	1010	4.201913	TGATT	7.8125	7.94607

cg2316742 ODZ2	GR-beta [T	1043	1047	4.201913	AATCA	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1310	1314	4.201913	AATAG	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1381	1385	4.201913	TTATT	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1433	1437	4.201913	TGATT	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1562	1566	4.201913	AATAA	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1668	1672	4.201913	TTATT	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1717	1721	4.201913	CTATT	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1903	1907	4.201913	AATAA	7.8125	7.94607
cg2316742 ODZ2	GR-beta [T	1915	1919	4.201913	CTATT	7.8125	7.94607
cg2316742 ODZ2	NF-AT1 [T	169	178	4.134416	TGAATT	0.08392	0.08485
cg2316742 ODZ2	c-Ets-2 [T	903	911	4.091811	AATAAG	0.16022	0.16243
cg2316742 ODZ2	c-Ets-2 [T	1968	1976	4.091811	TGTAAG	0.16022	0.16243
cg2316742 ODZ2	C/EBPalph	1954	1960	4.019783	GATTGC	0.48828	0.49358
cg2316742 ODZ2	c-Ets-2 [T	423	431	4.017001	AGAAAG	0.16022	0.16243
cg2316742 ODZ2	c-Ets-2 [T	450	458	4.017001	AGAAAG	0.16022	0.16243
cg2316742 ODZ2	c-Ets-2 [T	455	463	4.017001	GGAAAG	0.16022	0.16243
cg2316742 ODZ2	Pax-5 [T0	1335	1341	4.007279	AGGGCC	1.09863	1.07975
cg2316742 ODZ2	Pax-5 [T0	1336	1342	4.007279	GGGCCC	1.09863	1.07975
cg2316742 ODZ2	TFIID [T0	665	671	4.007279	TATTAA	1.09863	1.13456
cg2316742 ODZ2	TFIID [T0	728	734	4.007279	TAATAA	1.09863	1.13456
cg2316742 ODZ2	TFIID [T0	1592	1598	4.007279	TTTACA	1.09863	1.13456
cg2316742 ODZ2	TFIID [T0	1777	1783	4.007279	TTTTAA	1.09863	1.13456
cg2316742 ODZ2	TFIID [T0	1916	1922	4.007279	TATTAA	1.09863	1.13456
cg2316742 ODZ2	c-Jun [T00	1607	1613	3.807346	TTAGTC	0.24414	0.24526
cg2316742 ODZ2	GR [T050	608	614	3.763516	TGTTTC	0.73242	0.74251
cg2316742 ODZ2	GR [T050	924	930	3.763516	CAAAGA	0.73242	0.74251
cg2316742 ODZ2	NF-Y [T0	1862	1869	3.732121	ATTGGA	0.48828	0.48904
cg2316742 ODZ2	IRF-1 [T0	451	459	3.692688	GAAAGG	0.06866	0.06927
cg2316742 ODZ2	c-Ets-2 [T	401	409	3.518824	AAGAAG	0.18311	0.18304
cg2316742 ODZ2	c-Ets-2 [T	810	818	3.518824	TTCCTTC	0.18311	0.18304
cg2316742 ODZ2	c-Ets-2 [T	1396	1404	3.518824	TTCCTTC	0.18311	0.18304
cg2316742 ODZ2	HNF-3alph	736	743	3.500065	AAAAAA	0.27466	0.28532
cg2316742 ODZ2	HNF-3alph	1590	1597	3.500065	TATTTAC	0.27466	0.28532
cg2316742 ODZ2	c-Ets-1 [T	1171	1177	3.462376	CAGGAA	0.61035	0.60765
cg2316742 ODZ2	ATF-2 [T0	572	581	3.454345	TCTACG	0.01907	0.01902
cg2316742 ODZ2	T3R-beta1	1527	1535	3.370634	GAGAGG	0.27466	0.2755
cg2316742 ODZ2	GR-beta [T	632	636	3.361531	AATCT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	664	668	3.361531	ATATT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	965	969	3.361531	AATCT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1328	1332	3.361531	AATCT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1387	1391	3.361531	AATCT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1589	1593	3.361531	ATATT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1628	1632	3.361531	AGATT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1880	1884	3.361531	AGATT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1897	1901	3.361531	AATAT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1907	1911	3.361531	AGATT	3.90625	3.99611
cg2316742 ODZ2	GR-beta [T	1975	1979	3.361531	AATAT	3.90625	3.99611
cg2316742 ODZ2	T3R-beta1	1620	1628	3.332047	CTAAGG	0.27466	0.2755

cg2316742	ODZ2	AP-2alpha	1076	1081	3.229049	AGAGGC	0.48828	0.48238
cg2316742	ODZ2	POU2F2 (	300	310	3.116744	TGTTTT	0.02575	0.0265
cg2316742	ODZ2	TFIID [T0	627	633	3.075094	TGCAAA	0.12207	0.12409
cg2316742	ODZ2	c-Ets-2 [T	1654	1662	3.020647	TACAAG	0.06104	0.06231
cg2316742	ODZ2	Elk-1 [T00	424	432	2.987643	GAAAGG	0.07629	0.07656
cg2316742	ODZ2	Elk-1 [T00	456	464	2.987643	GAAAGG	0.07629	0.07656
cg2316742	ODZ2	c-Ets-2 [T	393	401	2.945838	GAAAAG	0.06104	0.06231
cg2316742	ODZ2	STAT4 [T	398	403	2.941176	GGAAAG	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	440	445	2.941176	GGAAAG	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	455	460	2.941176	GGAAAG	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	484	489	2.941176	GGAAAG	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	1173	1178	2.941176	GGAACA	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	1629	1634	2.941176	GATTCC	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	1659	1664	2.941176	GGAATA	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	1819	1824	2.941176	TGTTCC	2.92969	2.929
cg2316742	ODZ2	STAT4 [T	1973	1978	2.941176	GGAATA	2.92969	2.929
cg2316742	ODZ2	STAT1bet	172	181	2.898434	ATTTCC	0.0515	0.05191
cg2316742	ODZ2	STAT1bet	1036	1045	2.898434	ACTGGG	0.0515	0.05191
cg2316742	ODZ2	IRF-1 [T0	1395	1403	2.890712	TTTCCTT	0.07629	0.07756
cg2316742	ODZ2	TCF-4 [T0	920	929	2.859093	AATTCA	0.03433	0.0351
cg2316742	ODZ2	PR B [T00	1182	1188	2.80933	AACATT	0.73242	0.74818
cg2316742	ODZ2	PR A [T01	1182	1188	2.80933	AACATT	0.73242	0.74818
cg2316742	ODZ2	TBP [T00	1756	1765	2.807313	TTTATA	0.12207	0.12635
cg2316742	ODZ2	NF-kappa	549	559	2.757067	GGGGAA	0.01669	0.01625
cg2316742	ODZ2	AP-2alpha	1121	1126	2.550491	TGAGGC	0.48828	0.48266
cg2316742	ODZ2	c-Jun [T00	1316	1322	2.538231	TGACTT	0.48828	0.48929
cg2316742	ODZ2	NF-Y [T0	1262	1269	2.420868	CTACCA	0.21362	0.21485
cg2316742	ODZ2	C/EBPalp	1428	1434	2.371703	AATTGT	0.48828	0.49114
cg2316742	ODZ2	c-Jun [T00	1641	1647	2.345465	TGTGTC	0.48828	0.48929
cg2316742	ODZ2	c-Jun [T00	1979	1985	2.345465	TGACAC	0.48828	0.48929
cg2316742	ODZ2	AR [T000	1006	1014	2.267638	TGATTG	0.11444	0.11507
cg2316742	ODZ2	c-Ets-2 [T	1631	1639	2.217136	TTCCTC	0.16785	0.16856
cg2316742	ODZ2	GATA-1 [	847	852	2.176375	TATCCT	3.90625	3.92756
cg2316742	ODZ2	GATA-1 [	1276	1281	2.176375	AGGATA	3.90625	3.92756
cg2316742	ODZ2	GATA-1 [	1831	1836	2.176375	AGGATA	3.90625	3.92756
cg2316742	ODZ2	c-Ets-2 [T	479	487	2.142327	AGAGAG	0.16785	0.16856
cg2316742	ODZ2	LEF-1 [T0	1782	1789	2.004405	AAGCAA	0.18311	0.18582
cg2316742	ODZ2	GATA-1 [	861	866	2.001358	TATCCC	3.90625	3.92756
cg2316742	ODZ2	PR B [T00	255	261	1.892895	AACACT	0.12207	0.12429
cg2316742	ODZ2	PR B [T00	313	319	1.892895	AAGTGT	0.12207	0.12429
cg2316742	ODZ2	PR A [T01	255	261	1.892895	AACACT	0.12207	0.12429
cg2316742	ODZ2	PR A [T01	313	319	1.892895	AAGTGT	0.12207	0.12429
cg2316742	ODZ2	TFII-I [T0	1074	1079	1.824994	GGAGAG	0.48828	0.48408
cg2316742	ODZ2	FOXP3 [T	1594	1599	1.824994	TACAAC	0.48828	0.49451
cg2316742	ODZ2	p53 [T006	1553	1559	1.758307	GGGCAT	0.36621	0.36261
cg2316742	ODZ2	GR-beta [	112	116	1.680765	GAATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [	149	153	1.680765	GCATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [	170	174	1.680765	GAATT	3.90625	3.94936

cg2316742	ODZ2	GR-beta [T	235	239	1.680765	AATGC	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	363	367	1.680765	AATGC	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	808	812	1.680765	AATTC	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	909	913	1.680765	GAATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	920	924	1.680765	AATTC	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1250	1254	1.680765	AATGC	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1267	1271	1.680765	AATTC	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1292	1296	1.680765	GCATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1427	1431	1.680765	GAATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1494	1498	1.680765	GCATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1700	1704	1.680765	GAATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1860	1864	1.680765	GAATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1941	1945	1.680765	GAATT	3.90625	3.94936
cg2316742	ODZ2	GR-beta [T	1942	1946	1.680765	AATTC	3.90625	3.94936
cg2316742	ODZ2	c-Ets-2 [T	1186	1194	1.64415	TTCCTC	0.04578	0.04579
cg2316742	ODZ2	c-Ets-1 [T	396	402	1.641124	AAGGAA	0.36621	0.36952
cg2316742	ODZ2	c-Ets-1 [T	412	418	1.641124	AAGGAA	0.36621	0.36952
cg2316742	ODZ2	c-Ets-1 [T	438	444	1.641124	AAGGAA	0.36621	0.36952
cg2316742	ODZ2	c-Ets-1 [T	453	459	1.641124	AAGGAA	0.36621	0.36952
cg2316742	ODZ2	c-Ets-1 [T	1395	1401	1.641124	TTTCCTT	0.36621	0.36952
cg2316742	ODZ2	C/EBPbeta	143	146	1.639871	TTGG	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	176	179	1.639871	CCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	248	251	1.639871	TTGG	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	542	545	1.639871	TTGG	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	654	657	1.639871	CCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	766	769	1.639871	TTGG	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1016	1019	1.639871	CCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1072	1075	1.639871	TTGG	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1210	1213	1.639871	CCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1231	1234	1.639871	CCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1265	1268	1.639871	CCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1676	1679	1.639871	CCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1863	1866	1.639871	TTGG	15.625	15.72563
cg2316742	ODZ2	XBP-1 [T	683	688	1.583727	TGTCAT	0.97656	0.98146
cg2316742	ODZ2	XBP-1 [T	1301	1306	1.583727	TGTCAT	0.97656	0.98146
cg2316742	ODZ2	XBP-1 [T	1454	1459	1.583727	GGTCAT	0.97656	0.98146
cg2316742	ODZ2	XBP-1 [T	1978	1983	1.583727	ATGACA	0.97656	0.98146
cg2316742	ODZ2	TFIID [T0	1070	1076	1.537547	TTTTGG	0.73242	0.75096
cg2316742	ODZ2	c-Ets-1 [T	482	488	1.513038	GAGGAA	0.36621	0.36952
cg2316742	ODZ2	STAT4 [T	115	120	1.470588	TTTTCC	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	332	337	1.470588	TTTTCC	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	414	419	1.470588	GGAAAA	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	551	556	1.470588	GGAACT	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	650	655	1.470588	GTTTCC	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	808	813	1.470588	AATTCC	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	908	913	1.470588	GGAATT	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	1267	1272	1.470588	AATTCC	1.95312	1.96333
cg2316742	ODZ2	STAT4 [T	1394	1399	1.470588	GTTTCC	1.95312	1.96333

cg2316742	ODZ2	PR B [T00	60	66	1.404665	AACACT	0.36621	0.37023
cg2316742	ODZ2	PR A [T01	60	66	1.404665	AACACT	0.36621	0.37023
cg2316742	ODZ2	c-Ets-1 [T	116	122	1.384951	TTTCCT	0.36621	0.36952
cg2316742	ODZ2	C/EBPbeta	24	27	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	230	233	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	361	364	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	371	374	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	498	501	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	510	513	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	706	709	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	794	797	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	806	809	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	923	926	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1005	1008	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1315	1318	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1384	1387	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1449	1452	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1521	1524	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1536	1539	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1549	1552	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1616	1619	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1692	1695	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1839	1842	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1884	1887	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1894	1897	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1901	1904	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1911	1914	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1927	1930	1.366559	TCAA	15.625	15.72563
cg2316742	ODZ2	C/EBPbeta	1939	1942	1.366559	TTGA	15.625	15.72563
cg2316742	ODZ2	AP-2alpha	1481	1486	1.357116	GCCTGT	0.48828	0.48203
cg2316742	ODZ2	IRF-1 [T0	394	402	1.274173	AAAAGG	0.04578	0.04655
cg2316742	ODZ2	TCF-4 [T0	227	236	1.235198	GCTTTG	0.05722	0.05784
cg2316742	ODZ2	GATA-1 [	369	374	1.038567	TATCAA	1.95312	1.98662
cg2316742	ODZ2	GATA-1 [	1899	1904	1.038567	TATCAA	1.95312	1.98662
cg2316742	ODZ2	Elk-1 [T00	402	410	0.957025	AGAAGG	0.03052	0.03057
cg2316742	ODZ2	TBP [T00	303	312	0.935771	TTTATA	0.12207	0.12628
cg2316742	ODZ2	HNF-1A [	1344	1351	0.925521	CAATTA	0.48828	0.49664
cg2316742	ODZ2	GR-beta [	4	8	0.840383	TAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	87	91	0.840383	CAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	138	142	0.840383	CCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	203	207	0.840383	CCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	239	243	0.840383	CCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	326	330	0.840383	TAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	327	331	0.840383	AATTA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	471	475	0.840383	AATGA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	585	589	0.840383	AATTG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	590	594	0.840383	CAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [	591	595	0.840383	AATTG	7.8125	7.94706

cg2316742	ODZ2	GR-beta [T	685	689	0.840383	TCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	709	713	0.840383	AATTA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	759	763	0.840383	AATGG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	807	811	0.840383	CAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	856	860	0.840383	CCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	910	914	0.840383	AATTA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1058	1062	0.840383	AATTG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1067	1071	0.840383	TAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1160	1164	0.840383	AATGG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1216	1220	0.840383	TCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1266	1270	0.840383	CAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1344	1348	0.840383	CAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1345	1349	0.840383	AATTA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1409	1413	0.840383	AATGA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1418	1422	0.840383	AATGG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1428	1432	0.840383	AATTG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1451	1455	0.840383	AATGG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1537	1541	0.840383	CAATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1538	1542	0.840383	AATTA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1635	1639	0.840383	TCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1651	1655	0.840383	AATTA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1684	1688	0.840383	AATGA	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1743	1747	0.840383	TCATT	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1861	1865	0.840383	AATTG	7.8125	7.94706
cg2316742	ODZ2	GR-beta [T	1945	1949	0.840383	TCATT	7.8125	7.94706
cg2316742	ODZ2	Elk-1 [T00	406	414	0.822677	GGAAGG	0.03052	0.03057
cg2316742	ODZ2	Elk-1 [T00	428	436	0.822677	GGAAGG	0.03052	0.03057
cg2316742	ODZ2	Elk-1 [T00	432	440	0.822677	GGAAGG	0.03052	0.03057
cg2316742	ODZ2	POU2F1 [	1288	1298	0.818935	ATTTGC	0.01383	0.01413
cg2316742	ODZ2	GATA-1 [	1466	1471	0.758539	CTGATA	1.95312	1.98662
cg2316742	ODZ2	AP-2alpha	1464	1469	0.678558	GCCTGA	0.48828	0.48199
cg2316742	ODZ2	C/EBPalp	962	968	0.540941	CACAAT	0.24414	0.24507
cg2316742	ODZ2	C/EBPalp	1866	1872	0.540941	GATTGT	0.24414	0.24507
cg2316742	ODZ2	PR B [T00	340	346	0.48823	AACTGT	0.12207	0.12407
cg2316742	ODZ2	PR A [T01	340	346	0.48823	AACTGT	0.12207	0.12407
cg2316742	ODZ2	c-Ets-1 [T	1130	1136	0.384261	TAGGAA	0.24414	0.24569
cg2316742	ODZ2	GATA-1 [	570	575	0.280028	TATCTA	0.97656	0.99875
cg2316742	ODZ2	GATA-1 [	926	931	0.280028	AAGATA	0.97656	0.99875
cg2316742	ODZ2	c-Ets-1 [T	404	410	0.256174	AAGGAA	0.24414	0.24569
cg2316742	ODZ2	c-Ets-1 [T	408	414	0.256174	AAGGAA	0.24414	0.24569
cg2316742	ODZ2	c-Ets-1 [T	426	432	0.256174	AAGGAA	0.24414	0.24569
cg2316742	ODZ2	c-Ets-1 [T	430	436	0.256174	AAGGAA	0.24414	0.24569
cg2316742	ODZ2	c-Ets-1 [T	434	440	0.256174	AAGGAA	0.24414	0.24569
cg2316742	ODZ2	c-Ets-1 [T	458	464	0.256174	AAGGAA	0.24414	0.24569
cg2316742	ODZ2	AP-2alpha	1473	1478	0.226186	GCCTGG	0.97656	0.95305
cg2316742	ODZ2	GR-alpha	269	273	0.207689	AAAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha	376	380	0.207689	AAAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha	395	399	0.207689	AAAGG	7.8125	7.81264

cg2316742	ODZ2	GR-alpha [	425	429	0.207689	AAAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	452	456	0.207689	AAAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	457	461	0.207689	AAAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	481	485	0.207689	AGAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	828	832	0.207689	CCTTT	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1076	1080	0.207689	AGAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1126	1130	0.207689	CCTTT	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1528	1532	0.207689	AGAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1665	1669	0.207689	CCTTT	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1753	1757	0.207689	CCTTT	7.8125	7.81264
cg2316742	ODZ2	HNF-1A [	2	9	0.143882	GTTAAT	0.24414	0.25261
cg2316742	ODZ2	PXR-1:RX	1611	1618	0.123583	TCAGTT	0.12207	0.12407
cg2316742	ODZ2	GATA-1 [	724	729	0.105011	GAGATA	0.97656	0.98738
cg2316742	ODZ2	GATA-1 [	979	984	0.105011	GAGATA	0.97656	0.98738
cg2316742	ODZ2	GATA-1 [	1412	1417	0.105011	GAGATA	0.97656	0.98738
cg2316742	ODZ2	GR-alpha [	560	564	0	CCTAT	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	789	793	0	CCTGT	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	850	854	0	CCTAT	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1084	1088	0	ATAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1274	1278	0	ACAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1482	1486	0	CCTGT	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1759	1763	0	ATAGG	7.8125	7.81264
cg2316742	ODZ2	GR-alpha [	1847	1851	0	ATAGG	7.8125	7.81264
cg2316742	ODZ2	XBP-1 [T0	1458	1463	0	ATGACT	0.97656	0.98127
cg2316742	ODZ2	XBP-1 [T0	1741	1746	0	AGTCAT	0.97656	0.98127
cg2316742	ODZ2	TFII-I [T0	398	403	0	GGAAAG	1.46484	1.45997
cg2316742	ODZ2	TFII-I [T0	440	445	0	GGAAAG	1.46484	1.45997
cg2316742	ODZ2	TFII-I [T0	455	460	0	GGAAAG	1.46484	1.45997
cg2316742	ODZ2	TFII-I [T0	484	489	0	GGAAAG	1.46484	1.45997
cg2316742	ODZ2	TFII-I [T0	1023	1028	0	GGACAG	1.46484	1.45997
cg2316742	ODZ2	TFII-I [T0	1202	1207	0	GGACAG	1.46484	1.45997
cg2316742	ODZ2	TFII-I [T0	1277	1282	0	GGATAG	1.46484	1.45997
cg2316742	ODZ2	TFII-I [T0	1832	1837	0	GGATAG	1.46484	1.45997
cg2316742	ODZ2	STAT4 [T	172	177	0	ATTTCC	0.48828	0.49387
cg2316742	ODZ2	STAT4 [T	273	278	0	GGAAAT	0.48828	0.49387
cg2316742	ODZ2	STAT4 [T	1040	1045	0	GGAAAT	0.48828	0.49387
cg2316742	ODZ2	STAT4 [T	1670	1675	0	ATTTCC	0.48828	0.49387
cg2316742	ODZ2	YY1 [T00	94	97	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	138	141	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	203	206	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	239	242	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	309	312	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	700	703	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	760	763	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	800	803	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	823	826	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	856	859	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00	945	948	0	CCAT	7.8125	7.81711

cg2316742	ODZ2	YY1 [T00(	1161	1164	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1404	1407	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1419	1422	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1452	1455	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1488	1491	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1573	1576	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1585	1588	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1772	1775	0	ATGG	7.8125	7.81711
cg2316742	ODZ2	YY1 [T00(	1991	1994	0	CCAT	7.8125	7.81711
cg2316742	ODZ2	ER-alpha [	135	139	0	TGACC	1.95312	1.9404
cg2316742	ODZ2	ER-alpha [	1454	1458	0	GGTCA	1.95312	1.9404
cg2316742	ODZ2	GATA-1 [	661	666	0	CAGATA	0.97656	0.98738
cg2316742	ODZ2	GATA-1 [	1026	1031	0	CAGATA	0.97656	0.98738
cg2316742	ODZ2	C/EBPbeta	58	61	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	70	73	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	86	89	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	91	94	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	154	157	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	191	194	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	207	210	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	242	245	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	299	302	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	524	527	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	527	530	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	530	533	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	534	537	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	538	541	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	587	590	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	589	592	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	593	596	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	595	598	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	612	615	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	615	618	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	628	631	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	682	685	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	690	693	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	778	781	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	901	904	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	963	966	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	993	996	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1009	1012	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1060	1063	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1255	1258	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1259	1262	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1290	1293	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1300	1303	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1307	1310	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1326	1329	0	ACAA	15.625	15.71349

cg2316742	ODZ2	C/EBPbeta	1343	1346	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1357	1360	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1423	1426	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1430	1433	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1438	1441	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1497	1500	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1499	1502	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1505	1508	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1582	1585	0	TTGC	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1595	1598	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1640	1643	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1655	1658	0	ACAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1721	1724	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1746	1749	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1784	1787	0	GCAA	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1811	1814	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1868	1871	0	TTGT	15.625	15.71349
cg2316742	ODZ2	C/EBPbeta	1956	1959	0	TTGC	15.625	15.71349
cg2316742	ODZ2	TFIID [T0	21	27	0	TTTTCAA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	230	236	0	TTGAAA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	302	308	0	TTTTATA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	351	357	0	TAGAAA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	731	737	0	TAAAAA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	1755	1761	0	TTTTATA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	1918	1924	0	TTAAAA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	1919	1925	0	TAAAAA	1.09863	1.13474
cg2316742	ODZ2	TFIID [T0	1927	1933	0	TCAAAA	1.09863	1.13474
cg2316742	ODZ2	FOXP3 [T	526	531	0	GTTGTT	1.46484	1.47315
cg2316742	ODZ2	FOXP3 [T	529	534	0	GTTGTT	1.46484	1.47315
cg2316742	ODZ2	FOXP3 [T	614	619	0	GTTGTG	1.46484	1.47315
cg2316742	ODZ2	FOXP3 [T	1810	1815	0	GTTGTG	1.46484	1.47315
cg2316742	ODZ2	GR-beta [T	5	9	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	88	92	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	113	117	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	127	131	0	AATGT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	171	175	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	501	505	0	ACATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	584	588	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	708	712	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	841	845	0	ACATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	919	923	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1002	1006	0	ACATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1057	1061	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1068	1072	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1097	1101	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1098	1102	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1183	1187	0	ACATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1286	1290	0	AAATT	3.90625	3.99611

cg2316742	ODZ2	GR-beta [T	1287	1291	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1370	1374	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1371	1375	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1603	1607	0	ACATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1650	1654	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1688	1692	0	AAATT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1689	1693	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1701	1705	0	AATTT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1853	1857	0	AATGT	3.90625	3.99611
cg2316742	ODZ2	GR-beta [T	1966	1970	0	AATGT	3.90625	3.99611
cg2316742	ODZ2	IRF-1 [T0	269	277	0	AAAGGG	0.00763	0.00776
cg2316742	ODZ2	GR [T050	520	526	0	TTTTTTG	0.36621	0.37562
cg2316742	ODZ2	GR [T050	678	684	0	CTTTTTG	0.36621	0.37562
cg2316742	ODZ2	GR [T050	1928	1934	0	CAAAAA	0.36621	0.37562
cg2316742	ODZ2	HNF-3alph	1558	1565	0	TAAAAAT	0.09155	0.09511
cg2316742	ODZ2	TCF-4E [T	1783	1789	0	AGCAAA	0.12207	0.12262
cg2316742	ODZ2	IRF-2 [T01	578	583	0	TCACTT	0.48828	0.49387
cg0720093	PLXNC1	HOXD9 [T	1956	1965	9.979471	AATATTA	0.2327	0.19979
cg0720093	PLXNC1	HOXD10 [	1956	1965	9.979471	AATATTA	0.2327	0.19979
cg0720093	PLXNC1	RAR-beta:	1822	1833	9.97066	TCTGGTC	0.06974	0.07677
cg0720093	PLXNC1	XBP-1 [T0	533	538	9.789909	ATGGCT	1.95312	1.94901
cg0720093	PLXNC1	XBP-1 [T0	976	981	9.789909	ATGGCT	1.95312	1.94901
cg0720093	PLXNC1	Elk-1 [T00	691	699	9.754368	TGATGGA	0.10681	0.11027
cg0720093	PLXNC1	PR B [T00	1363	1369	9.743489	GGGTGTT	1.09863	1.0981
cg0720093	PLXNC1	PR B [T00	1474	1480	9.743489	GTGTGTT	1.09863	1.0981
cg0720093	PLXNC1	PR B [T00	1522	1528	9.743489	TCGTGTT	1.09863	1.0981
cg0720093	PLXNC1	PR A [T01	1363	1369	9.743489	GGGTGTT	1.09863	1.0981
cg0720093	PLXNC1	PR A [T01	1474	1480	9.743489	GTGTGTT	1.09863	1.0981
cg0720093	PLXNC1	PR A [T01	1522	1528	9.743489	TCGTGTT	1.09863	1.0981
cg0720093	PLXNC1	HNF-1C [T	1001	1009	9.733135	GTTAATT	0.19836	0.18179
cg0720093	PLXNC1	c-Myb [T0	794	801	9.729271	TAACTGT	0.36621	0.34746
cg0720093	PLXNC1	LEF-1 [T0	944	951	9.72404	TGGCAA	0.21362	0.21229
cg0720093	PLXNC1	c-Ets-1 [T0	227	233	9.713162	ATTCCCC	0.36621	0.37402
cg0720093	PLXNC1	HNF-4alph	1022	1034	9.675138	AGGTTCC	0.01109	0.01049
cg0720093	PLXNC1	Elk-1 [T00	425	433	9.62002	GGAGGG	0.07629	0.0786
cg0720093	PLXNC1	HNF-1C [T	1488	1496	9.601936	AAAACT	0.19836	0.18179
cg0720093	PLXNC1	TFIID [T0	157	163	9.552105	TTTGGA	1.46484	1.37777
cg0720093	PLXNC1	TFIID [T0	196	202	9.552105	TTCCAA	1.46484	1.37777
cg0720093	PLXNC1	TFIID [T0	944	950	9.552105	TGGCAA	1.46484	1.37777
cg0720093	PLXNC1	TFIID [T0	1333	1339	9.552105	TGTGAA	1.46484	1.37777
cg0720093	PLXNC1	TFIID [T0	1347	1353	9.552105	TTTGGA	1.46484	1.37777
cg0720093	PLXNC1	TFIID [T0	1438	1444	9.552105	TTTGGT	1.46484	1.37777
cg0720093	PLXNC1	TFIID [T0	1743	1749	9.552105	TTCCAA	1.46484	1.37777
cg0720093	PLXNC1	Pax-5 [T0	1371	1377	9.552105	GGGCAA	1.46484	1.61918
cg0720093	PLXNC1	NF-1 [T00	1032	1039	9.535536	TTGGGC	0.73242	0.74634
cg0720093	PLXNC1	NF-AT1 [T	160	168	9.521781	GGAAAT	0.16785	0.16528
cg0720093	PLXNC1	NF-1 [T00	624	631	9.513281	TAAGCC	0.73242	0.74634
cg0720093	PLXNC1	FOXP3 [T	108	113	9.512894	ATAAAC	7.32422	7.22156

cg0720093	PLXNC1	FOXP3 [T	342	347	9.512894	GTTCTT	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	500	505	9.512894	GTTGGC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	597	602	9.512894	GTTGGT	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	705	710	9.512894	GTTGGC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	792	797	9.512894	AATAAC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	823	828	9.512894	ATAAAC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	835	840	9.512894	GAGAAC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	951	956	9.512894	GTTCTT	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	1086	1091	9.512894	ACCAAC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	1166	1171	9.512894	GTTTAC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	1372	1377	9.512894	GGCAAC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	1413	1418	9.512894	GTTCTT	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	1759	1764	9.512894	CAGAAC	7.32422	7.22156
cg0720093	PLXNC1	FOXP3 [T	1838	1843	9.512894	GTTATG	7.32422	7.22156
cg0720093	PLXNC1	TFII-I [T0	194	199	9.512894	GTTTCC	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	218	223	9.512894	CCTTCC	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	285	290	9.512894	AATTCC	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	367	372	9.512894	CGTTCC	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	429	434	9.512894	GGAAGG	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	434	439	9.512894	GGAAGG	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	654	659	9.512894	GGACTT	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	1307	1312	9.512894	GGATAC	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	1350	1355	9.512894	GGAAAC	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	1383	1388	9.512894	GGATTT	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	1419	1424	9.512894	GGAAAA	7.32422	7.44385
cg0720093	PLXNC1	TFII-I [T0	1639	1644	9.512894	TTGTCC	7.32422	7.44385
cg0720093	PLXNC1	c-Jun [T00	1534	1540	9.511322	GTGGTC	0.73242	0.7366
cg0720093	PLXNC1	TCF-4E [T	156	162	9.453578	CTTTGG	0.48828	0.46934
cg0720093	PLXNC1	c-Jun [T00	805	811	9.397655	ATTGTC	0.73242	0.7366
cg0720093	PLXNC1	NFI/CTF [	1943	1950	9.352332	CCAAGG	0.54932	0.55369
cg0720093	PLXNC1	c-Ets-1 [T	1114	1120	9.276861	TGGGAA	0.36621	0.37402
cg0720093	PLXNC1	c-Ets-1 [T	528	534	9.19359	TTGGAA	0.85449	0.84987
cg0720093	PLXNC1	RAR-alpha	374	386	9.192562	GGGGTC	0.02065	0.02209
cg0720093	PLXNC1	PXR-1:RX	1615	1622	9.122407	TGAACA	0.24414	0.24356
cg0720093	PLXNC1	PXR-1:RX	1898	1905	9.122407	GCTGTT	0.24414	0.24356
cg0720093	PLXNC1	HNF-1C [	1838	1846	9.094725	GTTATG	0.12207	0.10938
cg0720093	PLXNC1	c-Ets-1 [T	286	292	9.065503	ATTCCA	0.85449	0.84987
cg0720093	PLXNC1	c-Jun [T00	259	265	9.013496	CATGTC	0.61035	0.60549
cg0720093	PLXNC1	LEF-1 [T0	156	163	8.973041	CTTTGG	0.54932	0.53171
cg0720093	PLXNC1	GR [T050	1687	1693	8.971049	GTATTT	0.61035	0.5928
cg0720093	PLXNC1	c-Ets-2 [T	507	515	8.912323	GCCCAG	0.27466	0.27171
cg0720093	PLXNC1	c-Ets-2 [T	561	569	8.912323	GCCTAG	0.27466	0.27171
cg0720093	PLXNC1	PR B [T00	711	717	8.827054	ATCTGT	0.36621	0.35051
cg0720093	PLXNC1	PR B [T00	811	817	8.827054	AACAGA	0.36621	0.35051
cg0720093	PLXNC1	PR B [T00	1666	1672	8.827054	ATCTGT	0.36621	0.35051
cg0720093	PLXNC1	PR A [T01	711	717	8.827054	ATCTGT	0.36621	0.35051
cg0720093	PLXNC1	PR A [T01	811	817	8.827054	AACAGA	0.36621	0.35051
cg0720093	PLXNC1	PR A [T01	1666	1672	8.827054	ATCTGT	0.36621	0.35051

cg0720093	PLXNC1	NFI/CTF [	1344	1351	8.814757	TCATTTC	0.48828	0.48845
cg0720093	PLXNC1	Elk-1 [T00	844	852	8.797343	GGCTGG	0.24414	0.26271
cg0720093	PLXNC1	LEF-1 [T0	671	678	8.759086	TTGCAA	0.54932	0.53171
cg0720093	PLXNC1	XBP-1 [T	19	24	8.75604	ATGAAA	2.92969	2.75329
cg0720093	PLXNC1	XBP-1 [T	68	73	8.75604	ATGAAA	2.92969	2.75329
cg0720093	PLXNC1	XBP-1 [T	352	357	8.75604	ATGATA	2.92969	2.75329
cg0720093	PLXNC1	XBP-1 [T	716	721	8.75604	TTTCAT	2.92969	2.75329
cg0720093	PLXNC1	XBP-1 [T	892	897	8.75604	ATGAAA	2.92969	2.75329
cg0720093	PLXNC1	XBP-1 [T	1233	1238	8.75604	ATGATA	2.92969	2.75329
cg0720093	PLXNC1	XBP-1 [T	1614	1619	8.75604	ATGAAC	2.92969	2.75329
cg0720093	PLXNC1	XBP-1 [T	1674	1679	8.75604	TTTCAT	2.92969	2.75329
cg0720093	PLXNC1	c-Myb [T0	1398	1405	8.728118	AAACTT	0.30518	0.28602
cg0720093	PLXNC1	AR [T000	1699	1707	8.547269	GGACAT	0.10681	0.10838
cg0720093	PLXNC1	RAR-beta	145	154	8.541284	TGGGTT	0.26703	0.27434
cg0720093	PLXNC1	RAR-beta	1085	1094	8.541284	TACCAA	0.26703	0.27434
cg0720093	PLXNC1	c-Ets-1 [T	1742	1748	8.501115	GTTCCA	0.24414	0.23702
cg0720093	PLXNC1	IRF-1 [T0	195	203	8.497322	TTTCCA	0.20599	0.20245
cg0720093	PLXNC1	IRF-1 [T0	1415	1423	8.497322	TCTTGG	0.20599	0.20245
cg0720093	PLXNC1	HNF-1B [	84	92	8.379818	TTTCTA	0.11444	0.10456
cg0720093	PLXNC1	LEF-1 [T0	1637	1644	8.361499	CTTTGTC	0.15259	0.154
cg0720093	PLXNC1	HNF-3alp	101	108	8.343064	TATTTC	0.27466	0.23078
cg0720093	PLXNC1	HNF-3alp	788	795	8.343064	CTAAAA	0.27466	0.23078
cg0720093	PLXNC1	HNF-3alp	1622	1629	8.343064	CATTTA	0.27466	0.23078
cg0720093	PLXNC1	PR B [T00	169	175	8.338824	AACAGA	1.09863	1.09384
cg0720093	PLXNC1	PR B [T00	758	764	8.338824	AACAGA	1.09863	1.09384
cg0720093	PLXNC1	PR B [T00	1154	1160	8.338824	AACAGC	1.09863	1.09384
cg0720093	PLXNC1	PR B [T00	1617	1623	8.338824	AACAGC	1.09863	1.09384
cg0720093	PLXNC1	PR B [T00	1738	1744	8.338824	TTCTGTT	1.09863	1.09384
cg0720093	PLXNC1	PR B [T00	1897	1903	8.338824	TGCTGT	1.09863	1.09384
cg0720093	PLXNC1	PR A [T01	169	175	8.338824	AACAGA	1.09863	1.09384
cg0720093	PLXNC1	PR A [T01	758	764	8.338824	AACAGA	1.09863	1.09384
cg0720093	PLXNC1	PR A [T01	1154	1160	8.338824	AACAGC	1.09863	1.09384
cg0720093	PLXNC1	PR A [T01	1617	1623	8.338824	AACAGC	1.09863	1.09384
cg0720093	PLXNC1	PR A [T01	1738	1744	8.338824	TTCTGTT	1.09863	1.09384
cg0720093	PLXNC1	PR A [T01	1897	1903	8.338824	TGCTGT	1.09863	1.09384
cg0720093	PLXNC1	ATF3 [T0	77	84	8.313799	TGACAT	0.27466	0.27379
cg0720093	PLXNC1	GR-alpha [	218	222	8.281568	CCTTC	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	364	368	8.281568	CCTCG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	388	392	8.281568	GAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	399	403	8.281568	CGAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	402	406	8.281568	GGAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	425	429	8.281568	GGAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	430	434	8.281568	GAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	435	439	8.281568	GAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	629	633	8.281568	CAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	840	844	8.281568	CGAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1056	1060	8.281568	CAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1092	1096	8.281568	CCTTG	7.8125	8.20394

cg0720093	PLXNC1	GR-alpha [	1121	1125	8.281568	CCTTC	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1159	1163	8.281568	CCTCC	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1162	1166	8.281568	CCTTG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1180	1184	8.281568	CAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1355	1359	8.281568	CAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1377	1381	8.281568	CCTCG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1380	1384	8.281568	CGAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1564	1568	8.281568	CCTCC	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1576	1580	8.281568	CAAGG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1808	1812	8.281568	CCTTG	7.8125	8.20394
cg0720093	PLXNC1	GR-alpha [	1944	1948	8.281568	CAAGG	7.8125	8.20394
cg0720093	PLXNC1	c-Ets-1 [T	1024	1030	8.244941	GTTCCA	0.24414	0.2494
cg0720093	PLXNC1	IRF-1 [T0	156	164	8.151819	CTTTGG	0.25177	0.2462
cg0720093	PLXNC1	c-Jun [T00	1195	1201	8.128539	AATGTC	0.48828	0.47447
cg0720093	PLXNC1	c-Ets-1 [T	368	374	8.116854	GTTCCA	0.24414	0.2494
cg0720093	PLXNC1	VDR [T00	1611	1619	8.079962	TAAATG	0.24414	0.22992
cg0720093	PLXNC1	GR-alpha [	43	47	8.073878	CCTAG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	324	328	8.073878	GTAGG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	371	375	8.073878	CCAGG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	452	456	8.073878	CCAGG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	462	466	8.073878	CCTGC	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	466	470	8.073878	CCTGC	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	493	497	8.073878	CCTGC	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	509	513	8.073878	CCAGG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	556	560	8.073878	GCAGG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	562	566	8.073878	CCTAG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	563	567	8.073878	CTAGG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	571	575	8.073878	CCTGG	7.8125	8.20289
cg0720093	PLXNC1	GR-alpha [	932	936	8.073878	CCTGG	7.8125	8.20289
cg0720093	PLXNC1	TFIID [T0	9	15	8.014558	TTTGCTA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	67	73	8.014558	TATGAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	84	90	8.014558	TTTCTAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	158	164	8.014558	TTGGAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	195	201	8.014558	TTTCCAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	292	298	8.014558	TTTGCTA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	583	589	8.014558	TTTGTAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	659	665	8.014558	TAGCAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	671	677	8.014558	TTGCAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	716	722	8.014558	TTTCATA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	857	863	8.014558	TCAGAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1075	1081	8.014558	TTAGAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1149	1155	8.014558	TTGCAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1251	1257	8.014558	TTTGAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1348	1354	8.014558	TTGGAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1417	1423	8.014558	TTGGAA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1459	1465	8.014558	TTTGTGA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1674	1680	8.014558	TTTCATA	2.19727	1.99811
cg0720093	PLXNC1	TFIID [T0	1690	1696	8.014558	TTTGATA	2.19727	1.99811

cg0720093	PLXNC1	Pax-5 [T0	504	510	8.014558	GCTGCC	2.19727	2.42766
cg0720093	PLXNC1	Pax-5 [T0	559	565	8.014558	GGGCCT	2.19727	2.42766
cg0720093	PLXNC1	Pax-5 [T0	1938	1944	8.014558	GAGGCC	2.19727	2.42766
cg0720093	PLXNC1	C/EBPalph	1297	1303	8.006685	CATTGT	0.24414	0.23098
cg0720093	PLXNC1	c-Myb [T0	210	217	8.005241	TAACTC	0.21362	0.20997
cg0720093	PLXNC1	MAZ [T00	420	432	7.968539	AGATGG	0.00915	0.01027
cg0720093	PLXNC1	NF-AT2 [	1419	1428	7.779688	GGAAAA	0.08965	0.08482
cg0720093	PLXNC1	GATA-2 [	1307	1315	7.777778	GGATAC	0.30518	0.29346
cg0720093	PLXNC1	NF-AT1 [	191	199	7.72101	TTTGTTT	0.19836	0.19379
cg0720093	PLXNC1	NF-AT1 [	1350	1358	7.72101	GGAAAC	0.19836	0.19379
cg0720093	PLXNC1	LEF-1 [T0	1030	1037	7.6105	CTTTGG	0.21362	0.21504
cg0720093	PLXNC1	RBP-Jkap	1110	1121	7.593528	ACCGTG	0.02337	0.02319
cg0720093	PLXNC1	AR [T000	454	462	7.588908	AGGATG	0.25177	0.2544
cg0720093	PLXNC1	GR [T050	167	173	7.527031	CAAACA	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	188	194	7.527031	TGCTTT	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	199	205	7.527031	CAAACA	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	580	586	7.527031	ATATTT	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	591	597	7.527031	CAAATA	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	885	891	7.527031	TTATTT	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	972	978	7.527031	CAAAAT	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	1010	1016	7.527031	TTGTTT	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	1152	1158	7.527031	CAAACA	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	1248	1254	7.527031	TTGTTT	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	1328	1334	7.527031	CAAAAT	1.83105	1.71535
cg0720093	PLXNC1	GR [T050	1932	1938	7.527031	ATATTT	1.83105	1.71535
cg0720093	PLXNC1	RAR-beta	1114	1123	7.47824	TGGGAA	0.24414	0.25121
cg0720093	PLXNC1	C/EBPalph	1393	1399	7.465744	CATTGA	0.48828	0.45033
cg0720093	PLXNC1	AR [T000	247	255	7.429939	GGACAG	0.25177	0.2544
cg0720093	PLXNC1	C/EBPalph	763	769	7.396431	AATTGT	0.48828	0.45033
cg0720093	PLXNC1	p53 [T006	1601	1607	7.266844	GGGCTT	0.73242	0.79826
cg0720093	PLXNC1	XBP-1 [T	125	130	7.172312	ATGATT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	178	183	7.172312	ATTCAT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	237	242	7.172312	AATCAT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	306	311	7.172312	ATGAAG	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	338	343	7.172312	ATGAGT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	690	695	7.172312	ATGATG	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	1339	1344	7.172312	ATGAGT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	1662	1667	7.172312	CTTCAT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	1724	1729	7.172312	AATCAT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	1732	1737	7.172312	ATTCAT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	1794	1799	7.172312	ATGAGT	2.92969	2.7512
cg0720093	PLXNC1	XBP-1 [T	1841	1846	7.172312	ATGAAT	2.92969	2.7512
cg0720093	PLXNC1	TFIID [T	11	17	7.082373	TGCTAA	0.12207	0.11255
cg0720093	PLXNC1	IRF-1 [T0	1402	1410	7.041849	TTTCCC	0.1297	0.12685
cg0720093	PLXNC1	NFI/CTF [	1087	1094	7.014249	CCAACC	0.73242	0.74795
cg0720093	PLXNC1	HNF-3alp	14	21	7.000129	TAAAAA	0.82397	0.71909
cg0720093	PLXNC1	HNF-3alp	82	89	7.000129	TATTTCT	0.82397	0.71909
cg0720093	PLXNC1	HNF-3alp	581	588	7.000129	TATTTGT	0.82397	0.71909

cg0720093	PLXNC1	HNF-3alph	1952	1959	7.000129	GAAAAA	0.82397	0.71909
cg0720093	PLXNC1	c-Ets-1 [T	1402	1408	6.943262	TTTCCCC	0.73242	0.73732
cg0720093	PLXNC1	ENKTF-1	534	541	6.942764	TGGCTG	1.46484	1.56616
cg0720093	PLXNC1	ENKTF-1	944	951	6.942764	TGGCAA	1.46484	1.56616
cg0720093	PLXNC1	p53 [T006	1938	1944	6.938545	GAGGCC	1.09863	1.22478
cg0720093	PLXNC1	NF-AT1 [	191	200	6.890694	TTTGTTT	0.01907	0.01836
cg0720093	PLXNC1	C/EBPalph	1203	1209	6.786177	TATTGTA	0.73242	0.68282
cg0720093	PLXNC1	NFI/CTF [	198	205	6.786076	CCAAAC	0.73242	0.74795
cg0720093	PLXNC1	POU2F2 (	1477	1487	6.735173	TGTTTAA	0.04292	0.03779
cg0720093	PLXNC1	GATA-2 [	781	789	6.666667	ACAATA	0.24414	0.2357
cg0720093	PLXNC1	AR [T000	1636	1644	6.617912	ACTTTGT	0.19836	0.20813
cg0720093	PLXNC1	FOXP3 [T	774	779	6.581441	TAAAAC	0.97656	0.904
cg0720093	PLXNC1	FOXP3 [T	1136	1141	6.581441	GTTGAA	0.97656	0.904
cg0720093	PLXNC1	FOXP3 [T	1511	1516	6.581441	GTTGAA	0.97656	0.904
cg0720093	PLXNC1	TFII-I [T0	1548	1553	6.581441	CACTCC	0.97656	0.9991
cg0720093	PLXNC1	MEF-2A [	619	629	6.559479	TATTTA	0.02384	0.02083
cg0720093	PLXNC1	c-Myb [T0	1968	1975	6.539977	CAACTT	0.30518	0.30272
cg0720093	PLXNC1	XBP-1 [T	707	712	6.478682	TGGCAT	0.97656	0.99906
cg0720093	PLXNC1	C/EBPalph	262	268	6.460799	GTCAAT	0.48828	0.47407
cg0720093	PLXNC1	C/EBPalph	334	340	6.460799	GGCAAT	0.48828	0.47407
cg0720093	PLXNC1	c-Ets-1 [T	158	164	6.423689	TTGGAA	0.48828	0.48842
cg0720093	PLXNC1	c-Ets-1 [T	195	201	6.423689	TTTCCAA	0.48828	0.48842
cg0720093	PLXNC1	c-Ets-1 [T	1348	1354	6.423689	TTGGAA	0.48828	0.48842
cg0720093	PLXNC1	c-Ets-1 [T	1417	1423	6.423689	TTGGAA	0.48828	0.48842
cg0720093	PLXNC1	C/EBPalph	804	810	6.391486	AATTGT	0.48828	0.47407
cg0720093	PLXNC1	TCF-4E [T	190	196	6.302385	CTTTGTT	0.61035	0.59686
cg0720093	PLXNC1	TCF-4E [T	945	951	6.302385	GGCAAA	0.61035	0.59686
cg0720093	PLXNC1	GR-alpha [	137	141	6.263098	CCTTA	3.90625	3.89624
cg0720093	PLXNC1	GR-alpha [	320	324	6.263098	TAAGG	3.90625	3.89624
cg0720093	PLXNC1	GR-alpha [	477	481	6.263098	TAAGG	3.90625	3.89624
cg0720093	PLXNC1	GR-alpha [	651	655	6.263098	TAAGG	3.90625	3.89624
cg0720093	PLXNC1	GR-alpha [	1591	1595	6.263098	TAAGG	3.90625	3.89624
cg0720093	PLXNC1	GR-alpha [	1937	1941	6.263098	TGAGG	3.90625	3.89624
cg0720093	PLXNC1	C/EBPalph	104	110	6.245236	TTCAATA	0.97656	0.91422
cg0720093	PLXNC1	SRY [T00	1637	1645	6.176442	CTTTGTC	0.15259	0.14742
cg0720093	PLXNC1	IRF-1 [T0	1346	1354	6.078807	ATTTGGA	0.16785	0.16217
cg0720093	PLXNC1	GR-alpha [	223	227	6.055408	CCTGA	3.90625	3.89835
cg0720093	PLXNC1	GR-alpha [	378	382	6.055408	TCAGG	3.90625	3.89835
cg0720093	PLXNC1	GR-alpha [	744	748	6.055408	TCAGG	3.90625	3.89835
cg0720093	PLXNC1	GR-alpha [	1368	1372	6.055408	TTAGG	3.90625	3.89835
cg0720093	PLXNC1	GR-alpha [	1643	1647	6.055408	CCTAA	3.90625	3.89835
cg0720093	PLXNC1	GR-alpha [	1949	1953	6.055408	CCTGA	3.90625	3.89835
cg0720093	PLXNC1	C/EBPalph	1507	1513	5.996794	CATTGTT	0.97656	0.91422
cg0720093	PLXNC1	HOXD9 [T	880	889	5.898575	AAGTCT	0.05722	0.04686
cg0720093	PLXNC1	HOXD10 [	880	889	5.898575	AAGTCT	0.05722	0.04686
cg0720093	PLXNC1	p53 [T006	559	565	5.883561	GGGCCT	0.61035	0.68483
cg0720093	PLXNC1	STAT4 [T	218	223	5.882353	CCTTCC	0.48828	0.51201
cg0720093	PLXNC1	STAT4 [T	429	434	5.882353	GGAAGG	0.48828	0.51201

cg0720093	PLXNC1	STAT4 [T	434	439	5.882353	GGAAGG	0.48828	0.51201
cg0720093	PLXNC1	C/EBPalp	38	44	5.850545	AATTGC	0.97656	0.91422
cg0720093	PLXNC1	STAT1bet	1415	1424	5.796867	TCTTGG	0.1545	0.14881
cg0720093	PLXNC1	RXR-alpha	1363	1369	5.715466	GGGTGT	0.61035	0.65415
cg0720093	PLXNC1	c-Jun [T00	374	380	5.703976	GGGGTC	0.48828	0.49294
cg0720093	PLXNC1	ENKTF-1	1180	1187	5.687009	CAAGGC	0.73242	0.76357
cg0720093	PLXNC1	c-Ets-1 [T	219	225	5.686398	CTTCCCT	0.36621	0.38732
cg0720093	PLXNC1	c-Ets-1 [T	390	396	5.686398	AGGGAA	0.36621	0.38732
cg0720093	PLXNC1	c-Ets-1 [T	427	433	5.686398	AGGGAA	0.36621	0.38732
cg0720093	PLXNC1	c-Ets-1 [T	432	438	5.686398	AGGGAA	0.36621	0.38732
cg0720093	PLXNC1	HNF-1A [	208	215	5.610392	GTTAAC	0.24414	0.23087
cg0720093	PLXNC1	C/EBPalp	1	7	5.565669	GATTGT	0.73242	0.68229
cg0720093	PLXNC1	NFI/CTF [	235	242	5.558661	CCAATC	0.54932	0.55504
cg0720093	PLXNC1	NFI/CTF [	524	531	5.558661	GTGCTT	0.54932	0.55504
cg0720093	PLXNC1	TFIID [T0	33	39	5.544826	TGTTAA	0.73242	0.65314
cg0720093	PLXNC1	TFIID [T0	728	734	5.544826	TTTACC	0.73242	0.65314
cg0720093	PLXNC1	TFIID [T0	817	823	5.544826	TTCTAA	0.73242	0.65314
cg0720093	PLXNC1	TFIID [T0	1074	1080	5.544826	TTTAGA	0.73242	0.65314
cg0720093	PLXNC1	TFIID [T0	1679	1685	5.544826	TACTAA	0.73242	0.65314
cg0720093	PLXNC1	NF-AT1 [	1349	1358	5.512555	TGGAAA	0.05913	0.05666
cg0720093	PLXNC1	C/EBPalp	282	288	5.38654	ACCAAT	0.73242	0.68229
cg0720093	PLXNC1	RXR-alpha	327	333	5.271235	GGGTAG	0.61035	0.65415
cg0720093	PLXNC1	POU2F2 (	1811	1821	5.23012	TGCTTT	0.02432	0.02134
cg0720093	PLXNC1	HNF-1C [	83	91	5.214027	ATTTCT	0.04578	0.04128
cg0720093	PLXNC1	GR [T050	1244	1250	5.207533	GGTTTT	0.24414	0.24013
cg0720093	PLXNC1	GR [T050	1746	1752	5.207533	CAAAAC	0.24414	0.24013
cg0720093	PLXNC1	NF-Y [T0	232	239	5.094053	CCCCCA	0.36621	0.35921
cg0720093	PLXNC1	GR-beta [	53	57	5.042296	GTATT	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	485	489	5.042296	AATAC	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	601	605	5.042296	GTATT	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	633	637	5.042296	GTATT	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	1176	1180	5.042296	AATAC	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	1202	1206	5.042296	GTATT	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	1383	1387	5.042296	GGATT	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	1687	1691	5.042296	GTATT	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	1844	1848	5.042296	AATAC	3.90625	3.7093
cg0720093	PLXNC1	GR-beta [	1913	1917	5.042296	GTATT	3.90625	3.7093
cg0720093	PLXNC1	PXR-1:RX	1827	1834	5.032032	TGAACC	0.12207	0.11843
cg0720093	PLXNC1	C/EBPalp	56	62	5.024728	TTCAAT	0.97656	0.90302
cg0720093	PLXNC1	p53 [T006	1518	1524	5.020467	GGGCTC	0.48828	0.53921
cg0720093	PLXNC1	RAR-beta:	374	385	4.98533	GGGGTC	0.00966	0.01077
cg0720093	PLXNC1	c-Myb [T0	1542	1549	4.974489	CAACTG	0.30518	0.30087
cg0720093	PLXNC1	c-Ets-1 [T	693	699	4.910652	ATGGAA	0.48828	0.48026
cg0720093	PLXNC1	c-Jun [T00	77	83	4.883696	TGACAT	0.61035	0.60573
cg0720093	PLXNC1	c-Jun [T00	540	546	4.883696	TGACAT	0.61035	0.60573
cg0720093	PLXNC1	NF-1 [T00	1741	1748	4.880836	TGTTCC	0.24414	0.24345
cg0720093	PLXNC1	C/EBPalp	1894	1900	4.845599	AATTGC	0.97656	0.90302
cg0720093	PLXNC1	HNF-3alp	1607	1614	4.842999	TATTTA	0.09155	0.07438

cg0720093	PLXNC1	NF-AT1 [T	1418	1427	4.823485	TGGAAA	0.07629	0.07281
cg0720093	PLXNC1	p53 [T006	1034	1040	4.786849	GGGCAC	0.48828	0.53921
cg0720093	PLXNC1	c-Ets-1 [T	1770	1776	4.782565	GTGGAA	0.48828	0.48026
cg0720093	PLXNC1	C/EBPalph	634	640	4.776286	TATTGTT	0.97656	0.90302
cg0720093	PLXNC1	FOXP3 [T	148	153	4.756447	GTTTTT	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	638	643	4.756447	GTTGAT	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	662	667	4.756447	CAAAAC	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	755	760	4.756447	AAAAAC	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	808	813	4.756447	GTCAAC	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1245	1250	4.756447	GTTTTG	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1254	1259	4.756447	GAAAAC	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1323	1328	4.756447	CAAAAC	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1487	1492	4.756447	AAAAAC	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1526	1531	4.756447	GTTTTT	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1540	1545	4.756447	ATCAAC	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1670	1675	4.756447	GTTTTT	2.92969	2.82
cg0720093	PLXNC1	FOXP3 [T	1746	1751	4.756447	CAAAAC	2.92969	2.82
cg0720093	PLXNC1	TFII-I [T0	160	165	4.756447	GGAAAT	2.92969	2.89715
cg0720093	PLXNC1	TFII-I [T0	457	462	4.756447	ATGTCC	2.92969	2.89715
cg0720093	PLXNC1	TFII-I [T0	512	517	4.756447	GGAATG	2.92969	2.89715
cg0720093	PLXNC1	TFII-I [T0	530	535	4.756447	GGAATG	2.92969	2.89715
cg0720093	PLXNC1	TFII-I [T0	1699	1704	4.756447	GGACAT	2.92969	2.89715
cg0720093	PLXNC1	TFII-I [T0	1708	1713	4.756447	GGATAT	2.92969	2.89715
cg0720093	PLXNC1	PPAR-alph	242	252	4.727619	TGCTGG	0.03242	0.03494
cg0720093	PLXNC1	HNF-1A [	206	213	4.684871	ATGTTA	0.12207	0.10966
cg0720093	PLXNC1	c-Ets-1 [T	846	852	4.654478	CTGGAA	0.85449	0.8381
cg0720093	PLXNC1	c-Fos [T00	1341	1350	4.563121	GAGTCA	0.04578	0.04479
cg0720093	PLXNC1	T3R-beta1	280	288	4.481316	TCACCA	0.27466	0.27245
cg0720093	PLXNC1	GATA-2 [	1692	1700	4.444445	TGATAG	0.24414	0.23857
cg0720093	PLXNC1	AP-2alpha	42	47	4.438035	GCCTAG	0.97656	0.99839
cg0720093	PLXNC1	AP-2alpha	561	566	4.438035	GCCTAG	0.97656	0.99839
cg0720093	PLXNC1	STAT4 [T	367	372	4.411765	CGTTCC	1.95312	1.99838
cg0720093	PLXNC1	STAT4 [T	392	397	4.411765	GGAAGC	1.95312	1.99838
cg0720093	PLXNC1	STAT4 [T	512	517	4.411765	GGAATG	1.95312	1.99838
cg0720093	PLXNC1	STAT4 [T	530	535	4.411765	GGAATG	1.95312	1.99838
cg0720093	PLXNC1	STAT4 [T	566	571	4.411765	GGAAGC	1.95312	1.99838
cg0720093	PLXNC1	STAT4 [T	695	700	4.411765	GGAAGA	1.95312	1.99838
cg0720093	PLXNC1	STAT4 [T	848	853	4.411765	GGAAGA	1.95312	1.99838
cg0720093	PLXNC1	STAT4 [T	1772	1777	4.411765	GGAAGA	1.95312	1.99838
cg0720093	PLXNC1	p53 [T006	572	578	4.33696	CTGGCC	0.24414	0.28373
cg0720093	PLXNC1	GR-beta [T	0	4	4.201913	TGATT	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	59	63	4.201913	AATCG	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	100	104	4.201913	CTATT	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	107	111	4.201913	AATAA	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	126	130	4.201913	TGATT	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	225	229	4.201913	TGATT	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	237	241	4.201913	AATCA	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	274	278	4.201913	AATAG	7.8125	7.23274

cg0720093	PLXNC1	GR-beta [T	593	597	4.201913	AATAG	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	618	622	4.201913	CTATT	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	792	796	4.201913	AATAA	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	822	826	4.201913	AATAA	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	885	889	4.201913	TTATT	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	1130	1134	4.201913	AATAG	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	1606	1610	4.201913	TTATT	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	1724	1728	4.201913	AATCA	7.8125	7.23274
cg0720093	PLXNC1	GR-beta [T	1856	1860	4.201913	TGATT	7.8125	7.23274
cg0720093	PLXNC1	c-Ets-1 [T	510	516	4.154851	CAGGAA	0.24414	0.23719
cg0720093	PLXNC1	NF-AT1 [T	159	168	4.134416	TGGAAA	0.08392	0.07965
cg0720093	PLXNC1	p53 [T006	929	935	4.125254	GGGCCT	0.73242	0.82434
cg0720093	PLXNC1	SRY [T00	1752	1760	4.087393	CTTTGA	0.12207	0.11312
cg0720093	PLXNC1	TFIID [T0	122	128	4.007279	TTTATG	1.09863	0.94722
cg0720093	PLXNC1	TFIID [T0	344	350	4.007279	TCTTAA	1.09863	0.94722
cg0720093	PLXNC1	TFIID [T0	1046	1052	4.007279	TTTAAG	1.09863	0.94722
cg0720093	PLXNC1	TFIID [T0	1299	1305	4.007279	TTGTAA	1.09863	0.94722
cg0720093	PLXNC1	Pax-5 [T0	413	419	4.007279	ACTGCC	1.09863	1.18533
cg0720093	PLXNC1	Pax-5 [T0	1034	1040	4.007279	GGGCAC	1.09863	1.18533
cg0720093	PLXNC1	Pax-5 [T0	1601	1607	4.007279	GGGCTT	1.09863	1.18533
cg0720093	PLXNC1	AP-2alpha	1056	1061	3.970052	CAAGGC	0.97656	1.02535
cg0720093	PLXNC1	AP-2alpha	1180	1185	3.970052	CAAGGC	0.97656	1.02535
cg0720093	PLXNC1	AP-2alpha	1944	1949	3.970052	CAAGGC	0.97656	1.02535
cg0720093	PLXNC1	Elk-1 [T00	562	570	3.944668	CCTAGG	0.09155	0.08816
cg0720093	PLXNC1	GR [T050	154	160	3.763516	TTCTTTG	0.73242	0.6946
cg0720093	PLXNC1	GR [T050	662	668	3.763516	CAAAAC	0.73242	0.6946
cg0720093	PLXNC1	GR [T050	1323	1329	3.763516	CAAAAC	0.73242	0.6946
cg0720093	PLXNC1	p53 [T006	843	849	3.750231	GGGCTG	0.73242	0.82434
cg0720093	PLXNC1	c-Ets-1 [T	1653	1659	3.71855	GTTCCT	0.61035	0.61936
cg0720093	PLXNC1	c-Myb [T0	667	674	3.555283	CAACTT	0.12207	0.12166
cg0720093	PLXNC1	p53 [T006	413	419	3.516613	ACTGCC	0.73242	0.80362
cg0720093	PLXNC1	HNF-3alph	818	825	3.500065	TCTAAA	0.27466	0.23175
cg0720093	PLXNC1	HNF-3alph	1126	1133	3.500065	TGTAAA	0.27466	0.23175
cg0720093	PLXNC1	HNF-3alph	1921	1928	3.500065	TATAAA	0.27466	0.23175
cg0720093	PLXNC1	VDR [T00	1901	1909	3.462841	GTTCAC	0.21362	0.21283
cg0720093	PLXNC1	RXR-alph	1116	1122	3.392904	GGAACC	1.09863	1.1653
cg0720093	PLXNC1	ATF3 [T0	540	547	3.372402	TGACAT	0.09155	0.08824
cg0720093	PLXNC1	GR-beta [T	46	50	3.361531	AGATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	81	85	3.361531	ATATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	141	145	3.361531	AATCT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	580	584	3.361531	ATATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	724	728	3.361531	AGATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	783	787	3.361531	AATAT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	814	818	3.361531	AGATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	940	944	3.361531	AATCT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1710	1714	3.361531	ATATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1817	1821	3.361531	AGATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1925	1929	3.361531	AATAT	3.90625	3.51525

cg0720093	PLXNC1	GR-beta [	1932	1936	3.361531	ATATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [	1956	1960	3.361531	AATAT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [	1957	1961	3.361531	ATATT	3.90625	3.51525
cg0720093	PLXNC1	T3R-beta1	1821	1829	3.351341	TTCTGG	0.27466	0.27326
cg0720093	PLXNC1	T3R-beta1	264	272	3.332047	CAATGG	0.27466	0.27326
cg0720093	PLXNC1	T3R-beta1	1572	1580	3.332047	TCACCA	0.27466	0.27326
cg0720093	PLXNC1	PR B [T00	204	210	3.29756	AAATGT	0.24414	0.21408
cg0720093	PLXNC1	PR B [T00	701	707	3.29756	AAATGT	0.24414	0.21408
cg0720093	PLXNC1	PR A [T01	204	210	3.29756	AAATGT	0.24414	0.21408
cg0720093	PLXNC1	PR A [T01	701	707	3.29756	AAATGT	0.24414	0.21408
cg0720093	PLXNC1	AP-2alpha	331	336	3.229049	AGAGGC	0.48828	0.5124
cg0720093	PLXNC1	RXR-alpha	146	152	3.170788	GGGTTT	0.24414	0.24551
cg0720093	PLXNC1	TCF-4E [	672	678	3.151193	TGCAAA	0.24414	0.23169
cg0720093	PLXNC1	TCF-4E [	1752	1758	3.151193	CTTTGA	0.24414	0.23169
cg0720093	PLXNC1	PEA3 [T0	912	920	3.113548	TGGATG	0.01526	0.01408
cg0720093	PLXNC1	TFIID [T0	751	757	3.075094	TGCAAA	0.12207	0.11309
cg0720093	PLXNC1	p53 [T006	1371	1377	3.024997	GGGCAA	0.48828	0.53227
cg0720093	PLXNC1	C/EBPalph	1229	1235	2.981957	CACAAT	0.48828	0.47526
cg0720093	PLXNC1	c-Ets-2 [T	1654	1662	2.945838	TTCCTTT	0.06104	0.05567
cg0720093	PLXNC1	STAT4 [T	226	231	2.941176	GATTCC	2.92969	2.92382
cg0720093	PLXNC1	STAT4 [T	1023	1028	2.941176	GGTTCC	2.92969	2.92382
cg0720093	PLXNC1	STAT4 [T	1116	1121	2.941176	GGAACC	2.92969	2.92382
cg0720093	PLXNC1	STAT4 [T	1401	1406	2.941176	CTTTCC	2.92969	2.92382
cg0720093	PLXNC1	STAT4 [T	1652	1657	2.941176	TGTTCC	2.92969	2.92382
cg0720093	PLXNC1	STAT4 [T	1741	1746	2.941176	TGTTCC	2.92969	2.92382
cg0720093	PLXNC1	p53 [T006	504	510	2.813291	GCTGCC	0.48828	0.53227
cg0720093	PLXNC1	NF-1 [T00	1939	1946	2.813149	AGGCCC	0.24414	0.2566
cg0720093	PLXNC1	PR B [T00	634	640	2.80933	TATTGT	0.73242	0.66711
cg0720093	PLXNC1	PR B [T00	1505	1511	2.80933	AACATT	0.73242	0.66711
cg0720093	PLXNC1	PR B [T00	1507	1513	2.80933	CATTGT	0.73242	0.66711
cg0720093	PLXNC1	PR A [T01	634	640	2.80933	TATTGT	0.73242	0.66711
cg0720093	PLXNC1	PR A [T01	1505	1511	2.80933	AACATT	0.73242	0.66711
cg0720093	PLXNC1	PR A [T01	1507	1513	2.80933	CATTGT	0.73242	0.66711
cg0720093	PLXNC1	RXR-alpha	1087	1093	2.726556	CCAACC	0.85449	0.89683
cg0720093	PLXNC1	NF-AT1 [	1398	1406	2.619709	AAACTT	0.09155	0.08666
cg0720093	PLXNC1	AP-2alpha	1937	1942	2.550491	TGAGGC	0.48828	0.51216
cg0720093	PLXNC1	POU2F2 (	1856	1866	2.508421	TGATTT	0.01001	0.00847
cg0720093	PLXNC1	NF-AT1 [	1419	1427	2.449764	GGAAAA	0.09155	0.08666
cg0720093	PLXNC1	NF-AT2 [	1397	1406	2.430885	GAAACT	0.01144	0.01045
cg0720093	PLXNC1	VDR [T00	1823	1831	2.308561	CTGGTG	0.10681	0.1091
cg0720093	PLXNC1	GATA-2 [	648	656	2.222222	TGATAA	0.22888	0.21978
cg0720093	PLXNC1	GATA-1 [	255	260	2.176375	TATCCA	3.90625	3.79558
cg0720093	PLXNC1	GATA-1 [	1707	1712	2.176375	TGGATA	3.90625	3.79558
cg0720093	PLXNC1	GATA-1 [	1889	1894	2.176375	TATCGA	3.90625	3.79558
cg0720093	PLXNC1	LEF-1 [T0	190	197	2.004405	CTTTGTT	0.18311	0.17215
cg0720093	PLXNC1	GATA-1 [	1306	1311	2.001358	GGGATA	3.90625	3.79558
cg0720093	PLXNC1	AP-2alpha	1158	1163	1.871933	GCCTCC	0.97656	1.07805
cg0720093	PLXNC1	FOXP3 [T	1966	1971	1.824994	TACAAC	0.48828	0.46414

cg0720093	PLXNC1	TFII-I [T0	383	388	1.824994	GGAGAG	0.48828	0.51201
cg0720093	PLXNC1	TFII-I [T0	1594	1599	1.824994	GGAGAG	0.48828	0.51201
cg0720093	PLXNC1	C/EBPalph	780	786	1.761449	CACAAT	0.48828	0.46352
cg0720093	PLXNC1	RXR-alpha	375	381	1.696452	GGGTCA	0.48828	0.52093
cg0720093	PLXNC1	GR-beta [T	131	135	1.680765	AATTC	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	163	167	1.680765	AATTC	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	285	289	1.680765	AATTC	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	472	476	1.680765	GCATT	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	514	518	1.680765	AATGC	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	546	550	1.680765	AATGC	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	762	766	1.680765	GAATT	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	904	908	1.680765	AATGC	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	1296	1300	1.680765	GCATT	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	1392	1396	1.680765	GCATT	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	1435	1439	1.680765	GAATT	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	1456	1460	1.680765	GCATT	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	1621	1625	1.680765	GCATT	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	1731	1735	1.680765	AATTC	3.90625	3.70067
cg0720093	PLXNC1	GR-beta [T	1893	1897	1.680765	GAATT	3.90625	3.70067
cg0720093	PLXNC1	C/EBPbeta	158	161	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	198	201	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	235	238	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	283	286	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	501	504	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	528	531	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	598	601	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	628	631	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	706	709	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	965	968	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1032	1035	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1055	1058	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1087	1090	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1348	1351	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1417	1420	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1439	1442	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1485	1488	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1575	1578	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1706	1709	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1745	1748	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1943	1946	1.639871	CCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1972	1975	1.639871	TTGG	15.625	15.23827
cg0720093	PLXNC1	XBP-1 [T	76	81	1.583727	ATGACA	0.97656	0.94995
cg0720093	PLXNC1	XBP-1 [T	1536	1541	1.583727	GGTCAT	0.97656	0.94995
cg0720093	PLXNC1	TFIID [T0	875	881	1.537547	TGTAAA	0.73242	0.65627
cg0720093	PLXNC1	TFIID [T0	1418	1424	1.537547	TGGAAA	0.73242	0.65627
cg0720093	PLXNC1	TFIID [T0	1527	1533	1.537547	TTTTTCA	0.73242	0.65627
cg0720093	PLXNC1	TFIID [T0	1672	1678	1.537547	TTTTTCA	0.73242	0.65627
cg0720093	PLXNC1	TFIID [T0	1716	1722	1.537547	TACAAA	0.73242	0.65627

cg0720093	PLXNC1	TFIID [T0	1744	1750	1.537547	TCCAAA	0.73242	0.65627
cg0720093	PLXNC1	TFIID [T0	1879	1885	1.537547	TTTTACA	0.73242	0.65627
cg0720093	PLXNC1	TFIID [T0	1951	1957	1.537547	TGAAAA	0.73242	0.65627
cg0720093	PLXNC1	Pax-5 [T0	572	578	1.537547	CTGGCC	0.73242	0.83087
cg0720093	PLXNC1	NF-Y [T0	280	287	1.51343	TCACCA	0.18311	0.17671
cg0720093	PLXNC1	STAT4 [T	194	199	1.470588	GTTTCC	1.95312	1.90161
cg0720093	PLXNC1	STAT4 [T	285	290	1.470588	AATTCC	1.95312	1.90161
cg0720093	PLXNC1	STAT4 [T	1350	1355	1.470588	GGAAAC	1.95312	1.90161
cg0720093	PLXNC1	STAT4 [T	1419	1424	1.470588	GGAAAA	1.95312	1.90161
cg0720093	PLXNC1	GR [T050	1486	1492	1.444018	CAAAAA	0.12207	0.11476
cg0720093	PLXNC1	PR B [T00	1496	1502	1.404665	CAGTGT	0.36621	0.35143
cg0720093	PLXNC1	PR A [T01	1496	1502	1.404665	CAGTGT	0.36621	0.35143
cg0720093	PLXNC1	C/EBPbeta	57	60	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	105	108	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	166	169	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	263	266	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	300	303	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	639	642	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	809	812	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	889	892	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	984	987	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1137	1140	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1252	1255	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1322	1325	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1395	1398	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1512	1515	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1541	1544	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1555	1558	1.366559	TCAA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1691	1694	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1754	1757	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	C/EBPbeta	1936	1939	1.366559	TTGA	15.625	15.23827
cg0720093	PLXNC1	AP-2alpha	249	254	1.357116	ACAGGC	0.48828	0.51319
cg0720093	PLXNC1	AP-2alpha	1098	1103	1.357116	GCCTGT	0.48828	0.51319
cg0720093	PLXNC1	HNF-3alph	619	626	1.342935	TATTTTA	0.03052	0.02477
cg0720093	PLXNC1	PEA3 [T0	454	462	1.194633	AGGATG	0.06866	0.06787
cg0720093	PLXNC1	T3R-beta1	1561	1569	1.129976	TCACCT	0.07629	0.07886
cg0720093	PLXNC1	RAR-beta	1825	1834	1.063044	GGTGAA	0.03052	0.03086
cg0720093	PLXNC1	GATA-1 [	352	357	1.038567	ATGATA	1.95312	1.80234
cg0720093	PLXNC1	GATA-1 [	1233	1238	1.038567	ATGATA	1.95312	1.80234
cg0720093	PLXNC1	GATA-1 [	1691	1696	1.038567	TTGATA	1.95312	1.80234
cg0720093	PLXNC1	SRY [T00	190	198	0.999172	CTTTGTT	0.06104	0.0571
cg0720093	PLXNC1	TBP [T00	1917	1926	0.935771	TATATA	0.12207	0.10448
cg0720093	PLXNC1	GATA-1 [	647	652	0.863549	GTGATA	1.95312	1.80234
cg0720093	PLXNC1	GR-beta [	6	10	0.840383	TAATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [	18	22	0.840383	AATGA	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [	38	42	0.840383	AATTG	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [	72	76	0.840383	AATTA	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [	113	117	0.840383	CCATT	7.8125	7.2174

cg0720093	PLXNC1	GR-beta [T	130	134	0.840383	TAATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	265	269	0.840383	AATGG	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	284	288	0.840383	CAATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	289	293	0.840383	CCATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	337	341	0.840383	AATGA	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	532	536	0.840383	AATGG	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	689	693	0.840383	AATGA	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	763	767	0.840383	AATTG	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	803	807	0.840383	TAATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	804	808	0.840383	AATTG	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	975	979	0.840383	AATGG	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1003	1007	0.840383	TAATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1232	1236	0.840383	AATGA	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1338	1342	0.840383	AATGA	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1344	1348	0.840383	TCATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1567	1571	0.840383	CCATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1613	1617	0.840383	AATGA	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1726	1730	0.840383	TCATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1730	1734	0.840383	TAATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1734	1738	0.840383	TCATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1784	1788	0.840383	CCATT	7.8125	7.2174
cg0720093	PLXNC1	GR-beta [T	1894	1898	0.840383	AATTG	7.8125	7.2174
cg0720093	PLXNC1	TCF-4 [T0	1751	1760	0.76243	CCTTTGA	0.05722	0.05422
cg0720093	PLXNC1	AP-2alpha	1948	1953	0.678558	GCCTGA	0.48828	0.51196
cg0720093	PLXNC1	C/EBPalph	234	240	0.540941	CCCAATC	0.24414	0.24432
cg0720093	PLXNC1	PR B [T00	795	801	0.48823	AACTGTT	0.12207	0.11255
cg0720093	PLXNC1	PR A [T01	795	801	0.48823	AACTGTT	0.12207	0.11255
cg0720093	PLXNC1	c-Ets-1 [T0	564	570	0.384261	TAGGAA	0.24414	0.23743
cg0720093	PLXNC1	AP-1 [T00	1338	1346	0.348957	AATGAG	0.09155	0.08806
cg0720093	PLXNC1	GATA-1 [	785	790	0.280028	TATCTA	0.97656	0.8795
cg0720093	PLXNC1	GATA-1 [	1871	1876	0.280028	AAGATA	0.97656	0.8795
cg0720093	PLXNC1	GATA-1 [	1976	1981	0.280028	TATCTT	0.97656	0.8795
cg0720093	PLXNC1	AP-2alpha	570	575	0.226186	GCCTGG	0.97656	1.07867
cg0720093	PLXNC1	AP-2alpha	931	936	0.226186	GCCTGG	0.97656	1.07867
cg0720093	PLXNC1	GR-alpha [	120	124	0.207689	CCTTT	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	331	335	0.207689	AGAGG	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1291	1295	0.207689	CCTCT	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1303	1307	0.207689	AAAGG	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1515	1519	0.207689	AAAGG	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1656	1660	0.207689	CCTTT	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1751	1755	0.207689	CCTTT	7.8125	7.79817
cg0720093	PLXNC1	HNF-1A [	34	41	0.143882	GTTAAAT	0.24414	0.20853
cg0720093	PLXNC1	HNF-1A [	1001	1008	0.143882	GTTAATT	0.24414	0.20853
cg0720093	PLXNC1	GR-beta [T	7	11	0	AATTT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	37	41	0	AAATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	71	75	0	AAATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	162	166	0	AAATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	176	180	0	ACATT	3.90625	3.51525

cg0720093	PLXNC1	GR-beta [T	205	209	0	AATGT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	702	706	0	AATGT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1004	1008	0	AATTT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1195	1199	0	AATGT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1331	1335	0	AATGT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1436	1440	0	AATTT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1506	1510	0	ACATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1646	1650	0	AATGT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1684	1688	0	AATGT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1876	1880	0	ACATT	3.90625	3.51525
cg0720093	PLXNC1	GR-beta [T	1883	1887	0	ACATT	3.90625	3.51525
cg0720093	PLXNC1	XBP-1 [T0	1342	1347	0	AGTCAT	0.97656	0.94838
cg0720093	PLXNC1	TFIID [T0	787	793	0	TCTAAA	1.09863	0.95175
cg0720093	PLXNC1	TFIID [T0	1044	1050	0	TTTTTAA	1.09863	0.95175
cg0720093	PLXNC1	TFIID [T0	1073	1079	0	TTTTAGA	1.09863	0.95175
cg0720093	PLXNC1	TFIID [T0	1252	1258	0	TTGAAA	1.09863	0.95175
cg0720093	PLXNC1	TFIID [T0	1859	1865	0	TTTAAA	1.09863	0.95175
cg0720093	PLXNC1	TFIID [T0	1860	1866	0	TTAAAA	1.09863	0.95175
cg0720093	PLXNC1	TFIID [T0	1861	1867	0	TAAAAA	1.09863	0.95175
cg0720093	PLXNC1	c-Jun [T00	1340	1346	0	TGAGTC	0.12207	0.11843
cg0720093	PLXNC1	GR-alpha [	249	253	0	ACAGG	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	644	648	0	CCTGT	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1020	1024	0	ATAGG	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1099	1103	0	CCTGT	7.8125	7.79817
cg0720093	PLXNC1	GR-alpha [	1832	1836	0	CCTGT	7.8125	7.79817
cg0720093	PLXNC1	FOXP3 [T	665	670	0	AACAAC	1.46484	1.44953
cg0720093	PLXNC1	FOXP3 [T	862	867	0	AACAAC	1.46484	1.44953
cg0720093	PLXNC1	FOXP3 [T	1009	1014	0	GTTGTT	1.46484	1.44953
cg0720093	PLXNC1	FOXP3 [T	1145	1150	0	GTTGTT	1.46484	1.44953
cg0720093	PLXNC1	PR B [T00	1494	1500	0	AACAGT	0.36621	0.35051
cg0720093	PLXNC1	PR A [T01	1494	1500	0	AACAGT	0.36621	0.35051
cg0720093	PLXNC1	C/EBPbeta	3	6	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	10	13	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	32	35	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	40	43	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	192	195	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	202	205	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	293	296	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	335	338	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	490	493	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	519	522	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	584	587	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	590	593	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	608	611	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	636	639	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	661	664	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	666	669	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	671	674	0	TTGC	15.625	15.26275

cg0720093	PLXNC1	C/EBPbeta	673	676	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	752	755	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	765	768	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	781	784	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	806	809	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	863	866	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	870	873	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	907	910	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	946	949	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	971	974	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1007	1010	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1010	1013	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1014	1017	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1094	1097	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1146	1149	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1149	1152	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1151	1154	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1164	1167	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1179	1182	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1205	1208	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1230	1233	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1248	1251	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1276	1279	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1299	1302	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1327	1330	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1354	1357	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1373	1376	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1387	1390	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1460	1463	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1501	1504	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1503	1506	0	GCAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1509	1512	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1639	1642	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1717	1720	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1810	1813	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1849	1852	0	TTGT	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1896	1899	0	TTGC	15.625	15.26275
cg0720093	PLXNC1	C/EBPbeta	1967	1970	0	ACAA	15.625	15.26275
cg0720093	PLXNC1	YY1 [T00	113	116	0	CCAT	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	258	261	0	CCAT	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	266	269	0	ATGG	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	289	292	0	CCAT	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	422	425	0	ATGG	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	533	536	0	ATGG	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	578	581	0	CCAT	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	693	696	0	ATGG	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	976	979	0	ATGG	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	1552	1555	0	CCAT	7.8125	7.79459

cg0720093	PLXNC1	YY1 [T00	1567	1570	0	CCAT	7.8125	7.79459
cg0720093	PLXNC1	YY1 [T00	1784	1787	0	CCAT	7.8125	7.79459
cg0720093	PLXNC1	TFII-I [T0	247	252	0	GGACAG	1.46484	1.48598
cg0720093	PLXNC1	TFII-I [T0	254	259	0	CTATCC	1.46484	1.48598
cg0720093	PLXNC1	TFII-I [T0	1401	1406	0	CTTTCC	1.46484	1.48598
cg0720093	PLXNC1	STAT4 [T	160	165	0	GGAAAT	0.48828	0.46235
cg0720093	PLXNC1	ER-alpha [	376	380	0	GGTCA	1.95312	1.99744
cg0720093	PLXNC1	ER-alpha [	449	453	0	TGACC	1.95312	1.99744
cg0720093	PLXNC1	ER-alpha [	1427	1431	0	TGACC	1.95312	1.99744
cg0720093	PLXNC1	ER-alpha [	1536	1540	0	GGTCA	1.95312	1.99744
cg0720093	PLXNC1	RXR-alph	1827	1833	0	TGAACC	0.24414	0.24342
cg0720093	PLXNC1	GR [T050	753	759	0	CAAAAA	0.36621	0.33174
cg0720093	PLXNC1	GR [T050	1718	1724	0	CAAAAA	0.36621	0.33174
cg0720093	PLXNC1	LEF-1 [T0	1752	1759	0	CTTTGA	0.03052	0.02895
cg0720093	PLXNC1	GATA-1 [	1631	1636	0	CAGATA	0.97656	0.92541
cg0720093	PLXNC1	Pax-5 [T0	843	849	0	GGGCTG	1.09863	1.24633
cg0720093	PLXNC1	Pax-5 [T0	929	935	0	GGGCCT	1.09863	1.24633
cg0720093	PLXNC1	Pax-5 [T0	1518	1524	0	GGGCTC	1.09863	1.24633
cg0720093	PLXNC1	AP-2alpha	465	470	0	GCCTGC	0.97656	1.07867
cg0720093	PLXNC1	AP-2alpha	492	497	0	GCCTGC	0.97656	1.07867
cg0720093	PLXNC1	IRF-2 [T0	309	314	0	AAGTGA	0.48828	0.46235
cg0720093	PLXNC1	IRF-2 [T0	676	681	0	AAGTGA	0.48828	0.46235
cg0720093	PLXNC1	HNF-1A [	1623	1630	0	ATTTTA	0.24414	0.20853
cg2419255	PPAP2C	RAR-beta:	543	554	9.97066	GGGCGC	0.06974	0.07677
cg2419255	PPAP2C	RAR-beta:	1554	1565	9.97066	GGGCTC	0.06974	0.07677
cg2715857	PPAP2C	RAR-beta:	464	475	9.97066	GGGCGC	0.06974	0.07677
cg2715857	PPAP2C	RAR-beta:	1475	1486	9.97066	GGGCTC	0.06974	0.07677
cg0268666	PPAP2C	RAR-beta:	429	440	9.97066	GGGCGC	0.06974	0.07677
cg0268666	PPAP2C	RAR-beta:	1440	1451	9.97066	GGGCTC	0.06974	0.07677
cg2387614	PPAP2C	RAR-beta:	403	414	9.97066	GGGCGC	0.06974	0.07677
cg2387614	PPAP2C	RAR-beta:	1414	1425	9.97066	GGGCTC	0.06974	0.07677
cg0268666	PPAP2C	NF-kappa	1964	1975	9.948544	AGGCTG	0.02313	0.02417
cg2387614	PPAP2C	NF-kappa	1938	1949	9.948544	AGGCTG	0.02313	0.02417
cg2419255	PPAP2C	LEF-1 [T0	1957	1964	9.937995	TGCCAA	0.12207	0.1238
cg2715857	PPAP2C	LEF-1 [T0	1878	1885	9.937995	TGCCAA	0.12207	0.1238
cg0268666	PPAP2C	LEF-1 [T0	1843	1850	9.937995	TGCCAA	0.12207	0.1238
cg2387614	PPAP2C	LEF-1 [T0	1817	1824	9.937995	TGCCAA	0.12207	0.1238
cg2419255	PPAP2C	XBP-1 [T0	1110	1115	9.789909	ATGGCG	1.95312	1.94901
cg2715857	PPAP2C	XBP-1 [T0	1031	1036	9.789909	ATGGCG	1.95312	1.94901
cg0268666	PPAP2C	XBP-1 [T0	996	1001	9.789909	ATGGCG	1.95312	1.94901
cg2387614	PPAP2C	XBP-1 [T0	970	975	9.789909	ATGGCG	1.95312	1.94901
cg2419255	PPAP2C	PR B [T00	128	134	9.743489	AACACC	1.09863	1.0981
cg2419255	PPAP2C	PR B [T00	1429	1435	9.743489	AACACC	1.09863	1.0981
cg2419255	PPAP2C	PR B [T00	1893	1899	9.743489	CGGTGT	1.09863	1.0981
cg2419255	PPAP2C	PR A [T01	128	134	9.743489	AACACC	1.09863	1.0981
cg2419255	PPAP2C	PR A [T01	1429	1435	9.743489	AACACC	1.09863	1.0981
cg2419255	PPAP2C	PR A [T01	1893	1899	9.743489	CGGTGT	1.09863	1.0981
cg2715857	PPAP2C	PR B [T00	49	55	9.743489	AACACC	1.09863	1.0981

cg2715857	PPAP2C	PR B [T00	1350	1356	9.743489	AACACC	1.09863	1.0981
cg2715857	PPAP2C	PR B [T00	1814	1820	9.743489	CGGTGT	1.09863	1.0981
cg2715857	PPAP2C	PR A [T01	49	55	9.743489	AACACC	1.09863	1.0981
cg2715857	PPAP2C	PR A [T01	1350	1356	9.743489	AACACC	1.09863	1.0981
cg2715857	PPAP2C	PR A [T01	1814	1820	9.743489	CGGTGT	1.09863	1.0981
cg0268666	PPAP2C	PR B [T00	14	20	9.743489	AACACC	1.09863	1.0981
cg0268666	PPAP2C	PR B [T00	1315	1321	9.743489	AACACC	1.09863	1.0981
cg0268666	PPAP2C	PR B [T00	1779	1785	9.743489	CGGTGT	1.09863	1.0981
cg0268666	PPAP2C	PR A [T01	14	20	9.743489	AACACC	1.09863	1.0981
cg0268666	PPAP2C	PR A [T01	1315	1321	9.743489	AACACC	1.09863	1.0981
cg0268666	PPAP2C	PR A [T01	1779	1785	9.743489	CGGTGT	1.09863	1.0981
cg2387614	PPAP2C	PR B [T00	1289	1295	9.743489	AACACC	1.09863	1.0981
cg2387614	PPAP2C	PR B [T00	1753	1759	9.743489	CGGTGT	1.09863	1.0981
cg2387614	PPAP2C	PR A [T01	1289	1295	9.743489	AACACC	1.09863	1.0981
cg2387614	PPAP2C	PR A [T01	1753	1759	9.743489	CGGTGT	1.09863	1.0981
cg2419255	PPAP2C	c-Jun [T00	1614	1620	9.717135	TGACCT	0.73242	0.7366
cg2715857	PPAP2C	c-Jun [T00	1535	1541	9.717135	TGACCT	0.73242	0.7366
cg0268666	PPAP2C	c-Jun [T00	1500	1506	9.717135	TGACCT	0.73242	0.7366
cg2387614	PPAP2C	c-Jun [T00	1474	1480	9.717135	TGACCT	0.73242	0.7366
cg2419255	PPAP2C	NF-AT1 [	1268	1276	9.691726	CACGTT	0.16785	0.16528
cg2715857	PPAP2C	NF-AT1 [	1189	1197	9.691726	CACGTT	0.16785	0.16528
cg0268666	PPAP2C	NF-AT1 [	1154	1162	9.691726	CACGTT	0.16785	0.16528
cg2387614	PPAP2C	NF-AT1 [	1128	1136	9.691726	CACGTT	0.16785	0.16528
cg2419255	PPAP2C	RAR-beta	1095	1104	9.641259	TGGGAA	0.21362	0.22369
cg2715857	PPAP2C	RAR-beta	1016	1025	9.641259	TGGGAA	0.21362	0.22369
cg0268666	PPAP2C	RAR-beta	981	990	9.641259	TGGGAA	0.21362	0.22369
cg2387614	PPAP2C	RAR-beta	955	964	9.641259	TGGGAA	0.21362	0.22369
cg2419255	PPAP2C	Elk-1 [T00	465	473	9.62002	GGAGGG	0.07629	0.0786
cg2715857	PPAP2C	Elk-1 [T00	386	394	9.62002	GGAGGG	0.07629	0.0786
cg0268666	PPAP2C	Elk-1 [T00	351	359	9.62002	GGAGGG	0.07629	0.0786
cg0268666	PPAP2C	Elk-1 [T00	1976	1984	9.62002	CTTCCA	0.07629	0.0786
cg2387614	PPAP2C	Elk-1 [T00	325	333	9.62002	GGAGGG	0.07629	0.0786
cg2387614	PPAP2C	Elk-1 [T00	1950	1958	9.62002	CTTCCA	0.07629	0.0786
cg2419255	PPAP2C	TFIID [T0	1064	1070	9.552105	TTTCAC	1.46484	1.37777
cg2419255	PPAP2C	Pax-5 [T0	591	597	9.552105	GGCGCC	1.46484	1.61918
cg2419255	PPAP2C	Pax-5 [T0	623	629	9.552105	GGGCGC	1.46484	1.61918
cg2419255	PPAP2C	Pax-5 [T0	642	648	9.552105	TCCGCC	1.46484	1.61918
cg2419255	PPAP2C	Pax-5 [T0	1082	1088	9.552105	GGGCGC	1.46484	1.61918
cg2419255	PPAP2C	Pax-5 [T0	1620	1626	9.552105	GTGGCC	1.46484	1.61918
cg2715857	PPAP2C	TFIID [T0	985	991	9.552105	TTTCAC	1.46484	1.37777
cg2715857	PPAP2C	Pax-5 [T0	512	518	9.552105	GGCGCC	1.46484	1.61918
cg2715857	PPAP2C	Pax-5 [T0	544	550	9.552105	GGGCGC	1.46484	1.61918
cg2715857	PPAP2C	Pax-5 [T0	563	569	9.552105	TCCGCC	1.46484	1.61918
cg2715857	PPAP2C	Pax-5 [T0	1003	1009	9.552105	GGGCGC	1.46484	1.61918
cg2715857	PPAP2C	Pax-5 [T0	1541	1547	9.552105	GTGGCC	1.46484	1.61918
cg2715857	PPAP2C	Pax-5 [T0	1922	1928	9.552105	GGGCCA	1.46484	1.61918
cg0268666	PPAP2C	TFIID [T0	950	956	9.552105	TTTCAC	1.46484	1.37777
cg0268666	PPAP2C	Pax-5 [T0	477	483	9.552105	GGCGCC	1.46484	1.61918

cg0268666	PPAP2C	Pax-5 [T0	509	515	9.552105	GGGCGC	1.46484	1.61918
cg0268666	PPAP2C	Pax-5 [T0	528	534	9.552105	TCCGCC	1.46484	1.61918
cg0268666	PPAP2C	Pax-5 [T0	968	974	9.552105	GGGCGC	1.46484	1.61918
cg0268666	PPAP2C	Pax-5 [T0	1506	1512	9.552105	GTGGCC	1.46484	1.61918
cg0268666	PPAP2C	Pax-5 [T0	1887	1893	9.552105	GGGCCA	1.46484	1.61918
cg2387614	PPAP2C	TFIID [T0	924	930	9.552105	TTTCAC	1.46484	1.37777
cg2387614	PPAP2C	Pax-5 [T0	451	457	9.552105	GGCGCC	1.46484	1.61918
cg2387614	PPAP2C	Pax-5 [T0	483	489	9.552105	GGGCGC	1.46484	1.61918
cg2387614	PPAP2C	Pax-5 [T0	502	508	9.552105	TCCGCC	1.46484	1.61918
cg2387614	PPAP2C	Pax-5 [T0	942	948	9.552105	GGGCGC	1.46484	1.61918
cg2387614	PPAP2C	Pax-5 [T0	1480	1486	9.552105	GTGGCC	1.46484	1.61918
cg2387614	PPAP2C	Pax-5 [T0	1861	1867	9.552105	GGGCCA	1.46484	1.61918
cg2387614	PPAP2C	Pax-5 [T0	1982	1988	9.552105	TTAGCC	1.46484	1.61918
cg2419255	PPAP2C	NF-1 [T00	592	599	9.535536	GCGCCC	0.73242	0.74634
cg2715857	PPAP2C	NF-1 [T00	513	520	9.535536	GCGCCC	0.73242	0.74634
cg0268666	PPAP2C	NF-1 [T00	478	485	9.535536	GCGCCC	0.73242	0.74634
cg2387614	PPAP2C	NF-1 [T00	452	459	9.535536	GCGCCC	0.73242	0.74634
cg2715857	PPAP2C	NF-1 [T00	1926	1933	9.513281	CAAGCC	0.73242	0.74634
cg0268666	PPAP2C	NF-1 [T00	1891	1898	9.513281	CAAGCC	0.73242	0.74634
cg2387614	PPAP2C	NF-1 [T00	1865	1872	9.513281	CAAGCC	0.73242	0.74634
cg2387614	PPAP2C	NF-1 [T00	1977	1984	9.513281	TTGGGT	0.73242	0.74634
cg2419255	PPAP2C	FOXP3 [T	125	130	9.512894	CCCAAC	7.32422	7.22156
cg2419255	PPAP2C	FOXP3 [T	1426	1431	9.512894	AGCAAC	7.32422	7.22156
cg2419255	PPAP2C	FOXP3 [T	1452	1457	9.512894	AGCAAC	7.32422	7.22156
cg2419255	PPAP2C	FOXP3 [T	1713	1718	9.512894	GTTCTG	7.32422	7.22156
cg2419255	PPAP2C	FOXP3 [T	1832	1837	9.512894	GCCAAC	7.32422	7.22156
cg2419255	PPAP2C	FOXP3 [T	1897	1902	9.512894	GTTCTT	7.32422	7.22156
cg2419255	PPAP2C	TFII-I [T0	70	75	9.512894	CGTTCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	103	108	9.512894	GTGTCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	107	112	9.512894	CCGTCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	227	232	9.512894	CGGTCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	315	320	9.512894	GGAAGG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	469	474	9.512894	GGAAGG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	505	510	9.512894	GGACGG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	559	564	9.512894	GGACCG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	780	785	9.512894	GGACCG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	794	799	9.512894	GGACGG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	847	852	9.512894	GGAAAC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	879	884	9.512894	GGAAGG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	930	935	9.512894	AAATCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1006	1011	9.512894	GTGTCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1036	1041	9.512894	CGTTCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1192	1197	9.512894	GGAAAC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1238	1243	9.512894	CCATCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1271	1276	9.512894	GTTTCC	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1459	1464	9.512894	GGACTT	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1494	1499	9.512894	GGATGG	7.32422	7.44385
cg2419255	PPAP2C	TFII-I [T0	1695	1700	9.512894	GGAATT	7.32422	7.44385

cg2715857	PPAP2C	FOXP3 [T	46	51	9.512894	CCCAAC	7.32422	7.22156
cg2715857	PPAP2C	FOXP3 [T	1347	1352	9.512894	AGCAAC	7.32422	7.22156
cg2715857	PPAP2C	FOXP3 [T	1373	1378	9.512894	AGCAAC	7.32422	7.22156
cg2715857	PPAP2C	FOXP3 [T	1634	1639	9.512894	GTTCTG	7.32422	7.22156
cg2715857	PPAP2C	FOXP3 [T	1753	1758	9.512894	GCCAAC	7.32422	7.22156
cg2715857	PPAP2C	FOXP3 [T	1818	1823	9.512894	GTTCTT	7.32422	7.22156
cg2715857	PPAP2C	TFII-I [T0	24	29	9.512894	GTGTCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	28	33	9.512894	CCGTCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	148	153	9.512894	CGGTCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	236	241	9.512894	GGAAGG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	390	395	9.512894	GGAAGG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	426	431	9.512894	GGACGG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	480	485	9.512894	GGACCG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	701	706	9.512894	GGACCG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	715	720	9.512894	GGACGG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	768	773	9.512894	GGAAAC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	800	805	9.512894	GGAAGG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	851	856	9.512894	AAATCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	927	932	9.512894	GTGTCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	957	962	9.512894	CGTTCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	1113	1118	9.512894	GGAAAC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	1159	1164	9.512894	CCATCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	1192	1197	9.512894	GTTTCC	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	1380	1385	9.512894	GGACTT	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	1415	1420	9.512894	GGATGG	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	1616	1621	9.512894	GGAATT	7.32422	7.44385
cg2715857	PPAP2C	TFII-I [T0	1917	1922	9.512894	GGATGG	7.32422	7.44385
cg0268666	PPAP2C	FOXP3 [T	11	16	9.512894	CCCAAC	7.32422	7.22156
cg0268666	PPAP2C	FOXP3 [T	1312	1317	9.512894	AGCAAC	7.32422	7.22156
cg0268666	PPAP2C	FOXP3 [T	1338	1343	9.512894	AGCAAC	7.32422	7.22156
cg0268666	PPAP2C	FOXP3 [T	1599	1604	9.512894	GTTCTG	7.32422	7.22156
cg0268666	PPAP2C	FOXP3 [T	1718	1723	9.512894	GCCAAC	7.32422	7.22156
cg0268666	PPAP2C	FOXP3 [T	1783	1788	9.512894	GTTCTT	7.32422	7.22156
cg0268666	PPAP2C	TFII-I [T0	113	118	9.512894	CGGTCC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	201	206	9.512894	GGAAGG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	355	360	9.512894	GGAAGG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	391	396	9.512894	GGACGG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	445	450	9.512894	GGACCG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	666	671	9.512894	GGACCG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	680	685	9.512894	GGACGG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	733	738	9.512894	GGAAAC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	765	770	9.512894	GGAAGG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	816	821	9.512894	AAATCC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	892	897	9.512894	GTGTCC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	922	927	9.512894	CGTTCC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1078	1083	9.512894	GGAAAC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1124	1129	9.512894	CCATCC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1157	1162	9.512894	GTTTCC	7.32422	7.44385

cg0268666	PPAP2C	TFII-I [T0	1345	1350	9.512894	GGACTT	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1380	1385	9.512894	GGATGG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1581	1586	9.512894	GGAATT	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1882	1887	9.512894	GGATGG	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1975	1980	9.512894	CCTTCC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1979	1984	9.512894	CCATCC	7.32422	7.44385
cg0268666	PPAP2C	TFII-I [T0	1983	1988	9.512894	CCTTCC	7.32422	7.44385
cg2387614	PPAP2C	FOXP3 [T	1286	1291	9.512894	AGCAAC	7.32422	7.22156
cg2387614	PPAP2C	FOXP3 [T	1312	1317	9.512894	AGCAAC	7.32422	7.22156
cg2387614	PPAP2C	FOXP3 [T	1573	1578	9.512894	GTTCTG	7.32422	7.22156
cg2387614	PPAP2C	FOXP3 [T	1692	1697	9.512894	GCCAAC	7.32422	7.22156
cg2387614	PPAP2C	FOXP3 [T	1757	1762	9.512894	GTTCTT	7.32422	7.22156
cg2387614	PPAP2C	TFII-I [T0	87	92	9.512894	CGGTCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	175	180	9.512894	GGAAGG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	329	334	9.512894	GGAAGG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	365	370	9.512894	GGACGG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	419	424	9.512894	GGACCG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	640	645	9.512894	GGACCG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	654	659	9.512894	GGACGG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	707	712	9.512894	GGAAAC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	739	744	9.512894	GGAAGG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	790	795	9.512894	AAATCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	866	871	9.512894	GTGTCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	896	901	9.512894	CGTTCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1052	1057	9.512894	GGAAAC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1098	1103	9.512894	CCATCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1131	1136	9.512894	GTTTCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1319	1324	9.512894	GGACTT	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1354	1359	9.512894	GGATGG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1555	1560	9.512894	GGAATT	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1856	1861	9.512894	GGATGG	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1949	1954	9.512894	CCTTCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1953	1958	9.512894	CCATCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1957	1962	9.512894	CCTTCC	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1973	1978	9.512894	GGATTT	7.32422	7.44385
cg2387614	PPAP2C	TFII-I [T0	1992	1997	9.512894	AAATCC	7.32422	7.44385
cg2419255	PPAP2C	c-Jun [T00	1803	1809	9.511322	TGACCA	0.73242	0.7366
cg2715857	PPAP2C	c-Jun [T00	1724	1730	9.511322	TGACCA	0.73242	0.7366
cg0268666	PPAP2C	c-Jun [T00	1689	1695	9.511322	TGACCA	0.73242	0.7366
cg2387614	PPAP2C	c-Jun [T00	1663	1669	9.511322	TGACCA	0.73242	0.7366
cg2419255	PPAP2C	c-Jun [T00	1811	1817	9.442241	GCTGTC	0.73242	0.7366
cg2419255	PPAP2C	c-Jun [T00	1827	1833	9.442241	TGACAG	0.73242	0.7366
cg2715857	PPAP2C	c-Jun [T00	1732	1738	9.442241	GCTGTC	0.73242	0.7366
cg2715857	PPAP2C	c-Jun [T00	1748	1754	9.442241	TGACAG	0.73242	0.7366
cg0268666	PPAP2C	c-Jun [T00	1697	1703	9.442241	GCTGTC	0.73242	0.7366
cg0268666	PPAP2C	c-Jun [T00	1713	1719	9.442241	TGACAG	0.73242	0.7366
cg2387614	PPAP2C	c-Jun [T00	1671	1677	9.442241	GCTGTC	0.73242	0.7366
cg2387614	PPAP2C	c-Jun [T00	1687	1693	9.442241	TGACAG	0.73242	0.7366

cg2419255	PPAP2C	NFI/CTF [	141	148	9.352332	CCAAGG	0.54932	0.55369
cg2419255	PPAP2C	NFI/CTF [	942	949	9.352332	GTCCTT	0.54932	0.55369
cg2715857	PPAP2C	NFI/CTF [	62	69	9.352332	CCAAGG	0.54932	0.55369
cg2715857	PPAP2C	NFI/CTF [	863	870	9.352332	GTCCTT	0.54932	0.55369
cg0268666	PPAP2C	NFI/CTF [	27	34	9.352332	CCAAGG	0.54932	0.55369
cg0268666	PPAP2C	NFI/CTF [	828	835	9.352332	GTCCTT	0.54932	0.55369
cg2387614	PPAP2C	NFI/CTF [	1	8	9.352332	CCAAGG	0.54932	0.55369
cg2387614	PPAP2C	NFI/CTF [	802	809	9.352332	GTCCTT	0.54932	0.55369
cg2419255	PPAP2C	c-Ets-1 [T	1095	1101	9.276861	TGGGAA	0.36621	0.37402
cg2715857	PPAP2C	c-Ets-1 [T	1016	1022	9.276861	TGGGAA	0.36621	0.37402
cg0268666	PPAP2C	c-Ets-1 [T	981	987	9.276861	TGGGAA	0.36621	0.37402
cg2387614	PPAP2C	c-Ets-1 [T	955	961	9.276861	TGGGAA	0.36621	0.37402
cg2419255	PPAP2C	E2F-1 [T0	547	554	9.261732	GCGGCG	0.15259	0.16832
cg2715857	PPAP2C	E2F-1 [T0	468	475	9.261732	GCGGCG	0.15259	0.16832
cg0268666	PPAP2C	E2F-1 [T0	433	440	9.261732	GCGGCG	0.15259	0.16832
cg2387614	PPAP2C	E2F-1 [T0	407	414	9.261732	GCGGCG	0.15259	0.16832
cg2419255	PPAP2C	PPAR-alp	227	237	9.158357	CGGTCC	0.0515	0.05878
cg2419255	PPAP2C	PPAR-alp	1355	1365	9.158357	GGGCCC	0.0515	0.05878
cg2715857	PPAP2C	PPAR-alp	148	158	9.158357	CGGTCC	0.0515	0.05878
cg2715857	PPAP2C	PPAR-alp	1276	1286	9.158357	GGGCCC	0.0515	0.05878
cg0268666	PPAP2C	PPAR-alp	113	123	9.158357	CGGTCC	0.0515	0.05878
cg0268666	PPAP2C	PPAR-alp	1241	1251	9.158357	GGGCCC	0.0515	0.05878
cg2387614	PPAP2C	PPAR-alp	87	97	9.158357	CGGTCC	0.0515	0.05878
cg2387614	PPAP2C	PPAR-alp	1215	1225	9.158357	GGGCCC	0.0515	0.05878
cg2419255	PPAP2C	c-Ets-1 [T	1535	1541	9.148774	AGGGAA	0.85449	0.84987
cg2715857	PPAP2C	c-Ets-1 [T	1456	1462	9.148774	AGGGAA	0.85449	0.84987
cg0268666	PPAP2C	c-Ets-1 [T	1421	1427	9.148774	AGGGAA	0.85449	0.84987
cg2387614	PPAP2C	c-Ets-1 [T	1395	1401	9.148774	AGGGAA	0.85449	0.84987
cg2419255	PPAP2C	COUP-TF	1286	1298	9.093379	CCTTGA	0.01878	0.01921
cg2419255	PPAP2C	COUP-TF	1611	1623	9.093379	AGCTGA	0.01878	0.01921
cg2715857	PPAP2C	COUP-TF	1207	1219	9.093379	CCTTGA	0.01878	0.01921
cg2715857	PPAP2C	COUP-TF	1532	1544	9.093379	AGCTGA	0.01878	0.01921
cg0268666	PPAP2C	COUP-TF	1172	1184	9.093379	CCTTGA	0.01878	0.01921
cg0268666	PPAP2C	COUP-TF	1497	1509	9.093379	AGCTGA	0.01878	0.01921
cg2387614	PPAP2C	COUP-TF	1146	1158	9.093379	CCTTGA	0.01878	0.01921
cg2387614	PPAP2C	COUP-TF	1471	1483	9.093379	AGCTGA	0.01878	0.01921
cg2419255	PPAP2C	STAT5A [	911	923	9.080962	TCTTTTC	0.02816	0.02551
cg2715857	PPAP2C	STAT5A [	832	844	9.080962	TCTTTTC	0.02816	0.02551
cg0268666	PPAP2C	STAT5A [	797	809	9.080962	TCTTTTC	0.02816	0.02551
cg2387614	PPAP2C	STAT5A [	771	783	9.080962	TCTTTTC	0.02816	0.02551
cg2419255	PPAP2C	E2F-1 [T0	23	30	9.028527	GTCCCC	0.27466	0.30178
cg2419255	PPAP2C	E2F-1 [T0	207	214	9.028527	GTCCCC	0.27466	0.30178
cg2419255	PPAP2C	E2F-1 [T0	335	342	9.028527	GCGGGG	0.27466	0.30178
cg2419255	PPAP2C	E2F-1 [T0	396	403	9.028527	GCGGGG	0.27466	0.30178
cg2419255	PPAP2C	E2F-1 [T0	443	450	9.028527	GCGGGG	0.27466	0.30178
cg2419255	PPAP2C	E2F-1 [T0	746	753	9.028527	GCGGGG	0.27466	0.30178
cg2715857	PPAP2C	E2F-1 [T0	128	135	9.028527	GTCCCC	0.27466	0.30178
cg2715857	PPAP2C	E2F-1 [T0	256	263	9.028527	GCGGGG	0.27466	0.30178

cg2715857	PPAP2C	E2F-1 [T0	317	324	9.028527	GCGGGG	0.27466	0.30178
cg2715857	PPAP2C	E2F-1 [T0	364	371	9.028527	GCGGGG	0.27466	0.30178
cg2715857	PPAP2C	E2F-1 [T0	667	674	9.028527	GCGGGG	0.27466	0.30178
cg0268666	PPAP2C	E2F-1 [T0	93	100	9.028527	GTCCCC	0.27466	0.30178
cg0268666	PPAP2C	E2F-1 [T0	221	228	9.028527	GCGGGG	0.27466	0.30178
cg0268666	PPAP2C	E2F-1 [T0	282	289	9.028527	GCGGGG	0.27466	0.30178
cg0268666	PPAP2C	E2F-1 [T0	329	336	9.028527	GCGGGG	0.27466	0.30178
cg0268666	PPAP2C	E2F-1 [T0	632	639	9.028527	GCGGGG	0.27466	0.30178
cg2387614	PPAP2C	E2F-1 [T0	67	74	9.028527	GTCCCC	0.27466	0.30178
cg2387614	PPAP2C	E2F-1 [T0	195	202	9.028527	GCGGGG	0.27466	0.30178
cg2387614	PPAP2C	E2F-1 [T0	256	263	9.028527	GCGGGG	0.27466	0.30178
cg2387614	PPAP2C	E2F-1 [T0	303	310	9.028527	GCGGGG	0.27466	0.30178
cg2387614	PPAP2C	E2F-1 [T0	606	613	9.028527	GCGGGG	0.27466	0.30178
cg2419255	PPAP2C	c-Ets-1 [T	71	77	9.020687	GTTCCC	0.85449	0.84987
cg2419255	PPAP2C	c-Ets-1 [T	714	720	9.020687	GTTCCC	0.85449	0.84987
cg2715857	PPAP2C	c-Ets-1 [T	635	641	9.020687	GTTCCC	0.85449	0.84987
cg0268666	PPAP2C	c-Ets-1 [T	600	606	9.020687	GTTCCC	0.85449	0.84987
cg0268666	PPAP2C	c-Ets-1 [T	1969	1975	9.020687	GTTCCC	0.85449	0.84987
cg2387614	PPAP2C	c-Ets-1 [T	574	580	9.020687	GTTCCC	0.85449	0.84987
cg2387614	PPAP2C	c-Ets-1 [T	1943	1949	9.020687	GTTCCC	0.85449	0.84987
cg2419255	PPAP2C	GR [T050	928	934	8.971049	CAAAAT	0.61035	0.5928
cg2715857	PPAP2C	GR [T050	849	855	8.971049	CAAAAT	0.61035	0.5928
cg0268666	PPAP2C	GR [T050	814	820	8.971049	CAAAAT	0.61035	0.5928
cg2387614	PPAP2C	GR [T050	788	794	8.971049	CAAAAT	0.61035	0.5928
cg2419255	PPAP2C	c-Ets-1 [T	799	805	8.8926	GTTCCC	0.85449	0.84987
cg2715857	PPAP2C	c-Ets-1 [T	720	726	8.8926	GTTCCC	0.85449	0.84987
cg0268666	PPAP2C	c-Ets-1 [T	685	691	8.8926	GTTCCC	0.85449	0.84987
cg2387614	PPAP2C	c-Ets-1 [T	659	665	8.8926	GTTCCC	0.85449	0.84987
cg2419255	PPAP2C	NFI/CTF [	596	603	8.814757	CCAAAA	0.48828	0.48845
cg2419255	PPAP2C	NFI/CTF [	1942	1949	8.814757	TCACTT	0.48828	0.48845
cg2715857	PPAP2C	NFI/CTF [	517	524	8.814757	CCAAAA	0.48828	0.48845
cg2715857	PPAP2C	NFI/CTF [	1863	1870	8.814757	TCACTT	0.48828	0.48845
cg2715857	PPAP2C	NFI/CTF [	1930	1937	8.814757	CCAAGA	0.48828	0.48845
cg0268666	PPAP2C	NFI/CTF [	482	489	8.814757	CCAAAA	0.48828	0.48845
cg0268666	PPAP2C	NFI/CTF [	1828	1835	8.814757	TCACTT	0.48828	0.48845
cg0268666	PPAP2C	NFI/CTF [	1895	1902	8.814757	CCAAGA	0.48828	0.48845
cg2387614	PPAP2C	NFI/CTF [	456	463	8.814757	CCAAAA	0.48828	0.48845
cg2387614	PPAP2C	NFI/CTF [	1802	1809	8.814757	TCACTT	0.48828	0.48845
cg2387614	PPAP2C	NFI/CTF [	1869	1876	8.814757	CCAAGA	0.48828	0.48845
cg2419255	PPAP2C	RelA [T00	1189	1199	8.812531	CAGGGA	0.02432	0.02522
cg2715857	PPAP2C	RelA [T00	1110	1120	8.812531	CAGGGA	0.02432	0.02522
cg0268666	PPAP2C	RelA [T00	1075	1085	8.812531	CAGGGA	0.02432	0.02522
cg2387614	PPAP2C	RelA [T00	1049	1059	8.812531	CAGGGA	0.02432	0.02522
cg2419255	PPAP2C	Elk-1 [T00	311	319	8.797343	GGCGGG	0.24414	0.26271
cg2419255	PPAP2C	Elk-1 [T00	1972	1980	8.797343	GGGGGG	0.24414	0.26271
cg2715857	PPAP2C	Elk-1 [T00	232	240	8.797343	GGCGGG	0.24414	0.26271
cg2715857	PPAP2C	Elk-1 [T00	1893	1901	8.797343	GGGGGG	0.24414	0.26271
cg0268666	PPAP2C	Elk-1 [T00	197	205	8.797343	GGCGGG	0.24414	0.26271

cg0268666 PPAP2C	Elk-1 [T00	1858	1866	8.797343	GGGGGG	0.24414	0.26271
cg2387614 PPAP2C	Elk-1 [T00	171	179	8.797343	GGCGGG	0.24414	0.26271
cg2387614 PPAP2C	Elk-1 [T00	1832	1840	8.797343	GGGGGG	0.24414	0.26271
cg2419255 PPAP2C	NF-1 [T00	1560	1567	8.790071	TTGGGA	0.24414	0.24339
cg2419255 PPAP2C	NF-1 [T00	1955	1962	8.790071	CCTGCC	0.24414	0.24339
cg2715857 PPAP2C	NF-1 [T00	1481	1488	8.790071	TTGGGA	0.24414	0.24339
cg2715857 PPAP2C	NF-1 [T00	1876	1883	8.790071	CCTGCC	0.24414	0.24339
cg0268666 PPAP2C	NF-1 [T00	1446	1453	8.790071	TTGGGA	0.24414	0.24339
cg0268666 PPAP2C	NF-1 [T00	1841	1848	8.790071	CCTGCC	0.24414	0.24339
cg2387614 PPAP2C	NF-1 [T00	1420	1427	8.790071	TTGGGA	0.24414	0.24339
cg2387614 PPAP2C	NF-1 [T00	1815	1822	8.790071	CCTGCC	0.24414	0.24339
cg2419255 PPAP2C	XBP-1 [T	1105	1110	8.75604	ATGAAA	2.92969	2.75329
cg2715857 PPAP2C	XBP-1 [T	1026	1031	8.75604	ATGAAA	2.92969	2.75329
cg0268666 PPAP2C	XBP-1 [T	991	996	8.75604	ATGAAA	2.92969	2.75329
cg2387614 PPAP2C	XBP-1 [T	965	970	8.75604	ATGAAA	2.92969	2.75329
cg2419255 PPAP2C	STAT1bet	807	816	8.695301	CTTTCCT	0.22316	0.2175
cg2715857 PPAP2C	STAT1bet	728	737	8.695301	CTTTCCT	0.22316	0.2175
cg0268666 PPAP2C	STAT1bet	693	702	8.695301	CTTTCCT	0.22316	0.2175
cg2387614 PPAP2C	STAT1bet	667	676	8.695301	CTTTCCT	0.22316	0.2175
cg2419255 PPAP2C	RAR-beta	1388	1397	8.578216	CTAAAA	0.26703	0.27434
cg2715857 PPAP2C	RAR-beta	1309	1318	8.578216	CTAAAA	0.26703	0.27434
cg0268666 PPAP2C	RAR-beta	1274	1283	8.578216	CTAAAA	0.26703	0.27434
cg2387614 PPAP2C	RAR-beta	1248	1257	8.578216	CTAAAA	0.26703	0.27434
cg2419255 PPAP2C	p53 [T006	1554	1560	8.537081	GGGCTC	0.12207	0.13169
cg2419255 PPAP2C	p53 [T006	1678	1684	8.537081	GGGCTC	0.12207	0.13169
cg2715857 PPAP2C	p53 [T006	1475	1481	8.537081	GGGCTC	0.12207	0.13169
cg2715857 PPAP2C	p53 [T006	1599	1605	8.537081	GGGCTC	0.12207	0.13169
cg0268666 PPAP2C	p53 [T006	1440	1446	8.537081	GGGCTC	0.12207	0.13169
cg0268666 PPAP2C	p53 [T006	1564	1570	8.537081	GGGCTC	0.12207	0.13169
cg2387614 PPAP2C	p53 [T006	1414	1420	8.537081	GGGCTC	0.12207	0.13169
cg2387614 PPAP2C	p53 [T006	1538	1544	8.537081	GGGCTC	0.12207	0.13169
cg2419255 PPAP2C	AhR:Arnt	97	106	8.431005	GGGGGC	0.07439	0.08553
cg2715857 PPAP2C	AhR:Arnt	18	27	8.431005	GGGGGC	0.07439	0.08553
cg2387614 PPAP2C	HNF-3alph	1989	1996	8.343064	TTAAAA	0.27466	0.23078
cg2419255 PPAP2C	PR B [T00	1437	1443	8.338824	AACAGG	1.09863	1.09384
cg2419255 PPAP2C	PR A [T01	1437	1443	8.338824	AACAGG	1.09863	1.09384
cg2715857 PPAP2C	PR B [T00	1358	1364	8.338824	AACAGG	1.09863	1.09384
cg2715857 PPAP2C	PR A [T01	1358	1364	8.338824	AACAGG	1.09863	1.09384
cg0268666 PPAP2C	PR B [T00	1323	1329	8.338824	AACAGG	1.09863	1.09384
cg0268666 PPAP2C	PR B [T00	1965	1971	8.338824	GGCTGT	1.09863	1.09384
cg0268666 PPAP2C	PR A [T01	1323	1329	8.338824	AACAGG	1.09863	1.09384
cg0268666 PPAP2C	PR A [T01	1965	1971	8.338824	GGCTGT	1.09863	1.09384
cg2387614 PPAP2C	PR B [T00	1297	1303	8.338824	AACAGG	1.09863	1.09384
cg2387614 PPAP2C	PR B [T00	1939	1945	8.338824	GGCTGT	1.09863	1.09384
cg2387614 PPAP2C	PR A [T01	1297	1303	8.338824	AACAGG	1.09863	1.09384
cg2387614 PPAP2C	PR A [T01	1939	1945	8.338824	GGCTGT	1.09863	1.09384
cg2419255 PPAP2C	GR-alpha [	1	5	8.281568	GGAGG	7.8125	8.20394
cg2419255 PPAP2C	GR-alpha [	19	23	8.281568	CGAGG	7.8125	8.20394

cg2419255	PPAP2C	GR-alpha |	30	34	8.281568	CCTCC	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	40	44	8.281568	CCTCG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	44	48	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	51	55	8.281568	CGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	64	68	8.281568	CCTCC	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	115	119	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	142	146	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	194	198	8.281568	CCTCC	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	301	305	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	306	310	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	316	320	8.281568	GAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	321	325	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	324	328	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	329	333	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	339	343	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	347	351	8.281568	CGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	362	366	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	367	371	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	372	376	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	377	381	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	380	384	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	384	388	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	400	404	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	405	409	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	408	412	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	412	416	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	418	422	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	423	427	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	426	430	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	431	435	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	447	451	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	452	456	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	459	463	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	465	469	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	470	474	8.281568	GAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	478	482	8.281568	GAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	486	490	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	491	495	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	494	498	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	498	502	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	637	641	8.281568	CCTCG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	710	714	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	759	763	8.281568	GAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	762	766	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	811	815	8.281568	CCTCC	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	863	867	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	880	884	8.281568	GAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	944	948	8.281568	CCTTG	7.8125	8.20394

cg2419255	PPAP2C	GR-alpha |	977	981	8.281568	CCTCG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	989	993	8.281568	CCTTG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1205	1209	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1245	1249	8.281568	GGAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1286	1290	8.281568	CCTTG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1345	1349	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1382	1386	8.281568	CCTCC	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1477	1481	8.281568	CCTCG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1544	1548	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1550	1554	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1625	1629	8.281568	CCTCC	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1629	1633	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1651	1655	8.281568	CCTTG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1883	1887	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1931	1935	8.281568	CAAGG	7.8125	8.20394
cg2419255	PPAP2C	GR-alpha |	1948	1952	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	36	40	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	63	67	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	115	119	8.281568	CCTCC	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	222	226	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	227	231	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	237	241	8.281568	GAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	242	246	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	245	249	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	250	254	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	260	264	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	268	272	8.281568	CGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	283	287	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	288	292	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	293	297	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	298	302	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	301	305	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	305	309	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	321	325	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	326	330	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	329	333	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	333	337	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	339	343	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	344	348	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	347	351	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	352	356	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	368	372	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	373	377	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	380	384	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	386	390	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	391	395	8.281568	GAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	399	403	8.281568	GAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	407	411	8.281568	GGAGG	7.8125	8.20394

cg2715857	PPAP2C	GR-alpha |	412	416	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	415	419	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	419	423	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	558	562	8.281568	CCTCG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	631	635	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	680	684	8.281568	GAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	683	687	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	732	736	8.281568	CCTCC	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	784	788	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	801	805	8.281568	GAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	865	869	8.281568	CCTTG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	898	902	8.281568	CCTCG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	910	914	8.281568	CCTTG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1126	1130	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1166	1170	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1207	1211	8.281568	CCTTG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1266	1270	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1303	1307	8.281568	CCTCC	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1398	1402	8.281568	CCTCG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1465	1469	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1471	1475	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1546	1550	8.281568	CCTCC	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1550	1554	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1572	1576	8.281568	CCTTG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1804	1808	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1852	1856	8.281568	CAAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1869	1873	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1958	1962	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1971	1975	8.281568	GGAGG	7.8125	8.20394
cg2715857	PPAP2C	GR-alpha |	1985	1989	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1	5	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	28	32	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	80	84	8.281568	CCTCC	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	187	191	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	192	196	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	202	206	8.281568	GAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	207	211	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	210	214	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	215	219	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	225	229	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	233	237	8.281568	CGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	248	252	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	253	257	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	258	262	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	263	267	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	266	270	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	270	274	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	286	290	8.281568	GGAGG	7.8125	8.20394

cg0268666	PPAP2C	GR-alpha |	291	295	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	294	298	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	298	302	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	304	308	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	309	313	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	312	316	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	317	321	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	333	337	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	338	342	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	345	349	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	351	355	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	356	360	8.281568	GAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	364	368	8.281568	GAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	372	376	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	377	381	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	380	384	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	384	388	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	523	527	8.281568	CCTCG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	596	600	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	645	649	8.281568	GAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	648	652	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	697	701	8.281568	CCTCC	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	749	753	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	766	770	8.281568	GAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	830	834	8.281568	CCTTG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	863	867	8.281568	CCTCG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	875	879	8.281568	CCTTG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1091	1095	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1131	1135	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1172	1176	8.281568	CCTTG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1231	1235	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1268	1272	8.281568	CCTCC	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1363	1367	8.281568	CCTCG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1430	1434	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1436	1440	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1511	1515	8.281568	CCTCC	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1515	1519	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1537	1541	8.281568	CCTTG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1769	1773	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1817	1821	8.281568	CAAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1834	1838	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1923	1927	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1936	1940	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1950	1954	8.281568	GGAGG	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1975	1979	8.281568	CCTTC	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1983	1987	8.281568	CCTTC	7.8125	8.20394
cg0268666	PPAP2C	GR-alpha |	1989	1993	8.281568	CCTTG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	2	6	8.281568	CAAGG	7.8125	8.20394

cg2387614	PPAP2C	GR-alpha |	54	58	8.281568	CCTCC	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	161	165	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	166	170	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	176	180	8.281568	GAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	181	185	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	184	188	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	189	193	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	199	203	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	207	211	8.281568	CGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	222	226	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	227	231	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	232	236	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	237	241	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	240	244	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	244	248	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	260	264	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	265	269	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	268	272	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	272	276	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	278	282	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	283	287	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	286	290	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	291	295	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	307	311	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	312	316	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	319	323	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	325	329	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	330	334	8.281568	GAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	338	342	8.281568	GAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	346	350	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	351	355	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	354	358	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	358	362	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	497	501	8.281568	CCTCG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	570	574	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	619	623	8.281568	GAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	622	626	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	671	675	8.281568	CCTCC	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	723	727	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	740	744	8.281568	GAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	804	808	8.281568	CCTTG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	837	841	8.281568	CCTCG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	849	853	8.281568	CCTTG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	1065	1069	8.281568	CAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	1105	1109	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	1146	1150	8.281568	CCTTG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	1205	1209	8.281568	CAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha |	1242	1246	8.281568	CCTCC	7.8125	8.20394

cg2387614	PPAP2C	GR-alpha [	1337	1341	8.281568	CCTCG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1404	1408	8.281568	CAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1410	1414	8.281568	CAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1485	1489	8.281568	CCTCC	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1489	1493	8.281568	CAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1511	1515	8.281568	CCTTG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1743	1747	8.281568	CAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1791	1795	8.281568	CAAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1808	1812	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1897	1901	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1910	1914	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1924	1928	8.281568	GGAGG	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1949	1953	8.281568	CCTTC	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1957	1961	8.281568	CCTTC	7.8125	8.20394
cg2387614	PPAP2C	GR-alpha [	1963	1967	8.281568	CCTTG	7.8125	8.20394
cg2419255	PPAP2C	GCF [T00	1761	1769	8.256755	CTACTG	0.09155	0.09762
cg2715857	PPAP2C	GCF [T00	1682	1690	8.256755	CTACTG	0.09155	0.09762
cg0268666	PPAP2C	GCF [T00	1647	1655	8.256755	CTACTG	0.09155	0.09762
cg2387614	PPAP2C	GCF [T00	1621	1629	8.256755	CTACTG	0.09155	0.09762
cg2419255	PPAP2C	c-Jun [T00	1289	1295	8.242207	TGACCT	0.48828	0.47447
cg2419255	PPAP2C	c-Jun [T00	1938	1944	8.242207	GAGGTC	0.48828	0.47447
cg2715857	PPAP2C	c-Jun [T00	1210	1216	8.242207	TGACCT	0.48828	0.47447
cg2715857	PPAP2C	c-Jun [T00	1859	1865	8.242207	GAGGTC	0.48828	0.47447
cg0268666	PPAP2C	c-Jun [T00	1175	1181	8.242207	TGACCT	0.48828	0.47447
cg0268666	PPAP2C	c-Jun [T00	1824	1830	8.242207	GAGGTC	0.48828	0.47447
cg2387614	PPAP2C	c-Jun [T00	1149	1155	8.242207	TGACCT	0.48828	0.47447
cg2387614	PPAP2C	c-Jun [T00	1798	1804	8.242207	GAGGTC	0.48828	0.47447
cg2419255	PPAP2C	NF-AT1 [	804	812	8.223794	CGACTT	0.1297	0.12846
cg2419255	PPAP2C	NF-AT1 [	1886	1894	8.223794	GGAAAG	0.1297	0.12846
cg2715857	PPAP2C	NF-AT1 [	725	733	8.223794	CGACTT	0.1297	0.12846
cg2715857	PPAP2C	NF-AT1 [	1807	1815	8.223794	GGAAAG	0.1297	0.12846
cg0268666	PPAP2C	NF-AT1 [	690	698	8.223794	CGACTT	0.1297	0.12846
cg0268666	PPAP2C	NF-AT1 [	1772	1780	8.223794	GGAAAG	0.1297	0.12846
cg2387614	PPAP2C	NF-AT1 [	664	672	8.223794	CGACTT	0.1297	0.12846
cg2387614	PPAP2C	NF-AT1 [	1746	1754	8.223794	GGAAAG	0.1297	0.12846
cg2419255	PPAP2C	p53 [T006	1355	1361	8.208781	GGGCCC	0.48828	0.55336
cg2715857	PPAP2C	p53 [T006	1276	1282	8.208781	GGGCCC	0.48828	0.55336
cg0268666	PPAP2C	p53 [T006	1241	1247	8.208781	GGGCCC	0.48828	0.55336
cg2387614	PPAP2C	p53 [T006	1215	1221	8.208781	GGGCCC	0.48828	0.55336
cg2419255	PPAP2C	ENKTF-1	584	591	8.19852	TGGCCG	0.73242	0.80254
cg2419255	PPAP2C	ENKTF-1	1367	1374	8.19852	CGCTGC	0.73242	0.80254
cg2715857	PPAP2C	ENKTF-1	505	512	8.19852	TGGCCG	0.73242	0.80254
cg2715857	PPAP2C	ENKTF-1	1288	1295	8.19852	CGCTGC	0.73242	0.80254
cg0268666	PPAP2C	ENKTF-1	470	477	8.19852	TGGCCG	0.73242	0.80254
cg0268666	PPAP2C	ENKTF-1	1253	1260	8.19852	CGCTGC	0.73242	0.80254
cg2387614	PPAP2C	ENKTF-1	444	451	8.19852	TGGCCG	0.73242	0.80254
cg2387614	PPAP2C	ENKTF-1	1227	1234	8.19852	CGCTGC	0.73242	0.80254
cg2419255	PPAP2C	IRF-1 [T0	843	851	8.078284	GCCTGG	0.25177	0.2462

cg2715857	PPAP2C	IRF-1 [T0(	764	772	8.078284	GCCTGG/	0.25177	0.2462
cg0268666	PPAP2C	IRF-1 [T0(	729	737	8.078284	GCCTGG/	0.25177	0.2462
cg2387614	PPAP2C	IRF-1 [T0(	703	711	8.078284	GCCTGG/	0.25177	0.2462
cg2419255	PPAP2C	GR-alpha [	33	37	8.073878	CCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	76	80	8.073878	CCTGC	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	437	441	8.073878	CTAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	520	524	8.073878	GCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	582	586	8.073878	CCTGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	844	848	8.073878	CCTGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	860	864	8.073878	GCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	934	938	8.073878	CCTGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	953	957	8.073878	CCTGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1001	1005	8.073878	GTAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1010	1014	8.073878	CCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1028	1032	8.073878	CCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1087	1091	8.073878	CCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1134	1138	8.073878	CCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1165	1169	8.073878	CCTGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1188	1192	8.073878	CCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1198	1202	8.073878	CCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1326	1330	8.073878	GCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1331	1335	8.073878	CCTGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1418	1422	8.073878	CCTGC	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1484	1488	8.073878	CCTGC	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1507	1511	8.073878	CCTGC	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1519	1523	8.073878	GCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1634	1638	8.073878	GCAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1722	1726	8.073878	CCTAG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1745	1749	8.073878	GTAGG	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1912	1916	8.073878	CCTAC	7.8125	8.20289
cg2419255	PPAP2C	GR-alpha [	1955	1959	8.073878	CCTGC	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	358	362	8.073878	CTAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	441	445	8.073878	GCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	503	507	8.073878	CCTGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	765	769	8.073878	CCTGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	781	785	8.073878	GCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	855	859	8.073878	CCTGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	874	878	8.073878	CCTGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	922	926	8.073878	GTAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	931	935	8.073878	CCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	949	953	8.073878	CCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	1008	1012	8.073878	CCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	1055	1059	8.073878	CCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	1086	1090	8.073878	CCTGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	1109	1113	8.073878	CCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	1119	1123	8.073878	CCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	1247	1251	8.073878	GCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha [	1252	1256	8.073878	CCTGG	7.8125	8.20289

cg2715857	PPAP2C	GR-alpha |	1339	1343	8.073878	CCTGC	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1405	1409	8.073878	CCTGC	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1428	1432	8.073878	CCTGC	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1440	1444	8.073878	GCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1555	1559	8.073878	GCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1643	1647	8.073878	CCTAG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1666	1670	8.073878	GTAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1833	1837	8.073878	CCTAC	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1876	1880	8.073878	CCTGC	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1945	1949	8.073878	CCAGG	7.8125	8.20289
cg2715857	PPAP2C	GR-alpha |	1967	1971	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	323	327	8.073878	CTAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	406	410	8.073878	GCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	468	472	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	730	734	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	746	750	8.073878	GCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	820	824	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	839	843	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	887	891	8.073878	GTAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	896	900	8.073878	CCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	914	918	8.073878	CCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	973	977	8.073878	CCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1020	1024	8.073878	CCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1051	1055	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1074	1078	8.073878	CCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1084	1088	8.073878	CCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1212	1216	8.073878	GCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1217	1221	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1304	1308	8.073878	CCTGC	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1370	1374	8.073878	CCTGC	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1393	1397	8.073878	CCTGC	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1405	1409	8.073878	GCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1520	1524	8.073878	GCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1608	1612	8.073878	CCTAG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1631	1635	8.073878	GTAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1798	1802	8.073878	CCTAC	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1841	1845	8.073878	CCTGC	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1910	1914	8.073878	CCAGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1932	1936	8.073878	CCTGG	7.8125	8.20289
cg0268666	PPAP2C	GR-alpha |	1962	1966	8.073878	GCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	297	301	8.073878	CTAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	380	384	8.073878	GCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	442	446	8.073878	CCTGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	704	708	8.073878	CCTGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	720	724	8.073878	GCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	794	798	8.073878	CCTGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	813	817	8.073878	CCTGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha |	861	865	8.073878	GTAGG	7.8125	8.20289

cg2387614	PPAP2C	GR-alpha [	870	874	8.073878	CCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	888	892	8.073878	CCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	947	951	8.073878	CCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	994	998	8.073878	CCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1025	1029	8.073878	CCTGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1048	1052	8.073878	CCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1058	1062	8.073878	CCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1186	1190	8.073878	GCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1191	1195	8.073878	CCTGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1278	1282	8.073878	CCTGC	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1344	1348	8.073878	CCTGC	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1367	1371	8.073878	CCTGC	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1379	1383	8.073878	GCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1494	1498	8.073878	GCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1582	1586	8.073878	CCTAG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1605	1609	8.073878	GTAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1772	1776	8.073878	CCTAC	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1815	1819	8.073878	CCTGC	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1884	1888	8.073878	CCAGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1906	1910	8.073878	CCTGG	7.8125	8.20289
cg2387614	PPAP2C	GR-alpha [	1936	1940	8.073878	GCAGG	7.8125	8.20289
cg2419255	PPAP2C	TFIID [T0	1338	1344	8.014558	TCAGAA	2.19727	1.99811
cg2419255	PPAP2C	Pax-5 [T0	280	286	8.014558	GGAGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	572	578	8.014558	TCTGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	736	742	8.014558	GGAGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1016	1022	8.014558	GCAGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1023	1029	8.014558	TGTGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1124	1130	8.014558	TGTGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1145	1151	8.014558	GGAGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1177	1183	8.014558	GGGCAC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1354	1360	8.014558	TGGGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1355	1361	8.014558	GGGCCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1411	1417	8.014558	TCAGCC	2.19727	2.42766
cg2419255	PPAP2C	Pax-5 [T0	1525	1531	8.014558	GGGCAT	2.19727	2.42766
cg2715857	PPAP2C	TFIID [T0	1259	1265	8.014558	TCAGAA	2.19727	1.99811
cg2715857	PPAP2C	Pax-5 [T0	201	207	8.014558	GGAGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	493	499	8.014558	TCTGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	657	663	8.014558	GGAGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	937	943	8.014558	GCAGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	944	950	8.014558	TGTGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	1045	1051	8.014558	TGTGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	1066	1072	8.014558	GGAGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	1098	1104	8.014558	GGGCAC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	1275	1281	8.014558	TGGGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	1276	1282	8.014558	GGGCCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	1332	1338	8.014558	TCAGCC	2.19727	2.42766
cg2715857	PPAP2C	Pax-5 [T0	1446	1452	8.014558	GGGCAT	2.19727	2.42766
cg0268666	PPAP2C	TFIID [T0	1224	1230	8.014558	TCAGAA	2.19727	1.99811

cg0268666	PPAP2C	Pax-5 [T0	166	172	8.014558	GGAGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	458	464	8.014558	TCTGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	622	628	8.014558	GGAGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	902	908	8.014558	GCAGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	909	915	8.014558	TGTGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	1010	1016	8.014558	TGTGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	1031	1037	8.014558	GGAGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	1063	1069	8.014558	GGGCAC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	1240	1246	8.014558	TGGGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	1241	1247	8.014558	GGGCCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	1297	1303	8.014558	TCAGCC	2.19727	2.42766
cg0268666	PPAP2C	Pax-5 [T0	1411	1417	8.014558	GGGCAT	2.19727	2.42766
cg2387614	PPAP2C	TFIID [T0	1198	1204	8.014558	TCAGAA	2.19727	1.99811
cg2387614	PPAP2C	Pax-5 [T0	140	146	8.014558	GGAGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	432	438	8.014558	TCTGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	596	602	8.014558	GGAGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	876	882	8.014558	GCAGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	883	889	8.014558	TGTGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	984	990	8.014558	TGTGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	1005	1011	8.014558	GGAGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	1037	1043	8.014558	GGGCAC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	1214	1220	8.014558	TGGGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	1215	1221	8.014558	GGGCCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	1271	1277	8.014558	TCAGCC	2.19727	2.42766
cg2387614	PPAP2C	Pax-5 [T0	1385	1391	8.014558	GGGCAT	2.19727	2.42766
cg0268666	PPAP2C	NF-kappaI	1965	1975	7.941081	GGCTGT	0.0329	0.03642
cg2387614	PPAP2C	NF-kappaI	1939	1949	7.941081	GGCTGT	0.0329	0.03642
cg2419255	PPAP2C	ATF-1 [T0	266	276	7.870358	GAGTCA	0.07153	0.07126
cg2419255	PPAP2C	ETF [T002	283	293	7.870358	GCCCGC	0.07153	0.08737
cg2419255	PPAP2C	ETF [T002	604	614	7.870358	GCGGGT	0.07153	0.08737
cg2419255	PPAP2C	ETF [T002	1510	1520	7.870358	GCACGT	0.07153	0.08737
cg2419255	PPAP2C	ETF [T002	1671	1681	7.870358	GGTGGG	0.07153	0.08737
cg2715857	PPAP2C	ATF-1 [T0	187	197	7.870358	GAGTCA	0.07153	0.07126
cg2715857	PPAP2C	ETF [T002	204	214	7.870358	GCCCGC	0.07153	0.08737
cg2715857	PPAP2C	ETF [T002	525	535	7.870358	GCGGGT	0.07153	0.08737
cg2715857	PPAP2C	ETF [T002	1431	1441	7.870358	GCACGT	0.07153	0.08737
cg2715857	PPAP2C	ETF [T002	1592	1602	7.870358	GGTGGG	0.07153	0.08737
cg0268666	PPAP2C	ATF-1 [T0	152	162	7.870358	GAGTCA	0.07153	0.07126
cg0268666	PPAP2C	ETF [T002	169	179	7.870358	GCCCGC	0.07153	0.08737
cg0268666	PPAP2C	ETF [T002	490	500	7.870358	GCGGGT	0.07153	0.08737
cg0268666	PPAP2C	ETF [T002	1396	1406	7.870358	GCACGT	0.07153	0.08737
cg0268666	PPAP2C	ETF [T002	1557	1567	7.870358	GGTGGG	0.07153	0.08737
cg2387614	PPAP2C	ATF-1 [T0	126	136	7.870358	GAGTCA	0.07153	0.07126
cg2387614	PPAP2C	ETF [T002	143	153	7.870358	GCCCGC	0.07153	0.08737
cg2387614	PPAP2C	ETF [T002	464	474	7.870358	GCGGGT	0.07153	0.08737
cg2387614	PPAP2C	ETF [T002	1370	1380	7.870358	GCACGT	0.07153	0.08737
cg2387614	PPAP2C	ETF [T002	1531	1541	7.870358	GGTGGG	0.07153	0.08737
cg2419255	PPAP2C	p53 [T006	280	286	7.833758	GGAGCC	0.48828	0.55336

cg2419255	PPAP2C	p53 [T006	736	742	7.833758	GGAGCC	0.48828	0.55336
cg2419255	PPAP2C	p53 [T006	1145	1151	7.833758	GGAGCC	0.48828	0.55336
cg2715857	PPAP2C	p53 [T006	201	207	7.833758	GGAGCC	0.48828	0.55336
cg2715857	PPAP2C	p53 [T006	657	663	7.833758	GGAGCC	0.48828	0.55336
cg2715857	PPAP2C	p53 [T006	1066	1072	7.833758	GGAGCC	0.48828	0.55336
cg0268666	PPAP2C	p53 [T006	166	172	7.833758	GGAGCC	0.48828	0.55336
cg0268666	PPAP2C	p53 [T006	622	628	7.833758	GGAGCC	0.48828	0.55336
cg0268666	PPAP2C	p53 [T006	1031	1037	7.833758	GGAGCC	0.48828	0.55336
cg2387614	PPAP2C	p53 [T006	140	146	7.833758	GGAGCC	0.48828	0.55336
cg2387614	PPAP2C	p53 [T006	596	602	7.833758	GGAGCC	0.48828	0.55336
cg2387614	PPAP2C	p53 [T006	1005	1011	7.833758	GGAGCC	0.48828	0.55336
cg2419255	PPAP2C	RXR-alph	1371	1377	7.815913	GCCACC	0.24414	0.26389
cg2715857	PPAP2C	RXR-alph	1292	1298	7.815913	GCCACC	0.24414	0.26389
cg0268666	PPAP2C	RXR-alph	1257	1263	7.815913	GCCACC	0.24414	0.26389
cg2387614	PPAP2C	RXR-alph	1231	1237	7.815913	GCCACC	0.24414	0.26389
cg2419255	PPAP2C	EBF [T05	1147	1157	7.780217	AGCCCT	0.04196	0.04563
cg2715857	PPAP2C	EBF [T05	1068	1078	7.780217	AGCCCT	0.04196	0.04563
cg0268666	PPAP2C	EBF [T05	1033	1043	7.780217	AGCCCT	0.04196	0.04563
cg2387614	PPAP2C	EBF [T05	1007	1017	7.780217	AGCCCT	0.04196	0.04563
cg2419255	PPAP2C	IRF-1 [T0	1272	1280	7.732782	TTTCCG	0.14496	0.14723
cg2715857	PPAP2C	IRF-1 [T0	1193	1201	7.732782	TTTCCG	0.14496	0.14723
cg0268666	PPAP2C	IRF-1 [T0	1158	1166	7.732782	TTTCCG	0.14496	0.14723
cg2387614	PPAP2C	IRF-1 [T0	1132	1140	7.732782	TTTCCG	0.14496	0.14723
cg2419255	PPAP2C	EBF [T05	813	823	7.659914	TCCTCA	0.01144	0.0122
cg2715857	PPAP2C	EBF [T05	734	744	7.659914	TCCTCA	0.01144	0.0122
cg0268666	PPAP2C	EBF [T05	699	709	7.659914	TCCTCA	0.01144	0.0122
cg2387614	PPAP2C	EBF [T05	673	683	7.659914	TCCTCA	0.01144	0.0122
cg2419255	PPAP2C	c-Ets-1 [T	1693	1699	7.642098	TCGGAA	0.48828	0.48642
cg2715857	PPAP2C	c-Ets-1 [T	1614	1620	7.642098	TCGGAA	0.48828	0.48642
cg0268666	PPAP2C	c-Ets-1 [T	1579	1585	7.642098	TCGGAA	0.48828	0.48642
cg2387614	PPAP2C	c-Ets-1 [T	1553	1559	7.642098	TCGGAA	0.48828	0.48642
cg2419255	PPAP2C	NFI/CTF [	1556	1563	7.587343	GCTCTT	0.36621	0.36269
cg2715857	PPAP2C	NFI/CTF [	1477	1484	7.587343	GCTCTT	0.36621	0.36269
cg0268666	PPAP2C	NFI/CTF [	1442	1449	7.587343	GCTCTT	0.36621	0.36269
cg2387614	PPAP2C	NFI/CTF [	1416	1423	7.587343	GCTCTT	0.36621	0.36269
cg2419255	PPAP2C	GR [T050	597	603	7.527031	CAAAAG	1.83105	1.71535
cg2715857	PPAP2C	GR [T050	518	524	7.527031	CAAAAG	1.83105	1.71535
cg0268666	PPAP2C	GR [T050	483	489	7.527031	CAAAAG	1.83105	1.71535
cg2387614	PPAP2C	GR [T050	457	463	7.527031	CAAAAG	1.83105	1.71535
cg2419255	PPAP2C	PXR-1:RX	1394	1401	7.486257	CCCGTT	0.24414	0.24326
cg2715857	PPAP2C	PXR-1:RX	1315	1322	7.486257	CCCGTT	0.24414	0.24326
cg0268666	PPAP2C	PXR-1:RX	1280	1287	7.486257	CCCGTT	0.24414	0.24326
cg2387614	PPAP2C	PXR-1:RX	1254	1261	7.486257	CCCGTT	0.24414	0.24326
cg2419255	PPAP2C	RAR-beta	386	395	7.47824	AGGGTT	0.24414	0.25121
cg2419255	PPAP2C	RAR-beta	1636	1645	7.47824	AGGGTT	0.24414	0.25121
cg2419255	PPAP2C	RAR-beta	1710	1719	7.47824	AGGGTT	0.24414	0.25121
cg2715857	PPAP2C	RAR-beta	307	316	7.47824	AGGGTT	0.24414	0.25121
cg2715857	PPAP2C	RAR-beta	1557	1566	7.47824	AGGGTT	0.24414	0.25121

cg2715857	PPAP2C	RAR-beta	1631	1640	7.47824	AGGGTT	0.24414	0.25121
cg0268666	PPAP2C	RAR-beta	272	281	7.47824	AGGGTT	0.24414	0.25121
cg0268666	PPAP2C	RAR-beta	1522	1531	7.47824	AGGGTT	0.24414	0.25121
cg0268666	PPAP2C	RAR-beta	1596	1605	7.47824	AGGGTT	0.24414	0.25121
cg2387614	PPAP2C	RAR-beta	246	255	7.47824	AGGGTT	0.24414	0.25121
cg2387614	PPAP2C	RAR-beta	1496	1505	7.47824	AGGGTT	0.24414	0.25121
cg2387614	PPAP2C	RAR-beta	1570	1579	7.47824	AGGGTT	0.24414	0.25121
cg2419255	PPAP2C	p53 [T006	591	597	7.458735	GGCGCC	0.73242	0.79826
cg2419255	PPAP2C	p53 [T006	623	629	7.458735	GGGCGC	0.73242	0.79826
cg2419255	PPAP2C	p53 [T006	1082	1088	7.458735	GGGCGC	0.73242	0.79826
cg2715857	PPAP2C	p53 [T006	512	518	7.458735	GGCGCC	0.73242	0.79826
cg2715857	PPAP2C	p53 [T006	544	550	7.458735	GGGCGC	0.73242	0.79826
cg2715857	PPAP2C	p53 [T006	1003	1009	7.458735	GGGCGC	0.73242	0.79826
cg0268666	PPAP2C	p53 [T006	477	483	7.458735	GGCGCC	0.73242	0.79826
cg0268666	PPAP2C	p53 [T006	509	515	7.458735	GGGCGC	0.73242	0.79826
cg0268666	PPAP2C	p53 [T006	968	974	7.458735	GGGCGC	0.73242	0.79826
cg2387614	PPAP2C	p53 [T006	451	457	7.458735	GGCGCC	0.73242	0.79826
cg2387614	PPAP2C	p53 [T006	483	489	7.458735	GGGCGC	0.73242	0.79826
cg2387614	PPAP2C	p53 [T006	942	948	7.458735	GGGCGC	0.73242	0.79826
cg2419255	PPAP2C	IRF-1 [T0	1770	1778	7.387351	TTTCCC	0.14496	0.14723
cg2715857	PPAP2C	IRF-1 [T0	1691	1699	7.387351	TTTCCC	0.14496	0.14723
cg0268666	PPAP2C	IRF-1 [T0	1656	1664	7.387351	TTTCCC	0.14496	0.14723
cg2387614	PPAP2C	IRF-1 [T0	1630	1638	7.387351	TTTCCC	0.14496	0.14723
cg2419255	PPAP2C	AR [T000	1003	1011	7.372454	AGGGTG	0.25177	0.2544
cg2715857	PPAP2C	AR [T000	924	932	7.372454	AGGGTG	0.25177	0.2544
cg0268666	PPAP2C	AR [T000	889	897	7.372454	AGGGTG	0.25177	0.2544
cg2387614	PPAP2C	AR [T000	863	871	7.372454	AGGGTG	0.25177	0.2544
cg2715857	PPAP2C	PPAR-alph	1940	1950	7.370536	GAGACC	0.04482	0.04884
cg0268666	PPAP2C	PPAR-alph	1905	1915	7.370536	GAGACC	0.04482	0.04884
cg2387614	PPAP2C	PPAR-alph	1879	1889	7.370536	GAGACC	0.04482	0.04884
cg2419255	PPAP2C	p53 [T006	668	674	7.266844	GGGCTG	0.73242	0.79826
cg2419255	PPAP2C	p53 [T006	1988	1994	7.266844	GGGCTG	0.73242	0.79826
cg2715857	PPAP2C	p53 [T006	589	595	7.266844	GGGCTG	0.73242	0.79826
cg2715857	PPAP2C	p53 [T006	1909	1915	7.266844	GGGCTG	0.73242	0.79826
cg0268666	PPAP2C	p53 [T006	554	560	7.266844	GGGCTG	0.73242	0.79826
cg0268666	PPAP2C	p53 [T006	1874	1880	7.266844	GGGCTG	0.73242	0.79826
cg2387614	PPAP2C	p53 [T006	528	534	7.266844	GGGCTG	0.73242	0.79826
cg2387614	PPAP2C	p53 [T006	1848	1854	7.266844	GGGCTG	0.73242	0.79826
cg2419255	PPAP2C	GCF [T00	58	66	7.186486	GCGCAG	0.45776	0.50397
cg2419255	PPAP2C	GCF [T00	89	97	7.186486	GCGCAG	0.45776	0.50397
cg2715857	PPAP2C	GCF [T00	10	18	7.186486	GCGCAG	0.45776	0.50397
cg2419255	PPAP2C	c-Jun [T00	662	668	7.178905	TGACCC	0.73242	0.73062
cg2715857	PPAP2C	c-Jun [T00	583	589	7.178905	TGACCC	0.73242	0.73062
cg0268666	PPAP2C	c-Jun [T00	548	554	7.178905	TGACCC	0.73242	0.73062
cg2387614	PPAP2C	c-Jun [T00	522	528	7.178905	TGACCC	0.73242	0.73062
cg2419255	PPAP2C	SRY [T00	1567	1575	7.175614	ACAGCA	0.30518	0.29547
cg2715857	PPAP2C	SRY [T00	1488	1496	7.175614	ACAGCA	0.30518	0.29547
cg0268666	PPAP2C	SRY [T00	1453	1461	7.175614	ACAGCA	0.30518	0.29547

cg2387614	PPAP2C	SRY [T00	1427	1435	7.175614	ACAGCA	0.30518	0.29547
cg2419255	PPAP2C	XBP-1 [T0	895	900	7.172312	CTTCAT	2.92969	2.7512
cg2419255	PPAP2C	XBP-1 [T0	1528	1533	7.172312	CATCAT	2.92969	2.7512
cg2419255	PPAP2C	XBP-1 [T0	1532	1537	7.172312	ATGAGG	2.92969	2.7512
cg2419255	PPAP2C	XBP-1 [T0	1798	1803	7.172312	ATGAGT	2.92969	2.7512
cg2419255	PPAP2C	XBP-1 [T0	1900	1905	7.172312	CTTCAT	2.92969	2.7512
cg2715857	PPAP2C	XBP-1 [T0	816	821	7.172312	CTTCAT	2.92969	2.7512
cg2715857	PPAP2C	XBP-1 [T0	1449	1454	7.172312	CATCAT	2.92969	2.7512
cg2715857	PPAP2C	XBP-1 [T0	1453	1458	7.172312	ATGAGG	2.92969	2.7512
cg2715857	PPAP2C	XBP-1 [T0	1719	1724	7.172312	ATGAGT	2.92969	2.7512
cg2715857	PPAP2C	XBP-1 [T0	1821	1826	7.172312	CTTCAT	2.92969	2.7512
cg0268666	PPAP2C	XBP-1 [T0	781	786	7.172312	CTTCAT	2.92969	2.7512
cg0268666	PPAP2C	XBP-1 [T0	1414	1419	7.172312	CATCAT	2.92969	2.7512
cg0268666	PPAP2C	XBP-1 [T0	1418	1423	7.172312	ATGAGG	2.92969	2.7512
cg0268666	PPAP2C	XBP-1 [T0	1684	1689	7.172312	ATGAGT	2.92969	2.7512
cg0268666	PPAP2C	XBP-1 [T0	1786	1791	7.172312	CTTCAT	2.92969	2.7512
cg2387614	PPAP2C	XBP-1 [T0	755	760	7.172312	CTTCAT	2.92969	2.7512
cg2387614	PPAP2C	XBP-1 [T0	1388	1393	7.172312	CATCAT	2.92969	2.7512
cg2387614	PPAP2C	XBP-1 [T0	1392	1397	7.172312	ATGAGG	2.92969	2.7512
cg2387614	PPAP2C	XBP-1 [T0	1658	1663	7.172312	ATGAGT	2.92969	2.7512
cg2387614	PPAP2C	XBP-1 [T0	1760	1765	7.172312	CTTCAT	2.92969	2.7512
cg2419255	PPAP2C	p53 [T006	1354	1360	7.153797	TGGGCC	1.09863	1.22478
cg2715857	PPAP2C	p53 [T006	1275	1281	7.153797	TGGGCC	1.09863	1.22478
cg0268666	PPAP2C	p53 [T006	1240	1246	7.153797	TGGGCC	1.09863	1.22478
cg2387614	PPAP2C	p53 [T006	1214	1220	7.153797	TGGGCC	1.09863	1.22478
cg2419255	PPAP2C	p53 [T006	1620	1626	7.150251	GTGGCC	1.09863	1.22478
cg2715857	PPAP2C	p53 [T006	1541	1547	7.150251	GTGGCC	1.09863	1.22478
cg0268666	PPAP2C	p53 [T006	1506	1512	7.150251	GTGGCC	1.09863	1.22478
cg2387614	PPAP2C	p53 [T006	1480	1486	7.150251	GTGGCC	1.09863	1.22478
cg2419255	PPAP2C	c-Ets-1 [T0	1190	1196	7.071349	AGGGAA	0.73242	0.73732
cg2715857	PPAP2C	c-Ets-1 [T0	1111	1117	7.071349	AGGGAA	0.73242	0.73732
cg0268666	PPAP2C	c-Ets-1 [T0	1076	1082	7.071349	AGGGAA	0.73242	0.73732
cg2387614	PPAP2C	c-Ets-1 [T0	1050	1056	7.071349	AGGGAA	0.73242	0.73732
cg2419255	PPAP2C	HNF-3alph	927	934	7.000129	TCAAAA	0.82397	0.71909
cg2715857	PPAP2C	HNF-3alph	848	855	7.000129	TCAAAA	0.82397	0.71909
cg0268666	PPAP2C	HNF-3alph	813	820	7.000129	TCAAAA	0.82397	0.71909
cg2387614	PPAP2C	HNF-3alph	787	794	7.000129	TCAAAA	0.82397	0.71909
cg2419255	PPAP2C	GCF [T00	827	835	6.987525	CAGCCG	0.45776	0.50397
cg2715857	PPAP2C	GCF [T00	748	756	6.987525	CAGCCG	0.45776	0.50397
cg0268666	PPAP2C	GCF [T00	713	721	6.987525	CAGCCG	0.45776	0.50397
cg2387614	PPAP2C	GCF [T00	687	695	6.987525	CAGCCG	0.45776	0.50397
cg2419255	PPAP2C	AhR [T01	686	696	6.981759	AGCGGC	0.02289	0.02402
cg2715857	PPAP2C	AhR [T01	607	617	6.981759	AGCGGC	0.02289	0.02402
cg0268666	PPAP2C	AhR [T01	572	582	6.981759	AGCGGC	0.02289	0.02402
cg2387614	PPAP2C	AhR [T01	546	556	6.981759	AGCGGC	0.02289	0.02402
cg2419255	PPAP2C	c-Ets-1 [T0	1770	1776	6.943262	TTTCCC	0.73242	0.73732
cg2715857	PPAP2C	c-Ets-1 [T0	1691	1697	6.943262	TTTCCC	0.73242	0.73732
cg0268666	PPAP2C	c-Ets-1 [T0	1656	1662	6.943262	TTTCCC	0.73242	0.73732

cg2387614	PPAP2C	c-Ets-1 [T(	1630	1636	6.943262	TTTCCCC	0.73242	0.73732
cg2419255	PPAP2C	ENKTF-1	623	630	6.942764	GGGCGC	1.46484	1.56616
cg2419255	PPAP2C	ENKTF-1	936	943	6.942764	TGGCGC(	1.46484	1.56616
cg2419255	PPAP2C	ENKTF-1	1082	1089	6.942764	GGGCGC	1.46484	1.56616
cg2419255	PPAP2C	ENKTF-1	1293	1300	6.942764	CTCTGCC	1.46484	1.56616
cg2715857	PPAP2C	ENKTF-1	544	551	6.942764	GGGCGC	1.46484	1.56616
cg2715857	PPAP2C	ENKTF-1	857	864	6.942764	TGGCGC(	1.46484	1.56616
cg2715857	PPAP2C	ENKTF-1	1003	1010	6.942764	GGGCGC	1.46484	1.56616
cg2715857	PPAP2C	ENKTF-1	1214	1221	6.942764	CTCTGCC	1.46484	1.56616
cg2715857	PPAP2C	ENKTF-1	1925	1932	6.942764	CCAAGC	1.46484	1.56616
cg0268666	PPAP2C	ENKTF-1	509	516	6.942764	GGGCGC	1.46484	1.56616
cg0268666	PPAP2C	ENKTF-1	822	829	6.942764	TGGCGC(	1.46484	1.56616
cg0268666	PPAP2C	ENKTF-1	968	975	6.942764	GGGCGC	1.46484	1.56616
cg0268666	PPAP2C	ENKTF-1	1179	1186	6.942764	CTCTGCC	1.46484	1.56616
cg0268666	PPAP2C	ENKTF-1	1890	1897	6.942764	CCAAGC	1.46484	1.56616
cg2387614	PPAP2C	ENKTF-1	483	490	6.942764	GGGCGC	1.46484	1.56616
cg2387614	PPAP2C	ENKTF-1	796	803	6.942764	TGGCGC(	1.46484	1.56616
cg2387614	PPAP2C	ENKTF-1	942	949	6.942764	GGGCGC	1.46484	1.56616
cg2387614	PPAP2C	ENKTF-1	1153	1160	6.942764	CTCTGCC	1.46484	1.56616
cg2387614	PPAP2C	ENKTF-1	1864	1871	6.942764	CCAAGC	1.46484	1.56616
cg2419255	PPAP2C	VDR [T00	1397	1405	6.925682	GTTCAG(	0.42725	0.41
cg2715857	PPAP2C	VDR [T00	1318	1326	6.925682	GTTCAG(	0.42725	0.41
cg0268666	PPAP2C	VDR [T00	1283	1291	6.925682	GTTCAG(	0.42725	0.41
cg2387614	PPAP2C	VDR [T00	1257	1265	6.925682	GTTCAG(	0.42725	0.41
cg2419255	PPAP2C	COUP-TF	1935	1947	6.820034	GGAGAG	0.00894	0.00923
cg2715857	PPAP2C	COUP-TF	1856	1868	6.820034	GGAGAG	0.00894	0.00923
cg0268666	PPAP2C	COUP-TF	1821	1833	6.820034	GGAGAG	0.00894	0.00923
cg2387614	PPAP2C	COUP-TF	1795	1807	6.820034	GGAGAG	0.00894	0.00923
cg2419255	PPAP2C	STAT5A [	1841	1853	6.810722	CATTTTC	0.01341	0.01217
cg2715857	PPAP2C	STAT5A [	1762	1774	6.810722	CATTTTC	0.01341	0.01217
cg0268666	PPAP2C	STAT5A [	1727	1739	6.810722	CATTTTC	0.01341	0.01217
cg2387614	PPAP2C	STAT5A [	1701	1713	6.810722	CATTTTC	0.01341	0.01217
cg2715857	PPAP2C	NFI/CTF [	1925	1932	6.786076	CCAAGC	0.73242	0.74795
cg0268666	PPAP2C	NFI/CTF [	1890	1897	6.786076	CCAAGC	0.73242	0.74795
cg2387614	PPAP2C	NFI/CTF [	1864	1871	6.786076	CCAAGC	0.73242	0.74795
cg2419255	PPAP2C	c-Ets-2 [T(	1038	1046	6.695187	TTCCTAT	0.09155	0.08559
cg2715857	PPAP2C	c-Ets-2 [T(	959	967	6.695187	TTCCTAT	0.09155	0.08559
cg0268666	PPAP2C	c-Ets-2 [T(	924	932	6.695187	TTCCTAT	0.09155	0.08559
cg2387614	PPAP2C	c-Ets-2 [T(	898	906	6.695187	TTCCTAT	0.09155	0.08559
cg2419255	PPAP2C	FOXP3 [T	1389	1394	6.581441	TAAAAC	0.97656	0.904
cg2419255	PPAP2C	FOXP3 [T	1463	1468	6.581441	TTCAAC	0.97656	0.904
cg2419255	PPAP2C	TFII-I [T0	820	825	6.581441	GGAGTG	0.97656	0.9991
cg2419255	PPAP2C	TFII-I [T0	1255	1260	6.581441	GGAGTG	0.97656	0.9991
cg2715857	PPAP2C	FOXP3 [T	1310	1315	6.581441	TAAAAC	0.97656	0.904
cg2715857	PPAP2C	FOXP3 [T	1384	1389	6.581441	TTCAAC	0.97656	0.904
cg2715857	PPAP2C	TFII-I [T0	741	746	6.581441	GGAGTG	0.97656	0.9991
cg2715857	PPAP2C	TFII-I [T0	1176	1181	6.581441	GGAGTG	0.97656	0.9991
cg0268666	PPAP2C	FOXP3 [T	1275	1280	6.581441	TAAAAC	0.97656	0.904

cg0268666	PPAP2C	FOXP3 [T	1349	1354	6.581441	TTCAAC	0.97656	0.904
cg0268666	PPAP2C	TFII-I [T0	706	711	6.581441	GGAGTG	0.97656	0.9991
cg0268666	PPAP2C	TFII-I [T0	1141	1146	6.581441	GGAGTG	0.97656	0.9991
cg2387614	PPAP2C	FOXP3 [T	1249	1254	6.581441	TAAAAC	0.97656	0.904
cg2387614	PPAP2C	FOXP3 [T	1323	1328	6.581441	TTCAAC	0.97656	0.904
cg2387614	PPAP2C	TFII-I [T0	680	685	6.581441	GGAGTG	0.97656	0.9991
cg2387614	PPAP2C	TFII-I [T0	1115	1120	6.581441	GGAGTG	0.97656	0.9991
cg2419255	PPAP2C	RXR-alpha	1004	1010	6.563693	GGGTGT	0.24414	0.25119
cg2715857	PPAP2C	RXR-alpha	925	931	6.563693	GGGTGT	0.24414	0.25119
cg0268666	PPAP2C	RXR-alpha	890	896	6.563693	GGGTGT	0.24414	0.25119
cg2387614	PPAP2C	RXR-alpha	864	870	6.563693	GGGTGT	0.24414	0.25119
cg2419255	PPAP2C	p53 [T006	1016	1022	6.563521	GCAGCC	0.48828	0.54643
cg2715857	PPAP2C	p53 [T006	937	943	6.563521	GCAGCC	0.48828	0.54643
cg0268666	PPAP2C	p53 [T006	902	908	6.563521	GCAGCC	0.48828	0.54643
cg2387614	PPAP2C	p53 [T006	876	882	6.563521	GCAGCC	0.48828	0.54643
cg2419255	PPAP2C	XBP-1 [T	1525	1530	6.478682	GGGCAT	0.97656	0.99906
cg2715857	PPAP2C	XBP-1 [T	1446	1451	6.478682	GGGCAT	0.97656	0.99906
cg0268666	PPAP2C	XBP-1 [T	1411	1416	6.478682	GGGCAT	0.97656	0.99906
cg2387614	PPAP2C	XBP-1 [T	1385	1390	6.478682	GGGCAT	0.97656	0.99906
cg2419255	PPAP2C	p53 [T006	884	890	6.400205	GGGCGA	0.48828	0.54643
cg2715857	PPAP2C	p53 [T006	805	811	6.400205	GGGCGA	0.48828	0.54643
cg0268666	PPAP2C	p53 [T006	770	776	6.400205	GGGCGA	0.48828	0.54643
cg2387614	PPAP2C	p53 [T006	744	750	6.400205	GGGCGA	0.48828	0.54643
cg2419255	PPAP2C	RAR-beta	1191	1200	6.39673	GGGAAA	0.18311	0.1857
cg2715857	PPAP2C	RAR-beta	1112	1121	6.39673	GGGAAA	0.18311	0.1857
cg0268666	PPAP2C	RAR-beta	1077	1086	6.39673	GGGAAA	0.18311	0.1857
cg2387614	PPAP2C	RAR-beta	1051	1060	6.39673	GGGAAA	0.18311	0.1857
cg2387614	PPAP2C	RAR-beta	1978	1987	6.39673	TGGGTT	0.18311	0.1857
cg2419255	PPAP2C	AR [T000	100	108	6.351833	GGCGTG	0.19836	0.20813
cg2715857	PPAP2C	AR [T000	21	29	6.351833	GGCGTG	0.19836	0.20813
cg2419255	PPAP2C	PPAR-alph	1216	1226	6.299891	CACTGG	0.03719	0.04058
cg2715857	PPAP2C	PPAR-alph	1137	1147	6.299891	CACTGG	0.03719	0.04058
cg0268666	PPAP2C	PPAR-alph	1102	1112	6.299891	CACTGG	0.03719	0.04058
cg2387614	PPAP2C	PPAR-alph	1076	1086	6.299891	CACTGG	0.03719	0.04058
cg2419255	PPAP2C	c-Jun [T00	1378	1384	6.293948	TGACCC	0.61035	0.6179
cg2715857	PPAP2C	c-Jun [T00	1299	1305	6.293948	TGACCC	0.61035	0.6179
cg0268666	PPAP2C	c-Jun [T00	1264	1270	6.293948	TGACCC	0.61035	0.6179
cg2387614	PPAP2C	c-Jun [T00	1238	1244	6.293948	TGACCC	0.61035	0.6179
cg2419255	PPAP2C	GR-alpha [	12	16	6.263098	CCTCA	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	359	363	6.263098	TGAGG	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	693	697	6.263098	TGAGG	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	699	703	6.263098	CCTCA	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	814	818	6.263098	CCTCA	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	870	874	6.263098	CCTTA	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	1157	1161	6.263098	TGAGG	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	1174	1178	6.263098	TGAGG	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	1250	1254	6.263098	CCTCA	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	1533	1537	6.263098	TGAGG	3.90625	3.89624

cg2419255	PPAP2C	GR-alpha [	1641	1645	6.263098	TGAGG	3.90625	3.89624
cg2419255	PPAP2C	GR-alpha [	1708	1712	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	280	284	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	614	618	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	620	624	6.263098	CCTCA	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	735	739	6.263098	CCTCA	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	791	795	6.263098	CCTTA	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	1078	1082	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	1095	1099	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	1171	1175	6.263098	CCTCA	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	1454	1458	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	1562	1566	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	1629	1633	6.263098	TGAGG	3.90625	3.89624
cg2715857	PPAP2C	GR-alpha [	1990	1994	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	245	249	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	579	583	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	585	589	6.263098	CCTCA	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	700	704	6.263098	CCTCA	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	756	760	6.263098	CCTTA	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	1043	1047	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	1060	1064	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	1136	1140	6.263098	CCTCA	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	1419	1423	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	1527	1531	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	1594	1598	6.263098	TGAGG	3.90625	3.89624
cg0268666	PPAP2C	GR-alpha [	1955	1959	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	219	223	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	553	557	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	559	563	6.263098	CCTCA	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	674	678	6.263098	CCTCA	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	730	734	6.263098	CCTTA	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1017	1021	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1034	1038	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1110	1114	6.263098	CCTCA	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1393	1397	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1501	1505	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1568	1572	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1929	1933	6.263098	TGAGG	3.90625	3.89624
cg2387614	PPAP2C	GR-alpha [	1987	1991	6.263098	CCTTA	3.90625	3.89624
cg2419255	PPAP2C	ETF [T002	427	437	6.253495	GAGGGG	0.00954	0.01147
cg2715857	PPAP2C	ETF [T002	348	358	6.253495	GAGGGG	0.00954	0.01147
cg0268666	PPAP2C	ETF [T002	313	323	6.253495	GAGGGG	0.00954	0.01147
cg2387614	PPAP2C	ETF [T002	287	297	6.253495	GAGGGG	0.00954	0.01147
cg2419255	PPAP2C	IRF-1 [T0(	808	816	6.24301	TTTCCTC	0.16785	0.16217
cg2715857	PPAP2C	IRF-1 [T0(	729	737	6.24301	TTTCCTC	0.16785	0.16217
cg0268666	PPAP2C	IRF-1 [T0(	694	702	6.24301	TTTCCTC	0.16785	0.16217
cg2387614	PPAP2C	IRF-1 [T0(	668	676	6.24301	TTTCCTC	0.16785	0.16217
cg2419255	PPAP2C	c-Fos [T00	1879	1888	6.236188	GAGTCA.	0.09155	0.09198

cg2715857	PPAP2C	c-Fos [T00	1800	1809	6.236188	GAGTCA	0.09155	0.09198
cg0268666	PPAP2C	c-Fos [T00	1765	1774	6.236188	GAGTCA	0.09155	0.09198
cg2387614	PPAP2C	c-Fos [T00	1739	1748	6.236188	GAGTCA	0.09155	0.09198
cg0268666	PPAP2C	PEA3 [T0	1977	1985	6.227095	TTCCAT	0.03815	0.03662
cg2387614	PPAP2C	PEA3 [T0	1951	1959	6.227095	TTCCAT	0.03815	0.03662
cg2419255	PPAP2C	c-Myb [T0	81	88	6.12608	AAACTT	0.21362	0.2053
cg2715857	PPAP2C	c-Myb [T0	2	9	6.12608	AAACTT	0.21362	0.2053
cg2419255	PPAP2C	RXR-alph	213	219	6.119461	GCGACC	0.73242	0.78318
cg2715857	PPAP2C	RXR-alph	134	140	6.119461	GCGACC	0.73242	0.78318
cg0268666	PPAP2C	RXR-alph	99	105	6.119461	GCGACC	0.73242	0.78318
cg2387614	PPAP2C	RXR-alph	73	79	6.119461	GCGACC	0.73242	0.78318
cg2419255	PPAP2C	MAZ [T00	407	419	6.11881	AGGAGG	0.00393	0.00438
cg2419255	PPAP2C	MAZ [T00	493	505	6.11881	AGGAGG	0.00393	0.00438
cg2715857	PPAP2C	MAZ [T00	328	340	6.11881	AGGAGG	0.00393	0.00438
cg2715857	PPAP2C	MAZ [T00	414	426	6.11881	AGGAGG	0.00393	0.00438
cg0268666	PPAP2C	MAZ [T00	293	305	6.11881	AGGAGG	0.00393	0.00438
cg0268666	PPAP2C	MAZ [T00	379	391	6.11881	AGGAGG	0.00393	0.00438
cg2387614	PPAP2C	MAZ [T00	267	279	6.11881	AGGAGG	0.00393	0.00438
cg2387614	PPAP2C	MAZ [T00	353	365	6.11881	AGGAGG	0.00393	0.00438
cg2419255	PPAP2C	GCF [T00	1014	1022	6.116216	GCGCAG	0.64087	0.72542
cg2715857	PPAP2C	GCF [T00	935	943	6.116216	GCGCAG	0.64087	0.72542
cg0268666	PPAP2C	GCF [T00	900	908	6.116216	GCGCAG	0.64087	0.72542
cg2387614	PPAP2C	GCF [T00	874	882	6.116216	GCGCAG	0.64087	0.72542
cg2419255	PPAP2C	AR [T000	1053	1061	6.110872	TTGCTG	0.24414	0.25115
cg2715857	PPAP2C	AR [T000	974	982	6.110872	TTGCTG	0.24414	0.25115
cg0268666	PPAP2C	AR [T000	939	947	6.110872	TTGCTG	0.24414	0.25115
cg2387614	PPAP2C	AR [T000	913	921	6.110872	TTGCTG	0.24414	0.25115
cg2715857	PPAP2C	p53 [T006	1922	1928	6.095267	GGGCCA	0.61035	0.68483
cg0268666	PPAP2C	p53 [T006	1887	1893	6.095267	GGGCCA	0.61035	0.68483
cg2387614	PPAP2C	p53 [T006	1861	1867	6.095267	GGGCCA	0.61035	0.68483
cg2419255	PPAP2C	GR-alpha [	390	394	6.055408	TTAGG	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	660	664	6.055408	CCTGA	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	816	820	6.055408	TCAGG	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	902	906	6.055408	TCAGG	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	919	923	6.055408	CCTAA	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	1150	1154	6.055408	CCTGA	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	1182	1186	6.055408	CCTGA	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	1252	1256	6.055408	TCAGG	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	1376	1380	6.055408	CCTGA	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	1699	1703	6.055408	TTAGG	3.90625	3.89835
cg2419255	PPAP2C	GR-alpha [	1849	1853	6.055408	CCTAA	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	311	315	6.055408	TTAGG	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	581	585	6.055408	CCTGA	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	737	741	6.055408	TCAGG	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	823	827	6.055408	TCAGG	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	840	844	6.055408	CCTAA	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	1071	1075	6.055408	CCTGA	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	1103	1107	6.055408	CCTGA	3.90625	3.89835

cg2715857	PPAP2C	GR-alpha [	1173	1177	6.055408	TCAGG	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	1297	1301	6.055408	CCTGA	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	1620	1624	6.055408	TTAGG	3.90625	3.89835
cg2715857	PPAP2C	GR-alpha [	1770	1774	6.055408	CCTAA	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	276	280	6.055408	TTAGG	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	546	550	6.055408	CCTGA	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	702	706	6.055408	TCAGG	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	788	792	6.055408	TCAGG	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	805	809	6.055408	CCTAA	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	1036	1040	6.055408	CCTGA	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	1068	1072	6.055408	CCTGA	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	1138	1142	6.055408	TCAGG	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	1262	1266	6.055408	CCTGA	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	1585	1589	6.055408	TTAGG	3.90625	3.89835
cg0268666	PPAP2C	GR-alpha [	1735	1739	6.055408	CCTAA	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	250	254	6.055408	TTAGG	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	520	524	6.055408	CCTGA	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	676	680	6.055408	TCAGG	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	762	766	6.055408	TCAGG	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	779	783	6.055408	CCTAA	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	1010	1014	6.055408	CCTGA	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	1042	1046	6.055408	CCTGA	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	1112	1116	6.055408	TCAGG	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	1236	1240	6.055408	CCTGA	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	1559	1563	6.055408	TTAGG	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	1709	1713	6.055408	CCTAA	3.90625	3.89835
cg2387614	PPAP2C	GR-alpha [	1970	1974	6.055408	TCAGG	3.90625	3.89835
cg2419255	PPAP2C	c-Ets-1 [T	845	851	6.039428	CTGGAA	0.36621	0.36174
cg2715857	PPAP2C	c-Ets-1 [T	766	772	6.039428	CTGGAA	0.36621	0.36174
cg0268666	PPAP2C	c-Ets-1 [T	731	737	6.039428	CTGGAA	0.36621	0.36174
cg2387614	PPAP2C	c-Ets-1 [T	705	711	6.039428	CTGGAA	0.36621	0.36174
cg2419255	PPAP2C	RXR-alpha	981	987	5.937582	GGCACC	0.73242	0.78318
cg2419255	PPAP2C	RXR-alpha	1160	1166	5.937582	GGGTGC	0.73242	0.78318
cg2419255	PPAP2C	RXR-alpha	1575	1581	5.937582	GGCACC	0.73242	0.78318
cg2715857	PPAP2C	RXR-alpha	902	908	5.937582	GGCACC	0.73242	0.78318
cg2715857	PPAP2C	RXR-alpha	1081	1087	5.937582	GGGTGC	0.73242	0.78318
cg2715857	PPAP2C	RXR-alpha	1496	1502	5.937582	GGCACC	0.73242	0.78318
cg0268666	PPAP2C	RXR-alpha	867	873	5.937582	GGCACC	0.73242	0.78318
cg0268666	PPAP2C	RXR-alpha	1046	1052	5.937582	GGGTGC	0.73242	0.78318
cg0268666	PPAP2C	RXR-alpha	1461	1467	5.937582	GGCACC	0.73242	0.78318
cg2387614	PPAP2C	RXR-alpha	841	847	5.937582	GGCACC	0.73242	0.78318
cg2387614	PPAP2C	RXR-alpha	1020	1026	5.937582	GGGTGC	0.73242	0.78318
cg2387614	PPAP2C	RXR-alpha	1435	1441	5.937582	GGCACC	0.73242	0.78318
cg2419255	PPAP2C	GCF [T00	545	553	5.917256	GCGCGG	0.64087	0.72542
cg2419255	PPAP2C	GCF [T00	564	572	5.917256	GCGCGG	0.64087	0.72542
cg2419255	PPAP2C	GCF [T00	587	595	5.917256	CCGCGG	0.64087	0.72542
cg2419255	PPAP2C	GCF [T00	832	840	5.917256	GCGCCG	0.64087	0.72542
cg2419255	PPAP2C	GCF [T00	1042	1050	5.917256	TATCAG	0.64087	0.72542

cg2715857	PPAP2C	GCF [T00	466	474	5.917256	GCGCGG	0.64087	0.72542
cg2715857	PPAP2C	GCF [T00	485	493	5.917256	GCGCGG	0.64087	0.72542
cg2715857	PPAP2C	GCF [T00	508	516	5.917256	CCGCGG	0.64087	0.72542
cg2715857	PPAP2C	GCF [T00	753	761	5.917256	GCGCCG	0.64087	0.72542
cg2715857	PPAP2C	GCF [T00	963	971	5.917256	TATCAG	0.64087	0.72542
cg0268666	PPAP2C	GCF [T00	431	439	5.917256	GCGCGG	0.64087	0.72542
cg0268666	PPAP2C	GCF [T00	450	458	5.917256	GCGCGG	0.64087	0.72542
cg0268666	PPAP2C	GCF [T00	473	481	5.917256	CCGCGG	0.64087	0.72542
cg0268666	PPAP2C	GCF [T00	718	726	5.917256	GCGCCG	0.64087	0.72542
cg0268666	PPAP2C	GCF [T00	928	936	5.917256	TATCAG	0.64087	0.72542
cg2387614	PPAP2C	GCF [T00	405	413	5.917256	GCGCGG	0.64087	0.72542
cg2387614	PPAP2C	GCF [T00	424	432	5.917256	GCGCGG	0.64087	0.72542
cg2387614	PPAP2C	GCF [T00	447	455	5.917256	CCGCGG	0.64087	0.72542
cg2387614	PPAP2C	GCF [T00	692	700	5.917256	GCGCCG	0.64087	0.72542
cg2387614	PPAP2C	GCF [T00	902	910	5.917256	TATCAG	0.64087	0.72542
cg2419255	PPAP2C	STAT4 [T	315	320	5.882353	GGAAGG	0.48828	0.51201
cg2419255	PPAP2C	STAT4 [T	469	474	5.882353	GGAAGG	0.48828	0.51201
cg2419255	PPAP2C	STAT4 [T	879	884	5.882353	GGAAGG	0.48828	0.51201
cg2715857	PPAP2C	STAT4 [T	236	241	5.882353	GGAAGG	0.48828	0.51201
cg2715857	PPAP2C	STAT4 [T	390	395	5.882353	GGAAGG	0.48828	0.51201
cg2715857	PPAP2C	STAT4 [T	800	805	5.882353	GGAAGG	0.48828	0.51201
cg0268666	PPAP2C	STAT4 [T	201	206	5.882353	GGAAGG	0.48828	0.51201
cg0268666	PPAP2C	STAT4 [T	355	360	5.882353	GGAAGG	0.48828	0.51201
cg0268666	PPAP2C	STAT4 [T	765	770	5.882353	GGAAGG	0.48828	0.51201
cg0268666	PPAP2C	STAT4 [T	1975	1980	5.882353	CCTTCC	0.48828	0.51201
cg0268666	PPAP2C	STAT4 [T	1983	1988	5.882353	CCTTCC	0.48828	0.51201
cg2387614	PPAP2C	STAT4 [T	175	180	5.882353	GGAAGG	0.48828	0.51201
cg2387614	PPAP2C	STAT4 [T	329	334	5.882353	GGAAGG	0.48828	0.51201
cg2387614	PPAP2C	STAT4 [T	739	744	5.882353	GGAAGG	0.48828	0.51201
cg2387614	PPAP2C	STAT4 [T	1949	1954	5.882353	CCTTCC	0.48828	0.51201
cg2387614	PPAP2C	STAT4 [T	1957	1962	5.882353	CCTTCC	0.48828	0.51201
cg2419255	PPAP2C	c-Myb [T0	1454	1461	5.841835	CAACTG	0.21362	0.2053
cg2715857	PPAP2C	c-Myb [T0	1375	1382	5.841835	CAACTG	0.21362	0.2053
cg0268666	PPAP2C	c-Myb [T0	1340	1347	5.841835	CAACTG	0.21362	0.2053
cg2387614	PPAP2C	c-Myb [T0	1314	1321	5.841835	CAACTG	0.21362	0.2053
cg2419255	PPAP2C	c-Ets-1 [T	1317	1323	5.814485	TGGGAA	0.36621	0.36174
cg2419255	PPAP2C	c-Ets-1 [T	1596	1602	5.814485	TGGGAA	0.36621	0.36174
cg2715857	PPAP2C	c-Ets-1 [T	1238	1244	5.814485	TGGGAA	0.36621	0.36174
cg2715857	PPAP2C	c-Ets-1 [T	1517	1523	5.814485	TGGGAA	0.36621	0.36174
cg0268666	PPAP2C	c-Ets-1 [T	1203	1209	5.814485	TGGGAA	0.36621	0.36174
cg0268666	PPAP2C	c-Ets-1 [T	1482	1488	5.814485	TGGGAA	0.36621	0.36174
cg2387614	PPAP2C	c-Ets-1 [T	1177	1183	5.814485	TGGGAA	0.36621	0.36174
cg2387614	PPAP2C	c-Ets-1 [T	1456	1462	5.814485	TGGGAA	0.36621	0.36174
cg2419255	PPAP2C	STAT1bet	1769	1778	5.796867	CTTTCC	0.1545	0.14881
cg2715857	PPAP2C	STAT1bet	1690	1699	5.796867	CTTTCC	0.1545	0.14881
cg0268666	PPAP2C	STAT1bet	1655	1664	5.796867	CTTTCC	0.1545	0.14881
cg2387614	PPAP2C	STAT1bet	1629	1638	5.796867	CTTTCC	0.1545	0.14881
cg2387614	PPAP2C	p53 [T006	1982	1988	5.720243	TTAGCC	0.61035	0.65765

cg2419255	PPAP2C	RXR-alpha	128	134	5.715466	AACACC	0.61035	0.65415
cg2715857	PPAP2C	RXR-alpha	49	55	5.715466	AACACC	0.61035	0.65415
cg0268666	PPAP2C	RXR-alpha	14	20	5.715466	AACACC	0.61035	0.65415
cg2419255	PPAP2C	c-Jun [T00	1334	1340	5.703976	GGGGTC	0.48828	0.49294
cg2715857	PPAP2C	c-Jun [T00	1255	1261	5.703976	GGGGTC	0.48828	0.49294
cg0268666	PPAP2C	c-Jun [T00	1220	1226	5.703976	GGGGTC	0.48828	0.49294
cg2387614	PPAP2C	c-Jun [T00	1194	1200	5.703976	GGGGTC	0.48828	0.49294
cg2419255	PPAP2C	ENKTF-1	1183	1190	5.687009	CTGAGC	0.73242	0.76357
cg2715857	PPAP2C	ENKTF-1	1104	1111	5.687009	CTGAGC	0.73242	0.76357
cg0268666	PPAP2C	ENKTF-1	1069	1076	5.687009	CTGAGC	0.73242	0.76357
cg2387614	PPAP2C	ENKTF-1	1043	1050	5.687009	CTGAGC	0.73242	0.76357
cg2419255	PPAP2C	c-Ets-1 [T	467	473	5.686398	AGGGAA	0.36621	0.38732
cg2419255	PPAP2C	c-Ets-1 [T	472	478	5.686398	AGGGAA	0.36621	0.38732
cg2715857	PPAP2C	c-Ets-1 [T	388	394	5.686398	AGGGAA	0.36621	0.38732
cg2715857	PPAP2C	c-Ets-1 [T	393	399	5.686398	AGGGAA	0.36621	0.38732
cg0268666	PPAP2C	c-Ets-1 [T	353	359	5.686398	AGGGAA	0.36621	0.38732
cg0268666	PPAP2C	c-Ets-1 [T	358	364	5.686398	AGGGAA	0.36621	0.38732
cg2387614	PPAP2C	c-Ets-1 [T	327	333	5.686398	AGGGAA	0.36621	0.38732
cg2387614	PPAP2C	c-Ets-1 [T	332	338	5.686398	AGGGAA	0.36621	0.38732
cg2419255	PPAP2C	c-Fos [T00	266	275	5.679695	GAGTCA	0.04578	0.04712
cg2715857	PPAP2C	c-Fos [T00	187	196	5.679695	GAGTCA	0.04578	0.04712
cg0268666	PPAP2C	c-Fos [T00	152	161	5.679695	GAGTCA	0.04578	0.04712
cg2387614	PPAP2C	c-Fos [T00	126	135	5.679695	GAGTCA	0.04578	0.04712
cg2419255	PPAP2C	NF-1 [T00	946	953	5.626299	TTGGAC	0.24414	0.25051
cg2715857	PPAP2C	NF-1 [T00	867	874	5.626299	TTGGAC	0.24414	0.25051
cg0268666	PPAP2C	NF-1 [T00	832	839	5.626299	TTGGAC	0.24414	0.25051
cg2387614	PPAP2C	NF-1 [T00	806	813	5.626299	TTGGAC	0.24414	0.25051
cg2419255	PPAP2C	AhR:Arnt	613	622	5.620669	GCGAGC	0.0515	0.05997
cg2715857	PPAP2C	AhR:Arnt	534	543	5.620669	GCGAGC	0.0515	0.05997
cg0268666	PPAP2C	AhR:Arnt	499	508	5.620669	GCGAGC	0.0515	0.05997
cg2387614	PPAP2C	AhR:Arnt	473	482	5.620669	GCGAGC	0.0515	0.05997
cg2419255	PPAP2C	c-Jun [T00	1257	1263	5.590308	AGTGTC	0.48828	0.49294
cg2419255	PPAP2C	c-Jun [T00	1754	1760	5.590308	AGCGTC	0.48828	0.49294
cg2715857	PPAP2C	c-Jun [T00	1178	1184	5.590308	AGTGTC	0.48828	0.49294
cg2715857	PPAP2C	c-Jun [T00	1675	1681	5.590308	AGCGTC	0.48828	0.49294
cg0268666	PPAP2C	c-Jun [T00	1143	1149	5.590308	AGTGTC	0.48828	0.49294
cg0268666	PPAP2C	c-Jun [T00	1640	1646	5.590308	AGCGTC	0.48828	0.49294
cg2387614	PPAP2C	c-Jun [T00	1117	1123	5.590308	AGTGTC	0.48828	0.49294
cg2387614	PPAP2C	c-Jun [T00	1614	1620	5.590308	AGCGTC	0.48828	0.49294
cg2419255	PPAP2C	c-Ets-1 [T	1974	1980	5.558311	GGGGAA	0.36621	0.38732
cg2715857	PPAP2C	c-Ets-1 [T	1895	1901	5.558311	GGGGAA	0.36621	0.38732
cg0268666	PPAP2C	c-Ets-1 [T	1860	1866	5.558311	GGGGAA	0.36621	0.38732
cg0268666	PPAP2C	c-Ets-1 [T	1984	1990	5.558311	CTTCCCC	0.36621	0.38732
cg2387614	PPAP2C	c-Ets-1 [T	1834	1840	5.558311	GGGGAA	0.36621	0.38732
cg2387614	PPAP2C	c-Ets-1 [T	1958	1964	5.558311	CTTCCCC	0.36621	0.38732
cg2715857	PPAP2C	GATA-2 [	1974	1982	5.555555	GGATAG	0.18311	0.18081
cg0268666	PPAP2C	GATA-2 [	1939	1947	5.555555	GGATAG	0.18311	0.18081
cg2387614	PPAP2C	GATA-2 [	1913	1921	5.555555	GGATAG	0.18311	0.18081

cg2419255	PPAP2C	p53 [T006	1411	1417	5.508538	TCAGCC	0.61035	0.65765
cg2715857	PPAP2C	p53 [T006	1332	1338	5.508538	TCAGCC	0.61035	0.65765
cg0268666	PPAP2C	p53 [T006	1297	1303	5.508538	TCAGCC	0.61035	0.65765
cg2387614	PPAP2C	p53 [T006	1271	1277	5.508538	TCAGCC	0.61035	0.65765
cg2419255	PPAP2C	E2F-1 [T0	715	722	5.476857	TTCCCC	0.03052	0.03364
cg2715857	PPAP2C	E2F-1 [T0	636	643	5.476857	TTCCCC	0.03052	0.03364
cg0268666	PPAP2C	E2F-1 [T0	601	608	5.476857	TTCCCC	0.03052	0.03364
cg2387614	PPAP2C	E2F-1 [T0	575	582	5.476857	TTCCCC	0.03052	0.03364
cg2419255	PPAP2C	C/EBPalph	1728	1734	5.455853	ATCAAT	0.73242	0.68229
cg2715857	PPAP2C	C/EBPalph	1649	1655	5.455853	ATCAAT	0.73242	0.68229
cg0268666	PPAP2C	C/EBPalph	1614	1620	5.455853	ATCAAT	0.73242	0.68229
cg2387614	PPAP2C	C/EBPalph	1588	1594	5.455853	ATCAAT	0.73242	0.68229
cg2419255	PPAP2C	c-Ets-1 [T	313	319	5.430224	CGGGAA	0.36621	0.38732
cg2419255	PPAP2C	c-Ets-1 [T	1488	1494	5.430224	CTTCCC	0.36621	0.38732
cg2715857	PPAP2C	c-Ets-1 [T	234	240	5.430224	CGGGAA	0.36621	0.38732
cg2715857	PPAP2C	c-Ets-1 [T	1409	1415	5.430224	CTTCCC	0.36621	0.38732
cg0268666	PPAP2C	c-Ets-1 [T	199	205	5.430224	CGGGAA	0.36621	0.38732
cg0268666	PPAP2C	c-Ets-1 [T	1374	1380	5.430224	CTTCCC	0.36621	0.38732
cg2387614	PPAP2C	c-Ets-1 [T	173	179	5.430224	CGGGAA	0.36621	0.38732
cg2387614	PPAP2C	c-Ets-1 [T	1348	1354	5.430224	CTTCCC	0.36621	0.38732
cg2419255	PPAP2C	IRF-1 [T0	1882	1890	5.309227	TCAAGG	0.22888	0.21959
cg2715857	PPAP2C	IRF-1 [T0	1803	1811	5.309227	TCAAGG	0.22888	0.21959
cg0268666	PPAP2C	IRF-1 [T0	1768	1776	5.309227	TCAAGG	0.22888	0.21959
cg2387614	PPAP2C	IRF-1 [T0	1742	1750	5.309227	TCAAGG	0.22888	0.21959
cg2419255	PPAP2C	RXR-alpha	606	612	5.271235	GGGTGG	0.61035	0.65415
cg2419255	PPAP2C	RXR-alpha	1593	1599	5.271235	GGGTGG	0.61035	0.65415
cg2419255	PPAP2C	RXR-alpha	1670	1676	5.271235	GGGTGG	0.61035	0.65415
cg2715857	PPAP2C	RXR-alpha	527	533	5.271235	GGGTGG	0.61035	0.65415
cg2715857	PPAP2C	RXR-alpha	1514	1520	5.271235	GGGTGG	0.61035	0.65415
cg2715857	PPAP2C	RXR-alpha	1591	1597	5.271235	GGGTGG	0.61035	0.65415
cg0268666	PPAP2C	RXR-alpha	492	498	5.271235	GGGTGG	0.61035	0.65415
cg0268666	PPAP2C	RXR-alpha	1479	1485	5.271235	GGGTGG	0.61035	0.65415
cg0268666	PPAP2C	RXR-alpha	1556	1562	5.271235	GGGTGG	0.61035	0.65415
cg2387614	PPAP2C	RXR-alpha	466	472	5.271235	GGGTGG	0.61035	0.65415
cg2387614	PPAP2C	RXR-alpha	1453	1459	5.271235	GGGTGG	0.61035	0.65415
cg2387614	PPAP2C	RXR-alpha	1530	1536	5.271235	GGGTGG	0.61035	0.65415
cg2419255	PPAP2C	ETF [T002	335	345	5.246906	GCGGGG	0.02861	0.03569
cg2419255	PPAP2C	ETF [T002	536	546	5.246906	GGGGGC	0.02861	0.03569
cg2419255	PPAP2C	ETF [T002	1414	1424	5.246906	GCCCCC	0.02861	0.03569
cg2715857	PPAP2C	ETF [T002	256	266	5.246906	GCGGGG	0.02861	0.03569
cg2715857	PPAP2C	ETF [T002	457	467	5.246906	GGGGGC	0.02861	0.03569
cg2715857	PPAP2C	ETF [T002	1335	1345	5.246906	GCCCCC	0.02861	0.03569
cg0268666	PPAP2C	ETF [T002	221	231	5.246906	GCGGGG	0.02861	0.03569
cg0268666	PPAP2C	ETF [T002	422	432	5.246906	GGGGGC	0.02861	0.03569
cg0268666	PPAP2C	ETF [T002	1300	1310	5.246906	GCCCCC	0.02861	0.03569
cg2387614	PPAP2C	ETF [T002	195	205	5.246906	GCGGGG	0.02861	0.03569
cg2387614	PPAP2C	ETF [T002	396	406	5.246906	GGGGGC	0.02861	0.03569
cg2387614	PPAP2C	ETF [T002	1274	1284	5.246906	GCCCCC	0.02861	0.03569

cg2419255	PPAP2C	c-Ets-2 [T	1881	1889	5.162974	GTCAAG	0.13733	0.13279
cg2715857	PPAP2C	c-Ets-2 [T	1802	1810	5.162974	GTCAAG	0.13733	0.13279
cg0268666	PPAP2C	c-Ets-2 [T	1767	1775	5.162974	GTCAAG	0.13733	0.13279
cg2387614	PPAP2C	c-Ets-2 [T	1741	1749	5.162974	GTCAAG	0.13733	0.13279
cg2419255	PPAP2C	p53 [T006	642	648	5.133514	TCCGCC	0.48828	0.53921
cg2715857	PPAP2C	p53 [T006	563	569	5.133514	TCCGCC	0.48828	0.53921
cg0268666	PPAP2C	p53 [T006	528	534	5.133514	TCCGCC	0.48828	0.53921
cg2387614	PPAP2C	p53 [T006	502	508	5.133514	TCCGCC	0.48828	0.53921
cg2419255	PPAP2C	AP-2alpha	1572	1577	5.100982	AAAGGC	0.97656	0.97517
cg2419255	PPAP2C	AP-2alpha	1888	1893	5.100982	AAAGGC	0.97656	0.97517
cg2715857	PPAP2C	AP-2alpha	1493	1498	5.100982	AAAGGC	0.97656	0.97517
cg2715857	PPAP2C	AP-2alpha	1809	1814	5.100982	AAAGGC	0.97656	0.97517
cg0268666	PPAP2C	AP-2alpha	1458	1463	5.100982	AAAGGC	0.97656	0.97517
cg0268666	PPAP2C	AP-2alpha	1774	1779	5.100982	AAAGGC	0.97656	0.97517
cg2387614	PPAP2C	AP-2alpha	1432	1437	5.100982	AAAGGC	0.97656	0.97517
cg2387614	PPAP2C	AP-2alpha	1748	1753	5.100982	AAAGGC	0.97656	0.97517
cg2419255	PPAP2C	USF2 [T0	1501	1510	5.052423	CAGACA	0.103	0.10797
cg2715857	PPAP2C	USF2 [T0	1422	1431	5.052423	CAGACA	0.103	0.10797
cg0268666	PPAP2C	USF2 [T0	1387	1396	5.052423	CAGACA	0.103	0.10797
cg2387614	PPAP2C	USF2 [T0	1361	1370	5.052423	CAGACA	0.103	0.10797
cg2419255	PPAP2C	GR-beta [	922	926	5.042296	AATAC	3.90625	3.7093
cg2419255	PPAP2C	GR-beta [	931	935	5.042296	AATCC	3.90625	3.7093
cg2419255	PPAP2C	GR-beta [	1170	1174	5.042296	GGATT	3.90625	3.7093
cg2419255	PPAP2C	GR-beta [	1702	1706	5.042296	GGATT	3.90625	3.7093
cg2715857	PPAP2C	GR-beta [	843	847	5.042296	AATAC	3.90625	3.7093
cg2715857	PPAP2C	GR-beta [	852	856	5.042296	AATCC	3.90625	3.7093
cg2715857	PPAP2C	GR-beta [	1091	1095	5.042296	GGATT	3.90625	3.7093
cg2715857	PPAP2C	GR-beta [	1623	1627	5.042296	GGATT	3.90625	3.7093
cg0268666	PPAP2C	GR-beta [	808	812	5.042296	AATAC	3.90625	3.7093
cg0268666	PPAP2C	GR-beta [	817	821	5.042296	AATCC	3.90625	3.7093
cg0268666	PPAP2C	GR-beta [	1056	1060	5.042296	GGATT	3.90625	3.7093
cg0268666	PPAP2C	GR-beta [	1588	1592	5.042296	GGATT	3.90625	3.7093
cg2387614	PPAP2C	GR-beta [	782	786	5.042296	AATAC	3.90625	3.7093
cg2387614	PPAP2C	GR-beta [	791	795	5.042296	AATCC	3.90625	3.7093
cg2387614	PPAP2C	GR-beta [	1030	1034	5.042296	GGATT	3.90625	3.7093
cg2387614	PPAP2C	GR-beta [	1562	1566	5.042296	GGATT	3.90625	3.7093
cg2387614	PPAP2C	GR-beta [	1973	1977	5.042296	GGATT	3.90625	3.7093
cg2387614	PPAP2C	GR-beta [	1993	1997	5.042296	AATCC	3.90625	3.7093
cg2419255	PPAP2C	PXR-1:RX	1747	1754	5.032032	AGGGTT	0.12207	0.11843
cg2715857	PPAP2C	PXR-1:RX	1668	1675	5.032032	AGGGTT	0.12207	0.11843
cg0268666	PPAP2C	PXR-1:RX	1633	1640	5.032032	AGGGTT	0.12207	0.11843
cg2387614	PPAP2C	PXR-1:RX	1607	1614	5.032032	AGGGTT	0.12207	0.11843
cg2419255	PPAP2C	NFI/CTF [	1204	1211	5.021086	CCAAGG	0.24414	0.25666
cg2715857	PPAP2C	NFI/CTF [	1125	1132	5.021086	CCAAGG	0.24414	0.25666
cg0268666	PPAP2C	NFI/CTF [	1090	1097	5.021086	CCAAGG	0.24414	0.25666
cg0268666	PPAP2C	NFI/CTF [	1987	1994	5.021086	CCCCTT	0.24414	0.25666
cg2387614	PPAP2C	NFI/CTF [	1064	1071	5.021086	CCAAGG	0.24414	0.25666
cg2387614	PPAP2C	NFI/CTF [	1961	1968	5.021086	CCCCTT	0.24414	0.25666

cg2419255	PPAP2C	USF1 [T0	1507	1516	4.993039	CCTGCA	0.04578	0.04763
cg2715857	PPAP2C	USF1 [T0	1428	1437	4.993039	CCTGCA	0.04578	0.04763
cg0268666	PPAP2C	USF1 [T0	1393	1402	4.993039	CCTGCA	0.04578	0.04763
cg2387614	PPAP2C	USF1 [T0	1367	1376	4.993039	CCTGCA	0.04578	0.04763
cg2419255	PPAP2C	RelA [T00	711	721	4.912503	GAGGTT	0.01001	0.01026
cg2715857	PPAP2C	RelA [T00	632	642	4.912503	GAGGTT	0.01001	0.01026
cg0268666	PPAP2C	RelA [T00	597	607	4.912503	GAGGTT	0.01001	0.01026
cg2387614	PPAP2C	RelA [T00	571	581	4.912503	GAGGTT	0.01001	0.01026
cg0268666	PPAP2C	c-Ets-1 [T	1976	1982	4.910652	CTTCCA	0.48828	0.48026
cg2387614	PPAP2C	c-Ets-1 [T	1950	1956	4.910652	CTTCCA	0.48828	0.48026
cg2419255	PPAP2C	AP-1 [T00	1876	1884	4.868583	CTGGAG	0.12207	0.12309
cg2715857	PPAP2C	AP-1 [T00	1797	1805	4.868583	CTGGAG	0.12207	0.12309
cg0268666	PPAP2C	AP-1 [T00	1762	1770	4.868583	CTGGAG	0.12207	0.12309
cg2387614	PPAP2C	AP-1 [T00	1736	1744	4.868583	CTGGAG	0.12207	0.12309
cg2419255	PPAP2C	RXR-alph	677	683	4.86724	GGGTCT	0.48828	0.51407
cg2715857	PPAP2C	RXR-alph	598	604	4.86724	GGGTCT	0.48828	0.51407
cg2715857	PPAP2C	RXR-alph	1940	1946	4.86724	GAGACC	0.48828	0.51407
cg0268666	PPAP2C	RXR-alph	563	569	4.86724	GGGTCT	0.48828	0.51407
cg0268666	PPAP2C	RXR-alph	1905	1911	4.86724	GAGACC	0.48828	0.51407
cg2387614	PPAP2C	RXR-alph	537	543	4.86724	GGGTCT	0.48828	0.51407
cg2387614	PPAP2C	RXR-alph	1879	1885	4.86724	GAGACC	0.48828	0.51407
cg2419255	PPAP2C	GCF [T00	276	284	4.846987	GCGCGG	0.27466	0.31905
cg2419255	PPAP2C	GCF [T00	292	300	4.846987	GCGCGG	0.27466	0.31905
cg2419255	PPAP2C	GCF [T00	559	567	4.846987	GGACCG	0.27466	0.31905
cg2715857	PPAP2C	GCF [T00	197	205	4.846987	GCGCGG	0.27466	0.31905
cg2715857	PPAP2C	GCF [T00	213	221	4.846987	GCGCGG	0.27466	0.31905
cg2715857	PPAP2C	GCF [T00	480	488	4.846987	GGACCG	0.27466	0.31905
cg0268666	PPAP2C	GCF [T00	162	170	4.846987	GCGCGG	0.27466	0.31905
cg0268666	PPAP2C	GCF [T00	178	186	4.846987	GCGCGG	0.27466	0.31905
cg0268666	PPAP2C	GCF [T00	445	453	4.846987	GGACCG	0.27466	0.31905
cg2387614	PPAP2C	GCF [T00	136	144	4.846987	GCGCGG	0.27466	0.31905
cg2387614	PPAP2C	GCF [T00	152	160	4.846987	GCGCGG	0.27466	0.31905
cg2387614	PPAP2C	GCF [T00	419	427	4.846987	GGACCG	0.27466	0.31905
cg2419255	PPAP2C	c-Ets-1 [T	877	883	4.782565	GTGGAA	0.48828	0.48026
cg2715857	PPAP2C	c-Ets-1 [T	798	804	4.782565	GTGGAA	0.48828	0.48026
cg0268666	PPAP2C	c-Ets-1 [T	763	769	4.782565	GTGGAA	0.48828	0.48026
cg2387614	PPAP2C	c-Ets-1 [T	737	743	4.782565	GTGGAA	0.48828	0.48026
cg2419255	PPAP2C	FOXP3 [T	1434	1439	4.756447	CAAAAC	2.92969	2.82
cg2419255	PPAP2C	FOXP3 [T	1639	1644	4.756447	GTTGAG	2.92969	2.82
cg2419255	PPAP2C	TFII-I [T0	1170	1175	4.756447	GGATTG	2.92969	2.89715
cg2419255	PPAP2C	TFII-I [T0	1702	1707	4.756447	GGATTG	2.92969	2.89715
cg2715857	PPAP2C	FOXP3 [T	1355	1360	4.756447	CAAAAC	2.92969	2.82
cg2715857	PPAP2C	FOXP3 [T	1560	1565	4.756447	GTTGAG	2.92969	2.82
cg2715857	PPAP2C	TFII-I [T0	1091	1096	4.756447	GGATTG	2.92969	2.89715
cg2715857	PPAP2C	TFII-I [T0	1623	1628	4.756447	GGATTG	2.92969	2.89715
cg0268666	PPAP2C	FOXP3 [T	1320	1325	4.756447	CAAAAC	2.92969	2.82
cg0268666	PPAP2C	FOXP3 [T	1525	1530	4.756447	GTTGAG	2.92969	2.82
cg0268666	PPAP2C	TFII-I [T0	1056	1061	4.756447	GGATTG	2.92969	2.89715

cg0268666	PPAP2C	TFII-I [T0	1588	1593	4.756447	GGATTG	2.92969	2.89715
cg2387614	PPAP2C	FOXP3 [T	1294	1299	4.756447	CAAAAC	2.92969	2.82
cg2387614	PPAP2C	FOXP3 [T	1499	1504	4.756447	GTTGAG	2.92969	2.82
cg2387614	PPAP2C	TFII-I [T0	1030	1035	4.756447	GGATTG	2.92969	2.89715
cg2387614	PPAP2C	TFII-I [T0	1562	1567	4.756447	GGATTG	2.92969	2.89715
cg2419255	PPAP2C	Ik-1 [T027	1087	1099	4.748597	CCAGGA	0.00313	0.00339
cg2715857	PPAP2C	Ik-1 [T027	1008	1020	4.748597	CCAGGA	0.00313	0.00339
cg0268666	PPAP2C	Ik-1 [T027	973	985	4.748597	CCAGGA	0.00313	0.00339
cg2387614	PPAP2C	Ik-1 [T027	947	959	4.748597	CCAGGA	0.00313	0.00339
cg2419255	PPAP2C	PPAR-alp	1419	1429	4.727619	CTGCCC	0.03242	0.03494
cg2715857	PPAP2C	PPAR-alp	1340	1350	4.727619	CTGCCC	0.03242	0.03494
cg0268666	PPAP2C	PPAR-alp	1305	1315	4.727619	CTGCCC	0.03242	0.03494
cg2387614	PPAP2C	PPAR-alp	1279	1289	4.727619	CTGCCC	0.03242	0.03494
cg2419255	PPAP2C	p53 [T006	54	60	4.645444	GGGCGC	0.24414	0.28373
cg2419255	PPAP2C	p53 [T006	543	549	4.645444	GGGCGC	0.24414	0.28373
cg2715857	PPAP2C	p53 [T006	464	470	4.645444	GGGCGC	0.24414	0.28373
cg0268666	PPAP2C	p53 [T006	429	435	4.645444	GGGCGC	0.24414	0.28373
cg2387614	PPAP2C	p53 [T006	403	409	4.645444	GGGCGC	0.24414	0.28373
cg2419255	PPAP2C	VDR [T00	1750	1758	4.617121	GTTCAG	0.37384	0.36855
cg2715857	PPAP2C	VDR [T00	1671	1679	4.617121	GTTCAG	0.37384	0.36855
cg0268666	PPAP2C	VDR [T00	1636	1644	4.617121	GTTCAG	0.37384	0.36855
cg2387614	PPAP2C	VDR [T00	1610	1618	4.617121	GTTCAG	0.37384	0.36855
cg2419255	PPAP2C	NF-kappa	115	125	4.600708	GGAGGG	0.03242	0.03571
cg2715857	PPAP2C	NF-kappa	36	46	4.600708	GGAGGG	0.03242	0.03571
cg0268666	PPAP2C	NF-kappa	1	11	4.600708	GGAGGG	0.03242	0.03571
cg2419255	PPAP2C	AP-1 [T00	263	271	4.553988	GCGGAG	0.03052	0.03196
cg2715857	PPAP2C	AP-1 [T00	184	192	4.553988	GCGGAG	0.03052	0.03196
cg0268666	PPAP2C	AP-1 [T00	149	157	4.553988	GCGGAG	0.03052	0.03196
cg2387614	PPAP2C	AP-1 [T00	123	131	4.553988	GCGGAG	0.03052	0.03196
cg2419255	PPAP2C	E2F-1 [T0	777	784	4.545253	GCGGGA	0.15259	0.16681
cg2419255	PPAP2C	E2F-1 [T0	791	798	4.545253	GCGGGA	0.15259	0.16681
cg2715857	PPAP2C	E2F-1 [T0	698	705	4.545253	GCGGGA	0.15259	0.16681
cg2715857	PPAP2C	E2F-1 [T0	712	719	4.545253	GCGGGA	0.15259	0.16681
cg0268666	PPAP2C	E2F-1 [T0	663	670	4.545253	GCGGGA	0.15259	0.16681
cg0268666	PPAP2C	E2F-1 [T0	677	684	4.545253	GCGGGA	0.15259	0.16681
cg2387614	PPAP2C	E2F-1 [T0	637	644	4.545253	GCGGGA	0.15259	0.16681
cg2387614	PPAP2C	E2F-1 [T0	651	658	4.545253	GCGGGA	0.15259	0.16681
cg2419255	PPAP2C	MAZ [T00	379	391	4.524062	AGGAGG	0.00188	0.00218
cg2715857	PPAP2C	MAZ [T00	300	312	4.524062	AGGAGG	0.00188	0.00218
cg0268666	PPAP2C	MAZ [T00	265	277	4.524062	AGGAGG	0.00188	0.00218
cg2387614	PPAP2C	MAZ [T00	239	251	4.524062	AGGAGG	0.00188	0.00218
cg2419255	PPAP2C	c-Ets-1 [T	1272	1278	4.487936	TTTCCG	0.85449	0.8381
cg2715857	PPAP2C	c-Ets-1 [T	1193	1199	4.487936	TTTCCG	0.85449	0.8381
cg0268666	PPAP2C	c-Ets-1 [T	1158	1164	4.487936	TTTCCG	0.85449	0.8381
cg2387614	PPAP2C	c-Ets-1 [T	1132	1138	4.487936	TTTCCG	0.85449	0.8381
cg2419255	PPAP2C	USF1 [T0	266	275	4.464121	GAGTCA	0.06866	0.06933
cg2715857	PPAP2C	USF1 [T0	187	196	4.464121	GAGTCA	0.06866	0.06933
cg0268666	PPAP2C	USF1 [T0	152	161	4.464121	GAGTCA	0.06866	0.06933

cg2387614	PPAP2C	USF1 [T0	126	135	4.464121	GAGTCA	0.06866	0.06933
cg2419255	PPAP2C	AP-2alpha	1721	1726	4.438035	GCCTAG	0.97656	0.99839
cg2715857	PPAP2C	AP-2alpha	1642	1647	4.438035	GCCTAG	0.97656	0.99839
cg0268666	PPAP2C	AP-2alpha	1607	1612	4.438035	GCCTAG	0.97656	0.99839
cg2387614	PPAP2C	AP-2alpha	1581	1586	4.438035	GCCTAG	0.97656	0.99839
cg2715857	PPAP2C	RXR-alpha	1954	1960	4.423008	GGGTGG	0.24414	0.25781
cg2715857	PPAP2C	RXR-alpha	1981	1987	4.423008	GGGTGG	0.24414	0.25781
cg0268666	PPAP2C	RXR-alpha	1919	1925	4.423008	GGGTGG	0.24414	0.25781
cg0268666	PPAP2C	RXR-alpha	1946	1952	4.423008	GGGTGG	0.24414	0.25781
cg2387614	PPAP2C	RXR-alpha	1893	1899	4.423008	GGGTGG	0.24414	0.25781
cg2387614	PPAP2C	RXR-alpha	1920	1926	4.423008	GGGTGG	0.24414	0.25781
cg2419255	PPAP2C	STAT4 [T	70	75	4.411765	CGTTCC	1.95312	1.99838
cg2419255	PPAP2C	STAT4 [T	474	479	4.411765	GGAAGA	1.95312	1.99838
cg2419255	PPAP2C	STAT4 [T	1036	1041	4.411765	CGTTCC	1.95312	1.99838
cg2419255	PPAP2C	STAT4 [T	1487	1492	4.411765	GCTTCC	1.95312	1.99838
cg2419255	PPAP2C	STAT4 [T	1598	1603	4.411765	GGAAGA	1.95312	1.99838
cg2419255	PPAP2C	STAT4 [T	1976	1981	4.411765	GGAAGA	1.95312	1.99838
cg2715857	PPAP2C	STAT4 [T	395	400	4.411765	GGAAGA	1.95312	1.99838
cg2715857	PPAP2C	STAT4 [T	957	962	4.411765	CGTTCC	1.95312	1.99838
cg2715857	PPAP2C	STAT4 [T	1408	1413	4.411765	GCTTCC	1.95312	1.99838
cg2715857	PPAP2C	STAT4 [T	1519	1524	4.411765	GGAAGA	1.95312	1.99838
cg2715857	PPAP2C	STAT4 [T	1897	1902	4.411765	GGAAGA	1.95312	1.99838
cg0268666	PPAP2C	STAT4 [T	360	365	4.411765	GGAAGA	1.95312	1.99838
cg0268666	PPAP2C	STAT4 [T	922	927	4.411765	CGTTCC	1.95312	1.99838
cg0268666	PPAP2C	STAT4 [T	1373	1378	4.411765	GCTTCC	1.95312	1.99838
cg0268666	PPAP2C	STAT4 [T	1484	1489	4.411765	GGAAGA	1.95312	1.99838
cg0268666	PPAP2C	STAT4 [T	1862	1867	4.411765	GGAAGA	1.95312	1.99838
cg2387614	PPAP2C	STAT4 [T	334	339	4.411765	GGAAGA	1.95312	1.99838
cg2387614	PPAP2C	STAT4 [T	896	901	4.411765	CGTTCC	1.95312	1.99838
cg2387614	PPAP2C	STAT4 [T	1347	1352	4.411765	GCTTCC	1.95312	1.99838
cg2387614	PPAP2C	STAT4 [T	1458	1463	4.411765	GGAAGA	1.95312	1.99838
cg2387614	PPAP2C	STAT4 [T	1836	1841	4.411765	GGAAGA	1.95312	1.99838
cg2419255	PPAP2C	RXR-alpha	118	124	4.24113	GGGTCC	0.97656	1.02803
cg2419255	PPAP2C	RXR-alpha	135	141	4.24113	GGGTCC	0.97656	1.02803
cg2419255	PPAP2C	RXR-alpha	1208	1214	4.24113	GGGACC	0.97656	1.02803
cg2715857	PPAP2C	RXR-alpha	39	45	4.24113	GGGTCC	0.97656	1.02803
cg2715857	PPAP2C	RXR-alpha	56	62	4.24113	GGGTCC	0.97656	1.02803
cg2715857	PPAP2C	RXR-alpha	1129	1135	4.24113	GGGACC	0.97656	1.02803
cg0268666	PPAP2C	RXR-alpha	4	10	4.24113	GGGTCC	0.97656	1.02803
cg0268666	PPAP2C	RXR-alpha	21	27	4.24113	GGGTCC	0.97656	1.02803
cg0268666	PPAP2C	RXR-alpha	1094	1100	4.24113	GGGACC	0.97656	1.02803
cg2387614	PPAP2C	RXR-alpha	1068	1074	4.24113	GGGACC	0.97656	1.02803
cg0268666	PPAP2C	NF-1 [T00	1991	1998	4.135372	TTGGGT	0.24414	0.25714
cg2387614	PPAP2C	NF-1 [T00	1965	1972	4.135372	TTGGGT	0.24414	0.25714
cg2419255	PPAP2C	p53 [T006	252	258	4.125254	CCGGCC	0.73242	0.82434
cg2419255	PPAP2C	p53 [T006	655	661	4.125254	CCGGCC	0.73242	0.82434
cg2419255	PPAP2C	p53 [T006	728	734	4.125254	GGGCCG	0.73242	0.82434
cg2419255	PPAP2C	p53 [T006	783	789	4.125254	CCGGCC	0.73242	0.82434

cg2419255	PPAP2C	p53 [T006	1199	1205	4.125254	CAGGCC	0.73242	0.82434
cg2419255	PPAP2C	p53 [T006	1952	1958	4.125254	GGGCCT	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	173	179	4.125254	CCGGCC	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	576	582	4.125254	CCGGCC	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	649	655	4.125254	GGGCCG	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	704	710	4.125254	CCGGCC	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	1120	1126	4.125254	CAGGCC	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	1873	1879	4.125254	GGGCCT	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	138	144	4.125254	CCGGCC	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	541	547	4.125254	CCGGCC	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	614	620	4.125254	GGGCCG	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	669	675	4.125254	CCGGCC	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	1085	1091	4.125254	CAGGCC	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	1838	1844	4.125254	GGGCCT	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	112	118	4.125254	CCGGCC	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	515	521	4.125254	CCGGCC	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	588	594	4.125254	GGGCCG	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	643	649	4.125254	CCGGCC	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	1059	1065	4.125254	CAGGCC	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	1812	1818	4.125254	GGGCCT	0.73242	0.82434
cg2419255	PPAP2C	Sp1 [T007	640	649	4.120098	CGTCCG	0.08965	0.10391
cg2715857	PPAP2C	Sp1 [T007	561	570	4.120098	CGTCCG	0.08965	0.10391
cg0268666	PPAP2C	Sp1 [T007	526	535	4.120098	CGTCCG	0.08965	0.10391
cg2387614	PPAP2C	Sp1 [T007	500	509	4.120098	CGTCCG	0.08965	0.10391
cg2419255	PPAP2C	p53 [T006	1177	1183	4.083527	GGGCAC	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	1098	1104	4.083527	GGGCAC	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	1063	1069	4.083527	GGGCAC	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	1037	1043	4.083527	GGGCAC	0.73242	0.82434
cg2419255	PPAP2C	RXR-alph	186	192	4.019014	AAGACC	0.97656	1.02803
cg2419255	PPAP2C	RXR-alph	1193	1199	4.019014	GAAACC	0.97656	1.02803
cg2715857	PPAP2C	RXR-alph	107	113	4.019014	AAGACC	0.97656	1.02803
cg2715857	PPAP2C	RXR-alph	1114	1120	4.019014	GAAACC	0.97656	1.02803
cg0268666	PPAP2C	RXR-alph	72	78	4.019014	AAGACC	0.97656	1.02803
cg0268666	PPAP2C	RXR-alph	1079	1085	4.019014	GAAACC	0.97656	1.02803
cg2387614	PPAP2C	RXR-alph	46	52	4.019014	AAGACC	0.97656	1.02803
cg2387614	PPAP2C	RXR-alph	1053	1059	4.019014	GAAACC	0.97656	1.02803
cg2419255	PPAP2C	STAT1bet	1882	1891	4.01053	TCAAGG	0.03433	0.03308
cg2715857	PPAP2C	STAT1bet	1803	1812	4.01053	TCAAGG	0.03433	0.03308
cg0268666	PPAP2C	STAT1bet	1768	1777	4.01053	TCAAGG	0.03433	0.03308
cg2387614	PPAP2C	STAT1bet	1742	1751	4.01053	TCAAGG	0.03433	0.03308
cg2419255	PPAP2C	Pax-5 [T0	668	674	4.007279	GGGCTG	1.09863	1.18533
cg2419255	PPAP2C	Pax-5 [T0	1554	1560	4.007279	GGGCTC	1.09863	1.18533
cg2419255	PPAP2C	Pax-5 [T0	1678	1684	4.007279	GGGCTC	1.09863	1.18533
cg2419255	PPAP2C	Pax-5 [T0	1988	1994	4.007279	GGGCTG	1.09863	1.18533
cg2715857	PPAP2C	Pax-5 [T0	589	595	4.007279	GGGCTG	1.09863	1.18533
cg2715857	PPAP2C	Pax-5 [T0	1475	1481	4.007279	GGGCTC	1.09863	1.18533
cg2715857	PPAP2C	Pax-5 [T0	1599	1605	4.007279	GGGCTC	1.09863	1.18533
cg2715857	PPAP2C	Pax-5 [T0	1909	1915	4.007279	GGGCTG	1.09863	1.18533

cg0268666	PPAP2C	Pax-5 [T0	554	560	4.007279	GGGCTG	1.09863	1.18533
cg0268666	PPAP2C	Pax-5 [T0	1440	1446	4.007279	GGGCTC	1.09863	1.18533
cg0268666	PPAP2C	Pax-5 [T0	1564	1570	4.007279	GGGCTC	1.09863	1.18533
cg0268666	PPAP2C	Pax-5 [T0	1874	1880	4.007279	GGGCTG	1.09863	1.18533
cg2387614	PPAP2C	Pax-5 [T0	528	534	4.007279	GGGCTG	1.09863	1.18533
cg2387614	PPAP2C	Pax-5 [T0	1414	1420	4.007279	GGGCTC	1.09863	1.18533
cg2387614	PPAP2C	Pax-5 [T0	1538	1544	4.007279	GGGCTC	1.09863	1.18533
cg2387614	PPAP2C	Pax-5 [T0	1848	1854	4.007279	GGGCTG	1.09863	1.18533
cg2419255	PPAP2C	USF2 [T0	1176	1185	4.003951	AGGGCA	0.01144	0.01199
cg2715857	PPAP2C	USF2 [T0	1097	1106	4.003951	AGGGCA	0.01144	0.01199
cg0268666	PPAP2C	USF2 [T0	1062	1071	4.003951	AGGGCA	0.01144	0.01199
cg2387614	PPAP2C	USF2 [T0	1036	1045	4.003951	AGGGCA	0.01144	0.01199
cg2419255	PPAP2C	AP-2alpha	142	147	3.970052	CAAGGC	0.97656	1.02535
cg2419255	PPAP2C	AP-2alpha	1285	1290	3.970052	GCCTTG	0.97656	1.02535
cg2419255	PPAP2C	AP-2alpha	1345	1350	3.970052	CAAGGC	0.97656	1.02535
cg2715857	PPAP2C	AP-2alpha	63	68	3.970052	CAAGGC	0.97656	1.02535
cg2715857	PPAP2C	AP-2alpha	1206	1211	3.970052	GCCTTG	0.97656	1.02535
cg2715857	PPAP2C	AP-2alpha	1266	1271	3.970052	CAAGGC	0.97656	1.02535
cg0268666	PPAP2C	AP-2alpha	28	33	3.970052	CAAGGC	0.97656	1.02535
cg0268666	PPAP2C	AP-2alpha	1171	1176	3.970052	GCCTTG	0.97656	1.02535
cg0268666	PPAP2C	AP-2alpha	1231	1236	3.970052	CAAGGC	0.97656	1.02535
cg2387614	PPAP2C	AP-2alpha	2	7	3.970052	CAAGGC	0.97656	1.02535
cg2387614	PPAP2C	AP-2alpha	1145	1150	3.970052	GCCTTG	0.97656	1.02535
cg2387614	PPAP2C	AP-2alpha	1205	1210	3.970052	CAAGGC	0.97656	1.02535
cg2419255	PPAP2C	p53 [T006	434	440	3.961937	GGGCTA	0.73242	0.82434
cg2715857	PPAP2C	p53 [T006	355	361	3.961937	GGGCTA	0.73242	0.82434
cg0268666	PPAP2C	p53 [T006	320	326	3.961937	GGGCTA	0.73242	0.82434
cg2387614	PPAP2C	p53 [T006	294	300	3.961937	GGGCTA	0.73242	0.82434
cg2419255	PPAP2C	c-Myb [T0	1465	1472	3.85204	CAACTG	0.09155	0.09116
cg2715857	PPAP2C	c-Myb [T0	1386	1393	3.85204	CAACTG	0.09155	0.09116
cg0268666	PPAP2C	c-Myb [T0	1351	1358	3.85204	CAACTG	0.09155	0.09116
cg2387614	PPAP2C	c-Myb [T0	1325	1332	3.85204	CAACTG	0.09155	0.09116
cg2419255	PPAP2C	c-Ets-1 [T	1037	1043	3.846637	GTTCCT	0.24414	0.23719
cg2715857	PPAP2C	c-Ets-1 [T	958	964	3.846637	GTTCCT	0.24414	0.23719
cg0268666	PPAP2C	c-Ets-1 [T	923	929	3.846637	GTTCCT	0.24414	0.23719
cg2387614	PPAP2C	c-Ets-1 [T	897	903	3.846637	GTTCCT	0.24414	0.23719
cg2419255	PPAP2C	NFI/CTF [	1543	1550	3.793671	CCAAGG	0.18311	0.19063
cg2419255	PPAP2C	NFI/CTF [	1628	1635	3.793671	CCAAGG	0.18311	0.19063
cg2715857	PPAP2C	NFI/CTF [	1464	1471	3.793671	CCAAGG	0.18311	0.19063
cg2715857	PPAP2C	NFI/CTF [	1549	1556	3.793671	CCAAGG	0.18311	0.19063
cg0268666	PPAP2C	NFI/CTF [	1429	1436	3.793671	CCAAGG	0.18311	0.19063
cg0268666	PPAP2C	NFI/CTF [	1514	1521	3.793671	CCAAGG	0.18311	0.19063
cg2387614	PPAP2C	NFI/CTF [	1403	1410	3.793671	CCAAGG	0.18311	0.19063
cg2387614	PPAP2C	NFI/CTF [	1488	1495	3.793671	CCAAGG	0.18311	0.19063
cg2419255	PPAP2C	GR [T050	1434	1440	3.763516	CAAAAC	0.73242	0.6946
cg2715857	PPAP2C	GR [T050	1355	1361	3.763516	CAAAAC	0.73242	0.6946
cg0268666	PPAP2C	GR [T050	1320	1326	3.763516	CAAAAC	0.73242	0.6946
cg2387614	PPAP2C	GR [T050	1294	1300	3.763516	CAAAAC	0.73242	0.6946

cg2419255	PPAP2C	IRF-1 [T0	1188	1196	3.689552	CCAGGG	0.06866	0.0661
cg2715857	PPAP2C	IRF-1 [T0	1109	1117	3.689552	CCAGGG	0.06866	0.0661
cg0268666	PPAP2C	IRF-1 [T0	1074	1082	3.689552	CCAGGG	0.06866	0.0661
cg2387614	PPAP2C	IRF-1 [T0	1048	1056	3.689552	CCAGGG	0.06866	0.0661
cg2419255	PPAP2C	c-Ets-1 [T	974	980	3.590463	GTTCCT	0.61035	0.61936
cg2715857	PPAP2C	c-Ets-1 [T	895	901	3.590463	GTTCCT	0.61035	0.61936
cg0268666	PPAP2C	c-Ets-1 [T	860	866	3.590463	GTTCCT	0.61035	0.61936
cg2387614	PPAP2C	c-Ets-1 [T	834	840	3.590463	GTTCCT	0.61035	0.61936
cg2419255	PPAP2C	p53 [T006	611	617	3.586914	GGGCGA	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006	532	538	3.586914	GGGCGA	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006	497	503	3.586914	GGGCGA	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006	471	477	3.586914	GGGCGA	0.73242	0.80362
cg2419255	PPAP2C	RXR-alph	723	729	3.574782	GGGTCG	1.09863	1.1653
cg2715857	PPAP2C	RXR-alph	644	650	3.574782	GGGTCG	1.09863	1.1653
cg0268666	PPAP2C	RXR-alph	609	615	3.574782	GGGTCG	1.09863	1.1653
cg2387614	PPAP2C	RXR-alph	583	589	3.574782	GGGTCG	1.09863	1.1653
cg2419255	PPAP2C	E2F-1 [T0	312	319	3.55167	GCGGGA	0.15259	0.16507
cg2715857	PPAP2C	E2F-1 [T0	233	240	3.55167	GCGGGA	0.15259	0.16507
cg0268666	PPAP2C	E2F-1 [T0	198	205	3.55167	GCGGGA	0.15259	0.16507
cg2387614	PPAP2C	E2F-1 [T0	172	179	3.55167	GCGGGA	0.15259	0.16507
cg2419255	PPAP2C	NF-AT1 [	846	855	3.445347	TGGAAA	0.07629	0.07204
cg2715857	PPAP2C	NF-AT1 [	767	776	3.445347	TGGAAA	0.07629	0.07204
cg0268666	PPAP2C	NF-AT1 [	732	741	3.445347	TGGAAA	0.07629	0.07204
cg2387614	PPAP2C	NF-AT1 [	706	715	3.445347	TGGAAA	0.07629	0.07204
cg2419255	PPAP2C	RXR-alph	36	42	3.392904	GGGTCC	1.09863	1.1653
cg2419255	PPAP2C	RXR-alph	1097	1103	3.392904	GGAACC	1.09863	1.1653
cg2419255	PPAP2C	RXR-alph	1220	1226	3.392904	GGGTCC	1.09863	1.1653
cg2419255	PPAP2C	RXR-alph	1441	1447	3.392904	GGGTGC	1.09863	1.1653
cg2715857	PPAP2C	RXR-alph	1018	1024	3.392904	GGAACC	1.09863	1.1653
cg2715857	PPAP2C	RXR-alph	1141	1147	3.392904	GGGTCC	1.09863	1.1653
cg2715857	PPAP2C	RXR-alph	1362	1368	3.392904	GGGTGC	1.09863	1.1653
cg0268666	PPAP2C	RXR-alph	983	989	3.392904	GGAACC	1.09863	1.1653
cg0268666	PPAP2C	RXR-alph	1106	1112	3.392904	GGGTCC	1.09863	1.1653
cg0268666	PPAP2C	RXR-alph	1327	1333	3.392904	GGGTGC	1.09863	1.1653
cg2387614	PPAP2C	RXR-alph	957	963	3.392904	GGAACC	1.09863	1.1653
cg2387614	PPAP2C	RXR-alph	1080	1086	3.392904	GGGTCC	1.09863	1.1653
cg2387614	PPAP2C	RXR-alph	1301	1307	3.392904	GGGTGC	1.09863	1.1653
cg2419255	PPAP2C	p53 [T006	99	105	3.375208	GGGCGT	0.73242	0.80362
cg2419255	PPAP2C	p53 [T006	284	290	3.375208	CCCGCC	0.73242	0.80362
cg2419255	PPAP2C	p53 [T006	310	316	3.375208	GGGCGG	0.73242	0.80362
cg2419255	PPAP2C	p53 [T006	333	339	3.375208	GGGCGG	0.73242	0.80362
cg2419255	PPAP2C	p53 [T006	394	400	3.375208	GGGCGG	0.73242	0.80362
cg2419255	PPAP2C	p53 [T006	441	447	3.375208	GGGCGG	0.73242	0.80362
cg2419255	PPAP2C	p53 [T006	538	544	3.375208	GGGCGG	0.73242	0.80362
cg2419255	PPAP2C	p53 [T006	744	750	3.375208	GGGCGG	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006	20	26	3.375208	GGGCGT	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006	205	211	3.375208	CCCGCC	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006	231	237	3.375208	GGGCGG	0.73242	0.80362

cg2715857	PPAP2C	p53 [T006'	254	260	3.375208	GGGCGG	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006'	315	321	3.375208	GGGCGG	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006'	362	368	3.375208	GGGCGG	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006'	459	465	3.375208	GGGCGG	0.73242	0.80362
cg2715857	PPAP2C	p53 [T006'	665	671	3.375208	GGGCGG	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006'	170	176	3.375208	CCCGCC(	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006'	196	202	3.375208	GGGCGG	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006'	219	225	3.375208	GGGCGG	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006'	280	286	3.375208	GGGCGG	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006'	327	333	3.375208	GGGCGG	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006'	424	430	3.375208	GGGCGG	0.73242	0.80362
cg0268666	PPAP2C	p53 [T006'	630	636	3.375208	GGGCGG	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006'	144	150	3.375208	CCCGCC(	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006'	170	176	3.375208	GGGCGG	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006'	193	199	3.375208	GGGCGG	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006'	254	260	3.375208	GGGCGG	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006'	301	307	3.375208	GGGCGG	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006'	398	404	3.375208	GGGCGG	0.73242	0.80362
cg2387614	PPAP2C	p53 [T006'	604	610	3.375208	GGGCGG	0.73242	0.80362
cg2419255	PPAP2C	T3R-beta1	353	361	3.370634	GAGAGG	0.27466	0.27326
cg2715857	PPAP2C	T3R-beta1	274	282	3.370634	GAGAGG	0.27466	0.27326
cg0268666	PPAP2C	T3R-beta1	239	247	3.370634	GAGAGG	0.27466	0.27326
cg2387614	PPAP2C	T3R-beta1	213	221	3.370634	GAGAGG	0.27466	0.27326
cg2419255	PPAP2C	NF-kappaI	709	720	3.321549	TGGAGG'	0.00513	0.00539
cg2715857	PPAP2C	NF-kappaI	630	641	3.321549	TGGAGG'	0.00513	0.00539
cg0268666	PPAP2C	NF-kappaI	595	606	3.321549	TGGAGG'	0.00513	0.00539
cg2387614	PPAP2C	NF-kappaI	569	580	3.321549	TGGAGG'	0.00513	0.00539
cg2419255	PPAP2C	c-Ets-2 [T(	975	983	3.2883	TTCCTCC	0.18311	0.18314
cg2715857	PPAP2C	c-Ets-2 [T(	896	904	3.2883	TTCCTCC	0.18311	0.18314
cg0268666	PPAP2C	c-Ets-2 [T(	861	869	3.2883	TTCCTCC	0.18311	0.18314
cg2387614	PPAP2C	c-Ets-2 [T(	835	843	3.2883	TTCCTCC	0.18311	0.18314
cg2419255	PPAP2C	AP-2alpha	703	708	3.229049	AGAGGC	0.48828	0.5124
cg2715857	PPAP2C	AP-2alpha	624	629	3.229049	AGAGGC	0.48828	0.5124
cg0268666	PPAP2C	AP-2alpha	589	594	3.229049	AGAGGC	0.48828	0.5124
cg2387614	PPAP2C	AP-2alpha	563	568	3.229049	AGAGGC	0.48828	0.5124
cg2419255	PPAP2C	RXR-alpha	1390	1396	3.170788	AAAACC'	0.24414	0.24551
cg2715857	PPAP2C	RXR-alpha	1311	1317	3.170788	AAAACC'	0.24414	0.24551
cg0268666	PPAP2C	RXR-alpha	1276	1282	3.170788	AAAACC'	0.24414	0.24551
cg2387614	PPAP2C	RXR-alpha	1250	1256	3.170788	AAAACC'	0.24414	0.24551
cg2419255	PPAP2C	MAZ [T00	334	346	3.162267	GGCGGG	0.00474	0.00544
cg2419255	PPAP2C	MAZ [T00	395	407	3.162267	GGCGGG	0.00474	0.00544
cg2419255	PPAP2C	MAZ [T00	442	454	3.162267	GGCGGG	0.00474	0.00544
cg2715857	PPAP2C	MAZ [T00	255	267	3.162267	GGCGGG	0.00474	0.00544
cg2715857	PPAP2C	MAZ [T00	316	328	3.162267	GGCGGG	0.00474	0.00544
cg2715857	PPAP2C	MAZ [T00	363	375	3.162267	GGCGGG	0.00474	0.00544
cg0268666	PPAP2C	MAZ [T00	220	232	3.162267	GGCGGG	0.00474	0.00544
cg0268666	PPAP2C	MAZ [T00	281	293	3.162267	GGCGGG	0.00474	0.00544
cg0268666	PPAP2C	MAZ [T00	328	340	3.162267	GGCGGG	0.00474	0.00544

cg2387614	PPAP2C	MAZ [T00	194	206	3.162267	GGCGGG	0.00474	0.00544
cg2387614	PPAP2C	MAZ [T00	255	267	3.162267	GGCGGG	0.00474	0.00544
cg2387614	PPAP2C	MAZ [T00	302	314	3.162267	GGCGGG	0.00474	0.00544
cg2419255	PPAP2C	Pax-5 [T0	611	617	3.075094	GGGCGA	0.12207	0.13819
cg2715857	PPAP2C	Pax-5 [T0	532	538	3.075094	GGGCGA	0.12207	0.13819
cg0268666	PPAP2C	Pax-5 [T0	497	503	3.075094	GGGCGA	0.12207	0.13819
cg2387614	PPAP2C	Pax-5 [T0	471	477	3.075094	GGGCGA	0.12207	0.13819
cg0268666	PPAP2C	c-Jun [T00	1992	1998	3.049104	TGGGTC	0.24414	0.2435
cg2387614	PPAP2C	c-Jun [T00	1966	1972	3.049104	TGGGTC	0.24414	0.2435
cg2419255	PPAP2C	p53 [T006	1023	1029	3.028543	TGTGCC	0.48828	0.53227
cg2419255	PPAP2C	p53 [T006	1124	1130	3.028543	TGTGCC	0.48828	0.53227
cg2715857	PPAP2C	p53 [T006	944	950	3.028543	TGTGCC	0.48828	0.53227
cg2715857	PPAP2C	p53 [T006	1045	1051	3.028543	TGTGCC	0.48828	0.53227
cg0268666	PPAP2C	p53 [T006	909	915	3.028543	TGTGCC	0.48828	0.53227
cg0268666	PPAP2C	p53 [T006	1010	1016	3.028543	TGTGCC	0.48828	0.53227
cg2387614	PPAP2C	p53 [T006	883	889	3.028543	TGTGCC	0.48828	0.53227
cg2387614	PPAP2C	p53 [T006	984	990	3.028543	TGTGCC	0.48828	0.53227
cg2419255	PPAP2C	STAT4 [T	713	718	2.941176	GGTTCC	2.92969	2.92382
cg2419255	PPAP2C	STAT4 [T	798	803	2.941176	GGTTCC	2.92969	2.92382
cg2419255	PPAP2C	STAT4 [T	807	812	2.941176	CTTTCC	2.92969	2.92382
cg2419255	PPAP2C	STAT4 [T	1097	1102	2.941176	GGAACC	2.92969	2.92382
cg2419255	PPAP2C	STAT4 [T	1319	1324	2.941176	GGAAGT	2.92969	2.92382
cg2419255	PPAP2C	STAT4 [T	1769	1774	2.941176	CTTTCC	2.92969	2.92382
cg2419255	PPAP2C	STAT4 [T	1886	1891	2.941176	GGAAAG	2.92969	2.92382
cg2715857	PPAP2C	STAT4 [T	634	639	2.941176	GGTTCC	2.92969	2.92382
cg2715857	PPAP2C	STAT4 [T	719	724	2.941176	GGTTCC	2.92969	2.92382
cg2715857	PPAP2C	STAT4 [T	728	733	2.941176	CTTTCC	2.92969	2.92382
cg2715857	PPAP2C	STAT4 [T	1018	1023	2.941176	GGAACC	2.92969	2.92382
cg2715857	PPAP2C	STAT4 [T	1240	1245	2.941176	GGAAGT	2.92969	2.92382
cg2715857	PPAP2C	STAT4 [T	1690	1695	2.941176	CTTTCC	2.92969	2.92382
cg2715857	PPAP2C	STAT4 [T	1807	1812	2.941176	GGAAAG	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	599	604	2.941176	GGTTCC	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	684	689	2.941176	GGTTCC	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	693	698	2.941176	CTTTCC	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	983	988	2.941176	GGAACC	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	1205	1210	2.941176	GGAAGT	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	1655	1660	2.941176	CTTTCC	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	1772	1777	2.941176	GGAAAG	2.92969	2.92382
cg0268666	PPAP2C	STAT4 [T	1968	1973	2.941176	TGTTCC	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	573	578	2.941176	GGTTCC	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	658	663	2.941176	GGTTCC	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	667	672	2.941176	CTTTCC	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	957	962	2.941176	GGAACC	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	1179	1184	2.941176	GGAAGT	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	1629	1634	2.941176	CTTTCC	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	1746	1751	2.941176	GGAAAG	2.92969	2.92382
cg2387614	PPAP2C	STAT4 [T	1942	1947	2.941176	TGTTCC	2.92969	2.92382
cg2419255	PPAP2C	USF1 [T0	270	279	2.862167	CACGTG	0.06294	0.06647

cg2715857	PPAP2C	USF1 [T0	191	200	2.862167	CACGTG	0.06294	0.06647
cg0268666	PPAP2C	USF1 [T0	156	165	2.862167	CACGTG	0.06294	0.06647
cg2387614	PPAP2C	USF1 [T0	130	139	2.862167	CACGTG	0.06294	0.06647
cg2419255	PPAP2C	p53 [T006	1525	1531	2.813291	GGGCAT	0.48828	0.53227
cg2715857	PPAP2C	p53 [T006	1446	1452	2.813291	GGGCAT	0.48828	0.53227
cg0268666	PPAP2C	p53 [T006	1411	1417	2.813291	GGGCAT	0.48828	0.53227
cg2387614	PPAP2C	p53 [T006	1385	1391	2.813291	GGGCAT	0.48828	0.53227
cg2419255	PPAP2C	NF-1 [T00	1200	1207	2.813149	AGGCCC	0.24414	0.2566
cg2715857	PPAP2C	NF-1 [T00	1121	1128	2.813149	AGGCCC	0.24414	0.2566
cg2715857	PPAP2C	NF-1 [T00	1921	1928	2.813149	GGGGCC	0.24414	0.2566
cg0268666	PPAP2C	NF-1 [T00	1086	1093	2.813149	AGGCCC	0.24414	0.2566
cg0268666	PPAP2C	NF-1 [T00	1886	1893	2.813149	GGGGCC	0.24414	0.2566
cg2387614	PPAP2C	NF-1 [T00	1060	1067	2.813149	AGGCCC	0.24414	0.2566
cg2387614	PPAP2C	NF-1 [T00	1860	1867	2.813149	GGGGCC	0.24414	0.2566
cg2419255	PPAP2C	HIF-1 [T0	954	962	2.735708	CTGGCA	0.04578	0.04719
cg2715857	PPAP2C	HIF-1 [T0	875	883	2.735708	CTGGCA	0.04578	0.04719
cg0268666	PPAP2C	HIF-1 [T0	840	848	2.735708	CTGGCA	0.04578	0.04719
cg2387614	PPAP2C	HIF-1 [T0	814	822	2.735708	CTGGCA	0.04578	0.04719
cg2419255	PPAP2C	RXR-alph	1479	1485	2.726556	TCGACC	0.85449	0.89683
cg2715857	PPAP2C	RXR-alph	1400	1406	2.726556	TCGACC	0.85449	0.89683
cg0268666	PPAP2C	RXR-alph	1365	1371	2.726556	TCGACC	0.85449	0.89683
cg2387614	PPAP2C	RXR-alph	1339	1345	2.726556	TCGACC	0.85449	0.89683
cg2419255	PPAP2C	MAZ [T00	301	313	2.655656	GGAGGG	0.00405	0.00469
cg2419255	PPAP2C	MAZ [T00	324	336	2.655656	GGAGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	222	234	2.655656	GGAGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	245	257	2.655656	GGAGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	187	199	2.655656	GGAGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	210	222	2.655656	GGAGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	161	173	2.655656	GGAGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	184	196	2.655656	GGAGGG	0.00405	0.00469
cg2419255	PPAP2C	c-Jun [T00	265	271	2.654872	GGAGTC	0.48828	0.48077
cg2419255	PPAP2C	c-Jun [T00	1878	1884	2.654872	GGAGTC	0.48828	0.48077
cg2715857	PPAP2C	c-Jun [T00	186	192	2.654872	GGAGTC	0.48828	0.48077
cg2715857	PPAP2C	c-Jun [T00	1799	1805	2.654872	GGAGTC	0.48828	0.48077
cg0268666	PPAP2C	c-Jun [T00	151	157	2.654872	GGAGTC	0.48828	0.48077
cg0268666	PPAP2C	c-Jun [T00	1764	1770	2.654872	GGAGTC	0.48828	0.48077
cg2387614	PPAP2C	c-Jun [T00	125	131	2.654872	GGAGTC	0.48828	0.48077
cg2387614	PPAP2C	c-Jun [T00	1738	1744	2.654872	GGAGTC	0.48828	0.48077
cg2419255	PPAP2C	ETF [T002	531	541	2.623453	GCGGGG	0.00715	0.0091
cg2715857	PPAP2C	ETF [T002	452	462	2.623453	GCGGGG	0.00715	0.0091
cg0268666	PPAP2C	ETF [T002	417	427	2.623453	GCGGGG	0.00715	0.0091
cg2387614	PPAP2C	ETF [T002	391	401	2.623453	GCGGGG	0.00715	0.0091
cg2419255	PPAP2C	AP-2alpha	1249	1254	2.550491	GCCTCA	0.48828	0.51216
cg2715857	PPAP2C	AP-2alpha	1170	1175	2.550491	GCCTCA	0.48828	0.51216
cg2715857	PPAP2C	AP-2alpha	1990	1995	2.550491	TGAGGC	0.48828	0.51216
cg0268666	PPAP2C	AP-2alpha	1135	1140	2.550491	GCCTCA	0.48828	0.51216
cg0268666	PPAP2C	AP-2alpha	1955	1960	2.550491	TGAGGC	0.48828	0.51216
cg2387614	PPAP2C	AP-2alpha	1109	1114	2.550491	GCCTCA	0.48828	0.51216

cg2387614	PPAP2C	AP-2alpha	1929	1934	2.550491	TGAGGC	0.48828	0.51216
cg2419255	PPAP2C	RXR-alph	1711	1717	2.544678	GGGTTC	0.85449	0.89683
cg2419255	PPAP2C	RXR-alph	1782	1788	2.544678	TTCACC	0.85449	0.89683
cg2419255	PPAP2C	RXR-alph	1862	1868	2.544678	GGGTGC	0.85449	0.89683
cg2715857	PPAP2C	RXR-alph	1632	1638	2.544678	GGGTTC	0.85449	0.89683
cg2715857	PPAP2C	RXR-alph	1703	1709	2.544678	TTCACC	0.85449	0.89683
cg2715857	PPAP2C	RXR-alph	1783	1789	2.544678	GGGTGC	0.85449	0.89683
cg0268666	PPAP2C	RXR-alph	1597	1603	2.544678	GGGTTC	0.85449	0.89683
cg0268666	PPAP2C	RXR-alph	1668	1674	2.544678	TTCACC	0.85449	0.89683
cg0268666	PPAP2C	RXR-alph	1748	1754	2.544678	GGGTGC	0.85449	0.89683
cg2387614	PPAP2C	RXR-alph	1571	1577	2.544678	GGGTTC	0.85449	0.89683
cg2387614	PPAP2C	RXR-alph	1642	1648	2.544678	TTCACC	0.85449	0.89683
cg2387614	PPAP2C	RXR-alph	1722	1728	2.544678	GGGTGC	0.85449	0.89683
cg2419255	PPAP2C	C/EBPalp	1903	1909	2.441016	CATTGA	0.48828	0.47439
cg2715857	PPAP2C	C/EBPalp	1824	1830	2.441016	CATTGA	0.48828	0.47439
cg0268666	PPAP2C	C/EBPalp	1789	1795	2.441016	CATTGA	0.48828	0.47439
cg2387614	PPAP2C	C/EBPalp	1763	1769	2.441016	CATTGA	0.48828	0.47439
cg2419255	PPAP2C	MAZ [T00	413	425	2.392122	GAGGGG	0.00405	0.00469
cg2419255	PPAP2C	MAZ [T00	454	466	2.392122	AGGGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	334	346	2.392122	GAGGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	375	387	2.392122	AGGGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	299	311	2.392122	GAGGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	340	352	2.392122	AGGGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	273	285	2.392122	GAGGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	314	326	2.392122	AGGGGG	0.00405	0.00469
cg2419255	PPAP2C	MAZ [T00	362	374	2.378507	GGAGGG	0.00405	0.00469
cg2419255	PPAP2C	MAZ [T00	367	379	2.378507	GGAGGG	0.00405	0.00469
cg2419255	PPAP2C	MAZ [T00	426	438	2.378507	GGAGGG	0.00405	0.00469
cg2419255	PPAP2C	MAZ [T00	447	459	2.378507	GGAGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	283	295	2.378507	GGAGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	288	300	2.378507	GGAGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	347	359	2.378507	GGAGGG	0.00405	0.00469
cg2715857	PPAP2C	MAZ [T00	368	380	2.378507	GGAGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	248	260	2.378507	GGAGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	253	265	2.378507	GGAGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	312	324	2.378507	GGAGGG	0.00405	0.00469
cg0268666	PPAP2C	MAZ [T00	333	345	2.378507	GGAGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	222	234	2.378507	GGAGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	227	239	2.378507	GGAGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	286	298	2.378507	GGAGGG	0.00405	0.00469
cg2387614	PPAP2C	MAZ [T00	307	319	2.378507	GGAGGG	0.00405	0.00469
cg2419255	PPAP2C	LEF-1 [T0	1568	1575	2.345041	CAGCAA	0.09155	0.09076
cg2715857	PPAP2C	LEF-1 [T0	1489	1496	2.345041	CAGCAA	0.09155	0.09076
cg0268666	PPAP2C	LEF-1 [T0	1454	1461	2.345041	CAGCAA	0.09155	0.09076
cg2387614	PPAP2C	LEF-1 [T0	1428	1435	2.345041	CAGCAA	0.09155	0.09076
cg2419255	PPAP2C	RXR-alph	1119	1125	2.322562	GGGTCT	0.85449	0.89683
cg2419255	PPAP2C	RXR-alph	1262	1268	2.322562	CAGACC	0.85449	0.89683
cg2715857	PPAP2C	RXR-alph	1040	1046	2.322562	GGGTCT	0.85449	0.89683

cg2715857	PPAP2C	RXR-alpha	1183	1189	2.322562	CAGACC	0.85449	0.89683
cg0268666	PPAP2C	RXR-alpha	1005	1011	2.322562	GGGTCT	0.85449	0.89683
cg0268666	PPAP2C	RXR-alpha	1148	1154	2.322562	CAGACC	0.85449	0.89683
cg2387614	PPAP2C	RXR-alpha	979	985	2.322562	GGGTCT	0.85449	0.89683
cg2387614	PPAP2C	RXR-alpha	1122	1128	2.322562	CAGACC	0.85449	0.89683
cg2715857	PPAP2C	GATA-1 [	1973	1978	2.176375	AGGATA	3.90625	3.79558
cg0268666	PPAP2C	GATA-1 [	1938	1943	2.176375	AGGATA	3.90625	3.79558
cg2387614	PPAP2C	GATA-1 [	1912	1917	2.176375	AGGATA	3.90625	3.79558
cg2419255	PPAP2C	RXR-alpha	1637	1643	1.87833	GGGTTG	0.12207	0.12517
cg2715857	PPAP2C	RXR-alpha	1558	1564	1.87833	GGGTTG	0.12207	0.12517
cg0268666	PPAP2C	RXR-alpha	1523	1529	1.87833	GGGTTG	0.12207	0.12517
cg2387614	PPAP2C	RXR-alpha	1497	1503	1.87833	GGGTTG	0.12207	0.12517
cg2419255	PPAP2C	AP-2alpha	29	34	1.871933	GCCTCC	0.97656	1.07805
cg2419255	PPAP2C	AP-2alpha	63	68	1.871933	GCCTCC	0.97656	1.07805
cg2419255	PPAP2C	AP-2alpha	863	868	1.871933	GGAGGC	0.97656	1.07805
cg2419255	PPAP2C	AP-2alpha	1245	1250	1.871933	GGAGGC	0.97656	1.07805
cg2715857	PPAP2C	AP-2alpha	784	789	1.871933	GGAGGC	0.97656	1.07805
cg2715857	PPAP2C	AP-2alpha	1166	1171	1.871933	GGAGGC	0.97656	1.07805
cg0268666	PPAP2C	AP-2alpha	749	754	1.871933	GGAGGC	0.97656	1.07805
cg0268666	PPAP2C	AP-2alpha	1131	1136	1.871933	GGAGGC	0.97656	1.07805
cg2387614	PPAP2C	AP-2alpha	723	728	1.871933	GGAGGC	0.97656	1.07805
cg2387614	PPAP2C	AP-2alpha	1105	1110	1.871933	GGAGGC	0.97656	1.07805
cg2419255	PPAP2C	NF-kappa	710	720	1.841416	GGAGGT	0.00572	0.00672
cg2715857	PPAP2C	NF-kappa	631	641	1.841416	GGAGGT	0.00572	0.00672
cg0268666	PPAP2C	NF-kappa	596	606	1.841416	GGAGGT	0.00572	0.00672
cg2387614	PPAP2C	NF-kappa	570	580	1.841416	GGAGGT	0.00572	0.00672
cg2419255	PPAP2C	TFII-I [T0	296	301	1.824994	GGAGAG	0.48828	0.51201
cg2419255	PPAP2C	TFII-I [T0	352	357	1.824994	GGAGAG	0.48828	0.51201
cg2419255	PPAP2C	TFII-I [T0	1857	1862	1.824994	GGAGAG	0.48828	0.51201
cg2419255	PPAP2C	TFII-I [T0	1935	1940	1.824994	GGAGAG	0.48828	0.51201
cg2715857	PPAP2C	TFII-I [T0	217	222	1.824994	GGAGAG	0.48828	0.51201
cg2715857	PPAP2C	TFII-I [T0	273	278	1.824994	GGAGAG	0.48828	0.51201
cg2715857	PPAP2C	TFII-I [T0	1778	1783	1.824994	GGAGAG	0.48828	0.51201
cg2715857	PPAP2C	TFII-I [T0	1856	1861	1.824994	GGAGAG	0.48828	0.51201
cg2715857	PPAP2C	TFII-I [T0	1937	1942	1.824994	GGAGAG	0.48828	0.51201
cg2715857	PPAP2C	TFII-I [T0	1948	1953	1.824994	GGAGAG	0.48828	0.51201
cg0268666	PPAP2C	TFII-I [T0	182	187	1.824994	GGAGAG	0.48828	0.51201
cg0268666	PPAP2C	TFII-I [T0	238	243	1.824994	GGAGAG	0.48828	0.51201
cg0268666	PPAP2C	TFII-I [T0	1743	1748	1.824994	GGAGAG	0.48828	0.51201
cg0268666	PPAP2C	TFII-I [T0	1821	1826	1.824994	GGAGAG	0.48828	0.51201
cg0268666	PPAP2C	TFII-I [T0	1902	1907	1.824994	GGAGAG	0.48828	0.51201
cg0268666	PPAP2C	TFII-I [T0	1913	1918	1.824994	GGAGAG	0.48828	0.51201
cg2387614	PPAP2C	TFII-I [T0	156	161	1.824994	GGAGAG	0.48828	0.51201
cg2387614	PPAP2C	TFII-I [T0	212	217	1.824994	GGAGAG	0.48828	0.51201
cg2387614	PPAP2C	TFII-I [T0	1717	1722	1.824994	GGAGAG	0.48828	0.51201
cg2387614	PPAP2C	TFII-I [T0	1795	1800	1.824994	GGAGAG	0.48828	0.51201
cg2387614	PPAP2C	TFII-I [T0	1876	1881	1.824994	GGAGAG	0.48828	0.51201
cg2387614	PPAP2C	TFII-I [T0	1887	1892	1.824994	GGAGAG	0.48828	0.51201

cg2419255	PPAP2C	p53 [T006	572	578	1.758307	TCTGCCC	0.36621	0.38097
cg2715857	PPAP2C	p53 [T006	493	499	1.758307	TCTGCCC	0.36621	0.38097
cg0268666	PPAP2C	p53 [T006	458	464	1.758307	TCTGCCC	0.36621	0.38097
cg2387614	PPAP2C	p53 [T006	432	438	1.758307	TCTGCCC	0.36621	0.38097
cg2419255	PPAP2C	Sp1 [T007	309	318	1.706745	GGGGCG	0.03242	0.03924
cg2715857	PPAP2C	Sp1 [T007	230	239	1.706745	GGGGCG	0.03242	0.03924
cg0268666	PPAP2C	Sp1 [T007	195	204	1.706745	GGGGCG	0.03242	0.03924
cg2387614	PPAP2C	Sp1 [T007	169	178	1.706745	GGGGCG	0.03242	0.03924
cg2419255	PPAP2C	RXR-alpha	551	557	1.696452	CGGACC	0.48828	0.52093
cg2419255	PPAP2C	RXR-alpha	661	667	1.696452	CTGACCC	0.48828	0.52093
cg2419255	PPAP2C	RXR-alpha	1335	1341	1.696452	GGGTCA	0.48828	0.52093
cg2419255	PPAP2C	RXR-alpha	1377	1383	1.696452	CTGACCC	0.48828	0.52093
cg2715857	PPAP2C	RXR-alpha	472	478	1.696452	CGGACC	0.48828	0.52093
cg2715857	PPAP2C	RXR-alpha	582	588	1.696452	CTGACCC	0.48828	0.52093
cg2715857	PPAP2C	RXR-alpha	1256	1262	1.696452	GGGTCA	0.48828	0.52093
cg2715857	PPAP2C	RXR-alpha	1298	1304	1.696452	CTGACCC	0.48828	0.52093
cg0268666	PPAP2C	RXR-alpha	437	443	1.696452	CGGACC	0.48828	0.52093
cg0268666	PPAP2C	RXR-alpha	547	553	1.696452	CTGACCC	0.48828	0.52093
cg0268666	PPAP2C	RXR-alpha	1221	1227	1.696452	GGGTCA	0.48828	0.52093
cg0268666	PPAP2C	RXR-alpha	1263	1269	1.696452	CTGACCC	0.48828	0.52093
cg0268666	PPAP2C	RXR-alpha	1993	1999	1.696452	GGGTCA	0.48828	0.52093
cg2387614	PPAP2C	RXR-alpha	411	417	1.696452	CGGACC	0.48828	0.52093
cg2387614	PPAP2C	RXR-alpha	521	527	1.696452	CTGACCC	0.48828	0.52093
cg2387614	PPAP2C	RXR-alpha	1195	1201	1.696452	GGGTCA	0.48828	0.52093
cg2387614	PPAP2C	RXR-alpha	1237	1243	1.696452	CTGACCC	0.48828	0.52093
cg2387614	PPAP2C	RXR-alpha	1967	1973	1.696452	GGGTCA	0.48828	0.52093
cg2419255	PPAP2C	GR-beta [T	1696	1700	1.680765	GAATT	3.90625	3.70067
cg2419255	PPAP2C	GR-beta [T	1731	1735	1.680765	AATGC	3.90625	3.70067
cg2715857	PPAP2C	GR-beta [T	1617	1621	1.680765	GAATT	3.90625	3.70067
cg2715857	PPAP2C	GR-beta [T	1652	1656	1.680765	AATGC	3.90625	3.70067
cg0268666	PPAP2C	GR-beta [T	1582	1586	1.680765	GAATT	3.90625	3.70067
cg0268666	PPAP2C	GR-beta [T	1617	1621	1.680765	AATGC	3.90625	3.70067
cg2387614	PPAP2C	GR-beta [T	1556	1560	1.680765	GAATT	3.90625	3.70067
cg2387614	PPAP2C	GR-beta [T	1591	1595	1.680765	AATGC	3.90625	3.70067
cg2419255	PPAP2C	c-Ets-2 [T	809	817	1.64415	TTCCTCC	0.04578	0.04602
cg2715857	PPAP2C	c-Ets-2 [T	730	738	1.64415	TTCCTCC	0.04578	0.04602
cg0268666	PPAP2C	c-Ets-2 [T	695	703	1.64415	TTCCTCC	0.04578	0.04602
cg2387614	PPAP2C	c-Ets-2 [T	669	677	1.64415	TTCCTCC	0.04578	0.04602
cg2419255	PPAP2C	c-Ets-1 [T	1884	1890	1.641124	AAGGAA	0.36621	0.35197
cg2715857	PPAP2C	c-Ets-1 [T	1805	1811	1.641124	AAGGAA	0.36621	0.35197
cg0268666	PPAP2C	c-Ets-1 [T	1770	1776	1.641124	AAGGAA	0.36621	0.35197
cg2387614	PPAP2C	c-Ets-1 [T	1744	1750	1.641124	AAGGAA	0.36621	0.35197
cg2419255	PPAP2C	C/EBPbeta	126	129	1.639871	CCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	141	144	1.639871	CCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	596	599	1.639871	CCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	946	949	1.639871	TTGG	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1204	1207	1.639871	CCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1433	1436	1.639871	CCAA	15.625	15.23827

cg2419255	PPAP2C	C/EBPbeta	1543	1546	1.639871	CCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1560	1563	1.639871	TTGG	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1628	1631	1.639871	CCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1833	1836	1.639871	CCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1946	1949	1.639871	TTGG	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1959	1962	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	47	50	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	62	65	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	517	520	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	867	870	1.639871	TTGG	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1125	1128	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1354	1357	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1464	1467	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1481	1484	1.639871	TTGG	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1549	1552	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1754	1757	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1867	1870	1.639871	TTGG	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1880	1883	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1925	1928	1.639871	CCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1930	1933	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	12	15	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	27	30	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	482	485	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	832	835	1.639871	TTGG	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1090	1093	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1319	1322	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1429	1432	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1446	1449	1.639871	TTGG	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1514	1517	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1719	1722	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1832	1835	1.639871	TTGG	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1845	1848	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1890	1893	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1895	1898	1.639871	CCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1991	1994	1.639871	TTGG	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1	4	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	456	459	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	806	809	1.639871	TTGG	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1064	1067	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1293	1296	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1403	1406	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1420	1423	1.639871	TTGG	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1488	1491	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1693	1696	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1806	1809	1.639871	TTGG	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1819	1822	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1864	1867	1.639871	CCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1869	1872	1.639871	CCAA	15.625	15.23827

cg2387614	PPAP2C	C/EBPbeta	1965	1968	1.639871	TTGG	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1977	1980	1.639871	TTGG	15.625	15.23827
cg2419255	PPAP2C	MAZ [T00	460	472	1.594748	GAGGGG	0.00143	0.00166
cg2419255	PPAP2C	MAZ [T00	481	493	1.594748	GGGGGG	0.00143	0.00166
cg2715857	PPAP2C	MAZ [T00	381	393	1.594748	GAGGGG	0.00143	0.00166
cg2715857	PPAP2C	MAZ [T00	402	414	1.594748	GGGGGG	0.00143	0.00166
cg0268666	PPAP2C	MAZ [T00	346	358	1.594748	GAGGGG	0.00143	0.00166
cg0268666	PPAP2C	MAZ [T00	367	379	1.594748	GGGGGG	0.00143	0.00166
cg2387614	PPAP2C	MAZ [T00	320	332	1.594748	GAGGGG	0.00143	0.00166
cg2387614	PPAP2C	MAZ [T00	341	353	1.594748	GGGGGG	0.00143	0.00166
cg2419255	PPAP2C	Pax-5 [T0(	54	60	1.537547	GGGCGC	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	99	105	1.537547	GGGCGT	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	284	290	1.537547	CCCGCC(	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	310	316	1.537547	GGGCGG	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	333	339	1.537547	GGGCGG	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	394	400	1.537547	GGGCGG	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	434	440	1.537547	GGGCTA	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	441	447	1.537547	GGGCGG	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	538	544	1.537547	GGGCGG	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	543	549	1.537547	GGGCGC	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	744	750	1.537547	GGGCGG	0.73242	0.83087
cg2419255	PPAP2C	Pax-5 [T0(	1547	1553	1.537547	GGGCAA	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	20	26	1.537547	GGGCGT	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	205	211	1.537547	CCCGCC(	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	231	237	1.537547	GGGCGG	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	254	260	1.537547	GGGCGG	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	315	321	1.537547	GGGCGG	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	355	361	1.537547	GGGCTA	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	362	368	1.537547	GGGCGG	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	459	465	1.537547	GGGCGG	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	464	470	1.537547	GGGCGC	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	665	671	1.537547	GGGCGG	0.73242	0.83087
cg2715857	PPAP2C	Pax-5 [T0(	1468	1474	1.537547	GGGCAA	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	170	176	1.537547	CCCGCC(	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	196	202	1.537547	GGGCGG	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	219	225	1.537547	GGGCGG	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	280	286	1.537547	GGGCGG	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	320	326	1.537547	GGGCTA	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	327	333	1.537547	GGGCGG	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	424	430	1.537547	GGGCGG	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	429	435	1.537547	GGGCGC	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	630	636	1.537547	GGGCGG	0.73242	0.83087
cg0268666	PPAP2C	Pax-5 [T0(	1433	1439	1.537547	GGGCAA	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0(	144	150	1.537547	CCCGCC(	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0(	170	176	1.537547	GGGCGG	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0(	193	199	1.537547	GGGCGG	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0(	254	260	1.537547	GGGCGG	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0(	294	300	1.537547	GGGCTA	0.73242	0.83087

cg2387614	PPAP2C	Pax-5 [T0	301	307	1.537547	GGGCGG	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0	398	404	1.537547	GGGCGG	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0	403	409	1.537547	GGGCGC	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0	604	610	1.537547	GGGCGG	0.73242	0.83087
cg2387614	PPAP2C	Pax-5 [T0	1407	1413	1.537547	GGGCAA	0.73242	0.83087
cg2419255	PPAP2C	Sp1 [T007	743	752	1.523913	CGGGCG	0.03242	0.03924
cg2715857	PPAP2C	Sp1 [T007	664	673	1.523913	CGGGCG	0.03242	0.03924
cg0268666	PPAP2C	Sp1 [T007	629	638	1.523913	CGGGCG	0.03242	0.03924
cg2387614	PPAP2C	Sp1 [T007	603	612	1.523913	CGGGCG	0.03242	0.03924
cg2419255	PPAP2C	c-Ets-1 [T	808	814	1.513038	TTTCCTC	0.36621	0.35197
cg2715857	PPAP2C	c-Ets-1 [T	729	735	1.513038	TTTCCTC	0.36621	0.35197
cg0268666	PPAP2C	c-Ets-1 [T	694	700	1.513038	TTTCCTC	0.36621	0.35197
cg2387614	PPAP2C	c-Ets-1 [T	668	674	1.513038	TTTCCTC	0.36621	0.35197
cg2419255	PPAP2C	STAT4 [T	847	852	1.470588	GGAAAC	1.95312	1.90161
cg2419255	PPAP2C	STAT4 [T	973	978	1.470588	AGTTCC	1.95312	1.90161
cg2419255	PPAP2C	STAT4 [T	1192	1197	1.470588	GGAAAC	1.95312	1.90161
cg2419255	PPAP2C	STAT4 [T	1271	1276	1.470588	GTTTCC	1.95312	1.90161
cg2419255	PPAP2C	STAT4 [T	1537	1542	1.470588	GGAACT	1.95312	1.90161
cg2419255	PPAP2C	STAT4 [T	1695	1700	1.470588	GGAATT	1.95312	1.90161
cg2715857	PPAP2C	STAT4 [T	768	773	1.470588	GGAAAC	1.95312	1.90161
cg2715857	PPAP2C	STAT4 [T	894	899	1.470588	AGTTCC	1.95312	1.90161
cg2715857	PPAP2C	STAT4 [T	1113	1118	1.470588	GGAAAC	1.95312	1.90161
cg2715857	PPAP2C	STAT4 [T	1192	1197	1.470588	GTTTCC	1.95312	1.90161
cg2715857	PPAP2C	STAT4 [T	1458	1463	1.470588	GGAACT	1.95312	1.90161
cg2715857	PPAP2C	STAT4 [T	1616	1621	1.470588	GGAATT	1.95312	1.90161
cg0268666	PPAP2C	STAT4 [T	733	738	1.470588	GGAAAC	1.95312	1.90161
cg0268666	PPAP2C	STAT4 [T	859	864	1.470588	AGTTCC	1.95312	1.90161
cg0268666	PPAP2C	STAT4 [T	1078	1083	1.470588	GGAAAC	1.95312	1.90161
cg0268666	PPAP2C	STAT4 [T	1157	1162	1.470588	GTTTCC	1.95312	1.90161
cg0268666	PPAP2C	STAT4 [T	1423	1428	1.470588	GGAACT	1.95312	1.90161
cg0268666	PPAP2C	STAT4 [T	1581	1586	1.470588	GGAATT	1.95312	1.90161
cg2387614	PPAP2C	STAT4 [T	707	712	1.470588	GGAAAC	1.95312	1.90161
cg2387614	PPAP2C	STAT4 [T	833	838	1.470588	AGTTCC	1.95312	1.90161
cg2387614	PPAP2C	STAT4 [T	1052	1057	1.470588	GGAAAC	1.95312	1.90161
cg2387614	PPAP2C	STAT4 [T	1131	1136	1.470588	GTTTCC	1.95312	1.90161
cg2387614	PPAP2C	STAT4 [T	1397	1402	1.470588	GGAACT	1.95312	1.90161
cg2387614	PPAP2C	STAT4 [T	1555	1560	1.470588	GGAATT	1.95312	1.90161
cg2419255	PPAP2C	USF1 [T0	1511	1520	1.431084	CACGTG	0.0248	0.02734
cg2715857	PPAP2C	USF1 [T0	1432	1441	1.431084	CACGTG	0.0248	0.02734
cg0268666	PPAP2C	USF1 [T0	1397	1406	1.431084	CACGTG	0.0248	0.02734
cg2387614	PPAP2C	USF1 [T0	1371	1380	1.431084	CACGTG	0.0248	0.02734
cg2419255	PPAP2C	C/EBPbeta	927	930	1.366559	TCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1173	1176	1.366559	TTGA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1288	1291	1.366559	TTGA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1464	1467	1.366559	TCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1640	1643	1.366559	TTGA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1729	1732	1.366559	TCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1826	1829	1.366559	TTGA	15.625	15.23827

cg2419255	PPAP2C	C/EBPbeta	1882	1885	1.366559	TCAA	15.625	15.23827
cg2419255	PPAP2C	C/EBPbeta	1905	1908	1.366559	TTGA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	848	851	1.366559	TCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1094	1097	1.366559	TTGA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1209	1212	1.366559	TTGA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1385	1388	1.366559	TCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1561	1564	1.366559	TTGA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1650	1653	1.366559	TCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1747	1750	1.366559	TTGA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1803	1806	1.366559	TCAA	15.625	15.23827
cg2715857	PPAP2C	C/EBPbeta	1826	1829	1.366559	TTGA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	813	816	1.366559	TCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1059	1062	1.366559	TTGA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1174	1177	1.366559	TTGA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1350	1353	1.366559	TCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1526	1529	1.366559	TTGA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1615	1618	1.366559	TCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1712	1715	1.366559	TTGA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1768	1771	1.366559	TCAA	15.625	15.23827
cg0268666	PPAP2C	C/EBPbeta	1791	1794	1.366559	TTGA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	787	790	1.366559	TCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1033	1036	1.366559	TTGA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1148	1151	1.366559	TTGA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1324	1327	1.366559	TCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1500	1503	1.366559	TTGA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1589	1592	1.366559	TCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1686	1689	1.366559	TTGA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1742	1745	1.366559	TCAA	15.625	15.23827
cg2387614	PPAP2C	C/EBPbeta	1765	1768	1.366559	TTGA	15.625	15.23827
cg2419255	PPAP2C	p53 [T006	342	348	1.270236	GGGCAC	0.12207	0.13816
cg2715857	PPAP2C	p53 [T006	263	269	1.270236	GGGCAC	0.12207	0.13816
cg0268666	PPAP2C	p53 [T006	228	234	1.270236	GGGCAC	0.12207	0.13816
cg2387614	PPAP2C	p53 [T006	202	208	1.270236	GGGCAC	0.12207	0.13816
cg2419255	PPAP2C	ENKTF-1	274	281	1.255756	TGGCGC	0.24414	0.27027
cg2419255	PPAP2C	ENKTF-1	1111	1118	1.255756	TGGCGC	0.24414	0.27027
cg2715857	PPAP2C	ENKTF-1	195	202	1.255756	TGGCGC	0.24414	0.27027
cg2715857	PPAP2C	ENKTF-1	1032	1039	1.255756	TGGCGC	0.24414	0.27027
cg0268666	PPAP2C	ENKTF-1	160	167	1.255756	TGGCGC	0.24414	0.27027
cg0268666	PPAP2C	ENKTF-1	997	1004	1.255756	TGGCGC	0.24414	0.27027
cg2387614	PPAP2C	ENKTF-1	134	141	1.255756	TGGCGC	0.24414	0.27027
cg2387614	PPAP2C	ENKTF-1	971	978	1.255756	TGGCGC	0.24414	0.27027
cg2419255	PPAP2C	Sp1 [T007	282	291	1.253855	AGCCCG	0.03242	0.03924
cg2715857	PPAP2C	Sp1 [T007	203	212	1.253855	AGCCCG	0.03242	0.03924
cg0268666	PPAP2C	Sp1 [T007	168	177	1.253855	AGCCCG	0.03242	0.03924
cg2387614	PPAP2C	Sp1 [T007	142	151	1.253855	AGCCCG	0.03242	0.03924
cg2715857	PPAP2C	T3R-beta1	1984	1992	1.129976	TGGAGG	0.07629	0.07886
cg0268666	PPAP2C	T3R-beta1	1949	1957	1.129976	TGGAGG	0.07629	0.07886
cg2387614	PPAP2C	T3R-beta1	1923	1931	1.129976	TGGAGG	0.07629	0.07886

cg2419255	PPAP2C	GCF [T00	1113	1121	1.070269	GCGCCG	0.18311	0.21473
cg2715857	PPAP2C	GCF [T00	1034	1042	1.070269	GCGCCG	0.18311	0.21473
cg0268666	PPAP2C	GCF [T00	999	1007	1.070269	GCGCCG	0.18311	0.21473
cg2387614	PPAP2C	GCF [T00	973	981	1.070269	GCGCCG	0.18311	0.21473
cg2419255	PPAP2C	RAR-beta	1747	1756	1.063044	AGGGTT	0.03052	0.03086
cg2715857	PPAP2C	RAR-beta	1668	1677	1.063044	AGGGTT	0.03052	0.03086
cg0268666	PPAP2C	RAR-beta	1633	1642	1.063044	AGGGTT	0.03052	0.03086
cg2387614	PPAP2C	RAR-beta	1607	1616	1.063044	AGGGTT	0.03052	0.03086
cg2419255	PPAP2C	HIF-1 [T0	166	174	1.003171	ACAGCA	0.09918	0.10583
cg2715857	PPAP2C	HIF-1 [T0	87	95	1.003171	ACAGCA	0.09918	0.10583
cg0268666	PPAP2C	HIF-1 [T0	52	60	1.003171	ACAGCA	0.09918	0.10583
cg2387614	PPAP2C	HIF-1 [T0	26	34	1.003171	ACAGCA	0.09918	0.10583
cg2419255	PPAP2C	RXR-alph	387	393	0.848226	GGGTTA	0.48828	0.51313
cg2419255	PPAP2C	RXR-alph	947	953	0.848226	TGGACC	0.48828	0.51313
cg2715857	PPAP2C	RXR-alph	308	314	0.848226	GGGTTA	0.48828	0.51313
cg2715857	PPAP2C	RXR-alph	868	874	0.848226	TGGACC	0.48828	0.51313
cg0268666	PPAP2C	RXR-alph	273	279	0.848226	GGGTTA	0.48828	0.51313
cg0268666	PPAP2C	RXR-alph	833	839	0.848226	TGGACC	0.48828	0.51313
cg2387614	PPAP2C	RXR-alph	247	253	0.848226	GGGTTA	0.48828	0.51313
cg2387614	PPAP2C	RXR-alph	807	813	0.848226	TGGACC	0.48828	0.51313
cg2387614	PPAP2C	RXR-alph	1979	1985	0.848226	GGGTTA	0.48828	0.51313
cg2419255	PPAP2C	GR-beta [	897	901	0.840383	TCATT	7.8125	7.2174
cg2419255	PPAP2C	GR-beta [	1061	1065	0.840383	CCATT	7.8125	7.2174
cg2419255	PPAP2C	GR-beta [	1109	1113	0.840383	AATGG	7.8125	7.2174
cg2419255	PPAP2C	GR-beta [	1315	1319	0.840383	AATGG	7.8125	7.2174
cg2419255	PPAP2C	GR-beta [	1697	1701	0.840383	AATTA	7.8125	7.2174
cg2419255	PPAP2C	GR-beta [	1797	1801	0.840383	AATGA	7.8125	7.2174
cg2419255	PPAP2C	GR-beta [	1902	1906	0.840383	TCATT	7.8125	7.2174
cg2715857	PPAP2C	GR-beta [	818	822	0.840383	TCATT	7.8125	7.2174
cg2715857	PPAP2C	GR-beta [	982	986	0.840383	CCATT	7.8125	7.2174
cg2715857	PPAP2C	GR-beta [	1030	1034	0.840383	AATGG	7.8125	7.2174
cg2715857	PPAP2C	GR-beta [	1236	1240	0.840383	AATGG	7.8125	7.2174
cg2715857	PPAP2C	GR-beta [	1618	1622	0.840383	AATTA	7.8125	7.2174
cg2715857	PPAP2C	GR-beta [	1718	1722	0.840383	AATGA	7.8125	7.2174
cg2715857	PPAP2C	GR-beta [	1823	1827	0.840383	TCATT	7.8125	7.2174
cg0268666	PPAP2C	GR-beta [	783	787	0.840383	TCATT	7.8125	7.2174
cg0268666	PPAP2C	GR-beta [	947	951	0.840383	CCATT	7.8125	7.2174
cg0268666	PPAP2C	GR-beta [	995	999	0.840383	AATGG	7.8125	7.2174
cg0268666	PPAP2C	GR-beta [	1201	1205	0.840383	AATGG	7.8125	7.2174
cg0268666	PPAP2C	GR-beta [	1583	1587	0.840383	AATTA	7.8125	7.2174
cg0268666	PPAP2C	GR-beta [	1683	1687	0.840383	AATGA	7.8125	7.2174
cg0268666	PPAP2C	GR-beta [	1788	1792	0.840383	TCATT	7.8125	7.2174
cg2387614	PPAP2C	GR-beta [	757	761	0.840383	TCATT	7.8125	7.2174
cg2387614	PPAP2C	GR-beta [	921	925	0.840383	CCATT	7.8125	7.2174
cg2387614	PPAP2C	GR-beta [	969	973	0.840383	AATGG	7.8125	7.2174
cg2387614	PPAP2C	GR-beta [	1175	1179	0.840383	AATGG	7.8125	7.2174
cg2387614	PPAP2C	GR-beta [	1557	1561	0.840383	AATTA	7.8125	7.2174
cg2387614	PPAP2C	GR-beta [	1657	1661	0.840383	AATGA	7.8125	7.2174

cg2387614	PPAP2C	GR-beta [	1762	1766	0.840383	TCATT	7.8125	7.2174
cg2419255	PPAP2C	GATA-1 [	1042	1047	0.758539	TATCAG	1.95312	1.80234
cg2715857	PPAP2C	GATA-1 [	963	968	0.758539	TATCAG	1.95312	1.80234
cg0268666	PPAP2C	GATA-1 [	928	933	0.758539	TATCAG	1.95312	1.80234
cg2387614	PPAP2C	GATA-1 [	902	907	0.758539	TATCAG	1.95312	1.80234
cg2419255	PPAP2C	Sp1 [T007	332	341	0.574521	GGGGCG	0.00763	0.0096
cg2419255	PPAP2C	Sp1 [T007	393	402	0.574521	GGGGCG	0.00763	0.0096
cg2419255	PPAP2C	Sp1 [T007	440	449	0.574521	GGGGCG	0.00763	0.0096
cg2715857	PPAP2C	Sp1 [T007	253	262	0.574521	GGGGCG	0.00763	0.0096
cg2715857	PPAP2C	Sp1 [T007	314	323	0.574521	GGGGCG	0.00763	0.0096
cg2715857	PPAP2C	Sp1 [T007	361	370	0.574521	GGGGCG	0.00763	0.0096
cg0268666	PPAP2C	Sp1 [T007	218	227	0.574521	GGGGCG	0.00763	0.0096
cg0268666	PPAP2C	Sp1 [T007	279	288	0.574521	GGGGCG	0.00763	0.0096
cg0268666	PPAP2C	Sp1 [T007	326	335	0.574521	GGGGCG	0.00763	0.0096
cg2387614	PPAP2C	Sp1 [T007	192	201	0.574521	GGGGCG	0.00763	0.0096
cg2387614	PPAP2C	Sp1 [T007	253	262	0.574521	GGGGCG	0.00763	0.0096
cg2387614	PPAP2C	Sp1 [T007	300	309	0.574521	GGGGCG	0.00763	0.0096
cg2419255	PPAP2C	HIF-1 [T0	1507	1515	0.543748	CCTGCA	0.04578	0.04961
cg2715857	PPAP2C	HIF-1 [T0	1428	1436	0.543748	CCTGCA	0.04578	0.04961
cg0268666	PPAP2C	HIF-1 [T0	1393	1401	0.543748	CCTGCA	0.04578	0.04961
cg2387614	PPAP2C	HIF-1 [T0	1367	1375	0.543748	CCTGCA	0.04578	0.04961
cg2419255	PPAP2C	C/EBPalph	1703	1709	0.540941	GATTGT	0.24414	0.24432
cg2715857	PPAP2C	C/EBPalph	1624	1630	0.540941	GATTGT	0.24414	0.24432
cg0268666	PPAP2C	C/EBPalph	1589	1595	0.540941	GATTGT	0.24414	0.24432
cg2387614	PPAP2C	C/EBPalph	1563	1569	0.540941	GATTGT	0.24414	0.24432
cg2419255	PPAP2C	AP-2alpha	581	586	0.226186	GCCTGG	0.97656	1.07867
cg2419255	PPAP2C	AP-2alpha	843	848	0.226186	GCCTGG	0.97656	1.07867
cg2419255	PPAP2C	AP-2alpha	1010	1015	0.226186	CCAGGC	0.97656	1.07867
cg2419255	PPAP2C	AP-2alpha	1028	1033	0.226186	CCAGGC	0.97656	1.07867
cg2419255	PPAP2C	AP-2alpha	1164	1169	0.226186	GCCTGG	0.97656	1.07867
cg2419255	PPAP2C	AP-2alpha	1198	1203	0.226186	CCAGGC	0.97656	1.07867
cg2419255	PPAP2C	AP-2alpha	1330	1335	0.226186	GCCTGG	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	502	507	0.226186	GCCTGG	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	764	769	0.226186	GCCTGG	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	931	936	0.226186	CCAGGC	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	949	954	0.226186	CCAGGC	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	1085	1090	0.226186	GCCTGG	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	1119	1124	0.226186	CCAGGC	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	1251	1256	0.226186	GCCTGG	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	467	472	0.226186	GCCTGG	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	729	734	0.226186	GCCTGG	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	896	901	0.226186	CCAGGC	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	914	919	0.226186	CCAGGC	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	1050	1055	0.226186	GCCTGG	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	1084	1089	0.226186	CCAGGC	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	1216	1221	0.226186	GCCTGG	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	441	446	0.226186	GCCTGG	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	703	708	0.226186	GCCTGG	0.97656	1.07867

cg2387614	PPAP2C	AP-2alpha	870	875	0.226186	CCAGGC	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	888	893	0.226186	CCAGGC	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	1024	1029	0.226186	GCCTGG	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	1058	1063	0.226186	CCAGGC	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	1190	1195	0.226186	GCCTGG	0.97656	1.07867
cg2419255	PPAP2C	p53 [T006	1547	1553	0.211706	GGGCAA	0.36621	0.40082
cg2715857	PPAP2C	p53 [T006	1468	1474	0.211706	GGGCAA	0.36621	0.40082
cg0268666	PPAP2C	p53 [T006	1433	1439	0.211706	GGGCAA	0.36621	0.40082
cg2387614	PPAP2C	p53 [T006	1407	1413	0.211706	GGGCAA	0.36621	0.40082
cg2419255	PPAP2C	AhR [T01	13	23	0.209179	CTCACG	0.00191	0.0021
cg2419255	PPAP2C	GR-alpha [	298	302	0.207689	AGAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	354	358	0.207689	AGAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	703	707	0.207689	AGAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1224	1228	0.207689	CCTTT	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1292	1296	0.207689	CCTCT	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1385	1389	0.207689	CCTCT	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1572	1576	0.207689	AAAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1859	1863	0.207689	AGAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1888	1892	0.207689	AAAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1937	1941	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	219	223	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	275	279	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	624	628	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1145	1149	0.207689	CCTTT	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1213	1217	0.207689	CCTCT	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1306	1310	0.207689	CCTCT	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1493	1497	0.207689	AAAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1780	1784	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1809	1813	0.207689	AAAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1858	1862	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1933	1937	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1950	1954	0.207689	AGAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1978	1982	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	184	188	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	240	244	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	589	593	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1110	1114	0.207689	CCTTT	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1178	1182	0.207689	CCTCT	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1271	1275	0.207689	CCTCT	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1458	1462	0.207689	AAAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1745	1749	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1774	1778	0.207689	AAAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1823	1827	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1898	1902	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1915	1919	0.207689	AGAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1943	1947	0.207689	AGAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	158	162	0.207689	AGAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	214	218	0.207689	AGAGG	7.8125	7.79817

cg2387614	PPAP2C	GR-alpha [	563	567	0.207689	AGAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1084	1088	0.207689	CCTTT	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1152	1156	0.207689	CCTCT	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1245	1249	0.207689	CCTCT	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1432	1436	0.207689	AAAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1719	1723	0.207689	AGAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1748	1752	0.207689	AAAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1797	1801	0.207689	AGAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1872	1876	0.207689	AGAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1889	1893	0.207689	AGAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1917	1921	0.207689	AGAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-beta [T	1742	1746	0	AATGT	3.90625	3.51525
cg2419255	PPAP2C	GR-beta [T	1840	1844	0	ACATT	3.90625	3.51525
cg2419255	PPAP2C	TFIID [T0	1387	1393	0	TCTAAA	1.09863	0.95175
cg2419255	PPAP2C	GR-alpha [	1021	1025	0	CCTGT	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1040	1044	0	CCTAT	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1438	1442	0	ACAGG	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1617	1621	0	CCTGT	7.8125	7.79817
cg2419255	PPAP2C	GR-alpha [	1787	1791	0	CCTGT	7.8125	7.79817
cg2419255	PPAP2C	C/EBPbeta	79	82	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	85	88	0	TTGC	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	991	994	0	TTGC	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1053	1056	0	TTGC	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1344	1347	0	ACAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1427	1430	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1453	1456	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1549	1552	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1570	1573	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1608	1611	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1653	1656	0	TTGC	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1705	1708	0	TTGT	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1794	1797	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1866	1869	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	C/EBPbeta	1930	1933	0	GCAA	15.625	15.26275
cg2419255	PPAP2C	YY1 [T00	204	207	0	ATGG	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1061	1064	0	CCAT	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1103	1106	0	CCAT	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1110	1113	0	ATGG	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1238	1241	0	CCAT	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1316	1319	0	ATGG	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1408	1411	0	CCAT	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1496	1499	0	ATGG	7.8125	7.79459
cg2419255	PPAP2C	YY1 [T00	1855	1858	0	ATGG	7.8125	7.79459
cg2419255	PPAP2C	C/EBPalph	1171	1177	0	GATTGA	0.24414	0.24342
cg2419255	PPAP2C	TFII-I [T0	807	812	0	CTTTCC	1.46484	1.48598
cg2419255	PPAP2C	TFII-I [T0	1056	1061	0	CTGTCC	1.46484	1.48598
cg2419255	PPAP2C	TFII-I [T0	1769	1774	0	CTTTCC	1.46484	1.48598
cg2419255	PPAP2C	TFII-I [T0	1886	1891	0	GGAAAG	1.46484	1.48598

cg2419255	PPAP2C	ER-alpha [	662	666	0	TGACC	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1289	1293	0	TGACC	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1306	1310	0	GGTCA	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1336	1340	0	GGTCA	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1378	1382	0	TGACC	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1498	1502	0	GGTCA	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1614	1618	0	TGACC	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1803	1807	0	TGACC	1.95312	1.99744
cg2419255	PPAP2C	ER-alpha [	1940	1944	0	GGTCA	1.95312	1.99744
cg2419255	PPAP2C	RXR-alph	1748	1754	0	GGGTTC	0.24414	0.24342
cg2419255	PPAP2C	TCF-4E [T	1569	1575	0	AGCAAA	0.12207	0.11933
cg2419255	PPAP2C	c-Myc [T0	270	275	0	CACGTG	0.48828	0.51196
cg2419255	PPAP2C	c-Myc [T0	1511	1516	0	CACGTG	0.48828	0.51196
cg2419255	PPAP2C	Pax-5 [T0	252	258	0	CCGGCC	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	342	348	0	GGGCAC	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	518	524	0	GGGCAG	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	655	661	0	CCGGCC	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	728	734	0	GGGCCG	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	783	789	0	CCGGCC	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	1199	1205	0	CAGGCC	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	1418	1424	0	CCTGCC	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	1517	1523	0	GGGCAG	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	1632	1638	0	GGGCAG	1.09863	1.24633
cg2419255	PPAP2C	Pax-5 [T0	1952	1958	0	GGGCCT	1.09863	1.24633
cg2419255	PPAP2C	p53 [T006	518	524	0	GGGCAG	0.36621	0.40082
cg2419255	PPAP2C	p53 [T006	1418	1424	0	CCTGCC	0.36621	0.40082
cg2419255	PPAP2C	p53 [T006	1517	1523	0	GGGCAG	0.36621	0.40082
cg2419255	PPAP2C	p53 [T006	1632	1638	0	GGGCAG	0.36621	0.40082
cg2419255	PPAP2C	AP-2alpha	1326	1331	0	GCAGGC	0.97656	1.07867
cg2419255	PPAP2C	AP-2alpha	1954	1959	0	GCCTGC	0.97656	1.07867
cg2419255	PPAP2C	GCF [T00	230	238	0	TCCCAG	0.09155	0.10999
cg2419255	PPAP2C	GCF [T00	287	295	0	GCCCCG	0.09155	0.10999
cg2419255	PPAP2C	Sp1 [T007	537	546	0	GGGGCG	0.00191	0.00246
cg2419255	PPAP2C	IRF-2 [T0	1308	1313	0	TCACTT	0.48828	0.46235
cg2419255	PPAP2C	IRF-2 [T0	1942	1947	0	TCACTT	0.48828	0.46235
cg2715857	PPAP2C	GR-beta [	1663	1667	0	AATGT	3.90625	3.51525
cg2715857	PPAP2C	GR-beta [	1761	1765	0	ACATT	3.90625	3.51525
cg2715857	PPAP2C	TFIID [T0	1308	1314	0	TCTAAA	1.09863	0.95175
cg2715857	PPAP2C	GR-alpha [	942	946	0	CCTGT	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	961	965	0	CCTAT	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1359	1363	0	ACAGG	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1538	1542	0	CCTGT	7.8125	7.79817
cg2715857	PPAP2C	GR-alpha [	1708	1712	0	CCTGT	7.8125	7.79817
cg2715857	PPAP2C	C/EBPbeta	0	3	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	6	9	0	TTGC	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	912	915	0	TTGC	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	974	977	0	TTGC	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1265	1268	0	ACAA	15.625	15.26275

cg2715857	PPAP2C	C/EBPbeta	1348	1351	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1374	1377	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1470	1473	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1491	1494	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1529	1532	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1574	1577	0	TTGC	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1626	1629	0	TTGT	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1715	1718	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1787	1790	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	C/EBPbeta	1851	1854	0	GCAA	15.625	15.26275
cg2715857	PPAP2C	YY1 [T00	125	128	0	ATGG	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	982	985	0	CCAT	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1024	1027	0	CCAT	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1031	1034	0	ATGG	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1159	1162	0	CCAT	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1237	1240	0	ATGG	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1329	1332	0	CCAT	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1417	1420	0	ATGG	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1776	1779	0	ATGG	7.8125	7.79459
cg2715857	PPAP2C	YY1 [T00	1919	1922	0	ATGG	7.8125	7.79459
cg2715857	PPAP2C	C/EBPalph	1092	1098	0	GATTGA	0.24414	0.24342
cg2715857	PPAP2C	TFII-I [T0	728	733	0	CTTTCC	1.46484	1.48598
cg2715857	PPAP2C	TFII-I [T0	977	982	0	CTGTCC	1.46484	1.48598
cg2715857	PPAP2C	TFII-I [T0	1690	1695	0	CTTTCC	1.46484	1.48598
cg2715857	PPAP2C	TFII-I [T0	1807	1812	0	GGAAAG	1.46484	1.48598
cg2715857	PPAP2C	TFII-I [T0	1974	1979	0	GGATAG	1.46484	1.48598
cg2715857	PPAP2C	ER-alpha [	583	587	0	TGACC	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1210	1214	0	TGACC	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1227	1231	0	GGTCA	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1257	1261	0	GGTCA	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1299	1303	0	TGACC	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1419	1423	0	GGTCA	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1535	1539	0	TGACC	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1724	1728	0	TGACC	1.95312	1.99744
cg2715857	PPAP2C	ER-alpha [	1861	1865	0	GGTCA	1.95312	1.99744
cg2715857	PPAP2C	RXR-alpha	1669	1675	0	GGGTTC	0.24414	0.24342
cg2715857	PPAP2C	TCF-4E [T	1490	1496	0	AGCAAA	0.12207	0.11933
cg2715857	PPAP2C	c-Myc [T0	191	196	0	CACGTG	0.48828	0.51196
cg2715857	PPAP2C	c-Myc [T0	1432	1437	0	CACGTG	0.48828	0.51196
cg2715857	PPAP2C	Pax-5 [T0	173	179	0	CCGGCC	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	263	269	0	GGGCAC	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	439	445	0	GGGCAG	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	576	582	0	CCGGCC	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	649	655	0	GGGCCG	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	704	710	0	CCGGCC	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	1120	1126	0	CAGGCC	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	1339	1345	0	CCTGCC	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	1438	1444	0	GGGCAG	1.09863	1.24633

cg2715857	PPAP2C	Pax-5 [T0	1553	1559	0	GGGCAG	1.09863	1.24633
cg2715857	PPAP2C	Pax-5 [T0	1873	1879	0	GGGCCT	1.09863	1.24633
cg2715857	PPAP2C	p53 [T006	439	445	0	GGGCAG	0.36621	0.40082
cg2715857	PPAP2C	p53 [T006	1339	1345	0	CCTGCC	0.36621	0.40082
cg2715857	PPAP2C	p53 [T006	1438	1444	0	GGGCAG	0.36621	0.40082
cg2715857	PPAP2C	p53 [T006	1553	1559	0	GGGCAG	0.36621	0.40082
cg2715857	PPAP2C	AP-2alpha	1247	1252	0	GCAGGC	0.97656	1.07867
cg2715857	PPAP2C	AP-2alpha	1875	1880	0	GCCTGC	0.97656	1.07867
cg2715857	PPAP2C	GCF [T00	151	159	0	TCCCAG	0.09155	0.10999
cg2715857	PPAP2C	GCF [T00	208	216	0	GCCCCG	0.09155	0.10999
cg2715857	PPAP2C	Sp1 [T007	458	467	0	GGGGCG	0.00191	0.00246
cg2715857	PPAP2C	IRF-2 [T01	1229	1234	0	TCACTT	0.48828	0.46235
cg2715857	PPAP2C	IRF-2 [T01	1863	1868	0	TCACTT	0.48828	0.46235
cg0268666	PPAP2C	GR-beta [T	1628	1632	0	AATGT	3.90625	3.51525
cg0268666	PPAP2C	GR-beta [T	1726	1730	0	ACATT	3.90625	3.51525
cg0268666	PPAP2C	TFIID [T0	1273	1279	0	TCTAAA	1.09863	0.95175
cg0268666	PPAP2C	GR-alpha [	907	911	0	CCTGT	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	926	930	0	CCTAT	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1324	1328	0	ACAGG	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1503	1507	0	CCTGT	7.8125	7.79817
cg0268666	PPAP2C	GR-alpha [	1673	1677	0	CCTGT	7.8125	7.79817
cg0268666	PPAP2C	C/EBPbeta	877	880	0	TTGC	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	939	942	0	TTGC	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1230	1233	0	ACAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1313	1316	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1339	1342	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1435	1438	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1456	1459	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1494	1497	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1539	1542	0	TTGC	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1591	1594	0	TTGT	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1680	1683	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1752	1755	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	C/EBPbeta	1816	1819	0	GCAA	15.625	15.26275
cg0268666	PPAP2C	YY1 [T00	90	93	0	ATGG	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	947	950	0	CCAT	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	989	992	0	CCAT	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	996	999	0	ATGG	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	1124	1127	0	CCAT	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	1202	1205	0	ATGG	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	1294	1297	0	CCAT	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	1382	1385	0	ATGG	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	1741	1744	0	ATGG	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	1884	1887	0	ATGG	7.8125	7.79459
cg0268666	PPAP2C	YY1 [T00	1979	1982	0	CCAT	7.8125	7.79459
cg0268666	PPAP2C	C/EBPalph	1057	1063	0	GATTGA	0.24414	0.24342
cg0268666	PPAP2C	TFII-I [T0	693	698	0	CTTTCC	1.46484	1.48598
cg0268666	PPAP2C	TFII-I [T0	942	947	0	CTGTCC	1.46484	1.48598

cg0268666	PPAP2C	TFII-I [T0	1655	1660	0	CTTTCC	1.46484	1.48598
cg0268666	PPAP2C	TFII-I [T0	1772	1777	0	GGAAAG	1.46484	1.48598
cg0268666	PPAP2C	TFII-I [T0	1939	1944	0	GGATAG	1.46484	1.48598
cg0268666	PPAP2C	ER-alpha [	548	552	0	TGACC	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1175	1179	0	TGACC	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1192	1196	0	GGTCA	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1222	1226	0	GGTCA	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1264	1268	0	TGACC	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1384	1388	0	GGTCA	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1500	1504	0	TGACC	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1689	1693	0	TGACC	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1826	1830	0	GGTCA	1.95312	1.99744
cg0268666	PPAP2C	ER-alpha [	1994	1998	0	GGTCA	1.95312	1.99744
cg0268666	PPAP2C	RXR-alpha	1634	1640	0	GGGTTC	0.24414	0.24342
cg0268666	PPAP2C	TCF-4E [T	1455	1461	0	AGCAAA	0.12207	0.11933
cg0268666	PPAP2C	c-Myc [T0	156	161	0	CACGTG	0.48828	0.51196
cg0268666	PPAP2C	c-Myc [T0	1397	1402	0	CACGTG	0.48828	0.51196
cg0268666	PPAP2C	Pax-5 [T0	138	144	0	CCGGCC	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	228	234	0	GGGCAC	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	404	410	0	GGGCAG	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	541	547	0	CCGGCC	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	614	620	0	GGGCCG	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	669	675	0	CCGGCC	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	1085	1091	0	CAGGCC	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	1304	1310	0	CCTGCC	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	1403	1409	0	GGGCAG	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	1518	1524	0	GGGCAG	1.09863	1.24633
cg0268666	PPAP2C	Pax-5 [T0	1838	1844	0	GGGCCT	1.09863	1.24633
cg0268666	PPAP2C	p53 [T006	404	410	0	GGGCAG	0.36621	0.40082
cg0268666	PPAP2C	p53 [T006	1304	1310	0	CCTGCC	0.36621	0.40082
cg0268666	PPAP2C	p53 [T006	1403	1409	0	GGGCAG	0.36621	0.40082
cg0268666	PPAP2C	p53 [T006	1518	1524	0	GGGCAG	0.36621	0.40082
cg0268666	PPAP2C	AP-2alpha	1212	1217	0	GCAGGC	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	1840	1845	0	GCCTGC	0.97656	1.07867
cg0268666	PPAP2C	AP-2alpha	1962	1967	0	GCAGGC	0.97656	1.07867
cg0268666	PPAP2C	GCF [T00	116	124	0	TCCCAG	0.09155	0.10999
cg0268666	PPAP2C	GCF [T00	173	181	0	GCCCCG	0.09155	0.10999
cg0268666	PPAP2C	Sp1 [T007	423	432	0	GGGGCG	0.00191	0.00246
cg0268666	PPAP2C	IRF-2 [T01	1194	1199	0	TCACTT	0.48828	0.46235
cg0268666	PPAP2C	IRF-2 [T01	1828	1833	0	TCACTT	0.48828	0.46235
cg2387614	PPAP2C	GR-beta [T	1602	1606	0	AATGT	3.90625	3.51525
cg2387614	PPAP2C	GR-beta [T	1700	1704	0	ACATT	3.90625	3.51525
cg2387614	PPAP2C	TFIID [T0	1247	1253	0	TCTAAA	1.09863	0.95175
cg2387614	PPAP2C	GR-alpha [	881	885	0	CCTGT	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	900	904	0	CCTAT	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1298	1302	0	ACAGG	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1477	1481	0	CCTGT	7.8125	7.79817
cg2387614	PPAP2C	GR-alpha [	1647	1651	0	CCTGT	7.8125	7.79817

cg2387614	PPAP2C	C/EBPbeta	851	854	0	TTGC	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	913	916	0	TTGC	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1204	1207	0	ACAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1287	1290	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1313	1316	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1409	1412	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1430	1433	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1468	1471	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1513	1516	0	TTGC	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1565	1568	0	TTGT	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1654	1657	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1726	1729	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	C/EBPbeta	1790	1793	0	GCAA	15.625	15.26275
cg2387614	PPAP2C	YY1 [T00	64	67	0	ATGG	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	921	924	0	CCAT	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	963	966	0	CCAT	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	970	973	0	ATGG	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	1098	1101	0	CCAT	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	1176	1179	0	ATGG	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	1268	1271	0	CCAT	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	1356	1359	0	ATGG	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	1715	1718	0	ATGG	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	1858	1861	0	ATGG	7.8125	7.79459
cg2387614	PPAP2C	YY1 [T00	1953	1956	0	CCAT	7.8125	7.79459
cg2387614	PPAP2C	C/EBPalph	1031	1037	0	GATTGA	0.24414	0.24342
cg2387614	PPAP2C	TFII-I [T0	667	672	0	CTTTCC	1.46484	1.48598
cg2387614	PPAP2C	TFII-I [T0	916	921	0	CTGTCC	1.46484	1.48598
cg2387614	PPAP2C	TFII-I [T0	1629	1634	0	CTTTCC	1.46484	1.48598
cg2387614	PPAP2C	TFII-I [T0	1746	1751	0	GGAAAG	1.46484	1.48598
cg2387614	PPAP2C	TFII-I [T0	1913	1918	0	GGATAG	1.46484	1.48598
cg2387614	PPAP2C	ER-alpha [	522	526	0	TGACC	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1149	1153	0	TGACC	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1166	1170	0	GGTCA	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1196	1200	0	GGTCA	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1238	1242	0	TGACC	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1358	1362	0	GGTCA	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1474	1478	0	TGACC	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1663	1667	0	TGACC	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1800	1804	0	GGTCA	1.95312	1.99744
cg2387614	PPAP2C	ER-alpha [	1968	1972	0	GGTCA	1.95312	1.99744
cg2387614	PPAP2C	RXR-alpha	1608	1614	0	GGGTTC	0.24414	0.24342
cg2387614	PPAP2C	TCF-4E [T	1429	1435	0	AGCAAA	0.12207	0.11933
cg2387614	PPAP2C	c-Myc [T0	130	135	0	CACGTG	0.48828	0.51196
cg2387614	PPAP2C	c-Myc [T0	1371	1376	0	CACGTG	0.48828	0.51196
cg2387614	PPAP2C	Pax-5 [T0	112	118	0	CCGGCC	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	202	208	0	GGGCAC	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	378	384	0	GGGCAG	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	515	521	0	CCGGCC	1.09863	1.24633

cg2387614	PPAP2C	Pax-5 [T0	588	594	0	GGGCCG	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	643	649	0	CCGGCC	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	1059	1065	0	CAGGCC	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	1278	1284	0	CCTGCC	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	1377	1383	0	GGGCAG	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	1492	1498	0	GGGCAG	1.09863	1.24633
cg2387614	PPAP2C	Pax-5 [T0	1812	1818	0	GGGCCT	1.09863	1.24633
cg2387614	PPAP2C	p53 [T006	378	384	0	GGGCAG	0.36621	0.40082
cg2387614	PPAP2C	p53 [T006	1278	1284	0	CCTGCC	0.36621	0.40082
cg2387614	PPAP2C	p53 [T006	1377	1383	0	GGGCAG	0.36621	0.40082
cg2387614	PPAP2C	p53 [T006	1492	1498	0	GGGCAG	0.36621	0.40082
cg2387614	PPAP2C	AP-2alpha	1186	1191	0	GCAGGC	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	1814	1819	0	GCCTGC	0.97656	1.07867
cg2387614	PPAP2C	AP-2alpha	1936	1941	0	GCAGGC	0.97656	1.07867
cg2387614	PPAP2C	GCF [T00	90	98	0	TCCCAG	0.09155	0.10999
cg2387614	PPAP2C	GCF [T00	147	155	0	GCCCCG	0.09155	0.10999
cg2387614	PPAP2C	Sp1 [T007	397	406	0	GGGGCG	0.00191	0.00246
cg2387614	PPAP2C	IRF-2 [T0	1168	1173	0	TCACTT	0.48828	0.46235
cg2387614	PPAP2C	IRF-2 [T0	1802	1807	0	TCACTT	0.48828	0.46235
cg1906430	PRDM1	c-Ets-1 [T	167	173	9.969337	TGGGAA	0.24414	0.2459
cg1906430	PRDM1	c-Ets-1 [T	241	247	9.841249	AGGGAA	0.24414	0.2459
cg1906430	PRDM1	STAT1bet	1441	1450	9.807397	CTTTCC	0.14877	0.1495
cg1906430	PRDM1	XBP-1 [T	1212	1217	9.789909	ATGGCG	1.95312	1.95208
cg1906430	PRDM1	XBP-1 [T	1530	1535	9.789909	ATGTCT	1.95312	1.95208
cg1906430	PRDM1	NF-AT2 [	782	791	9.755755	TTTTTTT	0.08774	0.08903
cg1906430	PRDM1	NF-AT2 [	1657	1666	9.755755	GGAAAA	0.08774	0.08903
cg1906430	PRDM1	PR B [T00	1987	1993	9.743489	TTGTGT	1.09863	1.10292
cg1906430	PRDM1	PR A [T01	1987	1993	9.743489	TTGTGT	1.09863	1.10292
cg1906430	PRDM1	c-Myb [T0	1503	1510	9.729271	AACAGT	0.36621	0.37054
cg1906430	PRDM1	c-Ets-1 [T	61	67	9.713162	GGGGAA	0.36621	0.36441
cg1906430	PRDM1	RAR-beta	1740	1749	9.622793	TGGGTT	0.21362	0.21243
cg1906430	PRDM1	RAR-beta	412	421	9.585862	ATGCAA	0.21362	0.21243
cg1906430	PRDM1	NF-AT1 [	536	544	9.557905	GGAAAA	0.16785	0.1682
cg1906430	PRDM1	TFIID [T0	20	26	9.552105	TTTGGA	1.46484	1.48472
cg1906430	PRDM1	TFIID [T0	287	293	9.552105	TTTGGT	1.46484	1.48472
cg1906430	PRDM1	TFIID [T0	511	517	9.552105	TGGGAA	1.46484	1.48472
cg1906430	PRDM1	TFIID [T0	533	539	9.552105	TTTGGA	1.46484	1.48472
cg1906430	PRDM1	TFIID [T0	908	914	9.552105	TTTCTCA	1.46484	1.48472
cg1906430	PRDM1	TFIID [T0	1518	1524	9.552105	TGGCAA	1.46484	1.48472
cg1906430	PRDM1	TFIID [T0	1691	1697	9.552105	TTTGGT	1.46484	1.48472
cg1906430	PRDM1	TFII-I [T0	23	28	9.512894	GGAAAA	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	53	58	9.512894	GGATTT	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	99	104	9.512894	TTGTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	169	174	9.512894	GGAATT	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	229	234	9.512894	GGAATT	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	243	248	9.512894	GGAATT	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	329	334	9.512894	TTTTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	346	351	9.512894	TTTTCC	7.32422	7.29728

cg1906430	PRDM1	TFII-I [T0	357	362	9.512894	TTTTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	536	541	9.512894	GGAAAA	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	613	618	9.512894	CCTTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	657	662	9.512894	TTTTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	704	709	9.512894	GGACAC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	786	791	9.512894	TTTTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	792	797	9.512894	TTTTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	993	998	9.512894	GGAACG	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	1002	1007	9.512894	GGACAA	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	1612	1617	9.512894	GTGTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	1657	1662	9.512894	GGAAAA	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	1824	1829	9.512894	GTGTCC	7.32422	7.29728
cg1906430	PRDM1	TFII-I [T0	1904	1909	9.512894	AATTCC	7.32422	7.29728
cg1906430	PRDM1	FOXP3 [T	3	8	9.512894	GTTTAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	141	146	9.512894	GTAAAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	499	504	9.512894	GTTGGG	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	723	728	9.512894	CAGAAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	808	813	9.512894	GTTGCC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	882	887	9.512894	GTTTAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1274	1279	9.512894	ACCAAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1300	1305	9.512894	GTTTAT	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1447	1452	9.512894	CTAAAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1500	1505	9.512894	GTAAAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1542	1547	9.512894	AGCAAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1702	1707	9.512894	GTTGGC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1774	1779	9.512894	GTTTAT	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1860	1865	9.512894	GTTTAT	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1977	1982	9.512894	AGCAAC	7.32422	7.35678
cg1906430	PRDM1	FOXP3 [T	1991	1996	9.512894	GTTTAC	7.32422	7.35678
cg1906430	PRDM1	TCF-4E [T	19	25	9.453578	CTTTGG	0.48828	0.49215
cg1906430	PRDM1	TCF-4E [T	1765	1771	9.453578	CTTTGA	0.48828	0.49215
cg1906430	PRDM1	LEF-1 [T0	1765	1772	9.422811	CTTTGA	0.21362	0.2139
cg1906430	PRDM1	c-Jun [T00	1569	1575	9.397655	ATTGTC	0.73242	0.73031
cg1906430	PRDM1	NFI/CTF [	1688	1695	9.352332	GTCTTT	0.54932	0.54821
cg1906430	PRDM1	POU2F2 (	1531	1541	9.350233	TGTCTTA	0.03433	0.03518
cg1906430	PRDM1	PEA3 [T0	1952	1960	9.340643	GGGATG	0.03052	0.03072
cg1906430	PRDM1	AP-1 [T00	962	970	9.290522	TATTAG	0.09155	0.09305
cg1906430	PRDM1	ATF [T00	1764	1775	9.257019	ACTTTG	0.07725	0.07724
cg1906430	PRDM1	RBP-Jkap	507	518	9.256527	CTGGTG	0.01884	0.01886
cg1906430	PRDM1	NF-AT1 [	1019	1027	9.248801	GGCCTT	0.22888	0.22959
cg1906430	PRDM1	c-Ets-1 [T	1969	1975	9.19359	TTGGAA	0.85449	0.85523
cg1906430	PRDM1	c-Myb [T0	1965	1972	9.110773	AAACTT	0.39673	0.40028
cg1906430	PRDM1	Egr-3 [T0	1556	1568	9.093379	TAGGGT	0.01878	0.01878
cg1906430	PRDM1	STAT5A [	1648	1660	9.080962	CTTTTTC	0.02816	0.02876
cg1906430	PRDM1	NFI/CTF [	1275	1282	9.042931	CCAACA	0.48828	0.48804
cg1906430	PRDM1	NF-AT2 [	342	351	9.016873	CCATTT	0.05341	0.05386
cg1906430	PRDM1	c-Jun [T00	1768	1774	9.013496	TGACGT	0.61035	0.61059
cg1906430	PRDM1	PXR-1:RX	1182	1189	8.998824	TGAACG	0.24414	0.2439

cg1906430	PRDM1	LEF-1 [T0	19	26	8.973041	CTTTGG	0.54932	0.55326
cg1906430	PRDM1	GR [T050	54	60	8.971049	GATTT	0.61035	0.61632
cg1906430	PRDM1	c-Myb [T0	1578	1585	8.947824	GAACTT	0.39673	0.40028
cg1906430	PRDM1	T3R-beta1	338	346	8.924046	TCACCC	0.2594	0.25766
cg1906430	PRDM1	HOXD9 [	199	208	8.847863	AAGTGC	0.04578	0.0476
cg1906430	PRDM1	HOXD10 [	199	208	8.847863	AAGTGC	0.04578	0.0476
cg1906430	PRDM1	NFI/CTF [	369	376	8.814757	CCAAGT	0.48828	0.48804
cg1906430	PRDM1	NFI/CTF [	530	537	8.814757	CCATTT	0.48828	0.48804
cg1906430	PRDM1	Elk-1 [T00	1469	1477	8.797343	CTTCCA	0.24414	0.24034
cg1906430	PRDM1	NF-1 [T00	1082	1089	8.790071	TTGGCA	0.24414	0.24467
cg1906430	PRDM1	NF-1 [T00	1517	1524	8.790071	TTGGCA	0.24414	0.24467
cg1906430	PRDM1	NF-AT1 [	513	521	8.769753	GGAAAG	0.22888	0.22959
cg1906430	PRDM1	XBP-1 [T	293	298	8.75604	ATGAGA	2.92969	2.9674
cg1906430	PRDM1	XBP-1 [T	444	449	8.75604	ATGAAA	2.92969	2.9674
cg1906430	PRDM1	XBP-1 [T	740	745	8.75604	ATGAGA	2.92969	2.9674
cg1906430	PRDM1	XBP-1 [T	1106	1111	8.75604	ATGAAA	2.92969	2.9674
cg1906430	PRDM1	XBP-1 [T	1461	1466	8.75604	TCTCAT	2.92969	2.9674
cg1906430	PRDM1	XBP-1 [T	1955	1960	8.75604	ATGAAA	2.92969	2.9674
cg1906430	PRDM1	XBP-1 [T	1974	1979	8.75604	ATGAGC	2.92969	2.9674
cg1906430	PRDM1	IRF-1 [T0	658	666	8.570857	TTTCCA	0.20599	0.20664
cg1906430	PRDM1	RAR-beta	1956	1965	8.55975	TGAAAA	0.26703	0.26657
cg1906430	PRDM1	NF-AT1 [	789	797	8.532897	TCCTTTT	0.10681	0.10725
cg1906430	PRDM1	IRF-1 [T0	1653	1661	8.497322	TCTTGG	0.20599	0.20664
cg1906430	PRDM1	c-Myb [T0	913	920	8.443873	CAACTG	0.30518	0.30924
cg1906430	PRDM1	c-Myb [T0	1480	1487	8.443873	CAACTG	0.30518	0.30924
cg1906430	PRDM1	c-Myb [T0	1979	1986	8.443873	CAACTG	0.30518	0.30924
cg1906430	PRDM1	HNF-3alp	245	252	8.343064	AATTTT	0.27466	0.28528
cg1906430	PRDM1	PR B [T00	324	330	8.338824	GGCTGT	1.09863	1.10009
cg1906430	PRDM1	PR B [T00	1616	1622	8.338824	CCCTGT	1.09863	1.10009
cg1906430	PRDM1	PR A [T01	324	330	8.338824	GGCTGT	1.09863	1.10009
cg1906430	PRDM1	PR A [T01	1616	1622	8.338824	CCCTGT	1.09863	1.10009
cg1906430	PRDM1	GR-alpha [	50	54	8.281568	GGAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	103	107	8.281568	CCTCC	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	335	339	8.281568	CCTTC	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	350	354	8.281568	CCTCC	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	467	471	8.281568	GGAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	470	474	8.281568	GGAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	613	617	8.281568	CCTTC	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	628	632	8.281568	CCTTG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	670	674	8.281568	CGAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	862	866	8.281568	CCTTG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	875	879	8.281568	CAAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	981	985	8.281568	GAAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	1096	1100	8.281568	CAAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	1120	1124	8.281568	GGAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	1234	1238	8.281568	GGAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	1248	1252	8.281568	CAAGG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	1349	1353	8.281568	CCTTG	7.8125	7.72956

cg1906430	PRDM1	GR-alpha [	1357	1361	8.281568	CCTTG	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	1458	1462	8.281568	CCTTC	7.8125	7.72956
cg1906430	PRDM1	GR-alpha [	1476	1480	8.281568	CCTTC	7.8125	7.72956
cg1906430	PRDM1	ENKTF-1	678	685	8.19852	TGGCGG	0.73242	0.71737
cg1906430	PRDM1	PXR-1:RX	759	766	8.180749	ATTGTTC	0.12207	0.12407
cg1906430	PRDM1	SRY [T00	1878	1886	8.174786	CTTTGCT	0.15259	0.15383
cg1906430	PRDM1	IRF-1 [T0	19	27	8.151819	CTTTGG	0.25177	0.25263
cg1906430	PRDM1	LEF-1 [T0	1944	1951	8.117221	TTTCAA	0.12207	0.1241
cg1906430	PRDM1	AR [T000	96	104	8.079301	AGCTTG	0.19836	0.19634
cg1906430	PRDM1	GR-alpha [	239	243	8.073878	CCAGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	321	325	8.073878	GCAGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	407	411	8.073878	GCAGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	543	547	8.073878	GCAGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	560	564	8.073878	CCTGC	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	692	696	8.073878	CCAGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	753	757	8.073878	CCAGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	1036	1040	8.073878	CCAGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	1194	1198	8.073878	CCTGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	1324	1328	8.073878	CCTGG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	1340	1344	8.073878	CCTAC	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	1608	1612	8.073878	CCTAG	7.8125	7.72238
cg1906430	PRDM1	GR-alpha [	1897	1901	8.073878	GCAGG	7.8125	7.72238
cg1906430	PRDM1	NF-AT2 [	1450	1459	8.023205	AACCAT	0.08965	0.09068
cg1906430	PRDM1	Pax-5 [T0	717	723	8.014558	TGTGCC	2.19727	2.14502
cg1906430	PRDM1	Pax-5 [T0	1040	1046	8.014558	GCTGCC	2.19727	2.14502
cg1906430	PRDM1	Pax-5 [T0	1595	1601	8.014558	TGGGCC	2.19727	2.14502
cg1906430	PRDM1	Pax-5 [T0	1596	1602	8.014558	GGGCCC	2.19727	2.14502
cg1906430	PRDM1	TFIID [T0	21	27	8.014558	TTGGAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	36	42	8.014558	TTTCTGA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	120	126	8.014558	TTTGTTA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	182	188	8.014558	TTTCAG	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	377	383	8.014558	TTTCTAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	482	488	8.014558	TTTGAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	534	540	8.014558	TTGGAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	633	639	8.014558	TTTGTG	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	644	650	8.014558	TTTCTGA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	1368	1374	8.014558	TCTGAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	1535	1541	8.014558	TTAGAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	1655	1661	8.014558	TTGGAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	1744	1750	8.014558	TTTCTAA	2.19727	2.24348
cg1906430	PRDM1	TFIID [T0	1944	1950	8.014558	TTTCAA	2.19727	2.24348
cg1906430	PRDM1	T3R-beta1	1559	1567	7.813363	GGTGGG	0.27466	0.27236
cg1906430	PRDM1	NF-AT2 [	653	662	7.779688	CAGCTT	0.08965	0.09068
cg1906430	PRDM1	RAR-alph	1810	1822	7.776192	GGGGTC	0.01627	0.01609
cg1906430	PRDM1	c-Ets-2 [T	359	367	7.76635	TTCCTGT	0.32043	0.32298
cg1906430	PRDM1	c-Ets-2 [T	988	996	7.76635	CCACAG	0.32043	0.32298
cg1906430	PRDM1	HNF-1B [	1715	1723	7.737819	TTTTTAA	0.09155	0.09368
cg1906430	PRDM1	E2F-1 [T0	1215	1222	7.604588	GCGGTA	0.45776	0.44878

cg1906430	PRDM1	NFI/CTF [	1047	1054	7.587343	CCAAGT	0.36621	0.36674
cg1906430	PRDM1	GR [T050	204	210	7.527031	CTATTT	1.83105	1.86007
cg1906430	PRDM1	GR [T050	630	636	7.527031	TTGTTT	1.83105	1.86007
cg1906430	PRDM1	GR [T050	1513	1519	7.527031	TATTTT	1.83105	1.86007
cg1906430	PRDM1	GR [T050	1678	1684	7.527031	TCTTTTG	1.83105	1.86007
cg1906430	PRDM1	NF-1 [T00	1525	1532	7.445595	TTGGCA	0.24414	0.24565
cg1906430	PRDM1	c-Myb [T0	514	521	7.442719	GAAAGT	0.42725	0.43114
cg1906430	PRDM1	PEA3 [T0	1122	1130	7.421728	AGGATG	0.34332	0.34161
cg1906430	PRDM1	PEA3 [T0	1236	1244	7.421728	AGGCAT	0.34332	0.34161
cg1906430	PRDM1	PEA3 [T0	1836	1844	7.421728	TGGATG	0.34332	0.34161
cg1906430	PRDM1	IRF-1 [T0	793	801	7.387351	TTTCCC	0.14496	0.14449
cg1906430	PRDM1	PPAR-alpl	1881	1891	7.370536	TGCTGG	0.04482	0.04393
cg1906430	PRDM1	NF-AT1 [	1438	1446	7.211175	TCTCTTT	0.15259	0.1548
cg1906430	PRDM1	c-Ets-1 [T	511	517	7.199436	TGGGAA	0.73242	0.73099
cg1906430	PRDM1	SRY [T00	1690	1698	7.175614	CTTTGG	0.30518	0.30739
cg1906430	PRDM1	XBP-1 [T	70	75	7.172312	CCTCAT	2.92969	2.97018
cg1906430	PRDM1	XBP-1 [T	172	177	7.172312	ATTCAT	2.92969	2.97018
cg1906430	PRDM1	XBP-1 [T	589	594	7.172312	CTTCAT	2.92969	2.97018
cg1906430	PRDM1	XBP-1 [T	1778	1783	7.172312	ATGAAG	2.92969	2.97018
cg1906430	PRDM1	p53 [T006	1595	1601	7.153797	TGGGCC	1.09863	1.07125
cg1906430	PRDM1	p53 [T006	1596	1602	7.153797	GGGCCC	1.09863	1.07125
cg1906430	PRDM1	NF-AT1 [	23	31	7.095752	GGAAAA	0.15259	0.1548
cg1906430	PRDM1	NF-AT1 [	326	334	7.095752	CTGTTTT	0.15259	0.1548
cg1906430	PRDM1	NF-AT1 [	354	362	7.095752	CTCTTTT	0.15259	0.1548
cg1906430	PRDM1	c-Ets-1 [T	1442	1448	7.071349	TTTCCCT	0.73242	0.73099
cg1906430	PRDM1	C/EBPalpl	1003	1009	7.00174	GACAAT	0.73242	0.74337
cg1906430	PRDM1	HNF-3alpl	114	121	7.000129	TCTAAA	0.82397	0.84946
cg1906430	PRDM1	HNF-3alpl	205	212	7.000129	TATTTGT	0.82397	0.84946
cg1906430	PRDM1	HNF-3alpl	580	587	7.000129	CATTTTT	0.82397	0.84946
cg1906430	PRDM1	HNF-3alpl	1107	1114	7.000129	TGAAAA	0.82397	0.84946
cg1906430	PRDM1	HNF-3alpl	1398	1405	7.000129	AGTAAA	0.82397	0.84946
cg1906430	PRDM1	HNF-3alpl	1513	1520	7.000129	TATTTT	0.82397	0.84946
cg1906430	PRDM1	IRF-1 [T0	509	517	6.968314	GGTGGG	0.1297	0.13036
cg1906430	PRDM1	RXR-alpha	1188	1194	6.967687	ACCACC	0.36621	0.36214
cg1906430	PRDM1	NF-1 [T00	901	908	6.948522	TTGGCT	0.48828	0.4856
cg1906430	PRDM1	c-Ets-1 [T	330	336	6.943262	TTTCCC	0.73242	0.73099
cg1906430	PRDM1	c-Ets-1 [T	793	799	6.943262	TTTCCC	0.73242	0.73099
cg1906430	PRDM1	ENKTF-1	1083	1090	6.942764	TGGCAG	1.46484	1.44228
cg1906430	PRDM1	ENKTF-1	1213	1220	6.942764	TGGCGG	1.46484	1.44228
cg1906430	PRDM1	STAT1bet	1454	1463	6.908963	ATTTCC	0.103	0.10372
cg1906430	PRDM1	C/EBPalpl	282	288	6.85549	TTCAAT	0.73242	0.74337
cg1906430	PRDM1	C/EBPalpl	1419	1425	6.85549	TTCAAT	0.73242	0.74337
cg1906430	PRDM1	E2F-1 [T0	551	558	6.839754	GGTTCC	0.30518	0.29782
cg1906430	PRDM1	C/EBPalpl	1624	1630	6.786177	TACAAT	0.73242	0.74337
cg1906430	PRDM1	c-Ets-1 [T	552	558	6.693449	GTTCCG	0.48828	0.48798
cg1906430	PRDM1	AR [T000	1114	1122	6.677479	GGACAT	0.19836	0.19597
cg1906430	PRDM1	c-Jun [T00	305	311	6.668031	CAAGTC	0.61035	0.60769
cg1906430	PRDM1	GATA-2 [	1625	1633	6.666667	ACAATA	0.24414	0.24583

cg1906430	PRDM1	HNF-1C [	834	842	6.596946	TTTTTTA	0.05341	0.05475
cg1906430	PRDM1	TFII-I [T0	1335	1340	6.581441	ATCTCC	0.97656	0.97366
cg1906430	PRDM1	FOXP3 [T	259	264	6.581441	GTTTTA	0.97656	0.99397
cg1906430	PRDM1	FOXP3 [T	1478	1483	6.581441	TTCAAC	0.97656	0.99397
cg1906430	PRDM1	FOXP3 [T	1667	1672	6.581441	GTTTTA	0.97656	0.99397
cg1906430	PRDM1	FOXP3 [T	1748	1753	6.581441	TAAAAC	0.97656	0.99397
cg1906430	PRDM1	XBP-1 [T	1269	1274	6.478682	ATGCCA	0.97656	0.97062
cg1906430	PRDM1	XBP-1 [T	1526	1531	6.478682	TGGCAT	0.97656	0.97062
cg1906430	PRDM1	c-Ets-1 [T	21	27	6.423689	TTGGAA	0.48828	0.48798
cg1906430	PRDM1	c-Ets-1 [T	534	540	6.423689	TTGGAA	0.48828	0.48798
cg1906430	PRDM1	c-Ets-1 [T	1655	1661	6.423689	TTGGAA	0.48828	0.48798
cg1906430	PRDM1	AR [T000	1143	1151	6.400417	GGACAG	0.19836	0.19597
cg1906430	PRDM1	RAR-beta	549	558	6.39673	TGGGTT	0.18311	0.183
cg1906430	PRDM1	C/EBPalp	1523	1529	6.391486	AATTGG	0.48828	0.49071
cg1906430	PRDM1	C/EBPalp	1568	1574	6.391486	AATTGT	0.48828	0.49071
cg1906430	PRDM1	C/EBPalp	1901	1907	6.391486	GCCAAT	0.48828	0.49071
cg1906430	PRDM1	TCF-4E [	1690	1696	6.302385	CTTTGG	0.61035	0.61344
cg1906430	PRDM1	TCF-4E [	1936	1942	6.302385	CTTTGT	0.61035	0.61344
cg1906430	PRDM1	TCF-4E [	1945	1951	6.302385	TTCAAA	0.61035	0.61344
cg1906430	PRDM1	c-Ets-1 [T	194	200	6.295602	ATGGAA	0.48828	0.48798
cg1906430	PRDM1	c-Ets-1 [T	576	582	6.295602	TTTCCA	0.48828	0.48798
cg1906430	PRDM1	GR-alpha [	46	50	6.263098	TGAGG	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	70	74	6.263098	CCTCA	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	215	219	6.263098	TGAGG	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	648	652	6.263098	TGAGG	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	804	808	6.263098	TGAGG	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	1068	1072	6.263098	TGAGG	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	1242	1246	6.263098	CCTTA	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	1352	1356	6.263098	TGAGG	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	1488	1492	6.263098	CCTCA	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	1636	1640	6.263098	TAAGG	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	1757	1761	6.263098	CCTCA	3.90625	3.91061
cg1906430	PRDM1	GR-alpha [	1908	1912	6.263098	CCTTA	3.90625	3.91061
cg1906430	PRDM1	TCF-4 [T0	1764	1773	6.262917	ACTTTG	0.04959	0.05016
cg1906430	PRDM1	IRF-1 [T0	347	355	6.24301	TTTCCT	0.16785	0.16909
cg1906430	PRDM1	PEA3 [T0	409	417	6.227095	AGGATG	0.03815	0.03849
cg1906430	PRDM1	SRY [T00	1943	1951	6.176442	GTTTCA	0.15259	0.15366
cg1906430	PRDM1	c-Ets-1 [T	658	664	6.167515	TTTCCA	0.36621	0.36731
cg1906430	PRDM1	c-Myb [T0	485	492	6.157321	GAAAGT	0.21362	0.21535
cg1906430	PRDM1	IRF-1 [T0	532	540	6.078807	ATTTGG	0.16785	0.16909
cg1906430	PRDM1	GR-alpha [	223	227	6.055408	CCTAA	3.90625	3.9065
cg1906430	PRDM1	GR-alpha [	1075	1079	6.055408	TCAGG	3.90625	3.9065
cg1906430	PRDM1	GR-alpha [	1228	1232	6.055408	TCAGG	3.90625	3.9065
cg1906430	PRDM1	GR-alpha [	1446	1450	6.055408	CCTAA	3.90625	3.9065
cg1906430	PRDM1	STAT4 [T	613	618	5.882353	CCTTCC	0.48828	0.48408
cg1906430	PRDM1	IRF-1 [T0	358	366	5.861409	TTTCCT	0.16785	0.16909
cg1906430	PRDM1	ATF-2 [T0	1767	1776	5.798107	TTGACG	0.11826	0.11873
cg1906430	PRDM1	STAT1bet	1653	1662	5.796867	TCTTGG	0.1545	0.1557

cg1906430	PRDM1	VDR [T00	762	770	5.771401	GTTCAG	0.42725	0.42999
cg1906430	PRDM1	VDR [T00	1178	1186	5.771401	ATTGTG	0.42725	0.42999
cg1906430	PRDM1	c-Jun [T00	687	693	5.703976	TGACCC	0.48828	0.48665
cg1906430	PRDM1	c-Jun [T00	1810	1816	5.703976	GGGGTC	0.48828	0.48665
cg1906430	PRDM1	NF-1 [T00	1091	1098	5.626299	GGGACC	0.24414	0.24258
cg1906430	PRDM1	c-Jun [T00	637	643	5.590308	TGACAC	0.48828	0.48665
cg1906430	PRDM1	NFI/CTF [	921	928	5.558661	CCAAGC	0.54932	0.55038
cg1906430	PRDM1	NFI/CTF [	1078	1085	5.558661	GGGATT	0.54932	0.55038
cg1906430	PRDM1	NFI/CTF [	1313	1320	5.558661	AAGATT	0.54932	0.55038
cg1906430	PRDM1	NFI/CTF [	1963	1970	5.558661	CCAAAC	0.54932	0.55038
cg1906430	PRDM1	c-Ets-1 [T	525	531	5.558311	CTTCCC	0.36621	0.3623
cg1906430	PRDM1	TFIID [T	113	119	5.544826	TTCTAA	0.73242	0.75085
cg1906430	PRDM1	TFIID [T	222	228	5.544826	TCCTAA	0.73242	0.75085
cg1906430	PRDM1	TFIID [T	1717	1723	5.544826	TTTAAC	0.73242	0.75085
cg1906430	PRDM1	TFIID [T	1745	1751	5.544826	TTCTAA	0.73242	0.75085
cg1906430	PRDM1	C/EBPalp	74	80	5.455853	ATCAAT	0.73242	0.74391
cg1906430	PRDM1	C/EBPalp	1430	1436	5.455853	CATTGC	0.73242	0.74391
cg1906430	PRDM1	AP-1 [T00	1134	1142	5.408943	TGACTC	0.09155	0.09214
cg1906430	PRDM1	NF-1 [T00	1898	1905	5.377909	CAGGCC	0.24414	0.24258
cg1906430	PRDM1	NF-AT1 [	1451	1459	5.354841	ACCATT	0.03815	0.03856
cg1906430	PRDM1	HNF-1C [	1714	1722	5.345227	CTTTTTA	0.07629	0.07817
cg1906430	PRDM1	MEF-2A [	205	215	5.321562	TATTTG	0.02003	0.02072
cg1906430	PRDM1	RXR-alph	414	420	5.271235	GCAACC	0.61035	0.6044
cg1906430	PRDM1	RXR-alph	1558	1564	5.271235	GGGTGG	0.61035	0.6044
cg1906430	PRDM1	C/EBPalp	1303	1309	5.240291	TATTGA	0.97656	0.99332
cg1906430	PRDM1	GR [T050	1688	1694	5.207533	GTCTTT	0.24414	0.24606
cg1906430	PRDM1	c-Jun [T00	160	166	5.193102	TGACTT	0.61035	0.61057
cg1906430	PRDM1	c-Jun [T00	1840	1846	5.193102	TGACTT	0.61035	0.61057
cg1906430	PRDM1	c-Ets-2 [T	1246	1254	5.162974	ACCAAG	0.13733	0.13828
cg1906430	PRDM1	c-Ets-2 [T	1906	1914	5.162974	TTCCTTA	0.13733	0.13828
cg1906430	PRDM1	NF-AT1 [	343	351	5.125037	CATTTT	0.05341	0.05402
cg1906430	PRDM1	NF-AT1 [	783	791	5.125037	TTTTTTT	0.05341	0.05402
cg1906430	PRDM1	NF-AT1 [	1657	1665	5.125037	GGAAAA	0.05341	0.05402
cg1906430	PRDM1	AP-2alpha	17	22	5.100982	GCCTTT	0.97656	0.97567
cg1906430	PRDM1	AP-2alpha	277	282	5.100982	GCCTTT	0.97656	0.97567
cg1906430	PRDM1	AP-2alpha	539	544	5.100982	AAAGGC	0.97656	0.97567
cg1906430	PRDM1	AP-2alpha	1016	1021	5.100982	AAAGGC	0.97656	0.97567
cg1906430	PRDM1	AP-2alpha	1020	1025	5.100982	GCCTTT	0.97656	0.97567
cg1906430	PRDM1	GR-beta [	53	57	5.042296	GGATT	3.90625	3.95351
cg1906430	PRDM1	GR-beta [	757	761	5.042296	GGATT	3.90625	3.95351
cg1906430	PRDM1	GR-beta [	961	965	5.042296	GTATT	3.90625	3.95351
cg1906430	PRDM1	GR-beta [	1011	1015	5.042296	GGATT	3.90625	3.95351
cg1906430	PRDM1	GR-beta [	1079	1083	5.042296	GGATT	3.90625	3.95351
cg1906430	PRDM1	GR-beta [	1198	1202	5.042296	GGATT	3.90625	3.95351
cg1906430	PRDM1	NFI/CTF [	1095	1102	5.021086	CCAAGG	0.24414	0.24103
cg1906430	PRDM1	HNF-1B [	835	843	4.953067	TTTTTA	0.04578	0.04699
cg1906430	PRDM1	c-Ets-1 [T	429	435	4.910652	CTTCCA	0.48828	0.49031
cg1906430	PRDM1	c-Fos [T00	1130	1139	4.907599	GATATG	0.02289	0.02308

cg1906430	PRDM1	XBP-1 [T0	694	699	4.894955	AGGCAT	0.97656	0.96979
cg1906430	PRDM1	XBP-1 [T0	1236	1241	4.894955	AGGCAT	0.97656	0.96979
cg1906430	PRDM1	NF-1 [T00	917	924	4.880836	TGTACCA	0.24414	0.24398
cg1906430	PRDM1	NF-1 [T00	1327	1334	4.880836	GGTGCCA	0.24414	0.24398
cg1906430	PRDM1	C/EBPalph	1405	1411	4.845599	AATTGAT	0.97656	0.99332
cg1906430	PRDM1	NF-AT1 [T	654	663	4.823485	AGCTTTT	0.07629	0.07704
cg1906430	PRDM1	NF-AT1 [T	1656	1665	4.823485	TGGAAAA	0.07629	0.07704
cg1906430	PRDM1	c-Ets-1 [T0	86	92	4.782565	GTGGAAG	0.48828	0.49031
cg1906430	PRDM1	NF-kappaB	521	531	4.773388	CGGTCTT	0.02432	0.02374
cg1906430	PRDM1	TFII-I [T0	66	71	4.756447	ATATCC	2.92969	2.93695
cg1906430	PRDM1	TFII-I [T0	711	716	4.756447	GGACTG	2.92969	2.93695
cg1906430	PRDM1	TFII-I [T0	757	762	4.756447	GGATTG	2.92969	2.93695
cg1906430	PRDM1	TFII-I [T0	1079	1084	4.756447	GGATTG	2.92969	2.93695
cg1906430	PRDM1	TFII-I [T0	1114	1119	4.756447	GGACAT	2.92969	2.93695
cg1906430	PRDM1	TFII-I [T0	1129	1134	4.756447	GGATAT	2.92969	2.93695
cg1906430	PRDM1	TFII-I [T0	1454	1459	4.756447	ATTTCC	2.92969	2.93695
cg1906430	PRDM1	TFII-I [T0	1971	1976	4.756447	GGAATG	2.92969	2.93695
cg1906430	PRDM1	FOXP3 [T	24	29	4.756447	GAAAAC	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	31	36	4.756447	GTTTTT	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	266	271	4.756447	GTTTTG	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	271	276	4.756447	GTTTTT	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	328	333	4.756447	GTTTTC	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	480	485	4.756447	GTTTTG	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	492	497	4.756447	GTTTTG	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	857	862	4.756447	AAAAAC	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	911	916	4.756447	CTCAAC	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	1371	1376	4.756447	GAAAAC	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	1643	1648	4.756447	GAAAAC	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	1760	1765	4.756447	CAAAAC	2.92969	2.96063
cg1906430	PRDM1	FOXP3 [T	1957	1962	4.756447	GAAAAC	2.92969	2.96063
cg1906430	PRDM1	PPAR-alph	699	709	4.727619	TTCTGGC	0.03242	0.03183
cg1906430	PRDM1	c-Ets-1 [T0	1033	1039	4.654478	CTTCCAC	0.85449	0.85764
cg1906430	PRDM1	c-Ets-1 [T0	1469	1475	4.654478	CTTCCAC	0.85449	0.85764
cg1906430	PRDM1	VDR [T00	1226	1234	4.617121	GTTCAGC	0.37384	0.37445
cg1906430	PRDM1	VDR [T00	1573	1581	4.617121	TCAGTGA	0.37384	0.37445
cg1906430	PRDM1	NF-kappaB	61	71	4.595042	GGGGAA	0.03242	0.03169
cg1906430	PRDM1	C/EBPalph	1080	1086	4.560723	GATTGGC	0.24414	0.24411
cg1906430	PRDM1	STAT4 [T	88	93	4.411765	GGAAGC	1.95312	1.94235
cg1906430	PRDM1	STAT4 [T	428	433	4.411765	TCTTCC	1.95312	1.94235
cg1906430	PRDM1	STAT4 [T	524	529	4.411765	TCTTCC	1.95312	1.94235
cg1906430	PRDM1	STAT4 [T	619	624	4.411765	TCTTCC	1.95312	1.94235
cg1906430	PRDM1	STAT4 [T	993	998	4.411765	GGAACG	1.95312	1.94235
cg1906430	PRDM1	STAT4 [T	1032	1037	4.411765	TCTTCC	1.95312	1.94235
cg1906430	PRDM1	STAT4 [T	1468	1473	4.411765	TCTTCC	1.95312	1.94235
cg1906430	PRDM1	STAT4 [T	1971	1976	4.411765	GGAATG	1.95312	1.94235
cg1906430	PRDM1	c-Ets-1 [T0	227	233	4.411026	AAGGAA	0.85449	0.85764
cg1906430	PRDM1	c-Ets-1 [T0	1249	1255	4.411026	AAGGAA	0.85449	0.85764
cg1906430	PRDM1	c-Ets-1 [T0	1905	1911	4.411026	ATTCCTT	0.85449	0.85764

cg1906430	PRDM1	p53 [T006	1603	1609	4.33696	CTGGCC	0.24414	0.23584
cg1906430	PRDM1	GR-beta [	204	208	4.201913	CTATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	249	253	4.201913	TTATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	374	378	4.201913	TGATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	771	775	4.201913	TGATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	1302	1306	4.201913	TTATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	1402	1406	4.201913	AATAA	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	1408	1412	4.201913	TGATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	1416	1420	4.201913	CTATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	1732	1736	4.201913	TTATT	7.8125	7.94607
cg1906430	PRDM1	GR-beta [	1983	1987	4.201913	TGATT	7.8125	7.94607
cg1906430	PRDM1	NF-Y [T0	1316	1323	4.186615	ATTGGG	0.18311	0.1853
cg1906430	PRDM1	NF-AT1 [	22	31	4.134416	TGGAAA	0.08392	0.08485
cg1906430	PRDM1	IRF-1 [T0	1442	1450	4.035054	TTTCCCT	0.1297	0.13087
cg1906430	PRDM1	RXR-alph	1741	1747	4.019014	GGGTTT	0.97656	0.9671
cg1906430	PRDM1	c-Ets-2 [T	224	232	4.017001	CTAAAG	0.16022	0.16243
cg1906430	PRDM1	c-Ets-2 [T	1024	1032	4.017001	TTCCTTT	0.16022	0.16243
cg1906430	PRDM1	EBF [T05	1191	1201	4.016439	ACCCCT	0.0248	0.02398
cg1906430	PRDM1	TFIID [T	248	254	4.007279	TTTATTA	1.09863	1.13456
cg1906430	PRDM1	TFIID [T	250	256	4.007279	TATTAA	1.09863	1.13456
cg1906430	PRDM1	TFIID [T	940	946	4.007279	TTTTAA	1.09863	1.13456
cg1906430	PRDM1	TFIID [T	1498	1504	4.007279	TAGTAA	1.09863	1.13456
cg1906430	PRDM1	TFIID [T	1669	1675	4.007279	TTTAAT	1.09863	1.13456
cg1906430	PRDM1	TFIID [T	1731	1737	4.007279	TTTATTA	1.09863	1.13456
cg1906430	PRDM1	TFIID [T	1775	1781	4.007279	TTTATG	1.09863	1.13456
cg1906430	PRDM1	AP-2alpha	875	880	3.970052	CAAGGC	0.97656	0.96469
cg1906430	PRDM1	AP-2alpha	1356	1361	3.970052	GCCTTG	0.97656	0.96469
cg1906430	PRDM1	AR [T000	1609	1617	3.814754	CTAGTG	0.06866	0.06828
cg1906430	PRDM1	c-Jun [T00	964	970	3.807346	TTAGTC	0.24414	0.24526
cg1906430	PRDM1	CREB [T0	1768	1776	3.80543	TGACGT	0.06104	0.06123
cg1906430	PRDM1	NFI/CTF [	17	24	3.793671	GCCTTT	0.18311	0.18109
cg1906430	PRDM1	GR [T050	265	271	3.763516	TGTTTT	0.73242	0.74251
cg1906430	PRDM1	GR [T050	479	485	3.763516	TGTTTT	0.73242	0.74251
cg1906430	PRDM1	GR [T050	491	497	3.763516	TGTTTT	0.73242	0.74251
cg1906430	PRDM1	GR [T050	1760	1766	3.763516	CAAAAC	0.73242	0.74251
cg1906430	PRDM1	GR [T050	1934	1940	3.763516	CTCTTT	0.73242	0.74251
cg1906430	PRDM1	p53 [T006	1886	1892	3.750231	GGGCTG	0.73242	0.71379
cg1906430	PRDM1	p53 [T006	1891	1897	3.750231	GGGCTG	0.73242	0.71379
cg1906430	PRDM1	AP-2alpha	1475	1480	3.743866	GCCTTC	0.48828	0.48238
cg1906430	PRDM1	IRF-1 [T0	1023	1031	3.692688	TTTCCTT	0.06866	0.06927
cg1906430	PRDM1	c-Ets-1 [T	1485	1491	3.590463	GTTCCT	0.61035	0.60765
cg1906430	PRDM1	C/EBPalp	758	764	3.555778	GATTGT	0.24414	0.24752
cg1906430	PRDM1	c-Myb [T0	1544	1551	3.555283	CAACTT	0.12207	0.12203
cg1906430	PRDM1	c-Ets-2 [T	1456	1464	3.518824	TTCCTT	0.18311	0.18304
cg1906430	PRDM1	NF-Y [T0	1081	1088	3.490142	ATTGGC	0.48828	0.48904
cg1906430	PRDM1	c-Ets-1 [T	991	997	3.462376	CAGGAA	0.61035	0.60765
cg1906430	PRDM1	NF-AT1 [	572	581	3.445347	GCGCTT	0.07629	0.07722
cg1906430	PRDM1	PXR-1:RX	1223	1230	3.395883	TCGGTT	0.12207	0.12271

cg1906430	PRDM1	RXR-alpha	550	556	3.392904	GGGTTC	1.09863	1.08572
cg1906430	PRDM1	RXR-alpha	686	692	3.392904	ATGACC	1.09863	1.08572
cg1906430	PRDM1	RXR-alpha	1811	1817	3.392904	GGGTCA	1.09863	1.08572
cg1906430	PRDM1	RXR-alpha	1927	1933	3.392904	GGGTAC	1.09863	1.08572
cg1906430	PRDM1	AR [T000	1821	1829	3.382886	AAAGTG	0.06866	0.06905
cg1906430	PRDM1	GR-beta [T	65	69	3.361531	AATAT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	186	190	3.361531	AGATT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1253	1257	3.361531	AATCT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1314	1318	3.361531	AGATT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1334	1338	3.361531	AATCT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1384	1388	3.361531	AATCT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1511	1515	3.361531	AATAT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1512	1516	3.361531	ATATT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1627	1631	3.361531	AATAT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1672	1676	3.361531	AATAT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1673	1677	3.361531	ATATT	3.90625	3.99611
cg1906430	PRDM1	IRF-1 [T0	330	338	3.352297	TTTCCCC	0.06866	0.06927
cg1906430	PRDM1	HNF-1B [	1506	1514	3.302045	AGTTAA	0.04578	0.0471
cg1906430	PRDM1	PR B [T00	726	732	3.29756	AACATT	0.24414	0.25122
cg1906430	PRDM1	PR A [T01	726	732	3.29756	AACATT	0.24414	0.25122
cg1906430	PRDM1	c-Ets-2 [T	1486	1494	3.2883	TTCCTCA	0.18311	0.18304
cg1906430	PRDM1	NF-Y [T0	1524	1531	3.263282	ATTGGC	0.48828	0.48904
cg1906430	PRDM1	c-Jun [T00	1134	1140	3.244843	TGACTC	0.24414	0.24403
cg1906430	PRDM1	AP-2alpha	383	388	3.229049	AGAGGC	0.48828	0.48238
cg1906430	PRDM1	AP-2alpha	597	602	3.229049	AGAGGC	0.48828	0.48238
cg1906430	PRDM1	AP-2alpha	973	978	3.229049	GCCTCT	0.48828	0.48238
cg1906430	PRDM1	AP-2alpha	1147	1152	3.229049	AGAGGC	0.48828	0.48238
cg1906430	PRDM1	AP-2alpha	1293	1298	3.229049	GCCTCT	0.48828	0.48238
cg1906430	PRDM1	AP-2alpha	1916	1921	3.229049	GCCTCT	0.48828	0.48238
cg1906430	PRDM1	RXR-alpha	1958	1964	3.170788	AAAACC	0.24414	0.24522
cg1906430	PRDM1	PEA3 [T0	441	449	3.113548	AGGATG	0.01526	0.01554
cg1906430	PRDM1	p53 [T006	717	723	3.028543	TGTGCC	0.48828	0.47786
cg1906430	PRDM1	C/EBPalph	1409	1415	3.014837	GATTGC	0.48828	0.4911
cg1906430	PRDM1	C/EBPalph	1177	1183	2.981957	CATTGT	0.48828	0.4911
cg1906430	PRDM1	c-Ets-2 [T	788	796	2.945838	TTCCTTT	0.06104	0.06231
cg1906430	PRDM1	STAT4 [T	63	68	2.941176	GGAATA	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	196	201	2.941176	GGAAAG	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	513	518	2.941176	GGAAAG	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	551	556	2.941176	GGTTCC	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	575	580	2.941176	CTTTCC	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	1022	1027	2.941176	CTTTCC	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	1251	1256	2.941176	GGAATC	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	1441	1446	2.941176	CTTTCC	2.92969	2.929
cg1906430	PRDM1	STAT4 [T	1484	1489	2.941176	TGTTCC	2.92969	2.929
cg1906430	PRDM1	IRF-1 [T0	1455	1463	2.890712	TTTCCTT	0.07629	0.07756
cg1906430	PRDM1	p53 [T006	1040	1046	2.813291	GCTGCC	0.48828	0.47786
cg1906430	PRDM1	NF-1 [T00	365	372	2.813149	TGGTCC	0.24414	0.24101
cg1906430	PRDM1	PR B [T00	758	764	2.80933	GATTGT	0.73242	0.74818

cg1906430	PRDM1	PR A [T01	758	764	2.80933	GATTGT	0.73242	0.74818
cg1906430	PRDM1	AR [T000	704	712	2.808697	GGACAC	0.06104	0.06058
cg1906430	PRDM1	AR [T000	1002	1010	2.808697	GGACAA	0.06104	0.06058
cg1906430	PRDM1	NF-AT1 [	535	544	2.756277	TGGAAA	0.05913	0.05995
cg1906430	PRDM1	c-Myb [T0	878	885	2.570796	GGCAGT	0.06104	0.06117
cg1906430	PRDM1	AP-2alpha	648	653	2.550491	TGAGGC	0.48828	0.48266
cg1906430	PRDM1	AP-2alpha	1352	1357	2.550491	TGAGGC	0.48828	0.48266
cg1906430	PRDM1	RXR-alph	337	343	2.544678	TTCACC	0.85449	0.84796
cg1906430	PRDM1	RXR-alph	1562	1568	2.544678	GGGTGA	0.85449	0.84796
cg1906430	PRDM1	PXR-1:RX	1577	1584	2.454225	TGAACT	0.12207	0.12266
cg1906430	PRDM1	NF-AT1 [	654	662	2.449764	AGCTTT	0.09155	0.0926
cg1906430	PRDM1	LEF-1 [T0	1878	1885	2.345041	CTTTGC	0.09155	0.09192
cg1906430	PRDM1	LEF-1 [T0	1936	1943	2.345041	CTTTGT	0.09155	0.09192
cg1906430	PRDM1	RXR-alph	673	679	2.322562	GGGTCT	0.85449	0.84796
cg1906430	PRDM1	Elk-1 [T00	614	622	2.299314	CTTCCT	0.09155	0.09114
cg1906430	PRDM1	LEF-1 [T0	1690	1697	2.21836	CTTTGG	0.18311	0.18582
cg1906430	PRDM1	GATA-1 [	67	72	2.176375	TATCCT	3.90625	3.92756
cg1906430	PRDM1	GATA-1 [	1754	1759	2.176375	TATCCT	3.90625	3.92756
cg1906430	PRDM1	Elk-1 [T00	620	628	2.164966	CTTCCT	0.05341	0.05317
cg1906430	PRDM1	c-Ets-2 [T	621	629	2.142327	TTCCTC	0.16785	0.16856
cg1906430	PRDM1	RelA [T00	60	70	2.119657	GGGGGA	0.00477	0.00477
cg1906430	PRDM1	NF-AT1 [	195	204	2.067208	TGGAAA	0.03815	0.03874
cg1906430	PRDM1	NF-kappa	61	72	2.044445	GGGGAA	0.00322	0.00317
cg1906430	PRDM1	HNF-1C [	1507	1515	1.940349	GTTAAA	0.02289	0.02363
cg1906430	PRDM1	GATA-1 [	1128	1133	1.896347	CGGATA	3.90625	3.92756
cg1906430	PRDM1	AP-2alpha	470	475	1.871933	GGAGGC	0.97656	0.95407
cg1906430	PRDM1	AP-2alpha	1234	1239	1.871933	GGAGGC	0.97656	0.95407
cg1906430	PRDM1	TBP [T00	888	897	1.871542	TTTATA	0.18311	0.18942
cg1906430	PRDM1	TFII-I [T0	235	240	1.824994	CTCTCC	0.48828	0.48408
cg1906430	PRDM1	TFII-I [T0	624	629	1.824994	CTCTCC	0.48828	0.48408
cg1906430	PRDM1	FOXP3 [T	1620	1625	1.824994	GTTGTA	0.48828	0.49451
cg1906430	PRDM1	NF-Y [T0	1899	1906	1.749852	AGGCCA	0.18311	0.18459
cg1906430	PRDM1	GR-beta [	170	174	1.680765	GAATT	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	171	175	1.680765	AATTC	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	230	234	1.680765	GAATT	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	231	235	1.680765	AATTC	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	244	248	1.680765	GAATT	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	696	700	1.680765	GCATT	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	851	855	1.680765	GCATT	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	1422	1426	1.680765	AATTC	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	1429	1433	1.680765	GCATT	3.90625	3.94936
cg1906430	PRDM1	GR-beta [	1904	1908	1.680765	AATTC	3.90625	3.94936
cg1906430	PRDM1	c-Ets-2 [T	348	356	1.64415	TTCCTC	0.04578	0.04579
cg1906430	PRDM1	c-Ets-1 [T	787	793	1.641124	TTTCCTT	0.36621	0.36952
cg1906430	PRDM1	c-Ets-1 [T	1023	1029	1.641124	TTTCCTT	0.36621	0.36952
cg1906430	PRDM1	c-Ets-1 [T	1455	1461	1.641124	TTTCCTT	0.36621	0.36952
cg1906430	PRDM1	C/EBPbeta	21	24	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	58	61	1.639871	TTGG	15.625	15.72563

cg1906430	PRDM1	C/EBPbeta	106	109	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	288	291	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	369	372	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	500	503	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	534	537	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	901	904	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	921	924	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1047	1050	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1082	1085	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1095	1098	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1247	1250	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1275	1278	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1317	1320	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1331	1334	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1517	1520	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1525	1528	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1655	1658	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1692	1695	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1703	1706	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1902	1905	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1963	1966	1.639871	CCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1969	1972	1.639871	TTGG	15.625	15.72563
cg1906430	PRDM1	XBP-1 [T	686	691	1.583727	ATGACC	0.97656	0.98146
cg1906430	PRDM1	XBP-1 [T	1812	1817	1.583727	GGTCAT	0.97656	0.98146
cg1906430	PRDM1	Pax-5 [T0	1344	1350	1.537547	CTTGCCC	0.73242	0.71311
cg1906430	PRDM1	Pax-5 [T0	1603	1609	1.537547	CTGGCCC	0.73242	0.71311
cg1906430	PRDM1	TFIID [T0	22	28	1.537547	TGGAAA	0.73242	0.75096
cg1906430	PRDM1	TFIID [T0	481	487	1.537547	TTTTGA	0.73242	0.75096
cg1906430	PRDM1	TFIID [T0	535	541	1.537547	TGGAAA	0.73242	0.75096
cg1906430	PRDM1	TFIID [T0	657	663	1.537547	TTTTCCA	0.73242	0.75096
cg1906430	PRDM1	TFIID [T0	1656	1662	1.537547	TGGAAA	0.73242	0.75096
cg1906430	PRDM1	TFIID [T0	1817	1823	1.537547	TGTAAA	0.73242	0.75096
cg1906430	PRDM1	IRF-1 [T0	192	200	1.529008	AAATGG	0.04578	0.04655
cg1906430	PRDM1	IRF-1 [T0	576	584	1.529008	TTTCCAT	0.04578	0.04655
cg1906430	PRDM1	c-Ets-1 [T	347	353	1.513038	TTTCCTC	0.36621	0.36952
cg1906430	PRDM1	STAT4 [T	23	28	1.470588	GGAAAA	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	169	174	1.470588	GGAATT	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	229	234	1.470588	GGAATT	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	243	248	1.470588	GGAATT	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	329	334	1.470588	TTTTCC	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	346	351	1.470588	TTTTCC	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	357	362	1.470588	TTTTCC	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	536	541	1.470588	GGAAAA	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	657	662	1.470588	TTTTCC	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	786	791	1.470588	TTTTCC	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	792	797	1.470588	TTTTCC	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	1657	1662	1.470588	GGAAAA	1.95312	1.96333
cg1906430	PRDM1	STAT4 [T	1904	1909	1.470588	AATTCC	1.95312	1.96333

cg1906430	PRDM1	GR [T050	271	277	1.444018	GTTTTTC	0.12207	0.1245
cg1906430	PRDM1	c-Ets-1 [T	358	364	1.384951	TTTCCTC	0.36621	0.36952
cg1906430	PRDM1	C/EBPbeta	75	78	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	283	286	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	483	486	1.366559	TTGA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	874	877	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	912	915	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1158	1161	1.366559	TTGA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1263	1266	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1305	1308	1.366559	TTGA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1351	1354	1.366559	TTGA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1407	1410	1.366559	TTGA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1420	1423	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1479	1482	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1583	1586	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1759	1762	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1767	1770	1.366559	TTGA	15.625	15.72563
cg1906430	PRDM1	C/EBPbeta	1946	1949	1.366559	TCAA	15.625	15.72563
cg1906430	PRDM1	IRF-1 [T0	787	795	1.274173	TTTCCTT	0.04578	0.04655
cg1906430	PRDM1	T3R-beta1	765	773	1.110682	CAGAGG	0.07629	0.07585
cg1906430	PRDM1	c-Ets-2 [T	615	623	1.071163	TTCCTCT	0.06104	0.06166
cg1906430	PRDM1	SRY [T00	1936	1944	0.999172	CTTTGTT	0.06104	0.06205
cg1906430	PRDM1	E2F-1 [T0	999	1006	0.993583	GCGGGA	0.03052	0.02978
cg1906430	PRDM1	HOXD9 [	244	253	0.954221	GAATTT	0.01526	0.01593
cg1906430	PRDM1	HOXD10 [	244	253	0.954221	GAATTT	0.01526	0.01593
cg1906430	PRDM1	GR-beta [	193	197	0.840383	AATGG	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	284	288	0.840383	CAATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	342	346	0.840383	CCATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	530	534	0.840383	CCATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	579	583	0.840383	CCATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	591	595	0.840383	TCATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1006	1010	0.840383	AATGG	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1111	1115	0.840383	AATGG	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1404	1408	0.840383	TAATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1405	1409	0.840383	AATTG	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1421	1425	0.840383	CAATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1452	1456	0.840383	CCATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1463	1467	0.840383	TCATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1494	1498	0.840383	TAATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1495	1499	0.840383	AATTA	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1523	1527	0.840383	AATTG	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1568	1572	0.840383	AATTG	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1696	1700	0.840383	TAATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1697	1701	0.840383	AATTA	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1903	1907	0.840383	CAATT	7.8125	7.94706
cg1906430	PRDM1	GR-beta [	1973	1977	0.840383	AATGA	7.8125	7.94706
cg1906430	PRDM1	GATA-1 [	1394	1399	0.758539	TATCAG	1.95312	1.98662
cg1906430	PRDM1	AP-2alpha	1228	1233	0.678558	TCAGGC	0.48828	0.48199

cg1906430	PRDM1	C/EBPalp	1315	1321	0.540941	GATTGG	0.24414	0.24507
cg1906430	PRDM1	TCF-4 [T0	1943	1952	0.53631	GTTTCA	0.01907	0.01932
cg1906430	PRDM1	PR B [T00	27	33	0.48823	AACAGT	0.12207	0.12407
cg1906430	PRDM1	PR B [T00	1481	1487	0.48823	AACTGT	0.12207	0.12407
cg1906430	PRDM1	PR B [T00	1503	1509	0.48823	AACAGT	0.12207	0.12407
cg1906430	PRDM1	PR A [T01	27	33	0.48823	AACAGT	0.12207	0.12407
cg1906430	PRDM1	PR A [T01	1481	1487	0.48823	AACTGT	0.12207	0.12407
cg1906430	PRDM1	PR A [T01	1503	1509	0.48823	AACAGT	0.12207	0.12407
cg1906430	PRDM1	AP-2alpha	692	697	0.226186	CCAGGC	0.97656	0.95305
cg1906430	PRDM1	AP-2alpha	1036	1041	0.226186	CCAGGC	0.97656	0.95305
cg1906430	PRDM1	p53 [T006	1344	1350	0.211706	CTTGCC	0.36621	0.35912
cg1906430	PRDM1	GR-alpha [	8	12	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	18	22	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	226	230	0.207689	AAAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	278	282	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	353	357	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	383	387	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	419	423	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	439	443	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	463	467	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	539	543	0.207689	AAAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	597	601	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	617	621	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	623	627	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	743	747	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	766	770	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	790	794	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	974	978	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1016	1020	0.207689	AAAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1021	1025	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1026	1030	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1087	1091	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1147	1151	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1285	1289	0.207689	AGAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1294	1298	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1376	1380	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1806	1810	0.207689	AAAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1828	1832	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1877	1881	0.207689	CCTTT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1917	1921	0.207689	CCTCT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1948	1952	0.207689	AAAGG	7.8125	7.81264
cg1906430	PRDM1	HNF-1A [	1507	1514	0.143882	GTTAAA	0.24414	0.25261
cg1906430	PRDM1	c-Ets-1 [T	614	620	0.128087	CTTCCT	0.24414	0.2429
cg1906430	PRDM1	c-Ets-1 [T	620	626	0.128087	CTTCCT	0.24414	0.2429
cg1906430	PRDM1	GATA-1 [	1364	1369	0.105011	TATCTC	0.97656	0.98738
cg1906430	PRDM1	GATA-1 [	1629	1634	0.105011	TATCTC	0.97656	0.98738
cg1906430	PRDM1	GR-alpha [	361	365	0	CCTGT	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	990	994	0	ACAGG	7.8125	7.81264

cg1906430	PRDM1	GR-alpha [	1555	1559	0	ATAGG	7.8125	7.81264
cg1906430	PRDM1	GR-alpha [	1617	1621	0	CCTGT	7.8125	7.81264
cg1906430	PRDM1	AP-2alpha	321	326	0	GCAGGC	0.97656	0.95305
cg1906430	PRDM1	AP-2alpha	543	548	0	GCAGGC	0.97656	0.95305
cg1906430	PRDM1	AP-2alpha	1897	1902	0	GCAGGC	0.97656	0.95305
cg1906430	PRDM1	XBP-1 [T0	966	971	0	AGTCAT	0.97656	0.98127
cg1906430	PRDM1	XBP-1 [T0	1133	1138	0	ATGACT	0.97656	0.98127
cg1906430	PRDM1	XBP-1 [T0	1839	1844	0	ATGACT	0.97656	0.98127
cg1906430	PRDM1	Pax-5 [T0	1886	1892	0	GGGCTG	1.09863	1.06846
cg1906430	PRDM1	Pax-5 [T0	1891	1897	0	GGGCTG	1.09863	1.06846
cg1906430	PRDM1	TFII-I [T0	196	201	0	GGAAAG	1.46484	1.45997
cg1906430	PRDM1	TFII-I [T0	513	518	0	GGAAAG	1.46484	1.45997
cg1906430	PRDM1	TFII-I [T0	575	580	0	CTTTCC	1.46484	1.45997
cg1906430	PRDM1	TFII-I [T0	1022	1027	0	CTTTCC	1.46484	1.45997
cg1906430	PRDM1	TFII-I [T0	1143	1148	0	GGACAG	1.46484	1.45997
cg1906430	PRDM1	TFII-I [T0	1441	1446	0	CTTTCC	1.46484	1.45997
cg1906430	PRDM1	TFII-I [T0	1753	1758	0	CTATCC	1.46484	1.45997
cg1906430	PRDM1	STAT4 [T	1454	1459	0	ATTTCC	0.48828	0.49387
cg1906430	PRDM1	YY1 [T00	194	197	0	ATGG	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	342	345	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	432	435	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	530	533	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	579	582	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	684	687	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	738	741	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	1007	1010	0	ATGG	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	1104	1107	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	1112	1115	0	ATGG	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	1118	1121	0	ATGG	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	1212	1215	0	ATGG	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	1452	1455	0	CCAT	7.8125	7.81711
cg1906430	PRDM1	YY1 [T00	1791	1794	0	ATGG	7.8125	7.81711
cg1906430	PRDM1	ER-alpha [	687	691	0	TGACC	1.95312	1.9404
cg1906430	PRDM1	ER-alpha [	1812	1816	0	GGTCA	1.95312	1.9404
cg1906430	PRDM1	GATA-1 [	1863	1868	0	TATCTG	0.97656	0.98738
cg1906430	PRDM1	C/EBPbeta	1	4	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	15	18	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	82	85	0	ACAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	99	102	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	121	124	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	208	211	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	269	272	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	275	278	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	302	305	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	304	307	0	GCAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	414	417	0	GCAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	478	481	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	490	493	0	TTGT	15.625	15.71349

cg1906430	PRDM1	C/EBPbeta	495	498	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	630	633	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	634	637	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	760	763	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	809	812	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	864	867	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1004	1007	0	ACAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1179	1182	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1308	1311	0	ACAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1345	1348	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1359	1362	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1411	1414	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1427	1430	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1432	1435	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1520	1523	0	GCAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1543	1546	0	GCAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1548	1551	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1570	1573	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1621	1624	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1625	1628	0	ACAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1682	1685	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1721	1724	0	ACAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1880	1883	0	TTGC	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1938	1941	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1941	1944	0	TTGT	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1978	1981	0	GCAA	15.625	15.71349
cg1906430	PRDM1	C/EBPbeta	1987	1990	0	TTGT	15.625	15.71349
cg1906430	PRDM1	TFIID [T0	280	286	0	TTTTCAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	834	840	0	TTTTTTA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	835	841	0	TTTTTAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	854	860	0	TTTAAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	855	861	0	TTAAAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	871	877	0	TTTTCAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	1260	1266	0	TTTTCAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	1536	1542	0	TAGAAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	1715	1721	0	TTTTTAA	1.09863	1.13474
cg1906430	PRDM1	TFIID [T0	1746	1752	0	TCTAAA	1.09863	1.13474
cg1906430	PRDM1	FOXP3 [T	0	5	0	GTTGTT	1.46484	1.47315
cg1906430	PRDM1	FOXP3 [T	477	482	0	GTTGTT	1.46484	1.47315
cg1906430	PRDM1	FOXP3 [T	489	494	0	GTTGTT	1.46484	1.47315
cg1906430	PRDM1	FOXP3 [T	1940	1945	0	GTTGTT	1.46484	1.47315
cg1906430	PRDM1	c-Myb [T0	473	480	0	GGCAGT	0.03052	0.03022
cg1906430	PRDM1	GR-beta [T	77	81	0	AATGT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	117	121	0	AAATT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	118	122	0	AATTT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	245	249	0	AATTT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	285	289	0	AATTT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	727	731	0	ACATT	3.90625	3.99611

cg1906430	PRDM1	GR-beta [T	814	818	0	ACATT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1176	1180	0	ACATT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1522	1526	0	AAATT	3.90625	3.99611
cg1906430	PRDM1	GR-beta [T	1567	1571	0	AAATT	3.90625	3.99611
cg1906430	PRDM1	PR B [T00	1277	1283	0	AACAGT	0.36621	0.36944
cg1906430	PRDM1	PR B [T00	1856	1862	0	CACTGT	0.36621	0.36944
cg1906430	PRDM1	PR A [T01	1277	1283	0	AACAGT	0.36621	0.36944
cg1906430	PRDM1	PR A [T01	1856	1862	0	CACTGT	0.36621	0.36944
cg1906430	PRDM1	GR [T050	11	17	0	TTTTTTG	0.36621	0.37562
cg1906430	PRDM1	TCF-4E [T	1878	1884	0	CTTTGC	0.12207	0.12262
cg1906430	PRDM1	HNF-1A [	835	842	0	TTTTTAA	0.24414	0.25261
cg1906430	PRDM1	HNF-1A [	1715	1722	0	TTTTTAA	0.24414	0.25261
cg1906430	PRDM1	IRF-2 [T0	371	376	0	AAGTGA	0.48828	0.49387
cg1906430	PRDM1	IRF-2 [T0	1781	1786	0	AAGTGA	0.48828	0.49387
cg1906430	PRDM1	IRF-2 [T0	1786	1791	0	AAGTGA	0.48828	0.49387
cg0735116	PSRC1	HNF-1C [	1706	1714	9.996165	GTTAGG	0.10681	0.09927
cg0735116	PSRC1	RAR-beta:	1476	1487	9.97066	TACCGT	0.06974	0.07677
cg0735116	PSRC1	c-Myb [T0	1616	1623	9.815171	GAACTT	0.36621	0.34605
cg0735116	PSRC1	XBP-1 [T	1824	1829	9.789909	ATGGCG	1.95312	1.94901
cg0735116	PSRC1	PR B [T00	1443	1449	9.743489	CGGTGT	1.09863	1.0981
cg0735116	PSRC1	PR B [T00	1504	1510	9.743489	GGGTGT	1.09863	1.0981
cg0735116	PSRC1	PR A [T01	1443	1449	9.743489	CGGTGT	1.09863	1.0981
cg0735116	PSRC1	PR A [T01	1504	1510	9.743489	GGGTGT	1.09863	1.0981
cg0735116	PSRC1	LEF-1 [T0	25	32	9.72404	AGACAA	0.21362	0.21229
cg0735116	PSRC1	LEF-1 [T0	388	395	9.72404	AGGCAA	0.21362	0.21229
cg0735116	PSRC1	c-Jun [T00	1754	1760	9.717135	CAGGTC	0.73242	0.7366
cg0735116	PSRC1	Elk-1 [T00	216	224	9.62002	CTTCCC	0.07629	0.0786
cg0735116	PSRC1	Elk-1 [T00	965	973	9.62002	GGAGGG	0.07629	0.0786
cg0735116	PSRC1	c-Ets-1 [T	696	702	9.585075	CGGGAA	0.36621	0.37402
cg0735116	PSRC1	TFIID [T0	726	732	9.552105	TTTCGA	1.46484	1.37777
cg0735116	PSRC1	TFIID [T0	1412	1418	9.552105	TGTGAA	1.46484	1.37777
cg0735116	PSRC1	Pax-5 [T0	489	495	9.552105	GCCGCC	1.46484	1.61918
cg0735116	PSRC1	Pax-5 [T0	520	526	9.552105	GGGCGG	1.46484	1.61918
cg0735116	PSRC1	Pax-5 [T0	1110	1116	9.552105	GGGCGC	1.46484	1.61918
cg0735116	PSRC1	Pax-5 [T0	1381	1387	9.552105	TTTGCC	1.46484	1.61918
cg0735116	PSRC1	Pax-5 [T0	1516	1522	9.552105	GTAGCC	1.46484	1.61918
cg0735116	PSRC1	Pax-5 [T0	1598	1604	9.552105	GTTGCC	1.46484	1.61918
cg0735116	PSRC1	Pax-5 [T0	1605	1611	9.552105	GGGCCA	1.46484	1.61918
cg0735116	PSRC1	NF-1 [T00	1108	1115	9.535536	TTGGGC	0.73242	0.74634
cg0735116	PSRC1	NF-AT1 [	1094	1102	9.521781	GGAAAT	0.16785	0.16528
cg0735116	PSRC1	NF-1 [T00	1318	1325	9.513281	CAACCC	0.73242	0.74634
cg0735116	PSRC1	FOXP3 [T	121	126	9.512894	ATAAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	465	470	9.512894	CCCAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	565	570	9.512894	GTTCTG	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	666	671	9.512894	CGCAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	683	688	9.512894	CGCAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	840	845	9.512894	GAGAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1045	1050	9.512894	CAGAAC	7.32422	7.22156

cg0735116	PSRC1	FOXP3 [T	1185	1190	9.512894	CTAAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1214	1219	9.512894	GTTCTC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1248	1253	9.512894	AAGAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1278	1283	9.512894	AGCAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1339	1344	9.512894	CAGAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1355	1360	9.512894	GTTTAG	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1426	1431	9.512894	GTTGGT	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1559	1564	9.512894	ACCAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1598	1603	9.512894	GTTGCC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1638	1643	9.512894	CAGAAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1740	1745	9.512894	GTTGGC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1922	1927	9.512894	GTTTAC	7.32422	7.22156
cg0735116	PSRC1	FOXP3 [T	1937	1942	9.512894	GGCAAC	7.32422	7.22156
cg0735116	PSRC1	TFII-I [T0	46	51	9.512894	GGAAAA	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	58	63	9.512894	GGATAA	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	100	105	9.512894	AAGTCC	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	237	242	9.512894	CCTTCC	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	246	251	9.512894	AAATCC	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	322	327	9.512894	GTATCC	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	445	450	9.512894	GGAACG	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	635	640	9.512894	GTGTCC	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	846	851	9.512894	CGTTCC	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	1164	1169	9.512894	TTTTCC	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	1454	1459	9.512894	GGATAA	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	1493	1498	9.512894	GGATTT	7.32422	7.44385
cg0735116	PSRC1	TFII-I [T0	1978	1983	9.512894	GGAATT	7.32422	7.44385
cg0735116	PSRC1	c-Jun [T00	87	93	9.442241	TGACAG	0.73242	0.7366
cg0735116	PSRC1	NFI/CTF [	97	104	9.352332	CCAAAG	0.54932	0.55369
cg0735116	PSRC1	NFI/CTF [	104	111	9.352332	CCAAGG	0.54932	0.55369
cg0735116	PSRC1	NFI/CTF [	335	342	9.352332	CCAAGG	0.54932	0.55369
cg0735116	PSRC1	LEF-1 [T0	95	102	9.313676	CCCCAA	0.21362	0.21229
cg0735116	PSRC1	c-Ets-1 [T	847	853	9.276861	GTTCCC	0.36621	0.37402
cg0735116	PSRC1	SRY [T00	1267	1275	9.264664	GGTGCA	0.12207	0.11857
cg0735116	PSRC1	RAR-alph	375	387	9.192562	GGGGTC	0.02065	0.02209
cg0735116	PSRC1	c-Myb [T0	1322	1329	9.110773	CCAAGT	0.39673	0.37851
cg0735116	PSRC1	c-Myb [T0	1345	1352	9.110773	CCAAGT	0.39673	0.37851
cg0735116	PSRC1	NFI/CTF [	466	473	9.042931	CCAACT	0.48828	0.48845
cg0735116	PSRC1	E2F-1 [T0	544	551	9.028527	CTCCCC	0.27466	0.30178
cg0735116	PSRC1	GR [T050	1506	1512	8.971049	GTGTTT	0.61035	0.5928
cg0735116	PSRC1	GR [T050	1540	1546	8.971049	GTATTT	0.61035	0.5928
cg0735116	PSRC1	GR [T050	1927	1933	8.971049	CAAATA	0.61035	0.5928
cg0735116	PSRC1	AP-1 [T00	1715	1723	8.94997	TCTAAG	0.24414	0.23028
cg0735116	PSRC1	Elk-1 [T00	642	650	8.931691	CTTCCC	0.24414	0.26271
cg0735116	PSRC1	c-Ets-1 [T	443	449	8.8926	CGGGAA	0.85449	0.84987
cg0735116	PSRC1	c-Myb [T0	993	1000	8.872587	GAACTC	0.39673	0.37851
cg0735116	PSRC1	c-Ets-1 [T	1652	1658	8.809329	CTGGAA	0.85449	0.84987
cg0735116	PSRC1	LEF-1 [T0	1758	1765	8.759086	TCACAA	0.54932	0.53171
cg0735116	PSRC1	XBP-1 [T	110	115	8.75604	TCTCAT	2.92969	2.75329

cg07351160	PSRC1	XBP-1 [T	151	156	8.75604	ATGAAA	2.92969	2.75329
cg07351160	PSRC1	XBP-1 [T	209	214	8.75604	TTTCAT	2.92969	2.75329
cg07351160	PSRC1	XBP-1 [T	1728	1733	8.75604	ATGAGA	2.92969	2.75329
cg07351160	PSRC1	XBP-1 [T	1830	1835	8.75604	ATGAAA	2.92969	2.75329
cg07351160	PSRC1	STAT1bet	926	935	8.695301	CTTTCC	0.22316	0.2175
cg07351160	PSRC1	STAT1bet	1090	1099	8.695301	GGGAGG	0.22316	0.2175
cg07351160	PSRC1	STAT1bet	1164	1173	8.695301	TTTTCCA	0.22316	0.2175
cg07351160	PSRC1	STAT1bet	1943	1952	8.695301	ATCAGG	0.22316	0.2175
cg07351160	PSRC1	IRF-1 [T0	1090	1098	8.661524	GGGAGG	0.20599	0.20245
cg07351160	PSRC1	c-Jun [T00	158	164	8.571705	CCAGTC	0.12207	0.1249
cg07351160	PSRC1	RAR-beta	1338	1347	8.55975	TCAGAA	0.26703	0.27434
cg07351160	PSRC1	RAR-beta	1158	1167	8.541284	TGGGTT	0.26703	0.27434
cg07351160	PSRC1	c-Myb [T0	1561	1568	8.529773	CAACTT	0.30518	0.28602
cg07351160	PSRC1	AhR:Arnt	897	906	8.431005	GTGCGC	0.07439	0.08553
cg07351160	PSRC1	c-Ets-1 [T	990	996	8.373028	ATGGAA	0.24414	0.23702
cg07351160	PSRC1	EBF [T05	480	490	8.349314	TGCCCT	0.03052	0.03497
cg07351160	PSRC1	HNF-3alp	1668	1675	8.343064	GTAAAA	0.27466	0.23078
cg07351160	PSRC1	PR B [T00	669	675	8.338824	AACAGG	1.09863	1.09384
cg07351160	PSRC1	PR B [T00	1581	1587	8.338824	CTCTGT	1.09863	1.09384
cg07351160	PSRC1	PR B [T00	1779	1785	8.338824	AACAGC	1.09863	1.09384
cg07351160	PSRC1	PR A [T01	669	675	8.338824	AACAGG	1.09863	1.09384
cg07351160	PSRC1	PR A [T01	1581	1587	8.338824	CTCTGT	1.09863	1.09384
cg07351160	PSRC1	PR A [T01	1779	1785	8.338824	AACAGC	1.09863	1.09384
cg07351160	PSRC1	IRF-1 [T0	313	321	8.316022	TTTCCTC	0.20599	0.20245
cg07351160	PSRC1	GR-alpha [	105	109	8.281568	CAAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	136	140	8.281568	GAAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	203	207	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	220	224	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	224	228	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	237	241	8.281568	CCTTC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	241	245	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	250	254	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	336	340	8.281568	CAAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	386	390	8.281568	GGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	415	419	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	439	443	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	455	459	8.281568	GGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	543	547	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	620	624	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	709	713	8.281568	CGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	791	795	8.281568	GGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	879	883	8.281568	CGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	965	969	8.281568	GGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	1091	1095	8.281568	GGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	1142	1146	8.281568	CGAGG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	1232	1236	8.281568	CCTCC	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	1370	1374	8.281568	CCTTG	7.8125	8.20394
cg07351160	PSRC1	GR-alpha [	1419	1423	8.281568	GGAGG	7.8125	8.20394

cg0735116	PSRC1	GR-alpha [	1432	1436	8.281568	CCTCG	7.8125	8.20394
cg0735116	PSRC1	GR-alpha [	1451	1455	8.281568	CGAGG	7.8125	8.20394
cg0735116	PSRC1	GR-alpha [	1464	1468	8.281568	GAAGG	7.8125	8.20394
cg0735116	PSRC1	GR-alpha [	1702	1706	8.281568	GGAGG	7.8125	8.20394
cg0735116	PSRC1	GR-alpha [	1736	1740	8.281568	GGAGG	7.8125	8.20394
cg0735116	PSRC1	GR-alpha [	1845	1849	8.281568	GGAGG	7.8125	8.20394
cg0735116	PSRC1	GR-alpha [	1975	1979	8.281568	GGAGG	7.8125	8.20394
cg0735116	PSRC1	c-Jun [T00	1333	1339	8.242207	TGACCT(	0.48828	0.47447
cg0735116	PSRC1	c-Jun [T00	1837	1843	8.242207	TGACCT(	0.48828	0.47447
cg0735116	PSRC1	ENKTF-1	959	966	8.19852	TGGCCA(	0.73242	0.80254
cg0735116	PSRC1	p53 [T006'	398	404	8.162057	AGCGCC(	0.48828	0.55336
cg0735116	PSRC1	c-Ets-1 [T(	1988	1994	8.116854	GTTCCA(	0.24414	0.2494
cg0735116	PSRC1	GR-alpha [	266	270	8.073878	GCAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	366	370	8.073878	CCAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	403	407	8.073878	CCAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	432	436	8.073878	CCTGC	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	483	487	8.073878	CCTGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	494	498	8.073878	CCTGC	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	501	505	8.073878	CCTGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	526	530	8.073878	CCTGC	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	597	601	8.073878	CCTGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	688	692	8.073878	CCTAG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	747	751	8.073878	CCTAC	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	933	937	8.073878	GTAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	962	966	8.073878	CCAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1125	1129	8.073878	GCAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1200	1204	8.073878	GTAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1295	1299	8.073878	GCAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1299	1303	8.073878	GCAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1685	1689	8.073878	CCTGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1698	1702	8.073878	CCTAG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1699	1703	8.073878	CTAGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1768	1772	8.073878	CCTGG	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1809	1813	8.073878	CCTAC	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1956	1960	8.073878	CCTAC	7.8125	8.20289
cg0735116	PSRC1	GR-alpha [	1991	1995	8.073878	CCAGG	7.8125	8.20289
cg0735116	PSRC1	TFIID [T0	1165	1171	8.014558	TTTCCAA	2.19727	1.99811
cg0735116	PSRC1	TFIID [T0	1509	1515	8.014558	TTTGTAA	2.19727	1.99811
cg0735116	PSRC1	TFIID [T0	1543	1549	8.014558	TTTGTAA	2.19727	1.99811
cg0735116	PSRC1	TFIID [T0	1589	1595	8.014558	TTTCTAA	2.19727	1.99811
cg0735116	PSRC1	TFIID [T0	1758	1764	8.014558	TCACAA	2.19727	1.99811
cg0735116	PSRC1	TFIID [T0	1924	1930	8.014558	TTACAA	2.19727	1.99811
cg0735116	PSRC1	Pax-5 [T0(	330	336	8.014558	TCTGCC(	2.19727	2.42766
cg0735116	PSRC1	Pax-5 [T0(	458	464	8.014558	GGGCTC(	2.19727	2.42766
cg0735116	PSRC1	Pax-5 [T0(	719	725	8.014558	GGGCTC(	2.19727	2.42766
cg0735116	PSRC1	Pax-5 [T0(	795	801	8.014558	GGGCTG	2.19727	2.42766
cg0735116	PSRC1	Pax-5 [T0(	1023	1029	8.014558	GGGCCG	2.19727	2.42766
cg0735116	PSRC1	Pax-5 [T0(	1481	1487	8.014558	TGTGCC(	2.19727	2.42766

cg0735116	PSRC1	MEF-2A [	43	53	7.982343	AGAGGA	0.04005	0.03447
cg0735116	PSRC1	ETF [T002	788	798	7.870358	GGGGGA	0.07153	0.08737
cg0735116	PSRC1	ETF [T002	1006	1016	7.870358	GCCCCG	0.07153	0.08737
cg0735116	PSRC1	c-Ets-2 [T	1696	1704	7.84116	TTCCTAC	0.32043	0.30792
cg0735116	PSRC1	c-Ets-2 [T	1942	1950	7.84116	CATCAG	0.32043	0.30792
cg0735116	PSRC1	p53 [T006	458	464	7.833758	GGGCTC	0.48828	0.55336
cg0735116	PSRC1	p53 [T006	719	725	7.833758	GGGCTC	0.48828	0.55336
cg0735116	PSRC1	c-Myb [T0	1168	1175	7.825375	CCAAGT	0.21362	0.20997
cg0735116	PSRC1	GATA-2 [	1749	1757	7.777778	AGATAC	0.30518	0.29346
cg0735116	PSRC1	NF-AT1 [	225	233	7.744746	CTCCTTT	0.19836	0.19379
cg0735116	PSRC1	NF-AT1 [	309	317	7.744746	TACCTTT	0.19836	0.19379
cg0735116	PSRC1	NF-AT1 [	583	591	7.744746	CACCTTT	0.19836	0.19379
cg0735116	PSRC1	EBF [T05	557	567	7.555934	TCCTCAC	0.01144	0.0122
cg0735116	PSRC1	GR [T050	391	397	7.527031	CAAAGC	1.83105	1.71535
cg0735116	PSRC1	GR [T050	1378	1384	7.527031	ATATTC	1.83105	1.71535
cg0735116	PSRC1	RAR-beta	881	890	7.47824	AGGGTT	0.24414	0.25121
cg0735116	PSRC1	LEF-1 [T0	1268	1275	7.396545	GTGCAA	0.21362	0.21504
cg0735116	PSRC1	IRF-1 [T0	587	595	7.299819	TTTCCAC	0.14496	0.14723
cg0735116	PSRC1	p53 [T006	89	95	7.266844	ACAGCC	0.73242	0.79826
cg0735116	PSRC1	p53 [T006	1284	1290	7.266844	GGGCTT	0.73242	0.79826
cg0735116	PSRC1	p53 [T006	1688	1694	7.266844	GGGCTG	0.73242	0.79826
cg0735116	PSRC1	NF-AT1 [	923	931	7.211175	TCTCTTT	0.15259	0.14325
cg0735116	PSRC1	SRY [T00	24	32	7.175614	GAGACA	0.30518	0.29547
cg0735116	PSRC1	XBP-1 [T	1462	1467	7.172312	ATGAAG	2.92969	2.7512
cg0735116	PSRC1	XBP-1 [T	1858	1863	7.172312	CCTCAT	2.92969	2.7512
cg0735116	PSRC1	p53 [T006	1605	1611	7.150251	GGGCCA	1.09863	1.22478
cg0735116	PSRC1	c-Myb [T0	279	286	7.127234	TCCAGT	0.18311	0.17765
cg0735116	PSRC1	NF-AT1 [	46	54	7.095752	GGAAAA	0.15259	0.14325
cg0735116	PSRC1	TFIID [T0	1890	1896	7.082373	TGCTAA	0.12207	0.11255
cg0735116	PSRC1	AR [T000	632	640	7.049779	CCTGTG	0.23651	0.23986
cg0735116	PSRC1	IRF-1 [T0	42	50	7.044985	TAGAGG	0.1297	0.12685
cg0735116	PSRC1	NFI/CTF [	1737	1744	7.014249	GAGGTT	0.73242	0.74795
cg0735116	PSRC1	C/EBPalp	1135	1141	7.00174	CATTGG	0.73242	0.68282
cg0735116	PSRC1	HNF-3alp	46	53	7.000129	GGAAAA	0.82397	0.71909
cg0735116	PSRC1	HNF-3alp	1541	1548	7.000129	TATTTGT	0.82397	0.71909
cg0735116	PSRC1	HNF-3alp	1925	1932	7.000129	TACAAA	0.82397	0.71909
cg0735116	PSRC1	GCF [T00	952	960	6.987525	GCGCGG	0.45776	0.50397
cg0735116	PSRC1	GCF [T00	1129	1137	6.987525	GCGCCG	0.45776	0.50397
cg0735116	PSRC1	c-Ets-1 [T	139	145	6.943262	GGGGAA	0.73242	0.73732
cg0735116	PSRC1	ENKTF-1	577	584	6.942764	CCAAGC	1.46484	1.56616
cg0735116	PSRC1	ENKTF-1	1138	1145	6.942764	TGGCCG	1.46484	1.56616
cg0735116	PSRC1	ENKTF-1	1603	1610	6.942764	CCGGGC	1.46484	1.56616
cg0735116	PSRC1	p53 [T006	1023	1029	6.938545	GGGCCG	1.09863	1.22478
cg0735116	PSRC1	AhR:Arnt	529	538	6.928166	GCACGC	0.0515	0.0599
cg0735116	PSRC1	PEA3 [T0	110	118	6.824411	TCTCATC	0.22888	0.22744
cg0735116	PSRC1	PEA3 [T0	495	503	6.824411	CTGCATC	0.22888	0.22744
cg0735116	PSRC1	COUP-TF	1834	1846	6.820034	AACTGA	0.00894	0.00923
cg0735116	PSRC1	c-Ets-1 [T	927	933	6.815175	TTTCCCC	0.73242	0.73732

cg0735116	PSRC1	C/EBPalph	1196	1202	6.786177	TATTGTA	0.73242	0.68282
cg0735116	PSRC1	NFI/CTF [	577	584	6.786076	CCAAGC	0.73242	0.74795
cg0735116	PSRC1	p53 [T006	1516	1522	6.775228	GTAGCC	1.09863	1.22478
cg0735116	PSRC1	NF-1 [T00	331	338	6.722386	CTGCCCA	0.24414	0.2565
cg0735116	PSRC1	NF-1 [T00	1137	1144	6.722386	TTGGCC	0.24414	0.2565
cg0735116	PSRC1	AR [T000	252	260	6.677479	TCCATGT	0.19836	0.20813
cg0735116	PSRC1	GATA-2 [	449	457	6.666667	CGATAC	0.24414	0.2357
cg0735116	PSRC1	Elk-1 [T00	811	819	6.598007	GGCCGG	0.06104	0.06731
cg0735116	PSRC1	FOXP3 [T	1776	1781	6.581441	TAAAAC	0.97656	0.904
cg0735116	PSRC1	TFII-I [T0	199	204	6.581441	CACTCC	0.97656	0.9991
cg0735116	PSRC1	TFII-I [T0	406	411	6.581441	GGAGTG	0.97656	0.9991
cg0735116	PSRC1	TFII-I [T0	571	576	6.581441	CACTCC	0.97656	0.9991
cg0735116	PSRC1	TFII-I [T0	591	596	6.581441	CACTCC	0.97656	0.9991
cg0735116	PSRC1	TFII-I [T0	1571	1576	6.581441	GGAGTG	0.97656	0.9991
cg0735116	PSRC1	TFII-I [T0	1900	1905	6.581441	CACTCC	0.97656	0.9991
cg0735116	PSRC1	PPAR-alph	189	199	6.51544	CGCTGG	0.03719	0.04058
cg0735116	PSRC1	NF-kappaB	837	847	6.500651	GGGGAG	0.03052	0.03409
cg0735116	PSRC1	XBP-1 [T	599	604	6.478682	TGGCAT	0.97656	0.99906
cg0735116	PSRC1	c-Myb [T0	1150	1157	6.454077	CTCAGTT	0.30518	0.30272
cg0735116	PSRC1	c-Ets-1 [T	1165	1171	6.423689	TTTCCAA	0.48828	0.48842
cg0735116	PSRC1	p53 [T006	1110	1116	6.403751	GGGCGC	0.48828	0.54643
cg0735116	PSRC1	TCF-4E [T	389	395	6.302385	GGCAAA	0.61035	0.59686
cg0735116	PSRC1	GR-alpha [	14	18	6.263098	TAAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	126	130	6.263098	CCTTA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	232	236	6.263098	CCTTA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	316	320	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	511	515	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	558	562	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	654	658	6.263098	CCTTA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	783	787	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	799	803	6.263098	TGAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	886	890	6.263098	TGAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1149	1153	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1174	1178	6.263098	TAAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1210	1214	6.263098	TGAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1255	1259	6.263098	TGAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1264	1268	6.263098	TGAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1336	1340	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1486	1490	6.263098	CCTTA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1674	1678	6.263098	TAAGG	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1851	1855	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	GR-alpha [	1858	1862	6.263098	CCTCA	3.90625	3.89624
cg0735116	PSRC1	POU2F2 (	1713	1723	6.233489	ATTCTAA	0.01431	0.01219
cg0735116	PSRC1	p53 [T006	489	495	6.188498	GCCGCC	0.61035	0.68483
cg0735116	PSRC1	p53 [T006	520	526	6.188498	GGGCGG	0.61035	0.68483
cg0735116	PSRC1	SRY [T00	1757	1765	6.176442	GTCACAA	0.15259	0.14742
cg0735116	PSRC1	c-Ets-1 [T	587	593	6.167515	TTTCCAC	0.36621	0.36174
cg0735116	PSRC1	NF-AT1 [	1161	1169	6.150044	GTTTTTT	0.06866	0.06621

cg0735116	PSRC1	IRF-1 [T0	1165	1173	6.078807	TTTCCA	0.16785	0.16217
cg0735116	PSRC1	GR-alpha [	171	175	6.055408	CCTGA	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	318	322	6.055408	TCAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	354	358	6.055408	TCAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	560	564	6.055408	TCAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	737	741	6.055408	TCAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	785	789	6.055408	TCAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1061	1065	6.055408	CCTAA	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1184	1188	6.055408	CCTAA	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1253	1257	6.055408	CCTGA	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1305	1309	6.055408	TTAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1488	1492	6.055408	TTAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1568	1572	6.055408	TTAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1707	1711	6.055408	TTAGG	3.90625	3.89835
cg0735116	PSRC1	GR-alpha [	1944	1948	6.055408	TCAGG	3.90625	3.89835
cg0735116	PSRC1	c-Myb [T0	1833	1840	6.04018	AAACTG	0.21362	0.2053
cg0735116	PSRC1	RXR-alpha	1951	1957	5.937582	ATTACC	0.73242	0.78318
cg0735116	PSRC1	GCF [T00	648	656	5.917256	GCGCCG	0.64087	0.72542
cg0735116	PSRC1	STAT4 [T	237	242	5.882353	CCTTCC	0.48828	0.51201
cg0735116	PSRC1	NF-AT1 [	141	149	5.77403	GGAAAG	0.06866	0.06621
cg0735116	PSRC1	VDR [T00	1309	1317	5.771401	GTTCAA	0.42725	0.41266
cg0735116	PSRC1	VDR [T00	1523	1531	5.771401	CCTCTG	0.42725	0.41266
cg0735116	PSRC1	HNF-1A [	1172	1179	5.754274	GTTAAG	0.24414	0.24293
cg0735116	PSRC1	RXR-alpha	1504	1510	5.715466	GGGTGT	0.61035	0.65415
cg0735116	PSRC1	c-Jun [T00	375	381	5.703976	GGGGTC	0.48828	0.49294
cg0735116	PSRC1	c-Ets-1 [T	216	222	5.686398	CTTCCCT	0.36621	0.38732
cg0735116	PSRC1	c-Ets-1 [T	967	973	5.686398	AGGGAA	0.36621	0.38732
cg0735116	PSRC1	NF-1 [T00	1427	1434	5.626299	TTGGTC	0.24414	0.25051
cg0735116	PSRC1	NFI/CTF [	770	777	5.558661	GTGATT	0.54932	0.55504
cg0735116	PSRC1	GATA-2 [	551	559	5.555555	CCACTA	0.18311	0.18081
cg0735116	PSRC1	TFIID [T0	1590	1596	5.544826	TTCTAA	0.73242	0.65314
cg0735116	PSRC1	TFIID [T0	1773	1779	5.544826	TGGTAA	0.73242	0.65314
cg0735116	PSRC1	Pax-5 [T0	398	404	5.544826	AGCGCC	0.73242	0.79
cg0735116	PSRC1	Pax-5 [T0	478	484	5.544826	ATTGCC	0.73242	0.79
cg0735116	PSRC1	p53 [T006	795	801	5.508538	GGGCTG	0.61035	0.65765
cg0735116	PSRC1	c-Ets-1 [T	642	648	5.430224	CTTCCC	0.36621	0.38732
cg0735116	PSRC1	IRF-1 [T0	1943	1951	5.404935	ATCAGG	0.22888	0.21959
cg0735116	PSRC1	MAZ [T00	217	229	5.321436	TTCCCTC	0.00459	0.00523
cg0735116	PSRC1	RAR-beta	562	571	5.31522	AGGGTT	0.15259	0.15813
cg0735116	PSRC1	IRF-1 [T0	229	237	5.309227	TTTCCTT	0.22888	0.21959
cg0735116	PSRC1	RXR-alpha	627	633	5.271235	CCCACC	0.61035	0.65415
cg0735116	PSRC1	RXR-alpha	1317	1323	5.271235	GCAACC	0.61035	0.65415
cg0735116	PSRC1	ETF [T002	712	722	5.246906	GGGGGC	0.02861	0.03569
cg0735116	PSRC1	GR [T050	1761	1767	5.207533	CAAAGA	0.24414	0.24013
cg0735116	PSRC1	GR [T050	1804	1810	5.207533	CAAAAC	0.24414	0.24013
cg0735116	PSRC1	c-Jun [T00	816	822	5.193102	GAAGTC	0.61035	0.60573
cg0735116	PSRC1	c-Ets-2 [T	230	238	5.162974	TTCCTTA	0.13733	0.13279
cg0735116	PSRC1	RXR-alpha	1032	1038	5.089356	AGCACC	0.48828	0.51407

cg0735116	PSRC1	GR-beta [T	18	22	5.042296	GGATT	3.90625	3.7093
cg0735116	PSRC1	GR-beta [T	247	251	5.042296	AATCC	3.90625	3.7093
cg0735116	PSRC1	GR-beta [T	780	784	5.042296	AATCC	3.90625	3.7093
cg0735116	PSRC1	GR-beta [T	1493	1497	5.042296	GGATT	3.90625	3.7093
cg0735116	PSRC1	GR-beta [T	1540	1544	5.042296	GTATT	3.90625	3.7093
cg0735116	PSRC1	GR-beta [T	1693	1697	5.042296	GTATT	3.90625	3.7093
cg0735116	PSRC1	GR-beta [T	1881	1885	5.042296	GTATT	3.90625	3.7093
cg0735116	PSRC1	GR-beta [T	1929	1933	5.042296	AATAC	3.90625	3.7093
cg0735116	PSRC1	E2F-1 [T0	415	422	5.042045	CCTCCCC	0.18311	0.20394
cg0735116	PSRC1	HOXD9 [T	1190	1199	5.035116	CACTTAT	0.00763	0.00669
cg0735116	PSRC1	HOXD10 [	1190	1199	5.035116	CACTTAT	0.00763	0.00669
cg0735116	PSRC1	IRF-1 [T0	927	935	4.932737	TTTCCCC	0.1297	0.12724
cg0735116	PSRC1	XBP-1 [T	1709	1714	4.894955	AGGCAT	0.97656	0.99839
cg0735116	PSRC1	AP-2alpha	1060	1065	4.890408	GCCTAA	0.97656	0.97517
cg0735116	PSRC1	AP-2alpha	1707	1712	4.890408	TTAGGC	0.97656	0.97517
cg0735116	PSRC1	RXR-alpha	193	199	4.86724	GGGTCTC	0.48828	0.51407
cg0735116	PSRC1	GCF [T00	913	921	4.846987	GCGCGG	0.27466	0.31905
cg0735116	PSRC1	c-Ets-1 [T	660	666	4.782565	CTTCCAC	0.48828	0.48026
cg0735116	PSRC1	FOXP3 [T	884	889	4.756447	GTTGAG	2.92969	2.82
cg0735116	PSRC1	FOXP3 [T	1102	1107	4.756447	GTTTTC	2.92969	2.82
cg0735116	PSRC1	FOXP3 [T	1161	1166	4.756447	GTTTTT	2.92969	2.82
cg0735116	PSRC1	FOXP3 [T	1470	1475	4.756447	GTTTTC	2.92969	2.82
cg0735116	PSRC1	FOXP3 [T	1678	1683	4.756447	GTTGAG	2.92969	2.82
cg0735116	PSRC1	FOXP3 [T	1804	1809	4.756447	CAAAAC	2.92969	2.82
cg0735116	PSRC1	TFII-I [T0	255	260	4.756447	ATGTCC	2.92969	2.89715
cg0735116	PSRC1	TFII-I [T0	1094	1099	4.756447	GGAAAT	2.92969	2.89715
cg0735116	PSRC1	TFII-I [T0	1854	1859	4.756447	CAGTCC	2.92969	2.89715
cg0735116	PSRC1	TFII-I [T0	1947	1952	4.756447	GGAAAT	2.92969	2.89715
cg0735116	PSRC1	c-Myb [T0	1329	1336	4.754782	TAACTGA	0.30518	0.30087
cg0735116	PSRC1	p53 [T006	998	1004	4.645444	CGCGCCC	0.24414	0.28373
cg0735116	PSRC1	c-Ets-1 [T	1695	1701	4.539113	ATTCCTA	0.85449	0.8381
cg0735116	PSRC1	T3R-beta1	81	89	4.481316	AGATGG	0.27466	0.27245
cg0735116	PSRC1	T3R-beta1	772	780	4.481316	GATTGG	0.27466	0.27245
cg0735116	PSRC1	GATA-2 [	58	66	4.444445	GGATAA	0.24414	0.23857
cg0735116	PSRC1	AP-2alpha	653	658	4.422424	GCCTTA	0.97656	0.99839
cg0735116	PSRC1	STAT4 [T	215	220	4.411765	TCTTCC	1.95312	1.99838
cg0735116	PSRC1	STAT4 [T	445	450	4.411765	GGAACG	1.95312	1.99838
cg0735116	PSRC1	STAT4 [T	539	544	4.411765	TCTTCC	1.95312	1.99838
cg0735116	PSRC1	STAT4 [T	659	664	4.411765	TCTTCC	1.95312	1.99838
cg0735116	PSRC1	STAT4 [T	846	851	4.411765	CGTTCC	1.95312	1.99838
cg0735116	PSRC1	STAT4 [T	969	974	4.411765	GGAAGA	1.95312	1.99838
cg0735116	PSRC1	c-Ets-1 [T	1976	1982	4.282938	GAGGAA	0.85449	0.8381
cg0735116	PSRC1	c-Myb [T0	1435	1442	4.270092	CGCAGT	0.06104	0.06232
cg0735116	PSRC1	MAZ [T00	786	798	4.264019	CAGGGG	0.00188	0.00218
cg0735116	PSRC1	RXR-alpha	166	172	4.24113	GGGTCCC	0.97656	1.02803
cg0735116	PSRC1	AP-2alpha	933	938	4.211849	GTAGGC	0.97656	1.02535
cg0735116	PSRC1	GR-beta [T	1	5	4.201913	AATAA	7.8125	7.23274
cg0735116	PSRC1	GR-beta [T	50	54	4.201913	AATAA	7.8125	7.23274

cg0735116	PSRC1	GR-beta [T	120	124	4.201913	AATAA	7.8125	7.23274
cg0735116	PSRC1	GR-beta [T	700	704	4.201913	AATCA	7.8125	7.23274
cg0735116	PSRC1	GR-beta [T	771	775	4.201913	TGATT	7.8125	7.23274
cg0735116	PSRC1	GR-beta [T	1656	1660	4.201913	AATAG	7.8125	7.23274
cg0735116	PSRC1	GR-beta [T	1672	1676	4.201913	AATAA	7.8125	7.23274
cg0735116	PSRC1	Sp1 [T007	487	496	4.197619	GAGCCG	0.08965	0.10391
cg0735116	PSRC1	NF-AT1 [T	583	592	4.134416	CACCTT	0.08392	0.07965
cg0735116	PSRC1	p53 [T006	738	744	4.125254	CAGGCC	0.73242	0.82434
cg0735116	PSRC1	C/EBPalph	477	483	4.019783	GATTGC	0.48828	0.46347
cg0735116	PSRC1	RXR-alpha	1763	1769	4.019014	AAGACC	0.97656	1.02803
cg0735116	PSRC1	TFIID [T0	1544	1550	4.007279	TTGTAA	1.09863	0.94722
cg0735116	PSRC1	TFIID [T0	1923	1929	4.007279	TTTACA	1.09863	0.94722
cg0735116	PSRC1	Pax-5 [T0	89	95	4.007279	ACAGCC	1.09863	1.18533
cg0735116	PSRC1	Pax-5 [T0	469	475	4.007279	ACTGCC	1.09863	1.18533
cg0735116	PSRC1	Pax-5 [T0	1284	1290	4.007279	GGGCTT	1.09863	1.18533
cg0735116	PSRC1	Pax-5 [T0	1688	1694	4.007279	GGGCTG	1.09863	1.18533
cg0735116	PSRC1	AP-2alpha	336	341	3.970052	CAAGGC	0.97656	1.02535
cg0735116	PSRC1	AP-2alpha	1369	1374	3.970052	GCCTTG	0.97656	1.02535
cg0735116	PSRC1	EBF [T05	782	792	3.842007	TCCTCA	0.0248	0.02839
cg0735116	PSRC1	GR [T050	28	34	3.763516	CAAAGA	0.73242	0.6946
cg0735116	PSRC1	GR [T050	1271	1277	3.763516	CAAAGA	0.73242	0.6946
cg0735116	PSRC1	p53 [T006	623	629	3.750231	CCAGCC	0.73242	0.82434
cg0735116	PSRC1	p53 [T006	831	837	3.750231	GGGCTG	0.73242	0.82434
cg0735116	PSRC1	AP-2alpha	1464	1469	3.743866	GAAGGC	0.48828	0.5124
cg0735116	PSRC1	p53 [T006	478	484	3.728319	ATTGCC	0.73242	0.80362
cg0735116	PSRC1	PEA3 [T0	1725	1733	3.710864	AGGATG	0.09155	0.08745
cg0735116	PSRC1	c-Ets-1 [T	1146	1152	3.590463	GTTCCT	0.61035	0.61936
cg0735116	PSRC1	RXR-alpha	369	375	3.574782	GGGTCG	1.09863	1.1653
cg0735116	PSRC1	C/EBPalph	772	778	3.555778	GATTGG	0.24414	0.23261
cg0735116	PSRC1	E2F-1 [T0	642	649	3.55167	CTTCCC	0.15259	0.16507
cg0735116	PSRC1	p53 [T006	469	475	3.516613	ACTGCC	0.73242	0.80362
cg0735116	PSRC1	Sp1 [T007	519	528	3.408439	GGGGCG	0.07439	0.08783
cg0735116	PSRC1	RXR-alpha	376	382	3.392904	GGGTCA	1.09863	1.1653
cg0735116	PSRC1	RXR-alpha	1666	1672	3.392904	GGGTAA	1.09863	1.1653
cg0735116	PSRC1	p53 [T006	530	536	3.375208	CACGCC	0.73242	0.80362
cg0735116	PSRC1	p53 [T006	714	720	3.375208	GGGCGG	0.73242	0.80362
cg0735116	PSRC1	p53 [T006	1003	1009	3.375208	CCCGCC	0.73242	0.80362
cg0735116	PSRC1	T3R-beta1	1393	1401	3.370634	TCACCT	0.27466	0.27326
cg0735116	PSRC1	GR-beta [T	350	354	3.361531	AGATT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [T	476	480	3.361531	AGATT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [T	731	735	3.361531	AATCT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [T	1120	1124	3.361531	AATAT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [T	1195	1199	3.361531	ATATT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [T	1206	1210	3.361531	ATATT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [T	1378	1382	3.361531	ATATT	3.90625	3.51525
cg0735116	PSRC1	IRF-1 [T0	137	145	3.352297	AAGGGG	0.06866	0.0661
cg0735116	PSRC1	PR B [T00	1594	1600	3.29756	AAATGT	0.24414	0.21408
cg0735116	PSRC1	PR A [T01	1594	1600	3.29756	AAATGT	0.24414	0.21408

cg0735116	PSRC1	c-Ets-2 [T(	314	322	3.2883	TTCCTCA	0.18311	0.18314
cg0735116	PSRC1	c-Ets-2 [T(	1147	1155	3.2883	TTCCTCA	0.18311	0.18314
cg0735116	PSRC1	PXR-1:RX	1306	1313	3.2723	TAGGTT(	0.12207	0.11883
cg0735116	PSRC1	AP-2alpha	64	69	3.229049	AGAGGC	0.48828	0.5124
cg0735116	PSRC1	AP-2alpha	505	510	3.229049	GCCTCT	0.48828	0.5124
cg0735116	PSRC1	AP-2alpha	1240	1245	3.229049	GCCTCT	0.48828	0.5124
cg0735116	PSRC1	AP-2alpha	1359	1364	3.229049	AGAGGC	0.48828	0.5124
cg0735116	PSRC1	AP-2alpha	1625	1630	3.229049	AGAGGC	0.48828	0.5124
cg0735116	PSRC1	AP-2alpha	1659	1664	3.229049	AGAGGC	0.48828	0.5124
cg0735116	PSRC1	RXR-alpha	1159	1165	3.170788	GGGTTT	0.24414	0.24551
cg0735116	PSRC1	TCF-4E [T	1269	1275	3.151193	TGCAAA(	0.24414	0.23169
cg0735116	PSRC1	c-Ets-1 [T(	813	819	3.102985	CCGGAA(	0.24414	0.26272
cg0735116	PSRC1	E2F-1 [T0	1787	1794	3.059334	GCGGTA	0.03052	0.03038
cg0735116	PSRC1	p53 [T006	1481	1487	3.028543	TGTGCC(	0.48828	0.53227
cg0735116	PSRC1	p53 [T006	1598	1604	3.024997	GTTGCC(	0.48828	0.53227
cg0735116	PSRC1	STAT4 [T(	141	146	2.941176	GGAAAG	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	228	233	2.941176	CTTTCC	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	312	317	2.941176	CTTTCC	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	586	591	2.941176	CTTTCC	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	641	646	2.941176	ACTTCC	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	698	703	2.941176	GGAATC	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	815	820	2.941176	GGAAGT	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	926	931	2.941176	CTTTCC	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	1145	1150	2.941176	GGTTCC	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	1654	1659	2.941176	GGAATA	2.92969	2.92382
cg0735116	PSRC1	STAT4 [T(	1694	1699	2.941176	TATTCC	2.92969	2.92382
cg0735116	PSRC1	AhR:Arnt	905	914	2.810335	GCTCGC(	0.01717	0.02068
cg0735116	PSRC1	NF-AT1 [T	1161	1170	2.756277	GTTTTTT	0.05913	0.05541
cg0735116	PSRC1	c-Ets-2 [T(	541	549	2.715313	TTCCTCC	0.07629	0.07844
cg0735116	PSRC1	c-Ets-2 [T(	1089	1097	2.715313	CGGGAG	0.07629	0.07844
cg0735116	PSRC1	c-Ets-2 [T(	1973	1981	2.715313	GGGGAG	0.07629	0.07844
cg0735116	PSRC1	AP-2alpha	886	891	2.550491	TGAGGC	0.48828	0.51216
cg0735116	PSRC1	AP-2alpha	1255	1260	2.550491	TGAGGC	0.48828	0.51216
cg0735116	PSRC1	RXR-alpha	357	363	2.544678	GGGTGC	0.85449	0.89683
cg0735116	PSRC1	RXR-alpha	563	569	2.544678	GGGTTCT	0.85449	0.89683
cg0735116	PSRC1	RXR-alpha	1340	1346	2.544678	AGAACC(	0.85449	0.89683
cg0735116	PSRC1	c-Jun [T00	1717	1723	2.538231	TAAGTCA	0.48828	0.48077
cg0735116	PSRC1	ENKTF-1	546	553	2.511511	CCCCGC(	0.12207	0.13847
cg0735116	PSRC1	HNF-4alph	98	110	2.392402	CAAAGT(	0.00167	0.00154
cg0735116	PSRC1	VDR [T00	1611	1619	2.308561	CCAGTGA	0.10681	0.1091
cg0735116	PSRC1	T3R-beta1	1914	1922	2.221365	TCACCA(	0.15259	0.15303
cg0735116	PSRC1	GATA-1 [	323	328	2.176375	TATCCA	3.90625	3.79558
cg0735116	PSRC1	GATA-1 [	448	453	2.176375	ACGATA	3.90625	3.79558
cg0735116	PSRC1	GATA-1 [	555	560	2.176375	TATCCT	3.90625	3.79558
cg0735116	PSRC1	GATA-1 [	1453	1458	2.176375	AGGATA	3.90625	3.79558
cg0735116	PSRC1	NF-1 [T00	1741	1748	2.067686	TTGGCA(	0.12207	0.12476
cg0735116	PSRC1	GATA-1 [	57	62	2.001358	GGGATA	3.90625	3.79558
cg0735116	PSRC1	NF-Y [T0(	1136	1143	1.976711	ATTGGC(	0.21362	0.20748

cg0735116	PSRC1	p53 [T006	1381	1387	1.970013	TTTGCC	0.36621	0.38097
cg0735116	PSRC1	PR B [T00	1188	1194	1.892895	AACACT	0.12207	0.1127
cg0735116	PSRC1	PR A [T01	1188	1194	1.892895	AACACT	0.12207	0.1127
cg0735116	PSRC1	RXR-alpha	882	888	1.87833	GGGTTG	0.12207	0.12517
cg0735116	PSRC1	AP-2alpha	386	391	1.871933	GGAGGC	0.97656	1.07805
cg0735116	PSRC1	TFII-I [T0	181	186	1.824994	CTCTCC	0.48828	0.51201
cg0735116	PSRC1	TFII-I [T0	297	302	1.824994	GGAGAG	0.48828	0.51201
cg0735116	PSRC1	TFII-I [T0	507	512	1.824994	CTCTCC	0.48828	0.51201
cg0735116	PSRC1	C/EBPalph	117	123	1.761449	CACAAT	0.48828	0.46352
cg0735116	PSRC1	p53 [T006	330	336	1.758307	TCTGCC	0.36621	0.38097
cg0735116	PSRC1	RXR-alpha	977	983	1.696452	CGGACC	0.48828	0.52093
cg0735116	PSRC1	GR-beta [T	4	8	1.680765	AATTC	3.90625	3.70067
cg0735116	PSRC1	GR-beta [T	1097	1101	1.680765	AATTC	3.90625	3.70067
cg0735116	PSRC1	GR-beta [T	1134	1138	1.680765	GCATT	3.90625	3.70067
cg0735116	PSRC1	GR-beta [T	1314	1318	1.680765	AATGC	3.90625	3.70067
cg0735116	PSRC1	GR-beta [T	1550	1554	1.680765	AATGC	3.90625	3.70067
cg0735116	PSRC1	GR-beta [T	1711	1715	1.680765	GCATT	3.90625	3.70067
cg0735116	PSRC1	GR-beta [T	1979	1983	1.680765	GAATT	3.90625	3.70067
cg0735116	PSRC1	GR-beta [T	1980	1984	1.680765	AATTC	3.90625	3.70067
cg0735116	PSRC1	c-Ets-2 [T	239	247	1.64415	TTCCTC	0.04578	0.04602
cg0735116	PSRC1	c-Ets-1 [T	229	235	1.641124	TTTCCTT	0.36621	0.35197
cg0735116	PSRC1	C/EBPbeta	97	100	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	104	107	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	244	247	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	335	338	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	466	469	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	577	580	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	774	777	1.639871	TTGG	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1108	1111	1.639871	TTGG	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1137	1140	1.639871	TTGG	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1168	1171	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1322	1325	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1345	1348	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1427	1430	1.639871	TTGG	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1560	1563	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1741	1744	1.639871	TTGG	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1803	1806	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1819	1822	1.639871	CCAA	15.625	15.23827
cg0735116	PSRC1	XBP-1 [T	377	382	1.583727	GGTCAT	0.97656	0.94995
cg0735116	PSRC1	TFIID [T0	1164	1170	1.537547	TTTTCCA	0.73242	0.65627
cg0735116	PSRC1	TFIID [T0	1545	1551	1.537547	TGTAAA	0.73242	0.65627
cg0735116	PSRC1	Pax-5 [T0	530	536	1.537547	CACGCC	0.73242	0.83087
cg0735116	PSRC1	Pax-5 [T0	714	720	1.537547	GGGCGG	0.73242	0.83087
cg0735116	PSRC1	Pax-5 [T0	998	1004	1.537547	CGCGCC	0.73242	0.83087
cg0735116	PSRC1	Pax-5 [T0	1003	1009	1.537547	CCCGCC	0.73242	0.83087
cg0735116	PSRC1	NF-Y [T0	773	780	1.51343	ATTGGT	0.18311	0.17671
cg0735116	PSRC1	c-Ets-1 [T	44	50	1.513038	GAGGAA	0.36621	0.35197
cg0735116	PSRC1	c-Ets-1 [T	313	319	1.513038	TTTCCTC	0.36621	0.35197

cg0735116	PSRC1	c-Ets-1 [T	1092	1098	1.513038	GAGGAA	0.36621	0.35197
cg0735116	PSRC1	E2F-1 [T0	678	685	1.490375	TCTCCC	0.06104	0.0656
cg0735116	PSRC1	STAT4 [T	46	51	1.470588	GGAAAA	1.95312	1.90161
cg0735116	PSRC1	STAT4 [T	992	997	1.470588	GGAACT	1.95312	1.90161
cg0735116	PSRC1	STAT4 [T	1164	1169	1.470588	TTTTCC	1.95312	1.90161
cg0735116	PSRC1	STAT4 [T	1978	1983	1.470588	GGAATT	1.95312	1.90161
cg0735116	PSRC1	STAT4 [T	1987	1992	1.470588	AGTTCC	1.95312	1.90161
cg0735116	PSRC1	PR B [T00	1572	1578	1.404665	GAGTGT	0.36621	0.35143
cg0735116	PSRC1	PR A [T01	1572	1578	1.404665	GAGTGT	0.36621	0.35143
cg0735116	PSRC1	c-Ets-1 [T	1945	1951	1.384951	CAGGAA	0.36621	0.35197
cg0735116	PSRC1	C/EBPbeta	752	755	1.366559	TCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	885	888	1.366559	TTGA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1118	1121	1.366559	TCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1209	1212	1.366559	TTGA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1246	1249	1.366559	TCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1311	1314	1.366559	TCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1372	1375	1.366559	TTGA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1632	1635	1.366559	TCAA	15.625	15.23827
cg0735116	PSRC1	C/EBPbeta	1679	1682	1.366559	TTGA	15.625	15.23827
cg0735116	PSRC1	AP-2alpha	670	675	1.357116	ACAGGC	0.48828	0.51319
cg0735116	PSRC1	ENKTF-1	870	877	1.255756	TGGCGG	0.24414	0.27027
cg0735116	PSRC1	ENKTF-1	1825	1832	1.255756	TGGCGA	0.24414	0.27027
cg0735116	PSRC1	C/EBPalph	1117	1123	1.220508	CTCAAT	0.24414	0.23153
cg0735116	PSRC1	C/EBPalph	1207	1213	1.220508	TATTGA	0.24414	0.23153
cg0735116	PSRC1	PEA3 [T0	1421	1429	1.194633	AGGATG	0.06866	0.06787
cg0735116	PSRC1	c-Ets-2 [T	41	49	1.071163	TTAGAG	0.06104	0.0583
cg0735116	PSRC1	GCF [T00	643	651	1.070269	TTCCCG	0.18311	0.21473
cg0735116	PSRC1	GR-beta [	3	7	0.840383	TAATT	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	150	154	0.840383	AATGA	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	211	215	0.840383	TCATT	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	326	330	0.840383	CCATT	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	1457	1461	0.840383	TAATT	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	1458	1462	0.840383	AATTA	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	1860	1864	0.840383	TCATT	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	1871	1875	0.840383	TAATT	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	1872	1876	0.840383	AATTA	7.8125	7.2174
cg0735116	PSRC1	GR-beta [	1950	1954	0.840383	AATTA	7.8125	7.2174
cg0735116	PSRC1	PXR-1:RX	1615	1622	0.818075	TGAACT	0.12207	0.11843
cg0735116	PSRC1	AP-2alpha	737	742	0.678558	TCAGGC	0.48828	0.51196
cg0735116	PSRC1	PEA3 [T0	1226	1234	0.597316	GTACAT	0.04578	0.04362
cg0735116	PSRC1	HNF-1A [	1325	1332	0.431647	AGTTTA	0.24414	0.21942
cg0735116	PSRC1	GATA-1 [	657	662	0.280028	TATCTT	0.97656	0.8795
cg0735116	PSRC1	GATA-1 [	1748	1753	0.280028	AAGATA	0.97656	0.8795
cg0735116	PSRC1	GR-alpha [	31	35	0.207689	AGAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	43	47	0.207689	AGAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	64	68	0.207689	AGAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	207	211	0.207689	CCTTT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	227	231	0.207689	CCTTT	7.8125	7.79817

cg0735116	PSRC1	GR-alpha [	311	315	0.207689	CCTTT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	506	510	0.207689	CCTCT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	585	589	0.207689	CCTTT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	724	728	0.207689	CCTTT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1015	1019	0.207689	CCTCT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1241	1245	0.207689	CCTCT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1359	1363	0.207689	AGAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1386	1390	0.207689	CCTCT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1396	1400	0.207689	CCTCT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1416	1420	0.207689	AAAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1499	1503	0.207689	AGAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1523	1527	0.207689	CCTCT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1625	1629	0.207689	AGAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1659	1663	0.207689	AGAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1840	1844	0.207689	CCTCT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1970	1974	0.207689	AAAGG	7.8125	7.79817
cg0735116	PSRC1	Elk-1 [T00	238	246	0.134348	CTTCCTC	0.06104	0.06399
cg0735116	PSRC1	c-Ets-1 [T	238	244	0.128087	CTTCCTC	0.24414	0.24982
cg0735116	PSRC1	c-Ets-1 [T	540	546	0.128087	CTTCCTC	0.24414	0.24982
cg0735116	PSRC1	GATA-1 [	1730	1735	0.105011	GAGATA	0.97656	0.92541
cg0735116	PSRC1	GR-beta [	1096	1100	0	AAATT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [	1595	1599	0	AATGT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [	1878	1882	0	AATGT	3.90625	3.51525
cg0735116	PSRC1	GR-beta [	1949	1953	0	AAATT	3.90625	3.51525
cg0735116	PSRC1	XBP-1 [T	160	165	0	AGTCAT	0.97656	0.94838
cg0735116	PSRC1	TFIID [T	1471	1477	0	TTTTCTA	1.09863	0.95175
cg0735116	PSRC1	TFIID [T	1965	1971	0	TCTAAA	1.09863	0.95175
cg0735116	PSRC1	GR-alpha [	75	79	0	CCTGT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	632	636	0	CCTGT	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	670	674	0	ACAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1723	1727	0	ACAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1733	1737	0	ATAGG	7.8125	7.79817
cg0735116	PSRC1	GR-alpha [	1753	1757	0	ACAGG	7.8125	7.79817
cg0735116	PSRC1	FOXP3 [T	1052	1057	0	GTTGTG	1.46484	1.44953
cg0735116	PSRC1	FOXP3 [T	1154	1159	0	GTTGTG	1.46484	1.44953
cg0735116	PSRC1	FOXP3 [T	1576	1581	0	GTTGTC	1.46484	1.44953
cg0735116	PSRC1	FOXP3 [T	1585	1590	0	GTTGTT	1.46484	1.44953
cg0735116	PSRC1	PR B [T00	36	42	0	TACTGT	0.36621	0.35051
cg0735116	PSRC1	PR A [T01	36	42	0	TACTGT	0.36621	0.35051
cg0735116	PSRC1	C/EBPbeta	27	30	0	ACAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	118	121	0	ACAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	361	364	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	390	393	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	395	398	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	479	482	0	TTGC	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	667	670	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	684	687	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1053	1056	0	TTGT	15.625	15.26275

cg0735116	PSRC1	C/EBPbeta	1155	1158	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1198	1201	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1270	1273	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1279	1282	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1317	1320	0	GCAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1382	1385	0	TTGC	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1510	1513	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1544	1547	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1565	1568	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1577	1580	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1586	1589	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1599	1602	0	TTGC	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1620	1623	0	TTGT	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1746	1749	0	ACAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1760	1763	0	ACAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1926	1929	0	ACAA	15.625	15.26275
cg0735116	PSRC1	C/EBPbeta	1938	1941	0	GCAA	15.625	15.26275
cg0735116	PSRC1	YY1 [T00	83	86	0	ATGG	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	164	167	0	ATGG	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	185	188	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	253	256	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	306	309	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	326	329	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	536	539	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	941	944	0	ATGG	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	990	993	0	ATGG	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	1235	1238	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	1648	1651	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	1824	1827	0	ATGG	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	1933	1936	0	CCAT	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	1935	1938	0	ATGG	7.8125	7.79459
cg0735116	PSRC1	YY1 [T00	1961	1964	0	ATGG	7.8125	7.79459
cg0735116	PSRC1	TFII-I [T0	141	146	0	GGAAAG	1.46484	1.48598
cg0735116	PSRC1	TFII-I [T0	228	233	0	CTTTCC	1.46484	1.48598
cg0735116	PSRC1	TFII-I [T0	312	317	0	CTTTCC	1.46484	1.48598
cg0735116	PSRC1	TFII-I [T0	554	559	0	CTATCC	1.46484	1.48598
cg0735116	PSRC1	TFII-I [T0	586	591	0	CTTTCC	1.46484	1.48598
cg0735116	PSRC1	TFII-I [T0	926	931	0	CTTTCC	1.46484	1.48598
cg0735116	PSRC1	STAT4 [T	1094	1099	0	GGAAAT	0.48828	0.46235
cg0735116	PSRC1	STAT4 [T	1947	1952	0	GGAAAT	0.48828	0.46235
cg0735116	PSRC1	c-Myb [T0	467	474	0	CAACTG	0.03052	0.03205
cg0735116	PSRC1	ER-alpha [	377	381	0	GGTCA	1.95312	1.99744
cg0735116	PSRC1	ER-alpha [	1333	1337	0	TGACC	1.95312	1.99744
cg0735116	PSRC1	ER-alpha [	1756	1760	0	GGTCA	1.95312	1.99744
cg0735116	PSRC1	ER-alpha [	1837	1841	0	TGACC	1.95312	1.99744
cg0735116	PSRC1	GATA-1 [	1408	1413	0	TATCTG	0.97656	0.92541
cg0735116	PSRC1	PXR-1:RX	1527	1534	0	TGAACT	0.12207	0.11255
cg0735116	PSRC1	Pax-5 [T0	623	629	0	CCAGCC	1.09863	1.24633

cg0735116	PSRC1	Pax-5 [T0	738	744	0	CAGGCC	1.09863	1.24633
cg0735116	PSRC1	Pax-5 [T0	831	837	0	GGGCTG	1.09863	1.24633
cg0735116	PSRC1	AP-2alpha	525	530	0	GCCTGC	0.97656	1.07867
cg0735116	PSRC1	AP-2alpha	1125	1130	0	GCAGGC	0.97656	1.07867
cg0735116	PSRC1	AP-2alpha	1295	1300	0	GCAGGC	0.97656	1.07867
cg0735116	PSRC1	AP-2alpha	1299	1304	0	GCAGGC	0.97656	1.07867
cg0735116	PSRC1	Sp1 [T007	713	722	0	GGGGCG	0.00191	0.00246
cg0735116	PSRC1	Sp1 [T007	1001	1010	0	GCCCCG	0.00191	0.00246
cg0735116	PSRC1	Elk-1 [T00	540	548	0	CTTCCTC	0.06104	0.06399
cg0735116	PSRC1	GATA-2 [	653	661	0	GCCTTAT	0.01526	0.0152
cg0261124	RAB21	PEA3 [T0	1350	1358	9.937959	CTCCATC	0.18311	0.18304
cg0261124	RAB21	HNF-1B [	895	903	9.830287	TGAGTA	0.12207	0.12399
cg0261124	RAB21	HNF-1B [	1093	1101	9.830287	TGTTACT	0.12207	0.12399
cg0261124	RAB21	XBP-1 [T	24	29	9.789909	CGCCAT	1.95312	1.95208
cg0261124	RAB21	XBP-1 [T	276	281	9.789909	ATGGCT	1.95312	1.95208
cg0261124	RAB21	XBP-1 [T	917	922	9.789909	AGCCAT	1.95312	1.95208
cg0261124	RAB21	XBP-1 [T	1341	1346	9.789909	ATGTCT	1.95312	1.95208
cg0261124	RAB21	PR B [T00	957	963	9.743489	GCGTGT	1.09863	1.10292
cg0261124	RAB21	PR B [T00	1844	1850	9.743489	TGGTGT	1.09863	1.10292
cg0261124	RAB21	PR A [T01	957	963	9.743489	GCGTGT	1.09863	1.10292
cg0261124	RAB21	PR A [T01	1844	1850	9.743489	TGGTGT	1.09863	1.10292
cg0261124	RAB21	c-Jun [T00	1487	1493	9.717135	TGACCT	0.73242	0.73031
cg0261124	RAB21	c-Ets-1 [T	584	590	9.713162	GGGGAA	0.36621	0.36441
cg0261124	RAB21	Elk-1 [T00	633	641	9.62002	GGAGGG	0.07629	0.07577
cg0261124	RAB21	RelA [T00	490	500	9.612409	TGGGGA	0.02813	0.0279
cg0261124	RAB21	HNF-1C [	1815	1823	9.601936	GTTATTC	0.19836	0.20229
cg0261124	RAB21	HNF-1C [	1387	1395	9.576203	TTACTTA	0.19836	0.20229
cg0261124	RAB21	RBP-Jkap	716	727	9.570372	TTTTCCC	0.01884	0.01886
cg0261124	RAB21	MAZ [T00	225	237	9.563287	TGTCGG	0.01425	0.014
cg0261124	RAB21	Pax-5 [T0	233	239	9.552105	GGGCGG	1.46484	1.43083
cg0261124	RAB21	Pax-5 [T0	255	261	9.552105	GGGCGG	1.46484	1.43083
cg0261124	RAB21	Pax-5 [T0	304	310	9.552105	GGGCGG	1.46484	1.43083
cg0261124	RAB21	Pax-5 [T0	459	465	9.552105	GGGCGC	1.46484	1.43083
cg0261124	RAB21	Pax-5 [T0	502	508	9.552105	GCCGCC	1.46484	1.43083
cg0261124	RAB21	TFIID [T0	528	534	9.552105	TGGCAA	1.46484	1.48472
cg0261124	RAB21	TFIID [T0	717	723	9.552105	TTTCCCA	1.46484	1.48472
cg0261124	RAB21	TFIID [T0	908	914	9.552105	TGGCAA	1.46484	1.48472
cg0261124	RAB21	TFIID [T0	1792	1798	9.552105	TGACAA	1.46484	1.48472
cg0261124	RAB21	TFIID [T0	1890	1896	9.552105	TTTGGA	1.46484	1.48472
cg0261124	RAB21	NF-1 [T00	1288	1295	9.535536	TTGGTCA	0.73242	0.73053
cg0261124	RAB21	HNF-1B [	839	847	9.522068	TTTGTAA	0.09155	0.09374
cg0261124	RAB21	TFII-I [T0	15	20	9.512894	GGAAGG	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	47	52	9.512894	GGATCG	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	61	66	9.512894	TTTTCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	106	111	9.512894	GGACTT	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	121	126	9.512894	CCTTCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	274	279	9.512894	GGATGG	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	353	358	9.512894	GGAAGG	7.32422	7.29728

cg0261124	RAB21	TFII-I [T0	493	498	9.512894	GGAAAC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	643	648	9.512894	GGAAGG	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	657	662	9.512894	AAGTCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	700	705	9.512894	CCGTCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	716	721	9.512894	TTTTCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	889	894	9.512894	TTGTCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1262	1267	9.512894	TTATCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1313	1318	9.512894	GGACTT	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1329	1334	9.512894	TTGTCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1352	1357	9.512894	CCATCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1461	1466	9.512894	GGATAA	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1754	1759	9.512894	GGAAAC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1772	1777	9.512894	AAATCC	7.32422	7.29728
cg0261124	RAB21	TFII-I [T0	1871	1876	9.512894	GGACAA	7.32422	7.29728
cg0261124	RAB21	FOXP3 [T	52	57	9.512894	GTTCTT	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	396	401	9.512894	GAGAAC	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	561	566	9.512894	GTTTAC	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	629	634	9.512894	GTTGGG	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	871	876	9.512894	GTTTAT	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1059	1064	9.512894	GCCAAC	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1167	1172	9.512894	GTTATC	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1247	1252	9.512894	GTTATT	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1527	1532	9.512894	CCCAAC	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1571	1576	9.512894	GAGAAC	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1784	1789	9.512894	CAGAAC	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1815	1820	9.512894	GTTATT	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1897	1902	9.512894	GTTTAG	7.32422	7.35678
cg0261124	RAB21	FOXP3 [T	1947	1952	9.512894	GTTCTT	7.32422	7.35678
cg0261124	RAB21	TCF-4E [T	1196	1202	9.453578	CTTTGA	0.48828	0.49215
cg0261124	RAB21	TCF-4E [T	1291	1297	9.453578	GTCAAA	0.48828	0.49215
cg0261124	RAB21	NFI/CTF [	1619	1626	9.352332	GACATT	0.54932	0.54821
cg0261124	RAB21	NF-AT1 [	106	114	9.248801	GGACTT	0.22888	0.22959
cg0261124	RAB21	VDR [T00	1337	1345	9.234242	GTTCAT	0.12207	0.12335
cg0261124	RAB21	AP-1 [T00	862	870	9.203282	TGACTA	0.24414	0.24693
cg0261124	RAB21	PPAR-alph	739	749	9.158357	GGGTCC	0.0515	0.04986
cg0261124	RAB21	STAT5A [	1251	1263	9.080962	TTAGGA	0.02816	0.02876
cg0261124	RAB21	c-Ets-1 [T	1685	1691	9.065503	ATTCCA	0.85449	0.85523
cg0261124	RAB21	USF2 [T0	432	441	9.056375	CAGGTG	0.1545	0.15287
cg0261124	RAB21	NFI/CTF [	626	633	9.042931	GCTGTT	0.48828	0.48804
cg0261124	RAB21	c-Myb [T0	1098	1105	9.024874	CTCAGT	0.39673	0.40028
cg0261124	RAB21	c-Ets-1 [T	668	674	9.020687	GTTCCC	0.85449	0.85523
cg0261124	RAB21	c-Jun [T00	76	82	9.013496	TGACGT	0.61035	0.61059
cg0261124	RAB21	GR [T050	814	820	8.971049	GTATTT	0.61035	0.61632
cg0261124	RAB21	GR [T050	820	826	8.971049	GATTTT	0.61035	0.61632
cg0261124	RAB21	GR [T050	1874	1880	8.971049	CAAATA	0.61035	0.61632
cg0261124	RAB21	c-Myb [T0	843	850	8.947824	TAACTT	0.39673	0.40028
cg0261124	RAB21	RelA [T00	583	593	8.944825	TGGGGA	0.02432	0.0241
cg0261124	RAB21	Elk-1 [T00	349	357	8.931691	TGGGGG	0.24414	0.24034

cg0261124	RAB21	c-Ets-2 [T	734	742	8.912323	TTCCTGC	0.27466	0.27495
cg0261124	RAB21	p53 [T006	91	97	8.912104	GGGCCC	0.12207	0.11837
cg0261124	RAB21	p53 [T006	468	474	8.912104	AGGGCC	0.12207	0.11837
cg0261124	RAB21	p53 [T006	646	652	8.912104	AGGGCC	0.12207	0.11837
cg0261124	RAB21	p53 [T006	647	653	8.912104	GGGCCC	0.12207	0.11837
cg0261124	RAB21	c-Myb [T0	1361	1368	8.872587	TAACTA	0.39673	0.40028
cg0261124	RAB21	NFI/CTF [	1887	1894	8.814757	TCATTTC	0.48828	0.48804
cg0261124	RAB21	c-Jun [T00	1454	1460	8.807683	GTTGTC	0.61035	0.61059
cg0261124	RAB21	NF-1 [T00	630	637	8.790071	TTGGGA	0.24414	0.24467
cg0261124	RAB21	MAZ [T00	628	640	8.765913	TGTTGG	0.01413	0.01385
cg0261124	RAB21	XBP-1 [T	970	975	8.75604	TTTCAT	2.92969	2.9674
cg0261124	RAB21	XBP-1 [T	1169	1174	8.75604	TATCAT	2.92969	2.9674
cg0261124	RAB21	XBP-1 [T	1337	1342	8.75604	GTTCAT	2.92969	2.9674
cg0261124	RAB21	XBP-1 [T	1445	1450	8.75604	GCTCAT	2.92969	2.9674
cg0261124	RAB21	XBP-1 [T	1885	1890	8.75604	GATCAT	2.92969	2.9674
cg0261124	RAB21	AP-1 [T00	1276	1284	8.566653	TGACTT	0.03052	0.03084
cg0261124	RAB21	NF-kappa	584	595	8.485421	GGGGAA	0.01526	0.01499
cg0261124	RAB21	LEF-1 [T0	1196	1203	8.457856	CTTTGA	0.15259	0.15214
cg0261124	RAB21	AhR:Arnt	141	150	8.431005	GAGGGC	0.07439	0.07225
cg0261124	RAB21	AhR:Arnt	980	989	8.431005	GCCTGC	0.07439	0.07225
cg0261124	RAB21	c-Ets-1 [T	881	887	8.373028	GTTCCA	0.24414	0.24529
cg0261124	RAB21	HNF-3alp	1114	1121	8.343064	GTAAAA	0.27466	0.28528
cg0261124	RAB21	HNF-3alp	1160	1167	8.343064	TTAAAA	0.27466	0.28528
cg0261124	RAB21	HNF-3alp	1418	1425	8.343064	TTAAAA	0.27466	0.28528
cg0261124	RAB21	PR B [T00	625	631	8.338824	GGCTGT	1.09863	1.10009
cg0261124	RAB21	PR B [T00	709	715	8.338824	GGCTGT	1.09863	1.10009
cg0261124	RAB21	PR B [T00	900	906	8.338824	AACAGG	1.09863	1.10009
cg0261124	RAB21	PR B [T00	1090	1096	8.338824	TGCTGT	1.09863	1.10009
cg0261124	RAB21	PR B [T00	1404	1410	8.338824	GCCTGT	1.09863	1.10009
cg0261124	RAB21	PR B [T00	1413	1419	8.338824	TTCTGTT	1.09863	1.10009
cg0261124	RAB21	PR A [T01	625	631	8.338824	GGCTGT	1.09863	1.10009
cg0261124	RAB21	PR A [T01	709	715	8.338824	GGCTGT	1.09863	1.10009
cg0261124	RAB21	PR A [T01	900	906	8.338824	AACAGG	1.09863	1.10009
cg0261124	RAB21	PR A [T01	1090	1096	8.338824	TGCTGT	1.09863	1.10009
cg0261124	RAB21	PR A [T01	1404	1410	8.338824	GCCTGT	1.09863	1.10009
cg0261124	RAB21	PR A [T01	1413	1419	8.338824	TTCTGTT	1.09863	1.10009
cg0261124	RAB21	IRF-1 [T0	62	70	8.316022	TTTCCTC	0.20599	0.20664
cg0261124	RAB21	GR-alpha	12	16	8.281568	GGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha	16	20	8.281568	GAAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha	35	39	8.281568	GGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha	65	69	8.281568	CCTCC	7.8125	7.72956
cg0261124	RAB21	GR-alpha	95	99	8.281568	CCTTC	7.8125	7.72956
cg0261124	RAB21	GR-alpha	121	125	8.281568	CCTTC	7.8125	7.72956
cg0261124	RAB21	GR-alpha	130	134	8.281568	CCTCG	7.8125	7.72956
cg0261124	RAB21	GR-alpha	137	141	8.281568	CGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha	140	144	8.281568	GGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha	208	212	8.281568	GAAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha	230	234	8.281568	GGAGG	7.8125	7.72956

cg0261124	RAB21	GR-alpha [	335	339	8.281568	CAAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	354	358	8.281568	GAAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	442	446	8.281568	CCTCG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	454	458	8.281568	GGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	480	484	8.281568	CCTCC	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	555	559	8.281568	CCTTC	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	617	621	8.281568	CGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	633	637	8.281568	GGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	644	648	8.281568	GAAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	927	931	8.281568	GGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	1018	1022	8.281568	CGAGG	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	1349	1353	8.281568	CCTCC	7.8125	7.72956
cg0261124	RAB21	GR-alpha [	1776	1780	8.281568	CCTTG	7.8125	7.72956
cg0261124	RAB21	p53 [T006	90	96	8.208781	GGGGCC	0.48828	0.47377
cg0261124	RAB21	p53 [T006	469	475	8.208781	GGGCCC	0.48828	0.47377
cg0261124	RAB21	ENKTF-1	277	284	8.19852	TGGCTG	0.73242	0.71737
cg0261124	RAB21	ENKTF-1	679	686	8.19852	TGGCTG	0.73242	0.71737
cg0261124	RAB21	HNF-1C [	1929	1937	8.193285	ATAGCT	0.19836	0.20224
cg0261124	RAB21	PXR-1:RX	1818	1825	8.180749	ATTGTT	0.12207	0.12407
cg0261124	RAB21	p53 [T006	155	161	8.162057	AGCGCC	0.48828	0.47377
cg0261124	RAB21	c-Jun [T00	1618	1624	8.128539	TGACAT	0.48828	0.49076
cg0261124	RAB21	GR-alpha [	9	13	8.073878	GTAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	125	129	8.073878	CCAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	325	329	8.073878	CCTAC	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	431	435	8.073878	GCAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	474	478	8.073878	CCTAC	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	507	511	8.073878	CCTGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	515	519	8.073878	CCTGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	522	526	8.073878	GTAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	581	585	8.073878	CCTGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	593	597	8.073878	CCAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	736	740	8.073878	CCTGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	744	748	8.073878	CCAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	952	956	8.073878	CCTAG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	953	957	8.073878	CTAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	981	985	8.073878	CCTGC	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1190	1194	8.073878	CCAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1266	1270	8.073878	CCTAC	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1333	1337	8.073878	CCAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1490	1494	8.073878	CCTGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1751	1755	8.073878	CCAGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1842	1846	8.073878	CCTGG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1880	1884	8.073878	CCTAG	7.8125	7.72238
cg0261124	RAB21	GR-alpha [	1881	1885	8.073878	CTAGG	7.8125	7.72238
cg0261124	RAB21	Pax-5 [T0	90	96	8.014558	GGGGCC	2.19727	2.14502
cg0261124	RAB21	Pax-5 [T0	116	122	8.014558	TCAGCC	2.19727	2.14502
cg0261124	RAB21	Pax-5 [T0	186	192	8.014558	GGGCTG	2.19727	2.14502
cg0261124	RAB21	Pax-5 [T0	317	323	8.014558	GGGCCG	2.19727	2.14502

cg0261124	RAB21	Pax-5 [T0	469	475	8.014558	GGGCCC	2.19727	2.14502
cg0261124	RAB21	Pax-5 [T0	601	607	8.014558	GGGCAG	2.19727	2.14502
cg0261124	RAB21	TFIID [T0	568	574	8.014558	TTTCCG	2.19727	2.24348
cg0261124	RAB21	TFIID [T0	790	796	8.014558	TTTCAG	2.19727	2.24348
cg0261124	RAB21	TFIID [T0	823	829	8.014558	TTTGCG	2.19727	2.24348
cg0261124	RAB21	TFIID [T0	839	845	8.014558	TTTGTA	2.19727	2.24348
cg0261124	RAB21	TFIID [T0	935	941	8.014558	TTTGAA	2.19727	2.24348
cg0261124	RAB21	TFIID [T0	1149	1155	8.014558	TTGGAA	2.19727	2.24348
cg0261124	RAB21	TFIID [T0	1735	1741	8.014558	TCTGAA	2.19727	2.24348
cg0261124	RAB21	C/EBPalp	1147	1153	8.006685	CATTGG	0.24414	0.24674
cg0261124	RAB21	C/EBPalp	1621	1627	8.006685	CATTGG	0.24414	0.24674
cg0261124	RAB21	MAZ [T00	449	461	7.982153	GAGCGG	0.00915	0.009
cg0261124	RAB21	ETF [T002	170	180	7.870358	GGGGCC	0.07153	0.06862
cg0261124	RAB21	ETF [T002	179	189	7.870358	GCGGTG	0.07153	0.06862
cg0261124	RAB21	HNF-1C [	894	902	7.864676	CTGAGT	0.19836	0.20224
cg0261124	RAB21	HNF-1C [	1094	1102	7.864676	GTTACT	0.19836	0.20224
cg0261124	RAB21	c-Ets-2 [T	796	804	7.84116	AATTAG	0.32043	0.32298
cg0261124	RAB21	c-Ets-2 [T	1749	1757	7.84116	TGCCAG	0.32043	0.32298
cg0261124	RAB21	E2F-1 [T0	999	1006	7.839654	GCGGGT	0.30518	0.3
cg0261124	RAB21	IRF-1 [T0	1750	1758	7.82345	GCCAGG	0.25177	0.25263
cg0261124	RAB21	T3R-beta1	1213	1221	7.813363	TCACCC	0.27466	0.27236
cg0261124	RAB21	NF-AT1 [	564	572	7.744746	TACCTT	0.19836	0.19941
cg0261124	RAB21	NF-AT1 [	1151	1159	7.744746	GGAAAG	0.19836	0.19941
cg0261124	RAB21	LEF-1 [T0	1290	1297	7.719635	GGTCAA	0.21362	0.21302
cg0261124	RAB21	AR [T000	886	894	7.623968	ATTTGT	0.25177	0.25079
cg0261124	RAB21	NFI/CTF [	766	773	7.587343	CCAAAT	0.36621	0.36674
cg0261124	RAB21	NFI/CTF [	1063	1070	7.587343	ACAATT	0.36621	0.36674
cg0261124	RAB21	NF-AT1 [	58	66	7.574801	CGCTTT	0.19836	0.19941
cg0261124	RAB21	c-Myb [T0	1756	1763	7.545286	AAACTG	0.42725	0.43114
cg0261124	RAB21	HNF-1B [	1388	1396	7.53234	TACTTA	0.09155	0.09368
cg0261124	RAB21	GR [T050	885	891	7.527031	CATTTC	1.83105	1.86007
cg0261124	RAB21	GR [T050	911	917	7.527031	CAAAAG	1.83105	1.86007
cg0261124	RAB21	GR [T050	1315	1321	7.527031	ACTTTC	1.83105	1.86007
cg0261124	RAB21	GR [T050	1627	1633	7.527031	ATGTTC	1.83105	1.86007
cg0261124	RAB21	GR [T050	1795	1801	7.527031	CAAAAT	1.83105	1.86007
cg0261124	RAB21	GR [T050	1964	1970	7.527031	TATTTC	1.83105	1.86007
cg0261124	RAB21	C/EBPalp	973	979	7.465744	CATTGC	0.48828	0.49653
cg0261124	RAB21	p53 [T006	459	465	7.458735	GGGCGC	0.73242	0.7186
cg0261124	RAB21	c-Myb [T0	1382	1389	7.442719	GTAAGT	0.42725	0.43114
cg0261124	RAB21	AR [T000	620	628	7.429939	GGACAG	0.25177	0.25079
cg0261124	RAB21	PXR-1:RX	329	336	7.362674	CTCGTT	0.24414	0.24395
cg0261124	RAB21	E2F-1 [T0	214	221	7.336545	GCTGCC	0.45776	0.44878
cg0261124	RAB21	HNF-1C [	1386	1394	7.313515	GTTACT	0.08392	0.08549
cg0261124	RAB21	HOXD9 [	1243	1252	7.270719	TGATGT	0.06866	0.07152
cg0261124	RAB21	HOXD10 [	1243	1252	7.270719	TGATGT	0.06866	0.07152
cg0261124	RAB21	p53 [T006	708	714	7.266844	GGGCTG	0.73242	0.7186
cg0261124	RAB21	c-Ets-1 [T	717	723	7.199436	TTTCCC	0.73242	0.73099
cg0261124	RAB21	GCF [T00	381	389	7.186486	GTGCTG	0.45776	0.44706

cg0261124	RAB21	c-Jun [T00	1000	1006	7.178905	CGGGTCA	0.73242	0.73173
cg0261124	RAB21	XBP-1 [T0	96	101	7.172312	CTTCAT	2.92969	2.97018
cg0261124	RAB21	XBP-1 [T0	1006	1011	7.172312	ACTCAT	2.92969	2.97018
cg0261124	RAB21	XBP-1 [T0	1808	1813	7.172312	ATGAAT	2.92969	2.97018
cg0261124	RAB21	c-Ets-1 [T0	110	116	7.071349	TTTCCCT	0.73242	0.73099
cg0261124	RAB21	IRF-1 [T0	489	497	7.041849	CTGGGGA	0.1297	0.13036
cg0261124	RAB21	HNF-3alph	1661	1668	7.000129	AATTTAC	0.82397	0.84946
cg0261124	RAB21	HNF-3alph	1762	1769	7.000129	CATTTTT	0.82397	0.84946
cg0261124	RAB21	HNF-3alph	1794	1801	7.000129	ACAAAA	0.82397	0.84946
cg0261124	RAB21	HNF-3alph	1859	1866	7.000129	AGAAAA	0.82397	0.84946
cg0261124	RAB21	HNF-3alph	1964	1971	7.000129	TATTTTG	0.82397	0.84946
cg0261124	RAB21	GCF [T00	846	854	6.987525	CTTCAGC	0.45776	0.44706
cg0261124	RAB21	c-Ets-1 [T0	491	497	6.943262	GGGGAA	0.73242	0.73099
cg0261124	RAB21	ENKTF-1	21	28	6.942764	AGACGC	1.46484	1.44228
cg0261124	RAB21	ENKTF-1	201	208	6.942764	TGGCTGT	1.46484	1.44228
cg0261124	RAB21	STAT1bet	109	118	6.908963	CTTTCCC	0.103	0.10372
cg0261124	RAB21	p53 [T006	177	183	6.891821	GGGCGG	1.09863	1.07125
cg0261124	RAB21	p53 [T006	1522	1528	6.891821	ACCGCCC	1.09863	1.07125
cg0261124	RAB21	c-Jun [T00	1288	1294	6.856451	TTGGTCA	0.73242	0.73173
cg0261124	RAB21	ATF-2 [T0	75	84	6.803907	CTGACGT	0.01907	0.01886
cg0261124	RAB21	AR [T000	1871	1879	6.760234	GGACAA	0.23651	0.23551
cg0261124	RAB21	NF-1 [T00	1056	1063	6.722386	CTGGCCA	0.24414	0.24147
cg0261124	RAB21	c-Myb [T0	1202	1209	6.719843	GGGAGT	0.30518	0.3056
cg0261124	RAB21	c-Jun [T00	993	999	6.668031	TGACTTC	0.61035	0.60769
cg0261124	RAB21	E2F-1 [T0	1519	1526	6.611004	ATTACCC	0.12207	0.12031
cg0261124	RAB21	TFII-I [T0	548	553	6.581441	ATCTCC	0.97656	0.97366
cg0261124	RAB21	TFII-I [T0	1603	1608	6.581441	ATCTCC	0.97656	0.97366
cg0261124	RAB21	FOXP3 [T	1848	1853	6.581441	GTTTTA	0.97656	0.99397
cg0261124	RAB21	IRF-1 [T0	1147	1155	6.535281	CATTGGA	0.19073	0.19127
cg0261124	RAB21	c-Ets-1 [T0	1149	1155	6.423689	TTGGAA	0.48828	0.48798
cg0261124	RAB21	HNF-1C [	838	846	6.400146	ATTTGTA	0.05341	0.05475
cg0261124	RAB21	TCF-4E [T	498	504	6.302385	CTTTGCC	0.61035	0.61344
cg0261124	RAB21	GR-alpha [	114	118	6.263098	CCTCA	3.90625	3.91061
cg0261124	RAB21	GR-alpha [	464	468	6.263098	CCTCA	3.90625	3.91061
cg0261124	RAB21	GR-alpha [	1199	1203	6.263098	TGAGG	3.90625	3.91061
cg0261124	RAB21	c-Myb [T0	729	736	6.259888	TGCAGTT	0.30518	0.3056
cg0261124	RAB21	p53 [T006	233	239	6.188498	GGGCGG	0.61035	0.594
cg0261124	RAB21	p53 [T006	255	261	6.188498	GGGCGG	0.61035	0.594
cg0261124	RAB21	p53 [T006	304	310	6.188498	GGGCGG	0.61035	0.594
cg0261124	RAB21	p53 [T006	502	508	6.188498	GCCGCCC	0.61035	0.594
cg0261124	RAB21	c-Myb [T0	1501	1508	6.157321	GTAAGTT	0.21362	0.21535
cg0261124	RAB21	c-Jun [T00	1792	1798	6.152811	TGACAAA	0.36621	0.37082
cg0261124	RAB21	NF-AT1 [T	713	721	6.150044	GTTTTTT	0.06866	0.06922
cg0261124	RAB21	RXR-alpha	474	480	6.119461	CCTACCC	0.73242	0.72249
cg0261124	RAB21	GCF [T00	679	687	6.116216	TGGCTGC	0.64087	0.6219
cg0261124	RAB21	IRF-1 [T0	568	576	6.078807	TTTCCGA	0.16785	0.16909
cg0261124	RAB21	GR-alpha [	74	78	6.055408	CCTGA	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	466	470	6.055408	TCAGG	3.90625	3.9065

cg0261124	RAB21	GR-alpha [	537	541	6.055408	TCAGG	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	651	655	6.055408	CCTGA	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	798	802	6.055408	TTAGG	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	831	835	6.055408	TTAGG	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	893	897	6.055408	CCTGA	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	1251	1255	6.055408	TTAGG	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	1324	1328	6.055408	CCTGA	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	1458	1462	6.055408	TCAGG	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	1607	1611	6.055408	CCTAA	3.90625	3.9065
cg0261124	RAB21	GR-alpha [	1911	1915	6.055408	TTAGG	3.90625	3.9065
cg0261124	RAB21	GCF [T00	212	220	5.917256	GCGCTG	0.64087	0.6219
cg0261124	RAB21	p53 [T006	317	323	5.883561	GGGCCG	0.61035	0.594
cg0261124	RAB21	STAT4 [T	15	20	5.882353	GGAAGG	0.48828	0.48408
cg0261124	RAB21	STAT4 [T	121	126	5.882353	CCTTCC	0.48828	0.48408
cg0261124	RAB21	STAT4 [T	353	358	5.882353	GGAAGG	0.48828	0.48408
cg0261124	RAB21	STAT4 [T	643	648	5.882353	GGAAGG	0.48828	0.48408
cg0261124	RAB21	VDR [T00	332	340	5.771401	GTTCAA	0.42725	0.42999
cg0261124	RAB21	VDR [T00	1821	1829	5.771401	GTTCAG	0.42725	0.42999
cg0261124	RAB21	POU2F2 (	1722	1732	5.731804	TATGTA	0.06437	0.06564
cg0261124	RAB21	ENKTF-1	1677	1684	5.687009	TGGCTC	0.73242	0.7249
cg0261124	RAB21	c-Ets-1 [T	635	641	5.686398	AGGGAA	0.36621	0.3623
cg0261124	RAB21	NF-1 [T00	1067	1074	5.626299	TTGGTC	0.24414	0.24258
cg0261124	RAB21	c-Ets-2 [T	899	907	5.624023	TAACAG	0.01526	0.0156
cg0261124	RAB21	T3R-beta1	590	598	5.591999	TCACCA	0.21362	0.21287
cg0261124	RAB21	c-Jun [T00	1825	1831	5.590308	AGTGTC	0.48828	0.48665
cg0261124	RAB21	c-Ets-1 [T	351	357	5.558311	GGGGAA	0.36621	0.3623
cg0261124	RAB21	c-Ets-1 [T	365	371	5.558311	GGGGAA	0.36621	0.3623
cg0261124	RAB21	c-Myb [T0	965	972	5.55549	CGCAGT	0.09155	0.09192
cg0261124	RAB21	Pax-5 [T0	155	161	5.544826	AGCGCC	0.73242	0.72046
cg0261124	RAB21	Pax-5 [T0	177	183	5.544826	GGGCGG	0.73242	0.72046
cg0261124	RAB21	Pax-5 [T0	1522	1528	5.544826	ACCGCC	0.73242	0.72046
cg0261124	RAB21	TFIID [T0	1158	1164	5.544826	TGTTAA	0.73242	0.75085
cg0261124	RAB21	TFIID [T0	1416	1422	5.544826	TGTTAA	0.73242	0.75085
cg0261124	RAB21	p53 [T006	116	122	5.508538	TCAGCC	0.61035	0.59991
cg0261124	RAB21	p53 [T006	186	192	5.508538	GGGCTG	0.61035	0.59991
cg0261124	RAB21	C/EBPalph	1172	1178	5.455853	CATTGA	0.73242	0.74391
cg0261124	RAB21	HOXD9 [	1118	1127	5.453039	AATAAA	0.04578	0.04743
cg0261124	RAB21	HOXD10 [	1118	1127	5.453039	AATAAA	0.04578	0.04743
cg0261124	RAB21	c-Ets-1 [T	262	268	5.430224	CGGGAA	0.36621	0.3623
cg0261124	RAB21	C/EBPalph	1062	1068	5.38654	AACAAT	0.73242	0.74391
cg0261124	RAB21	C/EBPalph	1065	1071	5.38654	AATTGG	0.73242	0.74391
cg0261124	RAB21	C/EBPalph	1282	1288	5.38654	ACCAAT	0.73242	0.74391
cg0261124	RAB21	C/EBPalph	1610	1616	5.38654	AATTGT	0.73242	0.74391
cg0261124	RAB21	C/EBPalph	1811	1817	5.38654	AATTGT	0.73242	0.74391
cg0261124	RAB21	p53 [T006	576	582	5.345221	TTCGCC	0.61035	0.59991
cg0261124	RAB21	c-Myb [T0	1893	1900	5.258734	GGAAGT	0.09155	0.09192
cg0261124	RAB21	AP-2alpha	1194	1199	5.100982	GCCTTT	0.97656	0.97567
cg0261124	RAB21	AP-2alpha	1294	1299	5.100982	AAAGGC	0.97656	0.97567

cg0261124	RAB21	AP-2alpha	1512	1517	5.100982	GCCTTT	0.97656	0.97567
cg0261124	RAB21	USF2 [T0	745	754	5.052423	CAGGTG	0.103	0.10178
cg0261124	RAB21	GR-beta [T	814	818	5.042296	GTATT	3.90625	3.95351
cg0261124	RAB21	GR-beta [T	1052	1056	5.042296	AATAC	3.90625	3.95351
cg0261124	RAB21	GR-beta [T	1773	1777	5.042296	AATCC	3.90625	3.95351
cg0261124	RAB21	GR-beta [T	1876	1880	5.042296	AATAC	3.90625	3.95351
cg0261124	RAB21	E2F-1 [T0	451	458	5.042045	GCGGGA	0.18311	0.17901
cg0261124	RAB21	c-Ets-1 [T	1891	1897	5.038739	TTGGAA	0.48828	0.49031
cg0261124	RAB21	RelA [T00	107	117	5.0365	GACTTT	0.01001	0.00994
cg0261124	RAB21	p53 [T006	249	255	5.020467	GGGCTC	0.48828	0.47747
cg0261124	RAB21	c-Jun [T00	747	753	5.000337	GGTGTC	0.61035	0.61057
cg0261124	RAB21	ATF3 [T0	5	12	4.941398	TGACGT	0.09155	0.09183
cg0261124	RAB21	c-Jun [T00	5	11	4.883696	TGACGT	0.61035	0.61057
cg0261124	RAB21	c-Ets-1 [T	568	574	4.872197	TTTCCG	0.48828	0.49031
cg0261124	RAB21	GCF [T00	151	159	4.846987	GGACAG	0.27466	0.26486
cg0261124	RAB21	GCF [T00	233	241	4.846987	GGGCGG	0.27466	0.26486
cg0261124	RAB21	HNF-3alph	1798	1805	4.842999	AATTTT	0.09155	0.09582
cg0261124	RAB21	c-Myb [T0	877	884	4.840682	GCAAGT	0.30518	0.30568
cg0261124	RAB21	HNF-1A [	1388	1395	4.828753	TACTTA	0.36621	0.37179
cg0261124	RAB21	c-Ets-1 [T	641	647	4.782565	GTGGAA	0.48828	0.49031
cg0261124	RAB21	c-Ets-1 [T	1135	1141	4.782565	CTTCCA	0.48828	0.49031
cg0261124	RAB21	C/EBPalph	1817	1823	4.776286	TATTGT	0.97656	0.99332
cg0261124	RAB21	C/EBPalph	1925	1931	4.776286	AACAAT	0.97656	0.99332
cg0261124	RAB21	TFII-I [T0	904	909	4.756447	GGAATG	2.92969	2.93695
cg0261124	RAB21	FOXP3 [T	713	718	4.756447	GTTTTT	2.92969	2.96063
cg0261124	RAB21	FOXP3 [T	931	936	4.756447	GTTTTT	2.92969	2.96063
cg0261124	RAB21	FOXP3 [T	1239	1244	4.756447	GTTTTG	2.92969	2.96063
cg0261124	RAB21	Sp1 [T007	500	509	4.675093	TTGCCG	0.08583	0.08339
cg0261124	RAB21	c-Ets-1 [T	122	128	4.654478	CTTCCA	0.85449	0.85764
cg0261124	RAB21	TCF-4 [T0	1289	1298	4.639022	TGGTCA	0.04196	0.04202
cg0261124	RAB21	HNF-1B [	1385	1393	4.569001	AGTTAC	0.05341	0.0549
cg0261124	RAB21	NF-AT1 [	493	501	4.566689	GGAAAC	0.06866	0.06925
cg0261124	RAB21	C/EBPalph	1327	1333	4.560723	GATTGT	0.24414	0.24411
cg0261124	RAB21	NF-kappaI	584	594	4.51387	GGGGAA	0.03242	0.03169
cg0261124	RAB21	T3R-beta1	830	838	4.481316	ATTAGG	0.27466	0.27551
cg0261124	RAB21	AP-2alpha	951	956	4.438035	GCCTAG	0.97656	0.96979
cg0261124	RAB21	AP-2alpha	953	958	4.438035	CTAGGC	0.97656	0.96979
cg0261124	RAB21	RXR-alpha	1452	1458	4.423008	GGGTTG	0.24414	0.24292
cg0261124	RAB21	STAT4 [T	264	269	4.411765	GGAAGC	1.95312	1.94235
cg0261124	RAB21	STAT4 [T	367	372	4.411765	GGAAGA	1.95312	1.94235
cg0261124	RAB21	STAT4 [T	904	909	4.411765	GGAATG	1.95312	1.94235
cg0261124	RAB21	STAT4 [T	1134	1139	4.411765	TCTTCC	1.95312	1.94235
cg0261124	RAB21	EBF [T054	463	473	4.334406	GCCTCA	0.00572	0.00551
cg0261124	RAB21	TCF-4 [T0	1195	1204	4.328832	CCTTTG	0.04196	0.04202
cg0261124	RAB21	PEA3 [T0	1624	1632	4.30818	TGGATG	0.13733	0.13791
cg0261124	RAB21	CREB [T0	76	84	4.261795	TGACGT	0.04578	0.04561
cg0261124	RAB21	RXR-alpha	739	745	4.24113	GGGTCC	0.97656	0.9671
cg0261124	RAB21	RXR-alpha	1001	1007	4.24113	GGGTCA	0.97656	0.9671

cg0261124	RAB21	RXR-alph	1380	1386	4.24113	GGGTAA	0.97656	0.9671
cg0261124	RAB21	AR [T000	151	159	4.241082	GGACAG	0.06866	0.06828
cg0261124	RAB21	Sp1 [T007	1520	1529	4.212075	TTACCG	0.08965	0.08686
cg0261124	RAB21	AP-2alpha	324	329	4.211849	GCCTAC	0.97656	0.96469
cg0261124	RAB21	AP-2alpha	522	527	4.211849	GTAGGC	0.97656	0.96469
cg0261124	RAB21	GR-beta [	588	592	4.201913	AATCA	7.8125	7.94607
cg0261124	RAB21	GR-beta [	819	823	4.201913	TGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	836	840	4.201913	TGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1024	1028	4.201913	CGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1118	1122	4.201913	AATAA	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1175	1179	4.201913	TGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1234	1238	4.201913	AATCA	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1248	1252	4.201913	TTATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1326	1330	4.201913	TGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1431	1435	4.201913	AATAG	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1539	1543	4.201913	AATAG	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1590	1594	4.201913	AATAG	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1637	1641	4.201913	CTATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1640	1644	4.201913	TTATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1683	1687	4.201913	TGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1695	1699	4.201913	CTATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1710	1714	4.201913	TGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1804	1808	4.201913	AATAA	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1816	1820	4.201913	TTATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1928	1932	4.201913	AATAG	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1960	1964	4.201913	TGATT	7.8125	7.94607
cg0261124	RAB21	GR-beta [	1963	1967	4.201913	TTATT	7.8125	7.94607
cg0261124	RAB21	NF-Y [T0	1148	1155	4.186615	ATTGGA	0.18311	0.1853
cg0261124	RAB21	CREB [T0	5	13	4.185436	TGACGT	0.06104	0.06123
cg0261124	RAB21	c-Ets-1 [T	902	908	4.154851	CAGGAA	0.24414	0.24526
cg0261124	RAB21	NF-1 [T00	1524	1531	4.135372	CGCCCC	0.24414	0.24154
cg0261124	RAB21	NF-AT1 [	1150	1159	4.134416	TGGAAA	0.08392	0.08485
cg0261124	RAB21	p53 [T006	171	177	4.125254	GGGCCG	0.73242	0.71379
cg0261124	RAB21	Sp1 [T007	254	263	4.120098	CGGGCG	0.08965	0.08686
cg0261124	RAB21	PXR-1:RX	1334	1341	4.090374	CAGGTT	0.12207	0.12119
cg0261124	RAB21	IRF-1 [T0	110	118	4.035054	TTTCCCT	0.1297	0.13087
cg0261124	RAB21	C/EBPalph	1025	1031	4.019783	GATTGA	0.48828	0.49358
cg0261124	RAB21	Pax-5 [T0	91	97	4.007279	GGGCCC	1.09863	1.07975
cg0261124	RAB21	Pax-5 [T0	468	474	4.007279	AGGGCC	1.09863	1.07975
cg0261124	RAB21	Pax-5 [T0	646	652	4.007279	AGGGCC	1.09863	1.07975
cg0261124	RAB21	Pax-5 [T0	647	653	4.007279	GGGCCC	1.09863	1.07975
cg0261124	RAB21	Pax-5 [T0	708	714	4.007279	GGGCTG	1.09863	1.07975
cg0261124	RAB21	TFIID [T0	1552	1558	4.007279	TAGTAA	1.09863	1.13456
cg0261124	RAB21	TFIID [T0	1641	1647	4.007279	TATTAA	1.09863	1.13456
cg0261124	RAB21	TFIID [T0	1663	1669	4.007279	TTTACA	1.09863	1.13456
cg0261124	RAB21	TFIID [T0	1765	1771	4.007279	TTTTAA	1.09863	1.13456
cg0261124	RAB21	TFIID [T0	1801	1807	4.007279	TTTAAT	1.09863	1.13456
cg0261124	RAB21	NF-AT2 [	493	502	3.973081	GGAAAC	0.01144	0.01159

cg0261124	RAB21	NF-Y [T0	1622	1629	3.95898	ATTGGA	0.18311	0.1853
cg0261124	RAB21	NF-kappa	105	116	3.878203	CGGACT	0.00608	0.00601
cg0261124	RAB21	c-Ets-1 [T	799	805	3.846637	TAGGAA	0.24414	0.24526
cg0261124	RAB21	c-Jun [T00	862	868	3.807346	TGACTA	0.24414	0.24526
cg0261124	RAB21	GR [T050	1238	1244	3.763516	AGTTTT	0.73242	0.74251
cg0261124	RAB21	p53 [T006	85	91	3.750231	GGGCTG	0.73242	0.71379
cg0261124	RAB21	p53 [T006	486	492	3.750231	GGGCTG	0.73242	0.71379
cg0261124	RAB21	AP-2alpha	208	213	3.743866	GAAGGC	0.48828	0.48238
cg0261124	RAB21	AP-2alpha	354	359	3.743866	GAAGGC	0.48828	0.48238
cg0261124	RAB21	AP-2alpha	554	559	3.743866	GCCTTC	0.48828	0.48238
cg0261124	RAB21	PEA3 [T0	517	525	3.710864	TGGATG	0.09155	0.09258
cg0261124	RAB21	p53 [T006	131	137	3.586914	CTCGCC	0.73242	0.7189
cg0261124	RAB21	RXR-alph	162	168	3.574782	GGGTCG	1.09863	1.08572
cg0261124	RAB21	c-Myb [T0	1529	1536	3.555283	CAACTT	0.12207	0.12203
cg0261124	RAB21	c-Ets-1 [T	733	739	3.462376	GTTCCT	0.61035	0.60765
cg0261124	RAB21	ATF-2 [T0	4	13	3.454345	GTGACG	0.01907	0.01902
cg0261124	RAB21	RXR-alph	1212	1218	3.392904	CTCACC	1.09863	1.08572
cg0261124	RAB21	p53 [T006	143	149	3.375208	GGGCGT	0.73242	0.7189
cg0261124	RAB21	T3R-beta1	421	429	3.370634	TCACCA	0.27466	0.2755
cg0261124	RAB21	GR-beta [	533	537	3.361531	AATCT	3.90625	3.99611
cg0261124	RAB21	GR-beta [	1010	1014	3.361531	ATATT	3.90625	3.99611
cg0261124	RAB21	GR-beta [	1466	1470	3.361531	AATAT	3.90625	3.99611
cg0261124	RAB21	GR-beta [	1602	1606	3.361531	AATCT	3.90625	3.99611
cg0261124	RAB21	GR-beta [	1903	1907	3.361531	AGATT	3.90625	3.99611
cg0261124	RAB21	PR B [T00	768	774	3.29756	AAATGT	0.24414	0.25122
cg0261124	RAB21	PR B [T00	1062	1068	3.29756	AACAAT	0.24414	0.25122
cg0261124	RAB21	PR B [T00	1163	1169	3.29756	AAATGT	0.24414	0.25122
cg0261124	RAB21	PR B [T00	1610	1616	3.29756	AATTGT	0.24414	0.25122
cg0261124	RAB21	PR B [T00	1811	1817	3.29756	AATTGT	0.24414	0.25122
cg0261124	RAB21	PR B [T00	1935	1941	3.29756	AACATT	0.24414	0.25122
cg0261124	RAB21	PR A [T01	768	774	3.29756	AAATGT	0.24414	0.25122
cg0261124	RAB21	PR A [T01	1062	1068	3.29756	AACAAT	0.24414	0.25122
cg0261124	RAB21	PR A [T01	1163	1169	3.29756	AAATGT	0.24414	0.25122
cg0261124	RAB21	PR A [T01	1610	1616	3.29756	AATTGT	0.24414	0.25122
cg0261124	RAB21	PR A [T01	1811	1817	3.29756	AATTGT	0.24414	0.25122
cg0261124	RAB21	PR A [T01	1935	1941	3.29756	AACATT	0.24414	0.25122
cg0261124	RAB21	POU2F2 (	1847	1857	3.116744	TGTTTTA	0.02575	0.0265
cg0261124	RAB21	Pax-5 [T0	131	137	3.075094	CTCGCC	0.12207	0.11895
cg0261124	RAB21	c-Jun [T00	1028	1034	3.049104	TGACCC	0.24414	0.24403
cg0261124	RAB21	Sp1 [T007	232	241	2.968348	AGGGCG	0.03433	0.03306
cg0261124	RAB21	HOXD9 [	1811	1820	2.949288	AATTGT	0.02289	0.02401
cg0261124	RAB21	HOXD10 [	1811	1820	2.949288	AATTGT	0.02289	0.02401
cg0261124	RAB21	STAT4 [T	109	114	2.941176	CTTTCC	2.92969	2.929
cg0261124	RAB21	STAT4 [T	567	572	2.941176	CTTTCC	2.92969	2.929
cg0261124	RAB21	STAT4 [T	586	591	2.941176	GGAATC	2.92969	2.929
cg0261124	RAB21	STAT4 [T	637	642	2.941176	GGAAGT	2.92969	2.929
cg0261124	RAB21	STAT4 [T	667	672	2.941176	TGTTCC	2.92969	2.929
cg0261124	RAB21	STAT4 [T	1151	1156	2.941176	GGAAAG	2.92969	2.929

cg0261124	RAB21	STAT4 [T	1684	1689	2.941176	GATTCC	2.92969	2.929
cg0261124	RAB21	STAT4 [T	1893	1898	2.941176	GGAAGT	2.92969	2.929
cg0261124	RAB21	IRF-1 [T0	717	725	2.93326	TTTCCC	0.07629	0.07756
cg0261124	RAB21	Sp1 [T007	176	185	2.842119	GGGGCG	0.03433	0.03306
cg0261124	RAB21	p53 [T006	601	607	2.813291	GGGCAG	0.48828	0.47786
cg0261124	RAB21	PR B [T00	1817	1823	2.80933	TATTGT	0.73242	0.74818
cg0261124	RAB21	PR B [T00	1925	1931	2.80933	AACAAT	0.73242	0.74818
cg0261124	RAB21	PR A [T01	1817	1823	2.80933	TATTGT	0.73242	0.74818
cg0261124	RAB21	PR A [T01	1925	1931	2.80933	AACAAT	0.73242	0.74818
cg0261124	RAB21	c-Ets-2 [T	63	71	2.715313	TTCCTC	0.07629	0.07593
cg0261124	RAB21	AP-2alpha	463	468	2.550491	GCCTCA	0.48828	0.48266
cg0261124	RAB21	c-Jun [T00	1276	1282	2.538231	TGACTT	0.48828	0.48929
cg0261124	RAB21	Sp1 [T007	303	312	2.491373	GGGGCG	0.04005	0.03892
cg0261124	RAB21	c-Jun [T00	1369	1375	2.345465	TGTGTC	0.48828	0.48929
cg0261124	RAB21	RXR-alpha	988	994	2.322562	GGGTCT	0.85449	0.84796
cg0261124	RAB21	E2F-1 [T0	499	506	2.294501	TTTGCC	0.06104	0.06059
cg0261124	RAB21	AR [T000	1326	1334	2.267638	TGATTG	0.11444	0.11507
cg0261124	RAB21	GATA-1 [	1263	1268	2.176375	TATCCT	3.90625	3.92756
cg0261124	RAB21	GATA-1 [	1460	1465	2.176375	AGGATA	3.90625	3.92756
cg0261124	RAB21	AP-2alpha	129	134	2.098119	GCCTCG	0.97656	0.95407
cg0261124	RAB21	PR B [T00	867	873	1.892895	AAGTGT	0.12207	0.12429
cg0261124	RAB21	PR A [T01	867	873	1.892895	AAGTGT	0.12207	0.12429
cg0261124	RAB21	AP-2alpha	35	40	1.871933	GGAGGC	0.97656	0.95407
cg0261124	RAB21	TFII-I [T0	1222	1227	1.824994	CTCTCC	0.48828	0.48408
cg0261124	RAB21	FOXP3 [T	1206	1211	1.824994	GTTGTA	0.48828	0.49451
cg0261124	RAB21	C/EBPalph	1536	1542	1.761449	CACAAT	0.48828	0.49438
cg0261124	RAB21	GR-beta [	573	577	1.680765	GAATT	3.90625	3.94936
cg0261124	RAB21	GR-beta [	574	578	1.680765	AATTC	3.90625	3.94936
cg0261124	RAB21	GR-beta [	795	799	1.680765	GAATT	3.90625	3.94936
cg0261124	RAB21	GR-beta [	828	832	1.680765	GAATT	3.90625	3.94936
cg0261124	RAB21	GR-beta [	1595	1599	1.680765	AATGC	3.90625	3.94936
cg0261124	RAB21	GR-beta [	1660	1664	1.680765	GAATT	3.90625	3.94936
cg0261124	RAB21	GR-beta [	1761	1765	1.680765	GCATT	3.90625	3.94936
cg0261124	RAB21	GR-beta [	1810	1814	1.680765	GAATT	3.90625	3.94936
cg0261124	RAB21	GR-beta [	1863	1867	1.680765	AATTC	3.90625	3.94936
cg0261124	RAB21	GR-beta [	1994	1998	1.680765	AATTC	3.90625	3.94936
cg0261124	RAB21	C/EBPbeta	630	633	1.639871	TTGG	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	766	769	1.639871	CCAA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1060	1063	1.639871	CCAA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1067	1070	1.639871	TTGG	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1149	1152	1.639871	TTGG	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1283	1286	1.639871	CCAA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1288	1291	1.639871	TTGG	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1528	1531	1.639871	CCAA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1623	1626	1.639871	TTGG	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1891	1894	1.639871	TTGG	15.625	15.72563
cg0261124	RAB21	XBP-1 [T	544	549	1.583727	TGTCAT	0.97656	0.98146
cg0261124	RAB21	XBP-1 [T	941	946	1.583727	ATGACC	0.97656	0.98146

cg0261124	RAB21	XBP-1 [T0	1371	1376	1.583727	TGTCAT	0.97656	0.98146
cg0261124	RAB21	XBP-1 [T0	1486	1491	1.583727	ATGACC	0.97656	0.98146
cg0261124	RAB21	XBP-1 [T0	1827	1832	1.583727	TGTCAT	0.97656	0.98146
cg0261124	RAB21	Pax-5 [T0	143	149	1.537547	GGGCGT	0.73242	0.71311
cg0261124	RAB21	TFIID [T0	934	940	1.537547	TTTTGA	0.73242	0.75096
cg0261124	RAB21	TFIID [T0	1113	1119	1.537547	TGTAAA	0.73242	0.75096
cg0261124	RAB21	TFIID [T0	1737	1743	1.537547	TGAAAA	0.73242	0.75096
cg0261124	RAB21	NF-Y [T0	1280	1287	1.51343	TTACCA	0.18311	0.18459
cg0261124	RAB21	c-Ets-1 [T	62	68	1.513038	TTTCCTC	0.36621	0.36952
cg0261124	RAB21	STAT4 [T	61	66	1.470588	TTTTCC	1.95312	1.96333
cg0261124	RAB21	STAT4 [T	493	498	1.470588	GGAAAC	1.95312	1.96333
cg0261124	RAB21	STAT4 [T	716	721	1.470588	TTTTCC	1.95312	1.96333
cg0261124	RAB21	STAT4 [T	732	737	1.470588	AGTTCC	1.95312	1.96333
cg0261124	RAB21	STAT4 [T	801	806	1.470588	GGAACT	1.95312	1.96333
cg0261124	RAB21	STAT4 [T	880	885	1.470588	AGTTCC	1.95312	1.96333
cg0261124	RAB21	STAT4 [T	1754	1759	1.470588	GGAAAC	1.95312	1.96333
cg0261124	RAB21	PR B [T00	664	670	1.404665	CAGTGT	0.36621	0.37023
cg0261124	RAB21	PR B [T00	752	758	1.404665	CAGTGT	0.36621	0.37023
cg0261124	RAB21	PR B [T00	1787	1793	1.404665	AACACT	0.36621	0.37023
cg0261124	RAB21	PR A [T01	664	670	1.404665	CAGTGT	0.36621	0.37023
cg0261124	RAB21	PR A [T01	752	758	1.404665	CAGTGT	0.36621	0.37023
cg0261124	RAB21	PR A [T01	1787	1793	1.404665	AACACT	0.36621	0.37023
cg0261124	RAB21	c-Ets-1 [T	1752	1758	1.384951	CAGGAA	0.36621	0.36952
cg0261124	RAB21	C/EBPbeta	334	337	1.366559	TCAA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	818	821	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	936	939	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1027	1030	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1045	1048	1.366559	TCAA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1174	1177	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1178	1181	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1198	1201	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1242	1245	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1275	1278	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1292	1295	1.366559	TCAA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1319	1322	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1631	1634	1.366559	TTGA	15.625	15.72563
cg0261124	RAB21	C/EBPbeta	1856	1859	1.366559	TCAA	15.625	15.72563
cg0261124	RAB21	AP-2alpha	541	546	1.357116	GCCTGT	0.48828	0.48203
cg0261124	RAB21	AP-2alpha	606	611	1.357116	GCCTGT	0.48828	0.48203
cg0261124	RAB21	AP-2alpha	622	627	1.357116	ACAGGC	0.48828	0.48203
cg0261124	RAB21	AP-2alpha	1404	1409	1.357116	GCCTGT	0.48828	0.48203
cg0261124	RAB21	HIF-1 [T0	683	691	1.296127	TGCGCA	0.09155	0.0902
cg0261124	RAB21	T3R-beta1	1346	1354	1.129976	TCACCT	0.07629	0.07585
cg0261124	RAB21	EBF [T05	578	588	1.088777	CGCCCT	0.00763	0.00736
cg0261124	RAB21	GATA-1 [	1169	1174	1.038567	TATCAT	1.95312	1.98662
cg0261124	RAB21	HNF-1A [	1357	1364	0.925521	CATTTA	0.48828	0.49664
cg0261124	RAB21	RXR-alpha	1027	1033	0.848226	TTGACC	0.48828	0.48333
cg0261124	RAB21	GR-beta [	26	30	0.840383	CCATT	7.8125	7.94706

cg0261124	RAB21	GR-beta [T	98	102	0.840383	TCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	721	725	0.840383	CCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	796	800	0.840383	AATTA	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	829	833	0.840383	AATTA	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	884	888	0.840383	CCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	906	910	0.840383	AATGG	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	940	944	0.840383	AATGA	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	972	976	0.840383	TCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1064	1068	0.840383	CAATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1065	1069	0.840383	AATTG	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1171	1175	0.840383	TCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1271	1275	0.840383	TAATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1284	1288	0.840383	CAATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1356	1360	0.840383	CCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1422	1426	0.840383	AATGG	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1517	1521	0.840383	TAATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1518	1522	0.840383	AATTA	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1548	1552	0.840383	TAATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1549	1553	0.840383	AATTA	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1609	1613	0.840383	TAATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1610	1614	0.840383	AATTG	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1807	1811	0.840383	AATGA	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1811	1815	0.840383	AATTG	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1829	1833	0.840383	TCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1887	1891	0.840383	TCATT	7.8125	7.94706
cg0261124	RAB21	GR-beta [T	1993	1997	0.840383	TAATT	7.8125	7.94706
cg0261124	RAB21	NF-Y [T0(	1066	1073	0.680578	ATTGGT(	0.09155	0.09259
cg0261124	RAB21	AP-2alpha	73	78	0.678558	GCCTGA	0.48828	0.48199
cg0261124	RAB21	AP-2alpha	537	542	0.678558	TCAGGC	0.48828	0.48199
cg0261124	RAB21	AP-2alpha	1323	1328	0.678558	GCCTGA	0.48828	0.48199
cg0261124	RAB21	c-Ets-2 [T(	10	18	0.572986	TAGGAG	0.00763	0.00769
cg0261124	RAB21	HNF-1A [	403	410	0.431647	AGTTTA/	0.24414	0.24974
cg0261124	RAB21	GATA-1 [	1439	1444	0.280028	TATCTA	0.97656	0.99875
cg0261124	RAB21	AP-2alpha	125	130	0.226186	CCAGGC	0.97656	0.95305
cg0261124	RAB21	AP-2alpha	1190	1195	0.226186	CCAGGC	0.97656	0.95305
cg0261124	RAB21	AP-2alpha	1841	1846	0.226186	GCCTGG	0.97656	0.95305
cg0261124	RAB21	GR-alpha [	31	35	0.207689	AGAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	43	47	0.207689	AGAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	566	570	0.207689	CCTTT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	779	783	0.207689	CCTTT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1122	1126	0.207689	AAAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1153	1157	0.207689	AAAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1195	1199	0.207689	CCTTT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1221	1225	0.207689	CCTCT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1294	1298	0.207689	AAAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1513	1517	0.207689	CCTTT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1706	1710	0.207689	CCTCT	7.8125	7.81264
cg0261124	RAB21	Elk-1 [T00	11	19	0.134348	AGGAGG	0.06104	0.06047

cg0261124	RAB21	c-Ets-1 [T	13	19	0.128087	GAGGAA	0.24414	0.2429
cg0261124	RAB21	GR-alpha [	542	546	0	CCTGT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	607	611	0	CCTGT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	622	626	0	ACAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	901	905	0	ACAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1111	1115	0	CCTGT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1140	1144	0	ACAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1395	1399	0	CCTGT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1405	1409	0	CCTGT	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1449	1453	0	ATAGG	7.8125	7.81264
cg0261124	RAB21	GR-alpha [	1540	1544	0	ATAGG	7.8125	7.81264
cg0261124	RAB21	AP-2alpha	980	985	0	GCCTGC	0.97656	0.95305
cg0261124	RAB21	XBP-1 [T	861	866	0	ATGACT	0.97656	0.98127
cg0261124	RAB21	Pax-5 [T0	85	91	0	GGGCTG	1.09863	1.06846
cg0261124	RAB21	Pax-5 [T0	171	177	0	GGGCCG	1.09863	1.06846
cg0261124	RAB21	Pax-5 [T0	249	255	0	GGGCTC	1.09863	1.06846
cg0261124	RAB21	Pax-5 [T0	486	492	0	GGGCTG	1.09863	1.06846
cg0261124	RAB21	TFII-I [T0	109	114	0	CTTTCC	1.46484	1.45997
cg0261124	RAB21	TFII-I [T0	151	156	0	GGACAG	1.46484	1.45997
cg0261124	RAB21	TFII-I [T0	567	572	0	CTTTCC	1.46484	1.45997
cg0261124	RAB21	TFII-I [T0	620	625	0	GGACAG	1.46484	1.45997
cg0261124	RAB21	TFII-I [T0	1151	1156	0	GGAAAG	1.46484	1.45997
cg0261124	RAB21	YY1 [T00	26	29	0	CCAT	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	276	279	0	ATGG	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	721	724	0	CCAT	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	884	887	0	CCAT	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	907	910	0	ATGG	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	919	922	0	CCAT	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	1352	1355	0	CCAT	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	1356	1359	0	CCAT	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	1423	1426	0	ATGG	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	1427	1430	0	CCAT	7.8125	7.81711
cg0261124	RAB21	YY1 [T00	1688	1691	0	CCAT	7.8125	7.81711
cg0261124	RAB21	ER-alpha [	942	946	0	TGACC	1.95312	1.9404
cg0261124	RAB21	ER-alpha [	1002	1006	0	GGTCA	1.95312	1.9404
cg0261124	RAB21	ER-alpha [	1028	1032	0	TGACC	1.95312	1.9404
cg0261124	RAB21	ER-alpha [	1290	1294	0	GGTCA	1.95312	1.9404
cg0261124	RAB21	ER-alpha [	1487	1491	0	TGACC	1.95312	1.9404
cg0261124	RAB21	GATA-1 [	1733	1738	0	TATCTG	0.97656	0.98738
cg0261124	RAB21	C/EBPbeta	400	403	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	412	415	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	500	503	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	530	533	0	GCAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	691	694	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	757	760	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	824	827	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	840	843	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	877	880	0	GCAA	15.625	15.71349

cg0261124	RAB21	C/EBPbeta	889	892	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	910	913	0	GCAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	949	952	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	975	978	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	997	1000	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1063	1066	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1207	1210	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1329	1332	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1455	1458	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1506	1509	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1533	1536	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1537	1540	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1612	1615	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1615	1618	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1666	1669	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1778	1781	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1794	1797	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1813	1816	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1819	1822	0	TTGT	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1873	1876	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1926	1929	0	ACAA	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1968	1971	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1972	1975	0	TTGC	15.625	15.71349
cg0261124	RAB21	C/EBPbeta	1987	1990	0	TTGC	15.625	15.71349
cg0261124	RAB21	TFIID [T0	933	939	0	TTTTTGA	1.09863	1.13474
cg0261124	RAB21	TFIID [T0	1764	1770	0	TTTTTAA	1.09863	1.13474
cg0261124	RAB21	TFIID [T0	1766	1772	0	TTTAAA	1.09863	1.13474
cg0261124	RAB21	TFIID [T0	1767	1773	0	TTAAAA	1.09863	1.13474
cg0261124	RAB21	TFIID [T0	1768	1774	0	TAAAAA	1.09863	1.13474
cg0261124	RAB21	TFIID [T0	1849	1855	0	TTTTAGA	1.09863	1.13474
cg0261124	RAB21	FOXP3 [T	690	695	0	GTTGTG	1.46484	1.47315
cg0261124	RAB21	FOXP3 [T	1454	1459	0	GTTGTC	1.46484	1.47315
cg0261124	RAB21	FOXP3 [T	1505	1510	0	GTTGTC	1.46484	1.47315
cg0261124	RAB21	FOXP3 [T	1614	1619	0	GTTGTG	1.46484	1.47315
cg0261124	RAB21	GR-beta [T	769	773	0	AATGT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1146	1150	0	ACATT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1164	1168	0	AATGT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1258	1262	0	AAATT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1259	1263	0	AATTT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1272	1276	0	AATTT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1285	1289	0	AATTT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1557	1561	0	AATGT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1620	1624	0	ACATT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1661	1665	0	AATTT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1797	1801	0	AAATT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1798	1802	0	AATTT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1862	1866	0	AAATT	3.90625	3.99611
cg0261124	RAB21	GR-beta [T	1936	1940	0	ACATT	3.90625	3.99611

cg0261124	RAB21	C/EBPalph	1176	1182	0	GATTGA	0.24414	0.2444
cg0261124	RAB21	GR [T050	932	938	0	TTTTTTG	0.36621	0.37562
cg0261124	RAB21	HNF-3alph	1696	1703	0	TATTTTT	0.09155	0.09511
cg0261124	RAB21	HNF-1A [	1159	1166	0	GTTAAA	0.24414	0.25261
cg0261124	RAB21	HNF-1A [	1417	1424	0	GTTAAA	0.24414	0.25261
cg0261124	RAB21	IRF-2 [T01	1047	1052	0	AAGTGA	0.48828	0.49387
cg0261124	RAB21	IRF-2 [T01	1742	1747	0	AAGTGA	0.48828	0.49387
cg0144284	RASSF5	NF-AT2 [	233	242	9.999272	GGAAAG	0.08774	0.08903
cg0144284	RASSF5	Elk-1 [T00	1843	1851	9.979803	ATCCGG	0.10681	0.10604
cg0144284	RASSF5	HOXD9 [	968	977	9.979471	TACTGG	0.2327	0.24089
cg0144284	RASSF5	HOXD9 [	1689	1698	9.979471	AACTGC	0.2327	0.24089
cg0144284	RASSF5	HOXD10 [	968	977	9.979471	TACTGG	0.2327	0.24089
cg0144284	RASSF5	HOXD10 [	1689	1698	9.979471	AACTGC	0.2327	0.24089
cg0144284	RASSF5	c-Ets-1 [T	678	684	9.969337	ATTCCC	0.24414	0.2459
cg0144284	RASSF5	c-Myb [T0	289	296	9.815171	ACAAGT	0.36621	0.3712
cg0144284	RASSF5	XBP-1 [T	186	191	9.789909	ATGGCT	1.95312	1.95208
cg0144284	RASSF5	XBP-1 [T	239	244	9.789909	AGACAT	1.95312	1.95208
cg0144284	RASSF5	XBP-1 [T	1360	1365	9.789909	AGCCAT	1.95312	1.95208
cg0144284	RASSF5	Elk-1 [T00	297	305	9.754368	CTTCCC	0.10681	0.10604
cg0144284	RASSF5	PR B [T00	457	463	9.743489	AACACA	1.09863	1.10292
cg0144284	RASSF5	PR B [T00	552	558	9.743489	TGGTGT	1.09863	1.10292
cg0144284	RASSF5	PR B [T00	894	900	9.743489	AACACC	1.09863	1.10292
cg0144284	RASSF5	PR A [T01	457	463	9.743489	AACACA	1.09863	1.10292
cg0144284	RASSF5	PR A [T01	552	558	9.743489	TGGTGT	1.09863	1.10292
cg0144284	RASSF5	PR A [T01	894	900	9.743489	AACACC	1.09863	1.10292
cg0144284	RASSF5	c-Myb [T0	1277	1284	9.729271	GAACTG	0.36621	0.37054
cg0144284	RASSF5	LEF-1 [T0	841	848	9.72404	AGACAA	0.21362	0.2139
cg0144284	RASSF5	LEF-1 [T0	1449	1456	9.72404	TGGCAA	0.21362	0.2139
cg0144284	RASSF5	c-Jun [T00	1861	1867	9.717135	TGACCT	0.73242	0.73031
cg0144284	RASSF5	EBF [T05	1528	1538	9.574945	ACACCA	0.06866	0.06676
cg0144284	RASSF5	Pax-5 [T0	997	1003	9.552105	GGGCGG	1.46484	1.43083
cg0144284	RASSF5	Pax-5 [T0	1510	1516	9.552105	GGGCGT	1.46484	1.43083
cg0144284	RASSF5	Pax-5 [T0	1909	1915	9.552105	GGGCCA	1.46484	1.43083
cg0144284	RASSF5	TFIID [T0	99	105	9.552105	TTTGGT	1.46484	1.48472
cg0144284	RASSF5	TFIID [T0	426	432	9.552105	TTTGGA	1.46484	1.48472
cg0144284	RASSF5	TFIID [T0	1168	1174	9.552105	TTTCTCA	1.46484	1.48472
cg0144284	RASSF5	TFIID [T0	1449	1455	9.552105	TGGCAA	1.46484	1.48472
cg0144284	RASSF5	TFIID [T0	1584	1590	9.552105	TTTCTCA	1.46484	1.48472
cg0144284	RASSF5	TFIID [T0	1770	1776	9.552105	TGGGAA	1.46484	1.48472
cg0144284	RASSF5	TFIID [T0	1832	1838	9.552105	TTTCTCA	1.46484	1.48472
cg0144284	RASSF5	NF-1 [T00	546	553	9.513281	TTGGCT	0.73242	0.73053
cg0144284	RASSF5	NF-1 [T00	1142	1149	9.513281	TTGGCT	0.73242	0.73053
cg0144284	RASSF5	TFII-I [T0	41	46	9.512894	CCTTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	71	76	9.512894	GGATTT	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	75	80	9.512894	TTTTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	143	148	9.512894	AAGTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	306	311	9.512894	GTTTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	345	350	9.512894	GGATAA	7.32422	7.29728

cg0144284	RASSF5	TFII-I [T0	463	468	9.512894	GTGTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	622	627	9.512894	GGACAC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	735	740	9.512894	GGACAA	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	777	782	9.512894	GGAAAC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	795	800	9.512894	GGAAAC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1121	1126	9.512894	CCTTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1138	1143	9.512894	GGATTT	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1213	1218	9.512894	GTGTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1252	1257	9.512894	GTTTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1285	1290	9.512894	GGAAAA	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1409	1414	9.512894	GTTTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1757	1762	9.512894	TTGTCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1772	1777	9.512894	GGAAAA	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1890	1895	9.512894	GTATCC	7.32422	7.29728
cg0144284	RASSF5	TFII-I [T0	1928	1933	9.512894	GGAAGG	7.32422	7.29728
cg0144284	RASSF5	FOXP3 [T	93	98	9.512894	GCCAAC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	197	202	9.512894	CCCAAC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	454	459	9.512894	AAGAAC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	471	476	9.512894	GAGAAC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	569	574	9.512894	GTTATT	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	697	702	9.512894	GTTCTT	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	753	758	9.512894	GTTATT	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	850	855	9.512894	CAGAAC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	982	987	9.512894	GTTCTC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	1201	1206	9.512894	GTTGGC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	1275	1280	9.512894	CAGAAC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	1316	1321	9.512894	GATAAC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	1949	1954	9.512894	GTTGCC	7.32422	7.35678
cg0144284	RASSF5	FOXP3 [T	1954	1959	9.512894	CATAAC	7.32422	7.35678
cg0144284	RASSF5	TCF-4E [T	46	52	9.453578	CTTTGA	0.48828	0.49215
cg0144284	RASSF5	TCF-4E [T	119	125	9.453578	CTTTGT	0.48828	0.49215
cg0144284	RASSF5	c-Jun [T00	213	219	9.442241	TGACAG	0.73242	0.73031
cg0144284	RASSF5	NFI/CTF [	96	103	9.352332	AACTTT	0.54932	0.54821
cg0144284	RASSF5	NFI/CTF [	618	625	9.352332	CCAAGG	0.54932	0.54821
cg0144284	RASSF5	NFI/CTF [	765	772	9.352332	CCAAGG	0.54932	0.54821
cg0144284	RASSF5	NF-AT2 [	1248	1257	9.268723	TTATGT	0.04578	0.04604
cg0144284	RASSF5	SRY [T00	46	54	9.264664	CTTTGA	0.12207	0.12265
cg0144284	RASSF5	c-Ets-1 [T	427	433	9.19359	TTGGAA	0.85449	0.85523
cg0144284	RASSF5	c-Ets-1 [T	1619	1625	9.19359	TTGGAA	0.85449	0.85523
cg0144284	RASSF5	c-Myb [T0	95	102	9.142015	CAACTT	0.39673	0.40028
cg0144284	RASSF5	HNF-1C [	1799	1807	9.094725	GTTAGG	0.12207	0.12495
cg0144284	RASSF5	HNF-1B [	241	249	9.06748	ACATTA	0.08392	0.0857
cg0144284	RASSF5	c-Myb [T0	302	309	9.024874	CTCAGT	0.39673	0.40028
cg0144284	RASSF5	PXR-1:RX	1666	1673	8.998824	GTTGTT	0.24414	0.2439
cg0144284	RASSF5	GR [T050	261	267	8.971049	GGCTTT	0.61035	0.61632
cg0144284	RASSF5	GR [T050	554	560	8.971049	GTGTTT	0.61035	0.61632
cg0144284	RASSF5	GR [T050	844	850	8.971049	CAAAGC	0.61035	0.61632
cg0144284	RASSF5	GR [T050	892	898	8.971049	CAAACA	0.61035	0.61632

cg0144284	RASSF5	GR [T050	1387	1393	8.971049	CAAAGC	0.61035	0.61632
cg0144284	RASSF5	GR [T050	1978	1984	8.971049	GTGTTT	0.61035	0.61632
cg0144284	RASSF5	c-Ets-2 [T	478	486	8.912323	TTCCTA	0.27466	0.27495
cg0144284	RASSF5	c-Ets-2 [T	1902	1910	8.912323	TTCCTG	0.27466	0.27495
cg0144284	RASSF5	p53 [T006	1340	1346	8.912104	AGGGCC	0.12207	0.11837
cg0144284	RASSF5	p53 [T006	1341	1347	8.912104	GGGCCC	0.12207	0.11837
cg0144284	RASSF5	PR B [T00	749	755	8.827054	AGCTGT	0.36621	0.36944
cg0144284	RASSF5	PR A [T01	749	755	8.827054	AGCTGT	0.36621	0.36944
cg0144284	RASSF5	NF-1 [T00	194	201	8.790071	CTTCCC	0.24414	0.24467
cg0144284	RASSF5	NF-AT1 [	473	481	8.769753	GAACTT	0.22888	0.22959
cg0144284	RASSF5	LEF-1 [T0	119	126	8.759086	CTTTGT	0.54932	0.55326
cg0144284	RASSF5	XBP-1 [T	114	119	8.75604	ATGATC	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	274	279	8.75604	ATGAGC	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	416	421	8.75604	TTTCAT	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	1170	1175	8.75604	TCTCAT	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	1357	1362	8.75604	ATGAGC	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	1374	1379	8.75604	ATGAAC	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	1586	1591	8.75604	TCTCAT	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	1632	1637	8.75604	ATGATA	2.92969	2.9674
cg0144284	RASSF5	XBP-1 [T	1783	1788	8.75604	ATGAGC	2.92969	2.9674
cg0144284	RASSF5	STAT1bet	791	800	8.695301	TGGGGG	0.22316	0.22446
cg0144284	RASSF5	STAT1bet	1281	1290	8.695301	TGTAGG	0.22316	0.22446
cg0144284	RASSF5	c-Jun [T00	1504	1510	8.571705	TGACTG	0.12207	0.12139
cg0144284	RASSF5	c-Jun [T00	1761	1767	8.571705	CCAGTC	0.12207	0.12139
cg0144284	RASSF5	NF-AT2 [	1285	1294	8.550786	GGAAAA	0.04959	0.05001
cg0144284	RASSF5	LEF-1 [T0	1728	1735	8.457856	CTTTGA	0.15259	0.15214
cg0144284	RASSF5	HOXD9 [	749	758	8.402327	AGCTGT	0.02289	0.02363
cg0144284	RASSF5	HOXD10	749	758	8.402327	AGCTGT	0.02289	0.02363
cg0144284	RASSF5	c-Ets-1 [T	284	290	8.373028	ATGGAA	0.24414	0.24529
cg0144284	RASSF5	LEF-1 [T0	735	742	8.361499	GGACAA	0.15259	0.15214
cg0144284	RASSF5	LEF-1 [T0	1755	1762	8.361499	CTTTGT	0.15259	0.15214
cg0144284	RASSF5	c-Ets-2 [T	1280	1288	8.339336	CTGTAG	0.13733	0.13681
cg0144284	RASSF5	PR B [T00	162	168	8.338824	CTCTGT	1.09863	1.10009
cg0144284	RASSF5	PR B [T00	651	657	8.338824	GCCTGT	1.09863	1.10009
cg0144284	RASSF5	PR B [T00	807	813	8.338824	AACAGC	1.09863	1.10009
cg0144284	RASSF5	PR A [T01	162	168	8.338824	CTCTGT	1.09863	1.10009
cg0144284	RASSF5	PR A [T01	651	657	8.338824	GCCTGT	1.09863	1.10009
cg0144284	RASSF5	PR A [T01	807	813	8.338824	AACAGC	1.09863	1.10009
cg0144284	RASSF5	GR-alpha	41	45	8.281568	CCTTC	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	79	83	8.281568	CCTCC	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	85	89	8.281568	GGAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	544	548	8.281568	CCTTG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	585	589	8.281568	GAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	619	623	8.281568	CAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	690	694	8.281568	CAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	693	697	8.281568	GGAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	766	770	8.281568	CAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha	936	940	8.281568	CCTCC	7.8125	7.72956

cg0144284	RASSF5	GR-alpha [	994	998	8.281568	CGAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1087	1091	8.281568	GGAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1121	1125	8.281568	CCTTC	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1176	1180	8.281568	GAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1236	1240	8.281568	CCTCC	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1345	1349	8.281568	CCTCC	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1402	1406	8.281568	GAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1611	1615	8.281568	CAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1732	1736	8.281568	GAAGG	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1789	1793	8.281568	CCTTC	7.8125	7.72956
cg0144284	RASSF5	GR-alpha [	1929	1933	8.281568	GAAGG	7.8125	7.72956
cg0144284	RASSF5	NF-AT2 [	71	80	8.245775	GGATTT	0.08965	0.09068
cg0144284	RASSF5	IRF-1 [T0	477	485	8.242487	TTTCCTA	0.25177	0.25263
cg0144284	RASSF5	IRF-1 [T0	1281	1289	8.242487	TGTAGG	0.25177	0.25263
cg0144284	RASSF5	NFI/CTF [	198	205	8.241664	CCAACC	0.18311	0.1823
cg0144284	RASSF5	HOXD9 [	565	574	8.224939	GGTTGT	0.08774	0.09025
cg0144284	RASSF5	HOXD10 [	565	574	8.224939	GGTTGT	0.08774	0.09025
cg0144284	RASSF5	NF-kappa	878	889	8.207376	GAGATC	0.01299	0.01272
cg0144284	RASSF5	ENKTF-1	147	154	8.19852	CCCTGC	0.73242	0.71737
cg0144284	RASSF5	ENKTF-1	433	440	8.19852	TGGCAG	0.73242	0.71737
cg0144284	RASSF5	SRY [T00	840	848	8.174786	CAGACA	0.15259	0.15383
cg0144284	RASSF5	SRY [T00	1728	1736	8.174786	CTTTGA	0.15259	0.15383
cg0144284	RASSF5	LEF-1 [T0	46	53	8.117221	CTTTGA	0.12207	0.1241
cg0144284	RASSF5	LEF-1 [T0	263	270	8.117221	CTTTGA	0.12207	0.1241
cg0144284	RASSF5	VDR [T00	1371	1379	8.079962	TCCATG	0.24414	0.24712
cg0144284	RASSF5	GR-alpha [	55	59	8.073878	CCTGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	82	86	8.073878	CCTGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	148	152	8.073878	CCTGC	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	202	206	8.073878	CCTAG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	229	233	8.073878	GTAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	335	339	8.073878	CCTGC	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	359	363	8.073878	CCTGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	435	439	8.073878	GCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	485	489	8.073878	CCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	535	539	8.073878	CCTGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	742	746	8.073878	GCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	855	859	8.073878	CCTAC	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	888	892	8.073878	CCTGC	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	950	954	8.073878	CCTGC	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	987	991	8.073878	CCTGC	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1046	1050	8.073878	CCTGC	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1050	1054	8.073878	CCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1060	1064	8.073878	GCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1258	1262	8.073878	CCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1282	1286	8.073878	GTAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1338	1342	8.073878	CCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1392	1396	8.073878	CCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1414	1418	8.073878	CCTGC	7.8125	7.72238

cg0144284	RASSF5	GR-alpha [	1514	1518	8.073878	GTAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1531	1535	8.073878	CCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1864	1868	8.073878	CCTGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1878	1882	8.073878	GCAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1945	1949	8.073878	CTAGG	7.8125	7.72238
cg0144284	RASSF5	GR-alpha [	1992	1996	8.073878	CCTGC	7.8125	7.72238
cg0144284	RASSF5	Pax-5 [T0(	59	65	8.014558	GGGCTT(	2.19727	2.14502
cg0144284	RASSF5	Pax-5 [T0(	325	331	8.014558	GGGCAT.	2.19727	2.14502
cg0144284	RASSF5	Pax-5 [T0(	1105	1111	8.014558	GGGCTG(	2.19727	2.14502
cg0144284	RASSF5	Pax-5 [T0(	1222	1228	8.014558	GGGCTG.	2.19727	2.14502
cg0144284	RASSF5	Pax-5 [T0(	1534	1540	8.014558	GGGCTG.	2.19727	2.14502
cg0144284	RASSF5	Pax-5 [T0(	1739	1745	8.014558	TCAGCC(	2.19727	2.14502
cg0144284	RASSF5	Pax-5 [T0(	1784	1790	8.014558	TGAGCC(	2.19727	2.14502
cg0144284	RASSF5	TFIID [T0	47	53	8.014558	TTTGAG/	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	264	270	8.014558	TTTGAA/	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	388	394	8.014558	TTTGAA/	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	416	422	8.014558	TTTCATA	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	477	483	8.014558	TTTCCTA	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	663	669	8.014558	TTTCTTA	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	721	727	8.014558	TTTCTTA	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	821	827	8.014558	TTTGAA/	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	1114	1120	8.014558	TTTGAA/	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	1272	1278	8.014558	TTTCAG/	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	1283	1289	8.014558	TAGGAA.	2.19727	2.24348
cg0144284	RASSF5	TFIID [T0	1384	1390	8.014558	TAGCAA.	2.19727	2.24348
cg0144284	RASSF5	RelA [T00	600	610	7.886423	GAGCTT(	0.02003	0.01979
cg0144284	RASSF5	ETF [T002	915	925	7.870358	GCCCCG(	0.07153	0.06862
cg0144284	RASSF5	ETF [T002	990	1000	7.870358	GCACCG.	0.07153	0.06862
cg0144284	RASSF5	p53 [T006'	9	15	7.853573	GGGCCA'	0.48828	0.47377
cg0144284	RASSF5	p53 [T006'	760	766	7.853573	ATGGCC(	0.48828	0.47377
cg0144284	RASSF5	c-Ets-2 [T(	1798	1806	7.84116	TGTTAG(	0.32043	0.32298
cg0144284	RASSF5	c-Myb [T0	1912	1919	7.825375	CCAAGT'	0.21362	0.21454
cg0144284	RASSF5	HNF-1B ['	377	385	7.737819	TGTTAA/	0.09155	0.09368
cg0144284	RASSF5	NF-AT1 ['	1249	1257	7.72101	TATGTTT	0.19836	0.19941
cg0144284	RASSF5	NFI/CTF [	1615	1622	7.587343	GCTATT(	0.36621	0.36674
cg0144284	RASSF5	c-Myb [T0	1109	1116	7.545286	TGCAGT'	0.42725	0.43114
cg0144284	RASSF5	c-Jun [T00	406	412	7.538568	GATGTC/	0.48828	0.48775
cg0144284	RASSF5	PPAR-alpl	54	64	7.529496	CCCTGG(	0.04482	0.04393
cg0144284	RASSF5	GR [T050'	738	744	7.527031	CAAAGC.	1.83105	1.86007
cg0144284	RASSF5	GR [T050'	805	811	7.527031	CAAACA(	1.83105	1.86007
cg0144284	RASSF5	GR [T050'	1465	1471	7.527031	CAAATA(	1.83105	1.86007
cg0144284	RASSF5	GR [T050'	1672	1678	7.527031	CAAACA.	1.83105	1.86007
cg0144284	RASSF5	GR [T050'	1726	1732	7.527031	TGCTTT(	1.83105	1.86007
cg0144284	RASSF5	RAR-beta	794	803	7.47824	GGGAAA	0.24414	0.24343
cg0144284	RASSF5	C/EBPalpl	593	599	7.465744	CATTGC/	0.48828	0.49653
cg0144284	RASSF5	c-Myb [T0	473	480	7.442719	GAACTT'	0.42725	0.43114
cg0144284	RASSF5	IRF-1 [T0(	361	369	7.387351	TGGGGG.	0.14496	0.14449
cg0144284	RASSF5	IRF-1 [T0(	791	799	7.387351	TGGGGG.	0.14496	0.14449

cg0144284	RASSF5	PPAR-alpl	1539	1549	7.370536	GAGTCC(	0.04482	0.04393
cg0144284	RASSF5	PXR-1:RX	1375	1382	7.362674	TGAACA'	0.24414	0.24395
cg0144284	RASSF5	NF-AT1 [1	233	241	7.211175	GGAAAG	0.15259	0.1548
cg0144284	RASSF5	c-Ets-1 [T(	1770	1776	7.199436	TGGGAA.	0.73242	0.73099
cg0144284	RASSF5	SRY [T00!	263	271	7.175614	CTTTGA/	0.30518	0.30739
cg0144284	RASSF5	SRY [T00!	734	742	7.175614	TGGACA.	0.30518	0.30739
cg0144284	RASSF5	SRY [T00!	1755	1763	7.175614	CTTTGTC	0.30518	0.30739
cg0144284	RASSF5	XBP-1 [T(	522	527	7.172312	ATTCAT	2.92969	2.97018
cg0144284	RASSF5	XBP-1 [T(	612	617	7.172312	ATGAAT	2.92969	2.97018
cg0144284	RASSF5	XBP-1 [T(	706	711	7.172312	ATGAAG	2.92969	2.97018
cg0144284	RASSF5	XBP-1 [T(	1092	1097	7.172312	ATGAAG	2.92969	2.97018
cg0144284	RASSF5	XBP-1 [T(	1174	1179	7.172312	ATGAAG	2.92969	2.97018
cg0144284	RASSF5	XBP-1 [T(	1472	1477	7.172312	CCTCAT	2.92969	2.97018
cg0144284	RASSF5	XBP-1 [T(	1475	1480	7.172312	CATCAT	2.92969	2.97018
cg0144284	RASSF5	XBP-1 [T(	1624	1629	7.172312	ATGAGT	2.92969	2.97018
cg0144284	RASSF5	PPAR-alpl	1505	1515	7.154987	GACTGG(	0.01431	0.01397
cg0144284	RASSF5	c-Ets-1 [T(	231	237	7.071349	AGGGAA	0.73242	0.73099
cg0144284	RASSF5	c-Ets-1 [T(	1410	1416	7.071349	TTTCCCT	0.73242	0.73099
cg0144284	RASSF5	AR [T000	1754	1762	7.049779	CCTTTGT	0.23651	0.23551
cg0144284	RASSF5	IRF-1 [T0(	1253	1261	7.041849	TTTCCCC	0.1297	0.13036
cg0144284	RASSF5	HNF-1B [	752	760	7.037014	TGTTATT	0.07629	0.07762
cg0144284	RASSF5	HNF-3alpl	413	420	7.000129	GATTTTC	0.82397	0.84946
cg0144284	RASSF5	HNF-3alpl	1772	1779	7.000129	GGAAAA	0.82397	0.84946
cg0144284	RASSF5	c-Ets-1 [T(	363	369	6.943262	GGGGAA	0.73242	0.73099
cg0144284	RASSF5	c-Ets-1 [T(	793	799	6.943262	GGGGAA	0.73242	0.73099
cg0144284	RASSF5	c-Ets-1 [T(	1253	1259	6.943262	TTTCCCC	0.73242	0.73099
cg0144284	RASSF5	ENKTF-1	547	554	6.942764	TGGCTT(	1.46484	1.44228
cg0144284	RASSF5	ENKTF-1	1326	1333	6.942764	CTCAGC(	1.46484	1.44228
cg0144284	RASSF5	ENKTF-1	1449	1456	6.942764	TGGCAA.	1.46484	1.44228
cg0144284	RASSF5	VDR [T00	0	8	6.925682	GTTCAG/	0.42725	0.43062
cg0144284	RASSF5	c-Jun [T00	1134	1140	6.787369	TGACGG.	0.73242	0.73173
cg0144284	RASSF5	C/EBPalpl	1617	1623	6.786177	TATTGG/	0.73242	0.74337
cg0144284	RASSF5	NFI/CTF [	547	554	6.786076	TGGCTT(	0.73242	0.73214
cg0144284	RASSF5	NFI/CTF [	804	811	6.786076	CCAAAC.	0.73242	0.73214
cg0144284	RASSF5	NFI/CTF [	1206	1213	6.786076	CAGCTT(	0.73242	0.73214
cg0144284	RASSF5	RXR-alpha	539	545	6.785809	GGGTAC(	0.36621	0.36214
cg0144284	RASSF5	p53 [T006'	1784	1790	6.778774	TGAGCC(	1.09863	1.07125
cg0144284	RASSF5	AR [T000	1210	1218	6.760234	TTGGTGT	0.23651	0.23551
cg0144284	RASSF5	NF-1 [T00	90	97	6.722386	CTGGCC/	0.24414	0.24147
cg0144284	RASSF5	c-Ets-2 [T(	772	780	6.695187	TCACAG(	0.09155	0.09289
cg0144284	RASSF5	AR [T000	222	230	6.675397	GGACAG	0.19836	0.19597
cg0144284	RASSF5	c-Fos [T00	1626	1635	6.660217	GAGTCA.	0.04578	0.04589
cg0144284	RASSF5	AR [T000	622	630	6.617912	GGACAC.	0.19836	0.19597
cg0144284	RASSF5	p53 [T006'	59	65	6.563521	GGGCTT(	0.48828	0.47541
cg0144284	RASSF5	p53 [T006'	1105	1111	6.563521	GGGCTG(	0.48828	0.47541
cg0144284	RASSF5	XBP-1 [T(	325	330	6.478682	GGGCAT	0.97656	0.97062
cg0144284	RASSF5	XBP-1 [T(	492	497	6.478682	TGGCAT	0.97656	0.97062
cg0144284	RASSF5	C/EBPalpl	1628	1634	6.460799	GTCAAT(	0.48828	0.49071

cg0144284	RASSF5	c-Fos [T00	1563	1572	6.448203	TGTGTG	0.04578	0.04589
cg0144284	RASSF5	C/EBPalp	1714	1720	6.391486	AATTGT	0.48828	0.49071
cg0144284	RASSF5	RAR-beta	1164	1173	6.378264	AGGGTT	0.18311	0.183
cg0144284	RASSF5	TCF-4E [T	98	104	6.302385	CTTTGG	0.61035	0.61344
cg0144284	RASSF5	TCF-4E [T	263	269	6.302385	CTTTGA	0.61035	0.61344
cg0144284	RASSF5	TCF-4E [T	1450	1456	6.302385	GGCAAA	0.61035	0.61344
cg0144284	RASSF5	TCF-4E [T	1728	1734	6.302385	CTTTGA	0.61035	0.61344
cg0144284	RASSF5	c-Jun [T00	1988	1994	6.293948	TGACCC	0.61035	0.60769
cg0144284	RASSF5	GR-alpha [	301	305	6.263098	CCTCA	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	310	314	6.263098	CCTTA	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	421	425	6.263098	TAAGG	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	513	517	6.263098	TAAGG	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	1472	1476	6.263098	CCTCA	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	1484	1488	6.263098	TGAGG	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	1577	1581	6.263098	CCTTA	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	1896	1900	6.263098	TGAGG	3.90625	3.91061
cg0144284	RASSF5	GR-alpha [	1906	1910	6.263098	TGAGG	3.90625	3.91061
cg0144284	RASSF5	c-Myb [T0	1688	1695	6.259888	GAACTG	0.30518	0.3056
cg0144284	RASSF5	c-Myb [T0	1722	1729	6.259888	TAACTG	0.30518	0.3056
cg0144284	RASSF5	IRF-1 [T0	76	84	6.24301	TTTCCTC	0.16785	0.16909
cg0144284	RASSF5	p53 [T006	997	1003	6.188498	GGGCGG	0.61035	0.594
cg0144284	RASSF5	SRY [T00	98	106	6.176442	CTTTGG	0.15259	0.15366
cg0144284	RASSF5	SRY [T00	1383	1391	6.176442	GTAGCA	0.15259	0.15366
cg0144284	RASSF5	NF-AT1 [	72	80	6.150044	GATTTT	0.06866	0.06922
cg0144284	RASSF5	RXR-alph	227	233	6.119461	GGGTAG	0.73242	0.72249
cg0144284	RASSF5	p53 [T006	1909	1915	6.095267	GGGCCA	0.61035	0.594
cg0144284	RASSF5	GR-alpha [	24	28	6.055408	TCAGG	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	139	143	6.055408	CCTAA	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	342	346	6.055408	TTAGG	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	449	453	6.055408	CCTAA	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	468	472	6.055408	CCTGA	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	480	484	6.055408	CCTAA	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	1147	1151	6.055408	TTAGG	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	1313	1317	6.055408	CCTGA	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	1800	1804	6.055408	TTAGG	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	1815	1819	6.055408	TCAGG	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	1894	1898	6.055408	CCTGA	3.90625	3.9065
cg0144284	RASSF5	GR-alpha [	1904	1908	6.055408	CCTGA	3.90625	3.9065
cg0144284	RASSF5	C/EBPalp	1674	1680	5.996794	AACAAT	0.97656	0.99
cg0144284	RASSF5	NF-kappa	879	889	5.986323	AGATCT	0.04053	0.03971
cg0144284	RASSF5	RXR-alph	444	450	5.937582	AGTACC	0.73242	0.72249
cg0144284	RASSF5	RXR-alph	1710	1716	5.937582	GGGTAA	0.73242	0.72249
cg0144284	RASSF5	STAT4 [T	41	46	5.882353	CCTTCC	0.48828	0.48408
cg0144284	RASSF5	STAT4 [T	1121	1126	5.882353	CCTTCC	0.48828	0.48408
cg0144284	RASSF5	STAT4 [T	1928	1933	5.882353	GGAAGG	0.48828	0.48408
cg0144284	RASSF5	IRF-1 [T0	773	781	5.861409	CACAGG	0.16785	0.16909
cg0144284	RASSF5	c-Ets-1 [T	194	200	5.814485	CTTCCC	0.36621	0.36731
cg0144284	RASSF5	c-Ets-1 [T	1069	1075	5.814485	TGGGAA	0.36621	0.36731

cg0144284	RASSF5	c-Ets-1 [T	1926	1932	5.814485	TGGGAA	0.36621	0.36731
cg0144284	RASSF5	VDR [T00	1669	1677	5.771401	GTTCAA	0.42725	0.42999
cg0144284	RASSF5	RXR-alpha	894	900	5.715466	AACACC	0.61035	0.6044
cg0144284	RASSF5	ENKTF-1	7	14	5.687009	CAGGGC	0.73242	0.7249
cg0144284	RASSF5	ENKTF-1	844	851	5.687009	CAAAGC	0.73242	0.7249
cg0144284	RASSF5	ENKTF-1	1143	1150	5.687009	TGGCTT	0.73242	0.7249
cg0144284	RASSF5	ENKTF-1	1387	1394	5.687009	CAAAGC	0.73242	0.7249
cg0144284	RASSF5	c-Ets-1 [T	297	303	5.686398	CTTCCC	0.36621	0.3623
cg0144284	RASSF5	RelA [T00	792	802	5.573947	GGGGGA	0.0124	0.0123
cg0144284	RASSF5	T3R-beta1	862	870	5.572705	TCACCC	0.21362	0.21287
cg0144284	RASSF5	NFI/CTF [	423	430	5.558661	AGGTTT	0.54932	0.55038
cg0144284	RASSF5	c-Ets-1 [T	883	889	5.558311	CTTCCC	0.36621	0.3623
cg0144284	RASSF5	T3R-beta1	907	915	5.553412	TCACCC	0.21362	0.21287
cg0144284	RASSF5	AP-1 [T00	1020	1028	5.54906	TGACTC	0.09155	0.09214
cg0144284	RASSF5	Pax-5 [T0	9	15	5.544826	GGGCCA	0.73242	0.72046
cg0144284	RASSF5	Pax-5 [T0	760	766	5.544826	ATGGCC	0.73242	0.72046
cg0144284	RASSF5	TFIID [T0	138	144	5.544826	TCCTAA	0.73242	0.75085
cg0144284	RASSF5	TFIID [T0	377	383	5.544826	TGTTAA	0.73242	0.75085
cg0144284	RASSF5	p53 [T006	1222	1228	5.508538	GGGCTG	0.61035	0.59991
cg0144284	RASSF5	p53 [T006	1534	1540	5.508538	GGGCTG	0.61035	0.59991
cg0144284	RASSF5	p53 [T006	1739	1745	5.508538	TCAGCC	0.61035	0.59991
cg0144284	RASSF5	HNF-1A [	1718	1725	5.466509	GTCTTA	0.24414	0.2469
cg0144284	RASSF5	C/EBPalph	1478	1484	5.455853	CATTGC	0.73242	0.74391
cg0144284	RASSF5	c-Ets-1 [T	603	609	5.430224	CTTCCC	0.36621	0.3623
cg0144284	RASSF5	c-Ets-1 [T	1122	1128	5.430224	CTTCCC	0.36621	0.3623
cg0144284	RASSF5	EBF [T05	52	62	5.399082	GACCCT	0.01907	0.0183
cg0144284	RASSF5	NF-1 [T00	1103	1110	5.377909	TTGGGC	0.24414	0.24258
cg0144284	RASSF5	NF-1 [T00	1816	1823	5.377909	CAGGCC	0.24414	0.24258
cg0144284	RASSF5	NF-kappa	793	804	5.351855	GGGGAA	0.00119	0.00116
cg0144284	RASSF5	IRF-1 [T0	1768	1776	5.351774	GATGGG	0.22888	0.23087
cg0144284	RASSF5	HNF-1C [	378	386	5.345227	GTTAAA	0.07629	0.07817
cg0144284	RASSF5	RXR-alpha	1459	1465	5.271235	CCCACC	0.61035	0.6044
cg0144284	RASSF5	RXR-alpha	1923	1929	5.271235	GGGTGG	0.61035	0.6044
cg0144284	RASSF5	ETF [T002	1215	1225	5.246906	GTCCGG	0.02861	0.02737
cg0144284	RASSF5	C/EBPalph	974	980	5.240291	TATTGA	0.97656	0.99332
cg0144284	RASSF5	NF-AT2 [	1772	1781	5.231211	GGAAAA	0.03815	0.03879
cg0144284	RASSF5	c-Jun [T00	173	179	5.193102	TGACTT	0.61035	0.61057
cg0144284	RASSF5	c-Jun [T00	251	257	5.193102	GAAGTC	0.61035	0.61057
cg0144284	RASSF5	p53 [T006	1510	1516	5.133514	GGGCGT	0.48828	0.47747
cg0144284	RASSF5	RXR-alpha	920	926	5.089356	GGGTGC	0.48828	0.484
cg0144284	RASSF5	RXR-alpha	1014	1020	5.089356	GGGTGC	0.48828	0.484
cg0144284	RASSF5	SRY [T00	119	127	5.086565	CTTTGTA	0.06104	0.06209
cg0144284	RASSF5	GR-beta [	71	75	5.042296	GGATT	3.90625	3.95351
cg0144284	RASSF5	GR-beta [	615	619	5.042296	AATCC	3.90625	3.95351
cg0144284	RASSF5	GR-beta [	671	675	5.042296	GTATT	3.90625	3.95351
cg0144284	RASSF5	GR-beta [	973	977	5.042296	GTATT	3.90625	3.95351
cg0144284	RASSF5	GR-beta [	1138	1142	5.042296	GGATT	3.90625	3.95351
cg0144284	RASSF5	GR-beta [	1266	1270	5.042296	GGATT	3.90625	3.95351

cg0144284	RASSF5	GR-beta [T	1438	1442	5.042296	GTATT	3.90625	3.95351
cg0144284	RASSF5	GR-beta [T	1735	1739	5.042296	GGATT	3.90625	3.95351
cg0144284	RASSF5	AP-1 [T00	1567	1575	4.990183	TGACTC	0.12207	0.12162
cg0144284	RASSF5	XBP-1 [T	608	613	4.894955	CGGCAT	0.97656	0.96979
cg0144284	RASSF5	AR [T000	735	743	4.890444	GGACAA	0.11444	0.11247
cg0144284	RASSF5	RelA [T00	880	890	4.885137	GATCTT	0.01001	0.00994
cg0144284	RASSF5	RXR-alpha	50	56	4.86724	GAGACC	0.48828	0.484
cg0144284	RASSF5	NF-Y [T0	1618	1625	4.867193	ATTGGA	0.36621	0.36847
cg0144284	RASSF5	HNF-3alph	1439	1446	4.842999	TATTTA	0.09155	0.09582
cg0144284	RASSF5	AP-1 [T00	530	538	4.815705	TGACTC	0.12207	0.12162
cg0144284	RASSF5	p53 [T006	1455	1461	4.786849	AGTGCC	0.48828	0.47747
cg0144284	RASSF5	TFII-I [T0	365	370	4.756447	GGAAAT	2.92969	2.93695
cg0144284	RASSF5	TFII-I [T0	429	434	4.756447	GGAATG	2.92969	2.93695
cg0144284	RASSF5	TFII-I [T0	1261	1266	4.756447	GGACTG	2.92969	2.93695
cg0144284	RASSF5	TFII-I [T0	1266	1271	4.756447	GGATTG	2.92969	2.93695
cg0144284	RASSF5	TFII-I [T0	1334	1339	4.756447	CAGTCC	2.92969	2.93695
cg0144284	RASSF5	TFII-I [T0	1621	1626	4.756447	GGAATG	2.92969	2.93695
cg0144284	RASSF5	TFII-I [T0	1803	1808	4.756447	GGAATG	2.92969	2.93695
cg0144284	RASSF5	FOXP3 [T	166	171	4.756447	GTTTTG	2.92969	2.96063
cg0144284	RASSF5	FOXP3 [T	655	660	4.756447	GTTTTT	2.92969	2.96063
cg0144284	RASSF5	FOXP3 [T	1037	1042	4.756447	GTTTTT	2.92969	2.96063
cg0144284	RASSF5	c-Myb [T0	978	985	4.754782	GACAGT	0.30518	0.30568
cg0144284	RASSF5	c-Ets-2 [T	39	47	4.589988	TTCCTTC	0.06866	0.06881
cg0144284	RASSF5	c-Ets-1 [T	1801	1807	4.539113	TAGGAA	0.85449	0.85764
cg0144284	RASSF5	RXR-alpha	1238	1244	4.423008	TCCACC	0.24414	0.24292
cg0144284	RASSF5	AP-2alpha	1576	1581	4.422424	GCCTTA	0.97656	0.96979
cg0144284	RASSF5	TCF-4 [T0	45	54	4.412902	CCTTTG	0.04196	0.04202
cg0144284	RASSF5	STAT4 [T	37	42	4.411765	TCTTCC	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	193	198	4.411765	TCTTCC	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	429	434	4.411765	GGAATG	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	602	607	4.411765	GCTTCC	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	882	887	4.411765	TCTTCC	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	1071	1076	4.411765	GGAAGA	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	1621	1626	4.411765	GGAATG	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	1803	1808	4.411765	GGAATG	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	1847	1852	4.411765	GGAAGA	1.95312	1.94235
cg0144284	RASSF5	STAT4 [T	1900	1905	4.411765	GCTTCC	1.95312	1.94235
cg0144284	RASSF5	RXR-alpha	1987	1993	4.24113	GTGACC	0.97656	0.9671
cg0144284	RASSF5	C/EBPalph	755	761	4.235345	TATTGA	0.48828	0.49358
cg0144284	RASSF5	C/EBPalph	1695	1701	4.235345	TATTGA	0.48828	0.49358
cg0144284	RASSF5	Sp1 [T007	996	1005	4.222204	AGGGCG	0.08965	0.08686
cg0144284	RASSF5	AP-2alpha	1514	1519	4.211849	GTAGGC	0.97656	0.96469
cg0144284	RASSF5	GR-beta [T	368	372	4.201913	AATAA	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	399	403	4.201913	CTATT	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	561	565	4.201913	AATAG	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	570	574	4.201913	TTATT	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	754	758	4.201913	TTATT	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	1467	1471	4.201913	AATAG	7.8125	7.94607

cg0144284	RASSF5	GR-beta [T	1616	1620	4.201913	CTATT	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	1649	1653	4.201913	AATCA	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	1694	1698	4.201913	CTATT	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	1702	1706	4.201913	CTATT	7.8125	7.94607
cg0144284	RASSF5	GR-beta [T	1968	1972	4.201913	TGATT	7.8125	7.94607
cg0144284	RASSF5	p53 [T006	649	655	4.125254	GGGCCT	0.73242	0.71379
cg0144284	RASSF5	c-Ets-2 [T	308	316	4.091811	TTCCTTA	0.16022	0.16243
cg0144284	RASSF5	IRF-1 [T0	229	237	4.035054	GTAGGG	0.1297	0.13087
cg0144284	RASSF5	IRF-1 [T0	1410	1418	4.035054	TTTCCCT	0.1297	0.13087
cg0144284	RASSF5	RXR-alpha	393	399	4.019014	AAGACC	0.97656	0.9671
cg0144284	RASSF5	RXR-alpha	796	802	4.019014	GAAACC	0.97656	0.9671
cg0144284	RASSF5	RXR-alpha	1165	1171	4.019014	GGGTTT	0.97656	0.9671
cg0144284	RASSF5	RXR-alpha	1822	1828	4.019014	AAGACC	0.97656	0.9671
cg0144284	RASSF5	c-Ets-2 [T	1752	1760	4.017001	TTCCTTT	0.16022	0.16243
cg0144284	RASSF5	Pax-5 [T0	1340	1346	4.007279	AGGGCC	1.09863	1.07975
cg0144284	RASSF5	Pax-5 [T0	1341	1347	4.007279	GGGCCC	1.09863	1.07975
cg0144284	RASSF5	Pax-5 [T0	1455	1461	4.007279	AGTGCC	1.09863	1.07975
cg0144284	RASSF5	TFIID [T0	703	709	4.007279	TTTATGA	1.09863	1.13456
cg0144284	RASSF5	USF2 [T0	743	752	4.003951	CAGGTG	0.01144	0.01129
cg0144284	RASSF5	AP-2alpha	1611	1616	3.970052	CAAGGC	0.97656	0.96469
cg0144284	RASSF5	HOXD9 [T	1776	1785	3.903508	AATATA	0.03052	0.03168
cg0144284	RASSF5	HOXD10 [	1776	1785	3.903508	AATATA	0.03052	0.03168
cg0144284	RASSF5	PPAR-alph	217	227	3.872523	AGCTGG	0.02575	0.02522
cg0144284	RASSF5	GR [T050	117	123	3.763516	ATCTTTC	0.73242	0.74251
cg0144284	RASSF5	GR [T050	165	171	3.763516	TGTTTTC	0.73242	0.74251
cg0144284	RASSF5	p53 [T006	912	918	3.750231	CCAGCC	0.73242	0.71379
cg0144284	RASSF5	p53 [T006	1426	1432	3.750231	CCAGCC	0.73242	0.71379
cg0144284	RASSF5	AP-2alpha	1402	1407	3.743866	GAAGGC	0.48828	0.48238
cg0144284	RASSF5	AP-2alpha	1929	1934	3.743866	GAAGGC	0.48828	0.48238
cg0144284	RASSF5	c-Ets-1 [T	1751	1757	3.71855	GTTCCTT	0.61035	0.60765
cg0144284	RASSF5	PEA3 [T0	373	381	3.710864	TGGATG	0.09155	0.09258
cg0144284	RASSF5	PEA3 [T0	1089	1097	3.710864	AGGATG	0.09155	0.09258
cg0144284	RASSF5	C/EBPalph	1267	1273	3.555778	GATTGT	0.24414	0.24752
cg0144284	RASSF5	RXR-alpha	906	912	3.392904	CTCACC	1.09863	1.08572
cg0144284	RASSF5	Elk-1 [T00	1901	1909	3.381796	CTTCCTC	0.04578	0.04588
cg0144284	RASSF5	T3R-beta1	741	749	3.370634	AGCAGG	0.27466	0.2755
cg0144284	RASSF5	GR-beta [T	105	109	3.361531	ATATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	125	129	3.361531	ATATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	205	209	3.361531	AGATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	412	416	3.361531	AGATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	520	524	3.361531	AGATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	643	647	3.361531	AATCT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	676	680	3.361531	AGATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	831	835	3.361531	AGATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	1298	1302	3.361531	AGATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [T	1776	1780	3.361531	AATAT	3.90625	3.99611
cg0144284	RASSF5	NF-Y [T0	1102	1109	3.353763	ATTGGG	0.48828	0.48904
cg0144284	RASSF5	GATA-2 [	1633	1641	3.333333	TGATAG	0.30518	0.30786

cg0144284	RASSF5	c-Jun [T00	1020	1026	3.244843	TGACTC1	0.24414	0.24403
cg0144284	RASSF5	AP-2alpha	258	263	3.229049	AGAGGC	0.48828	0.48238
cg0144284	RASSF5	AP-2alpha	811	816	3.229049	GCCTCT	0.48828	0.48238
cg0144284	RASSF5	AP-2alpha	1396	1401	3.229049	GCCTCT	0.48828	0.48238
cg0144284	RASSF5	Elk-1 [T00	42	50	3.121991	CTTCCTT	0.07629	0.07656
cg0144284	RASSF5	c-Ets-1 [T(	1845	1851	3.102985	CCGGAA(	0.24414	0.23981
cg0144284	RASSF5	USF1 [T0(	1550	1559	3.033037	CACGTG	0.06294	0.06201
cg0144284	RASSF5	C/EBPalph	832	838	3.014837	GATTGC	0.48828	0.4911
cg0144284	RASSF5	c-Ets-2 [T(	43	51	2.945838	TTCCTTT	0.06104	0.06231
cg0144284	RASSF5	STAT4 [T(	233	238	2.941176	GGAAAG	2.92969	2.929
cg0144284	RASSF5	STAT4 [T(	286	291	2.941176	GGAACA	2.92969	2.929
cg0144284	RASSF5	STAT4 [T(	296	301	2.941176	ACTTCC	2.92969	2.929
cg0144284	RASSF5	STAT4 [T(	476	481	2.941176	CTTTCC	2.92969	2.929
cg0144284	RASSF5	STAT4 [T(	677	682	2.941176	GATTCC	2.92969	2.929
cg0144284	RASSF5	STAT4 [T(	1750	1755	2.941176	TGTTCC	2.92969	2.929
cg0144284	RASSF5	STAT1bet	361	370	2.898434	TGGGGG	0.0515	0.05191
cg0144284	RASSF5	IRF-1 [T0(	307	315	2.890712	TTTCCTT	0.07629	0.07756
cg0144284	RASSF5	NF-1 [T00	1908	1915	2.813149	AGGGCC	0.24414	0.24101
cg0144284	RASSF5	PR B [T00	1267	1273	2.80933	GATTGT1	0.73242	0.74818
cg0144284	RASSF5	PR B [T00	1674	1680	2.80933	AACAAT(	0.73242	0.74818
cg0144284	RASSF5	PR B [T00	1795	1801	2.80933	CAATGT	0.73242	0.74818
cg0144284	RASSF5	PR A [T01	1267	1273	2.80933	GATTGT1	0.73242	0.74818
cg0144284	RASSF5	PR A [T01	1674	1680	2.80933	AACAAT(	0.73242	0.74818
cg0144284	RASSF5	PR A [T01	1795	1801	2.80933	CAATGT	0.73242	0.74818
cg0144284	RASSF5	NF-AT2 [1	365	374	2.800326	GGAAAT	0.03433	0.03494
cg0144284	RASSF5	c-Jun [T00	530	536	2.654872	TGACTC(	0.48828	0.48929
cg0144284	RASSF5	c-Jun [T00	1567	1573	2.654872	TGACTC(	0.48828	0.48929
cg0144284	RASSF5	c-Myb [T0	1405	1412	2.570796	GGCAGT	0.06104	0.06117
cg0144284	RASSF5	USF1 [T0(	1546	1555	2.556009	AGCACA(	0.02861	0.02812
cg0144284	RASSF5	AP-2alpha	1471	1476	2.550491	GCCTCA	0.48828	0.48266
cg0144284	RASSF5	AP-2alpha	1896	1901	2.550491	TGAGGC	0.48828	0.48266
cg0144284	RASSF5	RXR-alpha	861	867	2.544678	TTCACC(	0.85449	0.84796
cg0144284	RASSF5	RXR-alpha	1317	1323	2.544678	ATAACC(	0.85449	0.84796
cg0144284	RASSF5	NF-AT1 [1	1285	1293	2.449764	GGAAAA	0.09155	0.0926
cg0144284	RASSF5	C/EBPalph	1793	1799	2.441016	CTCAAT(	0.48828	0.49114
cg0144284	RASSF5	AR [T0004	460	468	2.37683	ACAGTG	0.11444	0.11507
cg0144284	RASSF5	HNF-1C [	753	761	2.372238	GTTATT(	0.04578	0.04709
cg0144284	RASSF5	C/EBPalph	1101	1107	2.371703	AATTGG(	0.48828	0.49114
cg0144284	RASSF5	RXR-alpha	1487	1493	2.322562	GGGTCT(	0.85449	0.84796
cg0144284	RASSF5	T3R-beta1	1982	1990	2.240658	TTGTGG1	0.15259	0.15262
cg0144284	RASSF5	LEF-1 [T0	98	105	2.21836	CTTTGG1	0.18311	0.18582
cg0144284	RASSF5	GATA-1 [	344	349	2.176375	AGGATA	3.90625	3.92756
cg0144284	RASSF5	GATA-1 [	1891	1896	2.176375	TATCCT	3.90625	3.92756
cg0144284	RASSF5	LEF-1 [T0	1384	1391	2.004405	TAGCAA	0.18311	0.18582
cg0144284	RASSF5	NF-AT1 [1	1772	1780	1.970716	GGAAAA	0.06866	0.07012
cg0144284	RASSF5	NF-AT1 [1	365	373	1.94698	GGAAAT	0.06866	0.07012
cg0144284	RASSF5	GATA-1 [	1842	1847	1.896347	TATCCG	3.90625	3.92756
cg0144284	RASSF5	AP-2alpha	85	90	1.871933	GGAGGC	0.97656	0.95407

cg0144284	RASSF5	TBP [T007	313	322	1.871542	TATCTAT	0.18311	0.18942
cg0144284	RASSF5	TFII-I [T0	516	521	1.824994	GGAGAG	0.48828	0.48408
cg0144284	RASSF5	TFII-I [T0	1154	1159	1.824994	GGAGAG	0.48828	0.48408
cg0144284	RASSF5	TFII-I [T0	1160	1165	1.824994	GGAGAG	0.48828	0.48408
cg0144284	RASSF5	TFII-I [T0	1304	1309	1.824994	GGAGAG	0.48828	0.48408
cg0144284	RASSF5	c-Ets-1 [T	477	483	1.769212	TTTCCTA	0.12207	0.12414
cg0144284	RASSF5	c-Ets-1 [T	1283	1289	1.769212	TAGGAA	0.12207	0.12414
cg0144284	RASSF5	C/EBPalph	1703	1709	1.761449	TATTGTC	0.48828	0.49438
cg0144284	RASSF5	p53 [T006	325	331	1.758307	GGGCAT	0.36621	0.36261
cg0144284	RASSF5	AR [T000	1867	1875	1.727468	GGACAG	0.09155	0.09119
cg0144284	RASSF5	GR-beta [T	592	596	1.680765	GCATT	3.90625	3.94936
cg0144284	RASSF5	HIF-1 [T0	1639	1647	1.646028	AGTGCA	0.09155	0.0902
cg0144284	RASSF5	c-Ets-2 [T	77	85	1.64415	TTCCTCC	0.04578	0.04579
cg0144284	RASSF5	c-Ets-1 [T	307	313	1.641124	TTTCCTT	0.36621	0.36952
cg0144284	RASSF5	C/EBPbeta	94	97	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	100	103	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	198	201	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	427	430	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	546	549	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	551	554	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	618	621	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	765	768	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	804	807	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1098	1101	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1103	1106	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1142	1145	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1202	1205	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1210	1213	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1302	1305	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1464	1467	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1619	1622	1.639871	TTGG	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1820	1823	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1912	1915	1.639871	CCAA	15.625	15.72563
cg0144284	RASSF5	XBP-1 [T	1497	1502	1.583727	ATGACA	0.97656	0.98146
cg0144284	RASSF5	XBP-1 [T	1806	1811	1.583727	ATGACA	0.97656	0.98146
cg0144284	RASSF5	XBP-1 [T	1860	1865	1.583727	ATGACC	0.97656	0.98146
cg0144284	RASSF5	TFIID [T0	823	829	1.537547	TGAAAA	0.73242	0.75096
cg0144284	RASSF5	c-Ets-1 [T	76	82	1.513038	TTTCCTC	0.36621	0.36952
cg0144284	RASSF5	STAT4 [T	75	80	1.470588	TTTTCC	1.95312	1.96333
cg0144284	RASSF5	STAT4 [T	306	311	1.470588	GTTTCC	1.95312	1.96333
cg0144284	RASSF5	STAT4 [T	777	782	1.470588	GGAAAC	1.95312	1.96333
cg0144284	RASSF5	STAT4 [T	795	800	1.470588	GGAAAC	1.95312	1.96333
cg0144284	RASSF5	STAT4 [T	1252	1257	1.470588	GTTTCC	1.95312	1.96333
cg0144284	RASSF5	STAT4 [T	1285	1290	1.470588	GGAAAA	1.95312	1.96333
cg0144284	RASSF5	STAT4 [T	1409	1414	1.470588	GTTTCC	1.95312	1.96333
cg0144284	RASSF5	STAT4 [T	1772	1777	1.470588	GGAAAA	1.95312	1.96333
cg0144284	RASSF5	GR [T050	1037	1043	1.444018	GTTTTTC	0.12207	0.1245
cg0144284	RASSF5	c-Ets-1 [T	775	781	1.384951	CAGGAA	0.36621	0.36952

cg0144284	RASSF5	C/EBPbeta	48	51	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	255	258	1.366559	TCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	265	268	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	389	392	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	558	561	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	757	760	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	822	825	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	976	979	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1115	1118	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1610	1613	1.366559	TCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1629	1632	1.366559	TCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1671	1674	1.366559	TCAA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1697	1700	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1730	1733	1.366559	TTGA	15.625	15.72563
cg0144284	RASSF5	C/EBPbeta	1794	1797	1.366559	TCAA	15.625	15.72563
cg0144284	RASSF5	AP-2alpha	651	656	1.357116	GCCTGT	0.48828	0.48203
cg0144284	RASSF5	TCF-4 [T0	1727	1736	1.151128	GCTTTGA	0.05722	0.05784
cg0144284	RASSF5	GATA-2 [	309	317	1.111111	TCCTTAT	0.09155	0.09208
cg0144284	RASSF5	GATA-1 [	1632	1637	1.038567	ATGATA	1.95312	1.98662
cg0144284	RASSF5	TBP [T007	1774	1783	0.935771	AAAATA	0.12207	0.12628
cg0144284	RASSF5	RXR-alpha	1351	1357	0.848226	GGGTCCA	0.48828	0.48333
cg0144284	RASSF5	GR-beta [T	12	16	0.840383	CCATT	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	273	277	0.840383	AATGA	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	322	326	0.840383	AATGG	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	371	375	0.840383	AATGG	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	431	435	0.840383	AATGG	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	868	872	0.840383	CCATT	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1101	1105	0.840383	AATTG	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1477	1481	0.840383	TCATT	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1623	1627	0.840383	AATGA	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1631	1635	0.840383	AATGA	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1677	1681	0.840383	AATGG	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1713	1717	0.840383	TAATT	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1714	1718	0.840383	AATTG	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1782	1786	0.840383	AATGA	7.8125	7.94706
cg0144284	RASSF5	GR-beta [T	1805	1809	0.840383	AATGA	7.8125	7.94706
cg0144284	RASSF5	Elk-1 [T00	38	46	0.822677	CTTCCTT	0.03052	0.03057
cg0144284	RASSF5	GATA-1 [	1314	1319	0.758539	CTGATA	1.95312	1.98662
cg0144284	RASSF5	TCF-4 [T0	262	271	0.698888	GCTTTGA	0.01907	0.01932
cg0144284	RASSF5	AP-2alpha	1815	1820	0.678558	TCAGGC	0.48828	0.48199
cg0144284	RASSF5	POU2F1 [	1970	1980	0.600959	ATTTGCA	0.00715	0.00734
cg0144284	RASSF5	c-Fos [T00	1016	1025	0.556493	GTGCTGA	0.01144	0.01141
cg0144284	RASSF5	AP-1 [T00	1623	1631	0.348957	AATGAG	0.09155	0.09215
cg0144284	RASSF5	HNF-1A [	241	248	0.287765	ACATTAA	0.24414	0.24974
cg0144284	RASSF5	GATA-1 [	313	318	0.280028	TATCTA	0.97656	0.99875
cg0144284	RASSF5	GATA-1 [	1849	1854	0.280028	AAGATA	0.97656	0.99875
cg0144284	RASSF5	c-Ets-1 [T	38	44	0.256174	CTTCCTT	0.24414	0.24569
cg0144284	RASSF5	c-Ets-1 [T	42	48	0.256174	CTTCCTT	0.24414	0.24569

cg0144284	RASSF5	AP-2alpha	358	363	0.226186	GCCTGG	0.97656	0.95305
cg0144284	RASSF5	AP-2alpha	1050	1055	0.226186	CCAGGC	0.97656	0.95305
cg0144284	RASSF5	AP-2alpha	1392	1397	0.226186	CCAGGC	0.97656	0.95305
cg0144284	RASSF5	GR-alpha [	45	49	0.207689	CCTTT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	258	262	0.207689	AGAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	383	387	0.207689	AAAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	785	789	0.207689	CCTCT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	812	816	0.207689	CCTCT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	939	943	0.207689	CCTCT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1156	1160	0.207689	AGAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1162	1166	0.207689	AGAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1323	1327	0.207689	CCTCT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1397	1401	0.207689	CCTCT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1754	1758	0.207689	CCTTT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1828	1832	0.207689	CCTCT	7.8125	7.81264
cg0144284	RASSF5	NF-kappa	793	803	0.112264	GGGGAA	0.00143	0.00138
cg0144284	RASSF5	GR-alpha [	6	10	0	ACAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	33	37	0	CCTGT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	224	228	0	ACAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	398	402	0	CCTAT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	562	566	0	ATAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	652	656	0	CCTGT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	774	778	0	ACAGG	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1561	1565	0	CCTGT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1744	1748	0	CCTAT	7.8125	7.81264
cg0144284	RASSF5	GR-alpha [	1885	1889	0	CCTGT	7.8125	7.81264
cg0144284	RASSF5	AP-2alpha	949	954	0	GCCTGC	0.97656	0.95305
cg0144284	RASSF5	AP-2alpha	1045	1050	0	GCCTGC	0.97656	0.95305
cg0144284	RASSF5	AP-2alpha	1060	1065	0	GCAGGC	0.97656	0.95305
cg0144284	RASSF5	AP-2alpha	1878	1883	0	GCAGGC	0.97656	0.95305
cg0144284	RASSF5	Pax-5 [T0	649	655	0	GGGCCT	1.09863	1.06846
cg0144284	RASSF5	Pax-5 [T0	912	918	0	CCAGCC	1.09863	1.06846
cg0144284	RASSF5	Pax-5 [T0	1426	1432	0	CCAGCC	1.09863	1.06846
cg0144284	RASSF5	TFII-I [T0	222	227	0	GGACAG	1.46484	1.45997
cg0144284	RASSF5	TFII-I [T0	233	238	0	GGAAAG	1.46484	1.45997
cg0144284	RASSF5	TFII-I [T0	476	481	0	CTTTCC	1.46484	1.45997
cg0144284	RASSF5	TFII-I [T0	1841	1846	0	CTATCC	1.46484	1.45997
cg0144284	RASSF5	TFII-I [T0	1867	1872	0	GGACAG	1.46484	1.45997
cg0144284	RASSF5	STAT4 [T	365	370	0	GGAAAT	0.48828	0.49387
cg0144284	RASSF5	c-Ets-1 [T	1901	1907	0	CTTCCTC	0.24414	0.2429
cg0144284	RASSF5	YY1 [T00	12	15	0	CCAT	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	186	189	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	284	287	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	323	326	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	372	375	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	432	435	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	760	763	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	868	871	0	CCAT	7.8125	7.81711

cg0144284	RASSF5	YY1 [T00	1196	1199	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1355	1358	0	CCAT	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1362	1365	0	CCAT	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1372	1375	0	CCAT	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1380	1383	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1448	1451	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1678	1681	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1769	1772	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1921	1924	0	ATGG	7.8125	7.81711
cg0144284	RASSF5	YY1 [T00	1953	1956	0	CCAT	7.8125	7.81711
cg0144284	RASSF5	ER-alpha [	926	930	0	TGACC	1.95312	1.9404
cg0144284	RASSF5	ER-alpha [	1861	1865	0	TGACC	1.95312	1.9404
cg0144284	RASSF5	ER-alpha [	1988	1992	0	TGACC	1.95312	1.9404
cg0144284	RASSF5	GATA-1 [	944	949	0	TATCTG	0.97656	0.98738
cg0144284	RASSF5	C/EBPbeta	121	124	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	169	172	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	289	292	0	ACAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	567	570	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	590	593	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	595	598	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	689	692	0	GCAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	737	740	0	ACAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	834	837	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	843	846	0	ACAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	891	894	0	GCAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1035	1038	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1041	1044	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1269	1272	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1386	1389	0	GCAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1451	1454	0	GCAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1480	1483	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1655	1658	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1667	1670	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1675	1678	0	ACAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1705	1708	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1716	1719	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1757	1760	0	TTGT	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1809	1812	0	ACAA	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1938	1941	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1950	1953	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1972	1975	0	TTGC	15.625	15.71349
cg0144284	RASSF5	C/EBPbeta	1982	1985	0	TTGT	15.625	15.71349
cg0144284	RASSF5	NF-1 [T00	761	768	0	TGGCCC	0.12207	0.11983
cg0144284	RASSF5	c-Jun [T00	1625	1631	0	TGAGTC	0.12207	0.12266
cg0144284	RASSF5	c-Fos [T00	526	535	0	ATGCTG	0.01144	0.01142
cg0144284	RASSF5	TFIID [T0	317	323	0	TATAAA	1.09863	1.13474
cg0144284	RASSF5	TFIID [T0	379	385	0	TTAAAA	1.09863	1.13474
cg0144284	RASSF5	TFIID [T0	814	820	0	TCTAAA	1.09863	1.13474

cg0144284	RASSF5	TFIID [T0	822	828	0	TTGAA	1.09863	1.13474
cg0144284	RASSF5	FOXP3 [T	566	571	0	GTTGTT	1.46484	1.47315
cg0144284	RASSF5	FOXP3 [T	1666	1671	0	GTTGTT	1.46484	1.47315
cg0144284	RASSF5	GR-beta [	241	245	0	ACATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [	818	822	0	AAATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [	819	823	0	AATTT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [	873	877	0	AATGT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [	1100	1104	0	AAATT	3.90625	3.99611
cg0144284	RASSF5	GR-beta [	1796	1800	0	AATGT	3.90625	3.99611
cg0144284	RASSF5	TCF-4E [	1385	1391	0	AGCAAA	0.12207	0.12262
cg0144284	RASSF5	HNF-1A [	378	385	0	GTTAAA	0.24414	0.25261
cg0144284	RASSF5	IRF-2 [T0	1651	1656	0	TCACTT	0.48828	0.49387
cg0144284	RASSF5	c-Myc [T0	1550	1555	0	CACGTG	0.48828	0.48199
cg1245001	RGMB	c-Ets-1 [T	1416	1422	9.969337	TGGGAA	0.24414	0.2459
cg0836780	RGMB	LEF-1 [T0	1889	1896	9.937995	AGCCAA	0.12207	0.12154
cg1245001	RGMB	LEF-1 [T0	981	988	9.937995	AGCCAA	0.12207	0.12154
cg0388534	RGMB	HNF-1B [	969	977	9.830287	TGAGTA	0.12207	0.12399
cg0836780	RGMB	STAT1bet	739	748	9.807397	AAATGG	0.14877	0.1495
cg0836780	RGMB	STAT1bet	1965	1974	9.807397	AGAGGG	0.14877	0.1495
cg1245001	RGMB	STAT1bet	1057	1066	9.807397	AGAGGG	0.14877	0.1495
cg1245001	RGMB	STAT1bet	1438	1447	9.807397	CTTTCCT	0.14877	0.1495
cg0836780	RGMB	XBP-1 [T	411	416	9.789909	CGCCAT	1.95312	1.95208
cg0836780	RGMB	XBP-1 [T	1211	1216	9.789909	ATGGCT	1.95312	1.95208
cg0836780	RGMB	XBP-1 [T	1340	1345	9.789909	ATGTCT	1.95312	1.95208
cg1245001	RGMB	XBP-1 [T	303	308	9.789909	ATGGCT	1.95312	1.95208
cg1245001	RGMB	XBP-1 [T	432	437	9.789909	ATGTCT	1.95312	1.95208
cg1245001	RGMB	XBP-1 [T	1720	1725	9.789909	AGCCAT	1.95312	1.95208
cg1245001	RGMB	XBP-1 [T	1895	1900	9.789909	ATGGCT	1.95312	1.95208
cg0388534	RGMB	XBP-1 [T	10	15	9.789909	ATGTCT	1.95312	1.95208
cg0388534	RGMB	PU.1 [T02	624	636	9.780929	TAACTT	0.00542	0.00541
cg0836780	RGMB	NF-1 [T00	1585	1592	9.761671	AGATCC	0.24414	0.24405
cg1245001	RGMB	NF-1 [T00	677	684	9.761671	AGATCC	0.24414	0.24405
cg1245001	RGMB	Elk-1 [T00	1771	1779	9.754368	TGATGG	0.10681	0.10604
cg1245001	RGMB	Elk-1 [T00	1792	1800	9.754368	TGAGGG	0.10681	0.10604
cg0836780	RGMB	PR B [T00	524	530	9.743489	AACACC	1.09863	1.10292
cg0836780	RGMB	PR B [T00	1303	1309	9.743489	TGGTGT	1.09863	1.10292
cg0836780	RGMB	PR A [T01	524	530	9.743489	AACACC	1.09863	1.10292
cg0836780	RGMB	PR A [T01	1303	1309	9.743489	TGGTGT	1.09863	1.10292
cg1245001	RGMB	PR B [T00	395	401	9.743489	TGGTGT	1.09863	1.10292
cg1245001	RGMB	PR A [T01	395	401	9.743489	TGGTGT	1.09863	1.10292
cg0388534	RGMB	PR B [T00	725	731	9.743489	GTGTGT	1.09863	1.10292
cg0388534	RGMB	PR B [T00	1573	1579	9.743489	AACACC	1.09863	1.10292
cg0388534	RGMB	PR A [T01	725	731	9.743489	GTGTGT	1.09863	1.10292
cg0388534	RGMB	PR A [T01	1573	1579	9.743489	AACACC	1.09863	1.10292
cg1245001	RGMB	AhR:Arnt	1218	1227	9.738501	TGGCGC	0.17929	0.17456
cg0388534	RGMB	c-Myb [T0	191	198	9.729271	AACAGT	0.36621	0.37054
cg0388534	RGMB	c-Myb [T0	534	541	9.729271	GAACTG	0.36621	0.37054
cg0836780	RGMB	LEF-1 [T0	206	213	9.72404	AGACAA	0.21362	0.2139

cg0836780	RGMB	LEF-1 [T0	1711	1718	9.72404	AGGCAA	0.21362	0.2139
cg1245001	RGMB	LEF-1 [T0	803	810	9.72404	AGGCAA	0.21362	0.2139
cg1245001	RGMB	LEF-1 [T0	1868	1875	9.72404	CTTTGCC	0.21362	0.2139
cg0388534	RGMB	LEF-1 [T0	1051	1058	9.72404	AGGCAA	0.21362	0.2139
cg1245001	RGMB	c-Jun [T00	1764	1770	9.717135	TGACCTC	0.73242	0.73031
cg0836780	RGMB	c-Ets-1 [T(	1497	1503	9.713162	GGGGAA	0.36621	0.36441
cg1245001	RGMB	c-Ets-1 [T(	589	595	9.713162	GGGGAA	0.36621	0.36441
cg0388534	RGMB	c-Myb [T0	994	1001	9.704537	CAACTA(	0.36621	0.37054
cg0388534	RGMB	RelA [T00	1044	1054	9.654376	TGGGGA.	0.02813	0.0279
cg0836780	RGMB	RAR-beta	21	30	9.641259	GGGGTT(	0.21362	0.21243
cg0836780	RGMB	RAR-beta	1899	1908	9.622793	AAAGAA	0.21362	0.21243
cg1245001	RGMB	RAR-beta	991	1000	9.622793	AAAGAA	0.21362	0.21243
cg0388534	RGMB	RAR-beta	1365	1374	9.622793	TAAAAA(	0.21362	0.21243
cg0388534	RGMB	Elk-1 [T00	1760	1768	9.62002	GGAGGG	0.07629	0.07577
cg0836780	RGMB	NF-kappaI	56	67	9.590046	CGGCGC'	0.01776	0.01758
cg0388534	RGMB	NF-AT1 [T	56	64	9.557905	GCATTTT	0.16785	0.1682
cg0836780	RGMB	Pax-5 [T0(	1837	1843	9.552105	TTAGCCC	1.46484	1.43083
cg0836780	RGMB	TFIID [T0	718	724	9.552105	TACCAA/	1.46484	1.48472
cg0836780	RGMB	TFIID [T0	792	798	9.552105	TTTCCCA	1.46484	1.48472
cg0836780	RGMB	TFIID [T0	922	928	9.552105	TTTGGA/	1.46484	1.48472
cg0836780	RGMB	TFIID [T0	1110	1116	9.552105	TTTCTCA	1.46484	1.48472
cg0836780	RGMB	TFIID [T0	1413	1419	9.552105	TGTGAA/	1.46484	1.48472
cg0836780	RGMB	TFIID [T0	1679	1685	9.552105	TTTGACA	1.46484	1.48472
cg1245001	RGMB	Pax-5 [T0(	929	935	9.552105	TTAGCCC	1.46484	1.43083
cg1245001	RGMB	Pax-5 [T0(	1328	1334	9.552105	GGGCAA	1.46484	1.43083
cg1245001	RGMB	Pax-5 [T0(	1637	1643	9.552105	TTGGCCC	1.46484	1.43083
cg1245001	RGMB	TFIID [T0	14	20	9.552105	TTTGGA/	1.46484	1.48472
cg1245001	RGMB	TFIID [T0	202	208	9.552105	TTTCTCA	1.46484	1.48472
cg1245001	RGMB	TFIID [T0	505	511	9.552105	TGTGAA/	1.46484	1.48472
cg1245001	RGMB	TFIID [T0	771	777	9.552105	TTTGACA	1.46484	1.48472
cg1245001	RGMB	TFIID [T0	1109	1115	9.552105	TTTGGG/	1.46484	1.48472
cg1245001	RGMB	TFIID [T0	1880	1886	9.552105	TTTCCCA	1.46484	1.48472
cg1245001	RGMB	TFIID [T0	1992	1998	9.552105	TTTGGA/	1.46484	1.48472
cg0388534	RGMB	Pax-5 [T0(	233	239	9.552105	GACGCC(	1.46484	1.43083
cg0388534	RGMB	Pax-5 [T0(	870	876	9.552105	TTTGCCC	1.46484	1.43083
cg0388534	RGMB	Pax-5 [T0(	1412	1418	9.552105	TTTGCCC	1.46484	1.43083
cg0388534	RGMB	TFIID [T0	45	51	9.552105	TGTGAA/	1.46484	1.48472
cg0388534	RGMB	TFIID [T0	128	134	9.552105	TGTCAA/	1.46484	1.48472
cg0388534	RGMB	TFIID [T0	1223	1229	9.552105	TTTCGG/	1.46484	1.48472
cg0388534	RGMB	TFIID [T0	1316	1322	9.552105	TGTGAA/	1.46484	1.48472
cg0388534	RGMB	TFIID [T0	1457	1463	9.552105	TGTCAA/	1.46484	1.48472
cg1245001	RGMB	NF-1 [T00	1161	1168	9.535536	CTGACC/	0.73242	0.73053
cg0388534	RGMB	NF-1 [T00	1859	1866	9.535536	TTGGGC(	0.73242	0.73053
cg1245001	RGMB	NF-AT1 [T	1461	1469	9.521781	TGCATTT	0.16785	0.1682
cg1245001	RGMB	NF-AT1 [T	1876	1884	9.521781	TGGATTT	0.16785	0.1682
cg0836780	RGMB	NF-1 [T00	879	886	9.513281	TTGGCTT	0.73242	0.73053
cg0388534	RGMB	NF-1 [T00	436	443	9.513281	TTGGGTT	0.73242	0.73053
cg0836780	RGMB	TFII-I [T0(	161	166	9.512894	AAATCC	7.32422	7.29728

cg0836780	RGMB	TFII-I [T0	195	200	9.512894	GGAATT	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	246	251	9.512894	TTTTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	288	293	9.512894	TTTTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	292	297	9.512894	CCTTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	307	312	9.512894	TTGTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	452	457	9.512894	GGAAAA	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	539	544	9.512894	GGAAAA	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	650	655	9.512894	GGAAAA	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	708	713	9.512894	GTGTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	765	770	9.512894	GTGTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	791	796	9.512894	GTTTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	952	957	9.512894	GTGTCC	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	1010	1015	9.512894	GGACAA	7.32422	7.29728
cg0836780	RGMB	TFII-I [T0	1572	1577	9.512894	AATTCC	7.32422	7.29728
cg0836780	RGMB	FOXP3 [T	31	36	9.512894	GATAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	261	266	9.512894	GAGAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	337	342	9.512894	GTTCTG	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	371	376	9.512894	CCCAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	609	614	9.512894	AAGAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	801	806	9.512894	GTTGCC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	878	883	9.512894	GTTGGC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	890	895	9.512894	GTTTAG	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	983	988	9.512894	CCCAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	1051	1056	9.512894	AAGAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	1263	1268	9.512894	ATAAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	1531	1536	9.512894	GTTGCT	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	1900	1905	9.512894	AAGAAC	7.32422	7.35678
cg0836780	RGMB	FOXP3 [T	1975	1980	9.512894	GTTTAG	7.32422	7.35678
cg1245001	RGMB	TFII-I [T0	44	49	9.512894	GTGTCC	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	102	107	9.512894	GGACAA	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	664	669	9.512894	AATTCC	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	1373	1378	9.512894	GGAAAA	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	1396	1401	9.512894	GGAAGG	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	1426	1431	9.512894	AATTCC	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	1600	1605	9.512894	TTATCC	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	1796	1801	9.512894	GGAAGG	7.32422	7.29728
cg1245001	RGMB	TFII-I [T0	1877	1882	9.512894	GGATTT	7.32422	7.29728
cg1245001	RGMB	FOXP3 [T	75	80	9.512894	CCCAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	143	148	9.512894	AAGAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	355	360	9.512894	ATAAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	623	628	9.512894	GTTGCT	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	992	997	9.512894	AAGAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1067	1072	9.512894	GTTTAG	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1141	1146	9.512894	GTTGGG	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1164	1169	9.512894	ACCAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1329	1334	9.512894	GGCAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1551	1556	9.512894	AAGAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1572	1577	9.512894	GTTTAG	7.32422	7.35678

cg1245001	RGMB	FOXP3 [T	1584	1589	9.512894	GTTCTT	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1777	1782	9.512894	AAGAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1846	1851	9.512894	CAGAAC	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1919	1924	9.512894	GTTTAG	7.32422	7.35678
cg1245001	RGMB	FOXP3 [T	1924	1929	9.512894	GTTGGT	7.32422	7.35678
cg0388534	RGMB	TFII-I [T0	59	64	9.512894	TTTTCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	178	183	9.512894	TTTTCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	214	219	9.512894	GGATTT	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	250	255	9.512894	GGAAAA	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	882	887	9.512894	TTATCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	950	955	9.512894	AATTCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1016	1021	9.512894	GGATTT	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1213	1218	9.512894	TTTTCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1231	1236	9.512894	CCATCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1289	1294	9.512894	GGAAAA	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1447	1452	9.512894	GGAAGG	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1497	1502	9.512894	AATTCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1521	1526	9.512894	CCTTCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1531	1536	9.512894	CCATCC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1547	1552	9.512894	GGACCG	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1617	1622	9.512894	GGAACG	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1869	1874	9.512894	GGAAAC	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1885	1890	9.512894	GGAAGG	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1901	1906	9.512894	GGAAGG	7.32422	7.29728
cg0388534	RGMB	TFII-I [T0	1943	1948	9.512894	GGACTT	7.32422	7.29728
cg0388534	RGMB	FOXP3 [T	38	43	9.512894	GTTTAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	188	193	9.512894	AAGAAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	653	658	9.512894	GGCAAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	729	734	9.512894	GTTTAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	989	994	9.512894	GTTGCC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	992	997	9.512894	GCCAAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	1027	1032	9.512894	GGCAAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	1129	1134	9.512894	GATAAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	1158	1163	9.512894	CATAAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	1332	1337	9.512894	AGCAAC	7.32422	7.35678
cg0388534	RGMB	FOXP3 [T	1858	1863	9.512894	GTTGGG	7.32422	7.35678
cg1245001	RGMB	Ik-1 [T027	1408	1420	9.497194	AAGGGA	0.02941	0.02907
cg0388534	RGMB	Ik-1 [T027	1524	1536	9.497194	TCCCAG	0.02941	0.02907
cg1245001	RGMB	TCF-4E [T	1991	1997	9.453578	CTTTGG	0.48828	0.49215
cg0388534	RGMB	TCF-4E [T	1195	1201	9.453578	CTTTGT	0.48828	0.49215
cg0388534	RGMB	TCF-4E [T	1799	1805	9.453578	GTCAAA	0.48828	0.49215
cg0388534	RGMB	TCF-4E [T	1814	1820	9.453578	CTTTGT	0.48828	0.49215
cg1245001	RGMB	c-Jun [T00	1592	1598	9.442241	GCTGTC	0.73242	0.73031
cg1245001	RGMB	NFI/CTF [	1633	1640	9.352332	GACCTT	0.54932	0.54821
cg0388534	RGMB	SRY [T00	1797	1805	9.264664	AGGTCA	0.12207	0.12265
cg0836780	RGMB	E2F-1 [T0	380	387	9.261732	GCGGAG	0.15259	0.14917
cg0388534	RGMB	HNF-1C [	751	759	9.253863	GTATGT	0.19836	0.20229
cg0388534	RGMB	VDR [T00	529	537	9.234242	GTCATG	0.12207	0.12335

cg0388534	RGMB	NF-AT2 [	1209	1218	9.228174	GTCTTT	0.05341	0.05386
cg1245001	RGMB	MEF-2A [	1188	1198	9.220261	TACTAA	0.07343	0.07563
cg0836780	RGMB	AP-1 [T00	1774	1782	9.203282	AATTAG	0.24414	0.24693
cg1245001	RGMB	AP-1 [T00	866	874	9.203282	AATTAG	0.24414	0.24693
cg0836780	RGMB	c-Ets-1 [T	826	832	9.19359	TTGGAA	0.85449	0.85523
cg0836780	RGMB	c-Ets-1 [T	923	929	9.19359	TTGGAA	0.85449	0.85523
cg1245001	RGMB	c-Ets-1 [T	15	21	9.19359	TTGGAA	0.85449	0.85523
cg0388534	RGMB	c-Ets-1 [T	1138	1144	9.19359	TTGGAA	0.85449	0.85523
cg0388534	RGMB	NF-AT1 [	1905	1913	9.18189	GGAAAG	0.22888	0.22959
cg1245001	RGMB	HNF-1B [	1927	1935	9.170219	GGTTAA	0.08392	0.0857
cg0388534	RGMB	NF-kappa	1650	1660	9.155163	GGGGAC	0.03576	0.0351
cg0836780	RGMB	c-Ets-1 [T	1121	1127	9.148774	AGGGAA	0.85449	0.85523
cg1245001	RGMB	c-Ets-1 [T	213	219	9.148774	AGGGAA	0.85449	0.85523
cg0388534	RGMB	c-Ets-1 [T	1962	1968	9.148774	AGGGAA	0.85449	0.85523
cg0836780	RGMB	c-Myb [T0	874	881	9.142015	CTAAGT	0.39673	0.40028
cg0388534	RGMB	c-Myb [T0	1754	1761	9.110773	AAACTT	0.39673	0.40028
cg0836780	RGMB	LEF-1 [T0	1148	1155	9.099721	CTTTGC	0.54932	0.55326
cg1245001	RGMB	LEF-1 [T0	240	247	9.099721	CTTTGC	0.54932	0.55326
cg0388534	RGMB	LEF-1 [T0	1195	1202	9.099721	CTTTGT	0.54932	0.55326
cg0836780	RGMB	NFI/CTF [	372	379	9.042931	CCAACT	0.48828	0.48804
cg0836780	RGMB	NFI/CTF [	1874	1881	9.042931	GCTGTT	0.48828	0.48804
cg1245001	RGMB	NFI/CTF [	966	973	9.042931	GCTGTT	0.48828	0.48804
cg0388534	RGMB	NF-AT1 [	1564	1572	9.042733	CAGATT	0.22888	0.22959
cg0836780	RGMB	c-Jun [T00	663	669	9.013496	TGACAT	0.61035	0.61059
cg0836780	RGMB	AP-1 [T00	961	969	9.002849	TTTAAG	0.24414	0.24693
cg1245001	RGMB	AP-1 [T00	53	61	9.002849	TTTAAG	0.24414	0.24693
cg1245001	RGMB	LEF-1 [T0	1108	1115	8.973041	CTTTGG	0.54932	0.55326
cg1245001	RGMB	LEF-1 [T0	1991	1998	8.973041	CTTTGG	0.54932	0.55326
cg0836780	RGMB	GR [T050	689	695	8.971049	GTGTTT	0.61035	0.61632
cg0388534	RGMB	GR [T050	471	477	8.971049	CAAATA	0.61035	0.61632
cg1245001	RGMB	c-Ets-1 [T	1427	1433	8.937416	ATTCCA	0.85449	0.85523
cg0388534	RGMB	c-Ets-1 [T	918	924	8.937416	GTGGAA	0.85449	0.85523
cg1245001	RGMB	Elk-1 [T00	1576	1584	8.931691	AGCGGG	0.24414	0.24034
cg0388534	RGMB	Elk-1 [T00	1897	1905	8.931691	AGGGGG	0.24414	0.24034
cg0388534	RGMB	IRF-1 [T0	1285	1293	8.916359	TTGTGG	0.09155	0.09147
cg0836780	RGMB	c-Ets-2 [T	1574	1582	8.912323	TTCCTG	0.27466	0.27495
cg1245001	RGMB	c-Ets-2 [T	666	674	8.912323	TTCCTG	0.27466	0.27495
cg1245001	RGMB	c-Ets-2 [T	1742	1750	8.912323	AGTTAG	0.27466	0.27495
cg0388534	RGMB	HNF-1C [	1814	1822	8.903584	CTTTGT	0.12207	0.12495
cg0388534	RGMB	Elk-1 [T00	1881	1889	8.897321	TCGCGG	0.24414	0.24034
cg0836780	RGMB	GATA-2 [	784	792	8.888889	GGATAT	0.22888	0.22993
cg0388534	RGMB	AP-1 [T00	737	745	8.82837	CTTAAG	0.24414	0.24693
cg0836780	RGMB	PR B [T00	1914	1920	8.827054	ATCTGT	0.36621	0.36944
cg0836780	RGMB	PR A [T01	1914	1920	8.827054	ATCTGT	0.36621	0.36944
cg1245001	RGMB	PR B [T00	1006	1012	8.827054	ATCTGT	0.36621	0.36944
cg1245001	RGMB	PR B [T00	1827	1833	8.827054	AGCTGT	0.36621	0.36944
cg1245001	RGMB	PR A [T01	1006	1012	8.827054	ATCTGT	0.36621	0.36944
cg1245001	RGMB	PR A [T01	1827	1833	8.827054	AGCTGT	0.36621	0.36944

cg0388534	RGMB	PR B [T00	787	793	8.827054	AACAGA	0.36621	0.36944
cg0388534	RGMB	PR A [T01	787	793	8.827054	AACAGA	0.36621	0.36944
cg1245001	RGMB	NFI/CTF [	1907	1914	8.814757	CCTTTT	0.48828	0.48804
cg0388534	RGMB	NFI/CTF [	1177	1184	8.814757	CCACTT	0.48828	0.48804
cg1245001	RGMB	NF-1 [T00	1110	1117	8.790071	TTGGGA	0.24414	0.24467
cg0836780	RGMB	E2F-1 [T0	1658	1665	8.76494	TGCTCC	0.27466	0.26875
cg1245001	RGMB	E2F-1 [T0	750	757	8.76494	TGCTCC	0.27466	0.26875
cg0388534	RGMB	E2F-1 [T0	1928	1935	8.76494	GCGGCG	0.27466	0.26875
cg0836780	RGMB	LEF-1 [T0	484	491	8.759086	CTTTGC	0.54932	0.55326
cg0836780	RGMB	LEF-1 [T0	494	501	8.759086	CTTTGC	0.54932	0.55326
cg0388534	RGMB	LEF-1 [T0	1814	1821	8.759086	CTTTGT	0.54932	0.55326
cg0836780	RGMB	XBP-1 [T	107	112	8.75604	ATGAGC	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	153	158	8.75604	TTTCAT	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	157	162	8.75604	ATGAAA	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	320	325	8.75604	ATGAGA	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	732	737	8.75604	TTTCAT	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	736	741	8.75604	ATGAAA	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	1188	1193	8.75604	TATCAT	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	1362	1367	8.75604	ATGAAA	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	1367	1372	8.75604	ATGAAA	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	1502	1507	8.75604	ATGAAA	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	1513	1518	8.75604	ATGAAA	2.92969	2.9674
cg0836780	RGMB	XBP-1 [T	1960	1965	8.75604	ATGAAA	2.92969	2.9674
cg1245001	RGMB	XBP-1 [T	280	285	8.75604	TATCAT	2.92969	2.9674
cg1245001	RGMB	XBP-1 [T	454	459	8.75604	ATGAAA	2.92969	2.9674
cg1245001	RGMB	XBP-1 [T	459	464	8.75604	ATGAAA	2.92969	2.9674
cg1245001	RGMB	XBP-1 [T	594	599	8.75604	ATGAAA	2.92969	2.9674
cg1245001	RGMB	XBP-1 [T	605	610	8.75604	ATGAAA	2.92969	2.9674
cg1245001	RGMB	XBP-1 [T	1052	1057	8.75604	ATGAAA	2.92969	2.9674
cg1245001	RGMB	XBP-1 [T	1403	1408	8.75604	ATGAAA	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	389	394	8.75604	ATGATC	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	532	537	8.75604	ATGAAC	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	769	774	8.75604	ATGAAA	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	902	907	8.75604	GCTCAT	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	1146	1151	8.75604	TATCAT	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	1155	1160	8.75604	TCTCAT	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	1237	1242	8.75604	GATCAT	2.92969	2.9674
cg0388534	RGMB	XBP-1 [T	1379	1384	8.75604	TCTCAT	2.92969	2.9674
cg0836780	RGMB	c-Myb [T0	570	577	8.728118	GAAAGT	0.30518	0.30924
cg0836780	RGMB	c-Myb [T0	727	734	8.728118	GTAAGT	0.30518	0.30924
cg0836780	RGMB	STAT1bet	646	655	8.695301	ACGTGG	0.22316	0.22446
cg0388534	RGMB	STAT1bet	1043	1052	8.695301	TTGGGG	0.22316	0.22446
cg0388534	RGMB	IRF-1 [T0	1214	1222	8.661524	TTTCCT	0.20599	0.20664
cg0388534	RGMB	IRF-1 [T0	1865	1873	8.661524	GCGAGG	0.20599	0.20664
cg0388534	RGMB	RAR-beta	437	446	8.55975	TGGGTT	0.26703	0.26657
cg0836780	RGMB	NF-AT1 [	243	251	8.532897	TCATTT	0.10681	0.10725
cg0836780	RGMB	c-Myb [T0	1013	1020	8.529773	CAACTT	0.30518	0.30924
cg1245001	RGMB	c-Myb [T0	105	112	8.529773	CAACTT	0.30518	0.30924

cg0836780	RGMB	c-Ets-1 [T	83	89	8.501115	GTTCCA	0.24414	0.24529
cg0388534	RGMB	IRF-1 [T0	1568	1576	8.497322	TTTCCA	0.20599	0.20664
cg0836780	RGMB	LEF-1 [T0	1075	1082	8.457856	CTTTGA	0.15259	0.15214
cg1245001	RGMB	LEF-1 [T0	167	174	8.457856	CTTTGA	0.15259	0.15214
cg0388534	RGMB	LEF-1 [T0	380	387	8.457856	CTTTGA	0.15259	0.15214
cg0388534	RGMB	c-Myb [T0	985	992	8.443873	TACAGT	0.30518	0.30924
cg0836780	RGMB	c-Myb [T0	1265	1272	8.412632	AAACTG	0.30518	0.30924
cg1245001	RGMB	c-Myb [T0	357	364	8.412632	AAACTG	0.30518	0.30924
cg1245001	RGMB	c-Ets-1 [T	1453	1459	8.373028	GTTCCA	0.24414	0.24529
cg0388534	RGMB	c-Ets-1 [T	276	282	8.373028	ATGGAA	0.24414	0.24529
cg1245001	RGMB	HNF-3alp	1496	1503	8.343064	TATTTG	0.27466	0.28528
cg1245001	RGMB	HNF-3alp	1499	1506	8.343064	TTGAAA	0.27466	0.28528
cg1245001	RGMB	HNF-3alp	1674	1681	8.343064	GATTTT	0.27466	0.28528
cg0388534	RGMB	HNF-3alp	1017	1024	8.343064	GATTTT	0.27466	0.28528
cg0388534	RGMB	HNF-3alp	1293	1300	8.343064	AATTTA	0.27466	0.28528
cg0836780	RGMB	PR B [T00	268	274	8.338824	AACAGC	1.09863	1.10009
cg0836780	RGMB	PR B [T00	1038	1044	8.338824	TCCTGTT	1.09863	1.10009
cg0836780	RGMB	PR B [T00	1708	1714	8.338824	AACAGG	1.09863	1.10009
cg0836780	RGMB	PR B [T00	1873	1879	8.338824	GGCTGT	1.09863	1.10009
cg0836780	RGMB	PR A [T01	268	274	8.338824	AACAGC	1.09863	1.10009
cg0836780	RGMB	PR A [T01	1038	1044	8.338824	TCCTGTT	1.09863	1.10009
cg0836780	RGMB	PR A [T01	1708	1714	8.338824	AACAGG	1.09863	1.10009
cg0836780	RGMB	PR A [T01	1873	1879	8.338824	GGCTGT	1.09863	1.10009
cg1245001	RGMB	PR B [T00	130	136	8.338824	TCCTGTT	1.09863	1.10009
cg1245001	RGMB	PR B [T00	800	806	8.338824	AACAGG	1.09863	1.10009
cg1245001	RGMB	PR B [T00	965	971	8.338824	GGCTGT	1.09863	1.10009
cg1245001	RGMB	PR B [T00	1934	1940	8.338824	TTCTGTT	1.09863	1.10009
cg1245001	RGMB	PR A [T01	130	136	8.338824	TCCTGTT	1.09863	1.10009
cg1245001	RGMB	PR A [T01	800	806	8.338824	AACAGG	1.09863	1.10009
cg1245001	RGMB	PR A [T01	965	971	8.338824	GGCTGT	1.09863	1.10009
cg1245001	RGMB	PR A [T01	1934	1940	8.338824	TTCTGTT	1.09863	1.10009
cg0388534	RGMB	PR B [T00	141	147	8.338824	AACAGA	1.09863	1.10009
cg0388534	RGMB	PR B [T00	280	286	8.338824	AACAGG	1.09863	1.10009
cg0388534	RGMB	PR B [T00	344	350	8.338824	AACAGA	1.09863	1.10009
cg0388534	RGMB	PR B [T00	1037	1043	8.338824	TGCTGTT	1.09863	1.10009
cg0388534	RGMB	PR B [T00	1854	1860	8.338824	TTCTGTT	1.09863	1.10009
cg0388534	RGMB	PR A [T01	141	147	8.338824	AACAGA	1.09863	1.10009
cg0388534	RGMB	PR A [T01	280	286	8.338824	AACAGG	1.09863	1.10009
cg0388534	RGMB	PR A [T01	344	350	8.338824	AACAGA	1.09863	1.10009
cg0388534	RGMB	PR A [T01	1037	1043	8.338824	TGCTGTT	1.09863	1.10009
cg0388534	RGMB	PR A [T01	1854	1860	8.338824	TTCTGTT	1.09863	1.10009
cg0388534	RGMB	E2F-1 [T0	1552	1559	8.336446	GCGGGT	0.15259	0.14963
cg0388534	RGMB	ATF3 [T0	525	532	8.313799	GTATGT	0.27466	0.27431
cg0388534	RGMB	PXR-1:RX	74	81	8.304332	TGAACA	0.12207	0.12266
cg0388534	RGMB	AR [T000	928	936	8.295755	AGCATG	0.10681	0.10625
cg0836780	RGMB	GR-alpha [	44	48	8.281568	CCTTC	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	50	54	8.281568	GGAGG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	70	74	8.281568	CCTTG	7.8125	7.72956

cg0836780	RGMB	GR-alpha [	87	91	8.281568	CAAGG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	112	116	8.281568	CCTTC	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	292	296	8.281568	CCTTC	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	429	433	8.281568	GGAGG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	772	776	8.281568	CCTTG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	842	846	8.281568	GAAGG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	1493	1497	8.281568	CCTTG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	1628	1632	8.281568	CCTTC	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	1643	1647	8.281568	CCTTG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	1686	1690	8.281568	GGAGG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	1798	1802	8.281568	CAAGG	7.8125	7.72956
cg0836780	RGMB	GR-alpha [	1870	1874	8.281568	GAAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	585	589	8.281568	CCTTG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	720	724	8.281568	CCTTC	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	735	739	8.281568	CCTTG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	778	782	8.281568	GGAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	890	894	8.281568	CAAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	962	966	8.281568	GAAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1247	1251	8.281568	GGAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1279	1283	8.281568	GGAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1285	1289	8.281568	GGAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1393	1397	8.281568	CAAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1397	1401	8.281568	GAAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1442	1446	8.281568	CCTTC	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1635	1639	8.281568	CCTTG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1797	1801	8.281568	GAAGG	7.8125	7.72956
cg1245001	RGMB	GR-alpha [	1873	1877	8.281568	CCTTG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	31	35	8.281568	CCTTG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	229	233	8.281568	CGAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	294	298	8.281568	GGAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	630	634	8.281568	CCTCC	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	800	804	8.281568	CCTTC	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	865	869	8.281568	GAAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1060	1064	8.281568	CGAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1086	1090	8.281568	CCTTG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1433	1437	8.281568	CCTTG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1448	1452	8.281568	GAAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1478	1482	8.281568	CCTCG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1521	1525	8.281568	CCTTC	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1689	1693	8.281568	CCTCC	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1693	1697	8.281568	CAAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1696	1700	8.281568	GGAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1730	1734	8.281568	GGAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1760	1764	8.281568	GGAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1790	1794	8.281568	CAAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1866	1870	8.281568	CGAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1886	1890	8.281568	GAAGG	7.8125	7.72956
cg0388534	RGMB	GR-alpha [	1902	1906	8.281568	GAAGG	7.8125	7.72956

cg0388534	RGMB	GR-alpha [	1917	1921	8.281568	CGAGG	7.8125	7.72956
cg1245001	RGMB	IRF-1 [T0	1743	1751	8.242487	GTTAGG	0.25177	0.25263
cg0388534	RGMB	c-Jun [T00	1090	1096	8.242207	GAGGTC	0.48828	0.49076
cg0388534	RGMB	c-Jun [T00	1796	1802	8.242207	GAGGTC	0.48828	0.49076
cg0388534	RGMB	HOXD9 [	701	710	8.224939	GGATTA	0.08774	0.09025
cg0388534	RGMB	HOXD10 [	701	710	8.224939	GGATTA	0.08774	0.09025
cg0388534	RGMB	NF-AT1 [	1047	1055	8.223794	GGAAAG	0.1297	0.12988
cg0836780	RGMB	ENKTF-1	408	415	8.19852	ACCCGC	0.73242	0.71737
cg0388534	RGMB	ENKTF-1	1713	1720	8.19852	TGGCAG	0.73242	0.71737
cg1245001	RGMB	AhR [T01	1087	1097	8.184723	CTCACG	0.04864	0.04833
cg0836780	RGMB	SRY [T00	205	213	8.174786	TAGACA	0.15259	0.15383
cg0836780	RGMB	SRY [T00	1075	1083	8.174786	CTTTGA	0.15259	0.15383
cg1245001	RGMB	SRY [T00	167	175	8.174786	CTTTGA	0.15259	0.15383
cg0836780	RGMB	p53 [T006	1984	1990	8.162057	GGGCGC	0.48828	0.47377
cg1245001	RGMB	p53 [T006	1076	1082	8.162057	GGGCGC	0.48828	0.47377
cg1245001	RGMB	IRF-1 [T0	1991	1999	8.151819	CTTTGG	0.25177	0.25263
cg0388534	RGMB	c-Jun [T00	615	621	8.128539	AATGTC	0.48828	0.49076
cg0388534	RGMB	c-Jun [T00	1455	1461	8.128539	AATGTC	0.48828	0.49076
cg0388534	RGMB	c-Jun [T00	1557	1563	8.128539	TGACAT	0.48828	0.49076
cg0836780	RGMB	NF-AT1 [	539	547	8.12076	GGAAAA	0.1297	0.12988
cg0388534	RGMB	LEF-1 [T0	477	484	8.117221	CTTTGA	0.12207	0.1241
cg0388534	RGMB	E2F-1 [T0	1065	1072	8.101379	GCGGTA	0.30518	0.3
cg0836780	RGMB	VDR [T00	352	360	8.079962	ATCCTG	0.24414	0.24712
cg0836780	RGMB	VDR [T00	913	921	8.079962	GTTCAA	0.24414	0.24712
cg0836780	RGMB	VDR [T00	1400	1408	8.079962	GTTCAG	0.24414	0.24712
cg1245001	RGMB	VDR [T00	5	13	8.079962	GTTCAA	0.24414	0.24712
cg1245001	RGMB	VDR [T00	492	500	8.079962	GTTCAG	0.24414	0.24712
cg1245001	RGMB	VDR [T00	1148	1156	8.079962	GTTCAA	0.24414	0.24712
cg0388534	RGMB	NF-kappa	1045	1055	8.076548	GGGGAA	0.0329	0.03218
cg0836780	RGMB	GR-alpha [	100	104	8.073878	CCTGC	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	165	169	8.073878	CCAGG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	192	196	8.073878	CTAGG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	203	207	8.073878	CCTAG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	753	757	8.073878	CTAGG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	900	904	8.073878	GTAGG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	1178	1182	8.073878	CCTGG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	1301	1305	8.073878	CCTGG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	1747	1751	8.073878	CCTGG	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	1950	1954	8.073878	CCTAC	7.8125	7.72238
cg0836780	RGMB	GR-alpha [	1954	1958	8.073878	CCTGC	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	270	274	8.073878	CCTGG	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	393	397	8.073878	CCTGG	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	839	843	8.073878	CCTGG	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	1042	1046	8.073878	CCTAC	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	1046	1050	8.073878	CCTGC	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	1156	1160	8.073878	CCTGC	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	1243	1247	8.073878	CTAGG	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	1257	1261	8.073878	GTAGG	7.8125	7.72238

cg1245001	RGMB	GR-alpha [	1275	1279	8.073878	CCTGG	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	1325	1329	8.073878	CCTGG	7.8125	7.72238
cg1245001	RGMB	GR-alpha [	1810	1814	8.073878	CCTGG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	211	215	8.073878	CCAGG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	650	654	8.073878	CCAGG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	813	817	8.073878	CCTAG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	886	890	8.073878	CCTAG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	1123	1127	8.073878	CCTAC	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	1655	1659	8.073878	CCTGC	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	1682	1686	8.073878	CCTGC	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	1715	1719	8.073878	GCAGG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	1721	1725	8.073878	CCAGG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	1726	1730	8.073878	GCAGG	7.8125	7.72238
cg0388534	RGMB	GR-alpha [	1933	1937	8.073878	GCAGG	7.8125	7.72238
cg0836780	RGMB	AR [T000	949	957	8.055836	CATGTG	0.19836	0.19634
cg1245001	RGMB	AR [T000	41	49	8.055836	CATGTG	0.19836	0.19634
cg1245001	RGMB	NF-AT2 [	1373	1382	8.023205	GGAAAA	0.08965	0.09068
cg0836780	RGMB	Pax-5 [T0	10	16	8.014558	GGGCTC	2.19727	2.14502
cg0836780	RGMB	Pax-5 [T0	979	985	8.014558	TCAGCC	2.19727	2.14502
cg0836780	RGMB	Pax-5 [T0	1488	1494	8.014558	TCTGCC	2.19727	2.14502
cg0836780	RGMB	Pax-5 [T0	1790	1796	8.014558	GAAGCC	2.19727	2.14502
cg0836780	RGMB	TFIID [T0	616	622	8.014558	TTAGAA	2.19727	2.24348
cg0836780	RGMB	TFIID [T0	851	857	8.014558	TTTGCT	2.19727	2.24348
cg0836780	RGMB	TFIID [T0	892	898	8.014558	TTAGAA	2.19727	2.24348
cg0836780	RGMB	TFIID [T0	1063	1069	8.014558	TTTGAG	2.19727	2.24348
cg0836780	RGMB	TFIID [T0	1512	1518	8.014558	TATGAA	2.19727	2.24348
cg0836780	RGMB	TFIID [T0	1924	1930	8.014558	TTTGAG	2.19727	2.24348
cg0836780	RGMB	TFIID [T0	1959	1965	8.014558	TATGAA	2.19727	2.24348
cg1245001	RGMB	Pax-5 [T0	71	77	8.014558	TCAGCC	2.19727	2.14502
cg1245001	RGMB	Pax-5 [T0	580	586	8.014558	TCTGCC	2.19727	2.14502
cg1245001	RGMB	Pax-5 [T0	882	888	8.014558	GAAGCC	2.19727	2.14502
cg1245001	RGMB	Pax-5 [T0	1125	1131	8.014558	GGGCAG	2.19727	2.14502
cg1245001	RGMB	TFIID [T0	155	161	8.014558	TTTGAG	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	604	610	8.014558	TATGAA	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1016	1022	8.014558	TTTGAG	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1051	1057	8.014558	TATGAA	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1350	1356	8.014558	TCTCAA	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1402	1408	8.014558	TATGAA	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1480	1486	8.014558	TTTGAT	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1498	1504	8.014558	TTTGAA	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1745	1751	8.014558	TAGGAA	2.19727	2.24348
cg1245001	RGMB	TFIID [T0	1993	1999	8.014558	TTGGAA	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	217	223	8.014558	TTTGCA	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	248	254	8.014558	TAGGAA	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	462	468	8.014558	TTTGTT	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	478	484	8.014558	TTTGAA	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	945	951	8.014558	TAAGAA	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	1131	1137	8.014558	TAACAA	2.19727	2.24348

cg0388534	RGMB	TFIID [T0	1314	1320	8.014558	TTTGTG	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	1568	1574	8.014558	TTTCCA	2.19727	2.24348
cg0388534	RGMB	TFIID [T0	1815	1821	8.014558	TTTGTA	2.19727	2.24348
cg0388534	RGMB	USF2 [T0	1466	1475	8.007902	AGAACA	0.01717	0.01695
cg0836780	RGMB	c-Myb [T0	1596	1603	8.005241	GGGAGT	0.21362	0.21454
cg1245001	RGMB	c-Myb [T0	688	695	8.005241	GGGAGT	0.21362	0.21454
cg1245001	RGMB	c-Myb [T0	1144	1151	8.005241	GGGAGT	0.21362	0.21454
cg1245001	RGMB	RelA [T00	1577	1587	8.005072	GCGGGA	0.02003	0.01979
cg0836780	RGMB	MEF-2A [	131	141	7.982343	TATTTTT	0.04005	0.04149
cg0836780	RGMB	MEF-2A [	1753	1763	7.982343	TATTTCT	0.04005	0.04149
cg1245001	RGMB	MEF-2A [	845	855	7.982343	TATTTCT	0.04005	0.04149
cg0388534	RGMB	HNF-1C [	968	976	7.864676	CTGAGT	0.19836	0.20224
cg0388534	RGMB	POU2F2 (	700	710	7.84518	TGGATT	0.01717	0.0176
cg0836780	RGMB	c-Ets-2 [T	190	198	7.84116	TTCTAG	0.32043	0.32298
cg0388534	RGMB	c-Ets-2 [T	952	960	7.84116	TTCCTA	0.32043	0.32298
cg0388534	RGMB	c-Ets-2 [T	1442	1450	7.84116	TTTCAG	0.32043	0.32298
cg0836780	RGMB	p53 [T006	10	16	7.833758	GGGCTC	0.48828	0.47377
cg0836780	RGMB	RXR-alph	367	373	7.815913	GCCACC	0.24414	0.24104
cg0836780	RGMB	GATA-2 [	939	947	7.777778	CCAGTA	0.30518	0.30758
cg1245001	RGMB	GATA-2 [	31	39	7.777778	CCAGTA	0.30518	0.30758
cg0388534	RGMB	GATA-2 [	1065	1073	7.777778	GCGGTA	0.30518	0.30758
cg1245001	RGMB	NF-AT1 [	1368	1376	7.744746	GGAAAG	0.19836	0.19941
cg0836780	RGMB	HNF-1B [	519	527	7.737819	TTTTTAA	0.09155	0.09368
cg0388534	RGMB	LEF-1 [T0	1798	1805	7.719635	GGTCAA	0.21362	0.21302
cg0836780	RGMB	AR [T000	762	770	7.623968	ATTGTG	0.25177	0.25079
cg0836780	RGMB	AR [T000	1010	1018	7.623968	GGACAA	0.25177	0.25079
cg1245001	RGMB	AR [T000	102	110	7.623968	GGACAA	0.25177	0.25079
cg0388534	RGMB	NFI/CTF [	635	642	7.587343	CCAAAA	0.36621	0.36674
cg0836780	RGMB	c-Jun [T00	460	466	7.538568	TGACAT	0.48828	0.48775
cg0836780	RGMB	GR [T050	266	272	7.527031	CAAACA	1.83105	1.86007
cg0836780	RGMB	GR [T050	492	498	7.527031	AGCTTT	1.83105	1.86007
cg0836780	RGMB	GR [T050	721	727	7.527031	CAAAAT	1.83105	1.86007
cg0836780	RGMB	GR [T050	1060	1066	7.527031	CCTTTT	1.83105	1.86007
cg0836780	RGMB	GR [T050	1676	1682	7.527031	CATTTT	1.83105	1.86007
cg0836780	RGMB	GR [T050	1892	1898	7.527031	CAAAGC	1.83105	1.86007
cg0836780	RGMB	GR [T050	1897	1903	7.527031	CAAAAG	1.83105	1.86007
cg0836780	RGMB	GR [T050	1916	1922	7.527031	CTGTTT	1.83105	1.86007
cg1245001	RGMB	GR [T050	152	158	7.527031	CCTTTT	1.83105	1.86007
cg1245001	RGMB	GR [T050	768	774	7.527031	CATTTT	1.83105	1.86007
cg1245001	RGMB	GR [T050	984	990	7.527031	CAAAGC	1.83105	1.86007
cg1245001	RGMB	GR [T050	989	995	7.527031	CAAAAG	1.83105	1.86007
cg1245001	RGMB	GR [T050	1008	1014	7.527031	CTGTTT	1.83105	1.86007
cg1245001	RGMB	GR [T050	1199	1205	7.527031	CAAAAT	1.83105	1.86007
cg1245001	RGMB	GR [T050	1495	1501	7.527031	CTATTT	1.83105	1.86007
cg1245001	RGMB	GR [T050	1556	1562	7.527031	CAAATA	1.83105	1.86007
cg1245001	RGMB	GR [T050	1891	1897	7.527031	CAAAAT	1.83105	1.86007
cg1245001	RGMB	GR [T050	1907	1913	7.527031	CCTTTT	1.83105	1.86007
cg1245001	RGMB	GR [T050	1979	1985	7.527031	TTATTT	1.83105	1.86007

cg1245001	RGMB	GR [T0507	1989	1995	7.527031	TGCTTTC	1.83105	1.86007
cg0388534	RGMB	GR [T0507	342	348	7.527031	CAAACA	1.83105	1.86007
cg0388534	RGMB	GR [T0507	378	384	7.527031	TGCTTTC	1.83105	1.86007
cg0388534	RGMB	GR [T0507	494	500	7.527031	ATGTTTC	1.83105	1.86007
cg0388534	RGMB	GR [T0507	636	642	7.527031	CAAAAG	1.83105	1.86007
cg0388534	RGMB	GR [T0507	832	838	7.527031	CAAAAT	1.83105	1.86007
cg0388534	RGMB	GR [T0507	1039	1045	7.527031	CTGTTTC	1.83105	1.86007
cg0836780	RGMB	RAR-beta	1121	1130	7.47824	AGGGAA	0.24414	0.24343
cg1245001	RGMB	RAR-beta	213	222	7.47824	AGGGAA	0.24414	0.24343
cg1245001	RGMB	C/EBPalph	1736	1742	7.465744	CATTGC	0.48828	0.49653
cg0388534	RGMB	C/EBPalph	219	225	7.465744	TGCAAT	0.48828	0.49653
cg0388534	RGMB	C/EBPalph	1263	1269	7.465744	CATTGA	0.48828	0.49653
cg0388534	RGMB	HNF-1B [	359	367	7.4296	TCCTTA	0.09155	0.09368
cg0388534	RGMB	PEA3 [T0	794	802	7.421728	AGGCAT	0.34332	0.34161
cg0388534	RGMB	PEA3 [T0	1529	1537	7.421728	GCCCAT	0.34332	0.34161
cg0836780	RGMB	C/EBPalph	824	830	7.396431	AATTGG	0.48828	0.49653
cg0388534	RGMB	C/EBPalph	1136	1142	7.396431	AATTGG	0.48828	0.49653
cg0836780	RGMB	IRF-1 [T0	448	456	7.387351	GGGGGG	0.14496	0.14449
cg0388534	RGMB	IRF-1 [T0	1043	1051	7.387351	TTGGGG	0.14496	0.14449
cg0836780	RGMB	PXR-1:RX	1397	1404	7.362674	CATGTT	0.24414	0.24395
cg1245001	RGMB	PXR-1:RX	489	496	7.362674	CATGTT	0.24414	0.24395
cg0388534	RGMB	E2F-1 [T0	1504	1511	7.336545	GCGGCA	0.45776	0.44878
cg0388534	RGMB	E2F-1 [T0	1655	1662	7.336545	CCTGCC	0.45776	0.44878
cg0388534	RGMB	E2F-1 [T0	1883	1890	7.336545	GCGGAA	0.45776	0.44878
cg0836780	RGMB	HNF-1C [	1401	1409	7.313515	TTCAGT	0.08392	0.08549
cg1245001	RGMB	HNF-1C [	493	501	7.313515	TTCAGT	0.08392	0.08549
cg0388534	RGMB	IRF-1 [T0	324	332	7.299819	GAGTGG	0.14496	0.14449
cg0388534	RGMB	NF-AT1 [	328	336	7.278086	GGAAAG	0.19836	0.19941
cg0388534	RGMB	c-Ets-1 [T	1498	1504	7.257837	ATTCCG	0.48828	0.4878
cg0836780	RGMB	c-Ets-1 [T	792	798	7.199436	TTTCCC	0.73242	0.73099
cg1245001	RGMB	c-Ets-1 [T	1880	1886	7.199436	TTTCCC	0.73242	0.73099
cg0836780	RGMB	SRY [T00	850	858	7.175614	CTTTGC	0.30518	0.30739
cg0388534	RGMB	SRY [T00	380	388	7.175614	CTTTGA	0.30518	0.30739
cg0388534	RGMB	SRY [T00	477	485	7.175614	CTTTGA	0.30518	0.30739
cg0836780	RGMB	XBP-1 [T	503	508	7.172312	ATGATG	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	582	587	7.172312	ATGATT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	946	951	7.172312	CTTCAT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	956	961	7.172312	CCTCAT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1247	1252	7.172312	CCTCAT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1347	1352	7.172312	ATTCAT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1359	1364	7.172312	ATGATG	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1611	1616	7.172312	ACTCAT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1620	1625	7.172312	CTTCAT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1737	1742	7.172312	ATTCAT	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1741	1746	7.172312	ATGAAG	2.92969	2.97018
cg0836780	RGMB	XBP-1 [T	1854	1859	7.172312	CATCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	38	43	7.172312	CTTCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	48	53	7.172312	CCTCAT	2.92969	2.97018

cg1245001	RGMB	XBP-1 [T	339	344	7.172312	CCTCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	439	444	7.172312	ATTCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	451	456	7.172312	ATGATG	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	703	708	7.172312	ACTCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	712	717	7.172312	CTTCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	829	834	7.172312	ATTCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	833	838	7.172312	ATGAAG	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	946	951	7.172312	CATCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	1621	1626	7.172312	CTTCAT	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	1819	1824	7.172312	ATGATG	2.92969	2.97018
cg1245001	RGMB	XBP-1 [T	1836	1841	7.172312	ATGATT	2.92969	2.97018
cg0388534	RGMB	XBP-1 [T	171	176	7.172312	ATGAAG	2.92969	2.97018
cg0388534	RGMB	XBP-1 [T	308	313	7.172312	AATCAT	2.92969	2.97018
cg0388534	RGMB	XBP-1 [T	551	556	7.172312	ATGAAG	2.92969	2.97018
cg0388534	RGMB	XBP-1 [T	744	749	7.172312	CATCAT	2.92969	2.97018
cg0388534	RGMB	XBP-1 [T	801	806	7.172312	CTTCAT	2.92969	2.97018
cg0388534	RGMB	XBP-1 [T	1769	1774	7.172312	ATGAAT	2.92969	2.97018
cg0836780	RGMB	HNF-1B [	599	607	7.148274	TTAGTA	0.07629	0.07762
cg0836780	RGMB	c-Myb [T0	1406	1413	7.127234	TAACTG	0.18311	0.18399
cg1245001	RGMB	c-Myb [T0	498	505	7.127234	TAACTG	0.18311	0.18399
cg1245001	RGMB	Ik-1 [T027	1234	1246	7.122895	TCCCAG	0.01064	0.01049
cg0836780	RGMB	c-Jun [T00	1940	1946	7.096776	GCAGTC	0.73242	0.73173
cg1245001	RGMB	c-Jun [T00	1032	1038	7.096776	GCAGTC	0.73242	0.73173
cg0836780	RGMB	NF-AT1 [	285	293	7.095752	TTCTTTT	0.15259	0.1548
cg0836780	RGMB	TFIID [T0	416	422	7.082373	TGCTAA	0.12207	0.12407
cg0836780	RGMB	TFIID [T0	1392	1398	7.082373	TTTAGC	0.12207	0.12407
cg1245001	RGMB	TFIID [T0	484	490	7.082373	TTTAGC	0.12207	0.12407
cg1245001	RGMB	NF-AT1 [	1747	1755	7.072017	GGAAAT	0.15259	0.1548
cg0836780	RGMB	c-Ets-1 [T	537	543	7.071349	AGGGAA	0.73242	0.73099
cg0836780	RGMB	c-Ets-1 [T	1967	1973	7.071349	AGGGAA	0.73242	0.73099
cg1245001	RGMB	c-Ets-1 [T	1059	1065	7.071349	AGGGAA	0.73242	0.73099
cg0388534	RGMB	c-Ets-1 [T	1450	1456	7.071349	AGGGAA	0.73242	0.73099
cg1245001	RGMB	c-Jun [T00	1492	1498	7.052189	TGACTA	0.73242	0.73173
cg0388534	RGMB	IRF-1 [T0	60	68	7.044985	TTTCCTC	0.1297	0.13036
cg1245001	RGMB	NFI/CTF [	1138	1145	7.014249	GAGGTT	0.73242	0.73214
cg0836780	RGMB	C/EBPalph	1665	1671	7.00174	CATTGT	0.73242	0.74337
cg1245001	RGMB	C/EBPalph	757	763	7.00174	CATTGT	0.73242	0.74337
cg0836780	RGMB	HNF-3alph	131	138	7.000129	TATTTTT	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	158	165	7.000129	TGAAAA	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	214	221	7.000129	AATTTTT	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	419	426	7.000129	TAAAAA	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	699	706	7.000129	GAAAAA	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	1452	1459	7.000129	CAAAAA	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	1676	1683	7.000129	CATTTT	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	1732	1739	7.000129	TATAAA	0.82397	0.84946
cg0836780	RGMB	HNF-3alph	1807	1814	7.000129	TGAAAA	0.82397	0.84946
cg1245001	RGMB	HNF-3alph	544	551	7.000129	CAAAAA	0.82397	0.84946
cg1245001	RGMB	HNF-3alph	768	775	7.000129	CATTTT	0.82397	0.84946

cg1245001	RGMB	HNF-3alp	824	831	7.000129	TATAAA	0.82397	0.84946
cg1245001	RGMB	HNF-3alp	899	906	7.000129	TGAAAA	0.82397	0.84946
cg1245001	RGMB	HNF-3alp	1198	1205	7.000129	ACAAAA	0.82397	0.84946
cg1245001	RGMB	HNF-3alp	1422	1429	7.000129	TCTAAA	0.82397	0.84946
cg1245001	RGMB	HNF-3alp	1646	1653	7.000129	TATTTA	0.82397	0.84946
cg1245001	RGMB	HNF-3alp	1963	1970	7.000129	GAAAAA	0.82397	0.84946
cg0388534	RGMB	HNF-3alp	480	487	7.000129	TGAAAA	0.82397	0.84946
cg0388534	RGMB	HNF-3alp	611	618	7.000129	TAAAAA	0.82397	0.84946
cg0388534	RGMB	HNF-3alp	831	838	7.000129	TCAAAA	0.82397	0.84946
cg0388534	RGMB	GCF [T00	1656	1664	6.987525	CTGCCG	0.45776	0.44706
cg0388534	RGMB	GCF [T00	1926	1934	6.987525	ATGCGG	0.45776	0.44706
cg0388534	RGMB	E2F-1 [T0	1987	1994	6.967231	GCGGGG	0.30518	0.29782
cg0836780	RGMB	c-Myb [T0	357	364	6.958029	GAACTT	0.18311	0.18399
cg0388534	RGMB	c-Ets-1 [T	1615	1621	6.949623	TCGGAA	0.73242	0.73099
cg0388534	RGMB	NF-1 [T00	332	339	6.948522	AGACCC	0.48828	0.4856
cg0836780	RGMB	c-Ets-1 [T	450	456	6.943262	GGGGAA	0.73242	0.73099
cg0388534	RGMB	c-Ets-1 [T	1045	1051	6.943262	GGGGAA	0.73242	0.73099
cg0836780	RGMB	ENKTF-1	363	370	6.942764	CGATGC	1.46484	1.44228
cg0836780	RGMB	ENKTF-1	1886	1893	6.942764	CTTAGC	1.46484	1.44228
cg1245001	RGMB	ENKTF-1	978	985	6.942764	CTTAGC	1.46484	1.44228
cg1245001	RGMB	ENKTF-1	1218	1225	6.942764	TGGCGC	1.46484	1.44228
cg1245001	RGMB	ENKTF-1	1306	1313	6.942764	TCGCGC	1.46484	1.44228
cg0836780	RGMB	HNF-1B [	1041	1049	6.912308	TGTTAA	0.07629	0.07762
cg0836780	RGMB	HNF-1B [	1306	1314	6.912308	TGTTAA	0.07629	0.07762
cg1245001	RGMB	HNF-1B [	133	141	6.912308	TGTTAA	0.07629	0.07762
cg1245001	RGMB	HNF-1B [	398	406	6.912308	TGTTAA	0.07629	0.07762
cg0388534	RGMB	p53 [T006	1063	1069	6.891821	GGGCGG	1.09863	1.07125
cg0388534	RGMB	p53 [T006	1576	1582	6.891821	ACCGCC	1.09863	1.07125
cg0388534	RGMB	MAZ [T00	1725	1737	6.888955	GGCAGG	0.00918	0.00907
cg1245001	RGMB	c-Jun [T00	1162	1168	6.856451	TGACCA	0.73242	0.73173
cg0836780	RGMB	C/EBPalp	594	600	6.85549	TTCAAT	0.73242	0.74337
cg0836780	RGMB	C/EBPalp	1569	1575	6.85549	TGCAAT	0.73242	0.74337
cg1245001	RGMB	C/EBPalp	661	667	6.85549	TGCAAT	0.73242	0.74337
cg0388534	RGMB	C/EBPalp	558	564	6.85549	AATTGC	0.73242	0.74337
cg0388534	RGMB	E2F-1 [T0	1624	1631	6.839754	GGTTCC	0.30518	0.29782
cg0388534	RGMB	c-Ets-1 [T	195	201	6.821536	GTTCCG	0.73242	0.73099
cg0836780	RGMB	c-Jun [T00	26	32	6.787369	TGACAG	0.73242	0.73173
cg0836780	RGMB	c-Jun [T00	818	824	6.787369	TGACAG	0.73242	0.73173
cg0836780	RGMB	C/EBPalp	1588	1594	6.786177	TCCAAT	0.73242	0.74337
cg1245001	RGMB	C/EBPalp	680	686	6.786177	TCCAAT	0.73242	0.74337
cg0836780	RGMB	NFI/CTF [	778	785	6.786076	CTGCTT	0.73242	0.73214
cg0388534	RGMB	NFI/CTF [	336	343	6.786076	CCAAAC	0.73242	0.73214
cg0388534	RGMB	NFI/CTF [	341	348	6.786076	CCAAAC	0.73242	0.73214
cg0388534	RGMB	NFI/CTF [	818	825	6.786076	TGGTTT	0.73242	0.73214
cg0388534	RGMB	NFI/CTF [	1039	1046	6.786076	CTGTTT	0.73242	0.73214
cg0388534	RGMB	RXR-alph	1516	1522	6.785809	GGGTAC	0.36621	0.36214
cg0836780	RGMB	AR [T000	304	312	6.760234	TTTTTGT	0.23651	0.23551
cg0836780	RGMB	AR [T000	705	713	6.760234	TATGTG	0.23651	0.23551

cg0836780	RGMB	ATF3 [T0	962	969	6.744803	TTAAGT	0.27466	0.27656
cg1245001	RGMB	ATF3 [T0	54	61	6.744803	TTAAGT	0.27466	0.27656
cg0388534	RGMB	ATF3 [T0	738	745	6.744803	TTAAGT	0.27466	0.27656
cg0836780	RGMB	POU2F2 (	959	969	6.735173	CATTTA	0.04292	0.04408
cg1245001	RGMB	POU2F2 (	51	61	6.735173	CATTTA	0.04292	0.04408
cg0388534	RGMB	NF-1 [T00	822	829	6.722386	TTGGGC	0.24414	0.24147
cg0388534	RGMB	IRF-1 [T0	179	187	6.699483	TTTCCT	0.19073	0.19127
cg0388534	RGMB	c-Ets-2 [T	19	27	6.695187	AAATAG	0.09155	0.09289
cg0388534	RGMB	c-Ets-2 [T	245	253	6.695187	TGATAG	0.09155	0.09289
cg0388534	RGMB	c-Ets-1 [T	1625	1631	6.693449	GTTCCG	0.48828	0.48798
cg0388534	RGMB	GATA-2 [	536	544	6.666667	ACTGTA	0.24414	0.24583
cg0388534	RGMB	IRF-1 [T0	246	254	6.625948	GATAGG	0.19073	0.19127
cg1245001	RGMB	RelA [T00	1877	1887	6.6175	GGATTT	0.01001	0.00989
cg0836780	RGMB	TFII-I [T0	686	691	6.581441	GGAGTG	0.97656	0.97366
cg0836780	RGMB	TFII-I [T0	1022	1027	6.581441	GGAGTG	0.97656	0.97366
cg0836780	RGMB	TFII-I [T0	1910	1915	6.581441	GGAGAT	0.97656	0.97366
cg0836780	RGMB	FOXP3 [T	233	238	6.581441	GTTGAA	0.97656	0.99397
cg0836780	RGMB	FOXP3 [T	574	579	6.581441	GTTTTA	0.97656	0.99397
cg0836780	RGMB	FOXP3 [T	1170	1175	6.581441	GTTTTA	0.97656	0.99397
cg0836780	RGMB	FOXP3 [T	1480	1485	6.581441	GTTTTA	0.97656	0.99397
cg1245001	RGMB	TFII-I [T0	114	119	6.581441	GGAGTG	0.97656	0.97366
cg1245001	RGMB	TFII-I [T0	1002	1007	6.581441	GGAGAT	0.97656	0.97366
cg1245001	RGMB	FOXP3 [T	262	267	6.581441	GTTTTA	0.97656	0.99397
cg1245001	RGMB	FOXP3 [T	572	577	6.581441	GTTTTA	0.97656	0.99397
cg1245001	RGMB	FOXP3 [T	1831	1836	6.581441	GTTTTA	0.97656	0.99397
cg0388534	RGMB	FOXP3 [T	1405	1410	6.581441	GTTGAA	0.97656	0.99397
cg0836780	RGMB	RXR-alph	0	6	6.563693	GGGTGT	0.24414	0.2434
cg0836780	RGMB	RXR-alph	903	909	6.563693	GGGTGT	0.24414	0.2434
cg0388534	RGMB	RXR-alph	1599	1605	6.563693	GACACC	0.24414	0.2434
cg0836780	RGMB	p53 [T006	1790	1796	6.563521	GAAGCC	0.48828	0.47541
cg1245001	RGMB	p53 [T006	882	888	6.563521	GAAGCC	0.48828	0.47541
cg0388534	RGMB	NF-AT1 [	1210	1218	6.562181	TCTTTTT	0.03815	0.03835
cg0836780	RGMB	PXR-1:RX	910	917	6.5446	TTCGTT	0.24414	0.24672
cg1245001	RGMB	PXR-1:RX	2	9	6.5446	TTCGTT	0.24414	0.24672
cg0836780	RGMB	IRF-1 [T0	646	654	6.497844	ACGTGG	0.19073	0.19127
cg0836780	RGMB	XBP-1 [T	365	370	6.478682	ATGCCA	0.97656	0.97062
cg0836780	RGMB	XBP-1 [T	1098	1103	6.478682	ATGCCC	0.97656	0.97062
cg0836780	RGMB	XBP-1 [T	1673	1678	6.478682	TGGCAT	0.97656	0.97062
cg1245001	RGMB	XBP-1 [T	190	195	6.478682	ATGCCC	0.97656	0.97062
cg1245001	RGMB	XBP-1 [T	765	770	6.478682	TGGCAT	0.97656	0.97062
cg0388534	RGMB	XBP-1 [T	1347	1352	6.478682	TGGCAT	0.97656	0.97062
cg0836780	RGMB	c-Myb [T0	373	380	6.454077	CAACTG	0.30518	0.3056
cg0388534	RGMB	c-Myb [T0	655	662	6.454077	CAACTG	0.30518	0.3056
cg1245001	RGMB	c-Ets-1 [T	1993	1999	6.423689	TTGGAA	0.48828	0.48798
cg0388534	RGMB	c-Ets-1 [T	1568	1574	6.423689	TTTCCA	0.48828	0.48798
cg0388534	RGMB	p53 [T006	1845	1851	6.400205	GTCGCC	0.48828	0.47541
cg0836780	RGMB	C/EBPalp	530	536	6.391486	GACAAT	0.48828	0.49071
cg0388534	RGMB	C/EBPalp	1202	1208	6.391486	GACAAT	0.48828	0.49071

cg0388534	RGMB	C/EBPalp	1205	1211	6.391486	AATTGT	0.48828	0.49071
cg1245001	RGMB	RAR-beta	1173	1182	6.378264	GAGAAA	0.18311	0.183
cg0836780	RGMB	TCF-4E [T	484	490	6.302385	CTTTGC	0.61035	0.61344
cg0836780	RGMB	TCF-4E [T	1075	1081	6.302385	CTTTGA	0.61035	0.61344
cg0836780	RGMB	TCF-4E [T	1712	1718	6.302385	GGCAAA	0.61035	0.61344
cg1245001	RGMB	TCF-4E [T	167	173	6.302385	CTTTGA	0.61035	0.61344
cg1245001	RGMB	TCF-4E [T	804	810	6.302385	GGCAAA	0.61035	0.61344
cg1245001	RGMB	TCF-4E [T	1868	1874	6.302385	CTTTGC	0.61035	0.61344
cg0388534	RGMB	TCF-4E [T	380	386	6.302385	CTTTGA	0.61035	0.61344
cg0388534	RGMB	TCF-4E [T	461	467	6.302385	CTTTGTT	0.61035	0.61344
cg0388534	RGMB	TCF-4E [T	477	483	6.302385	CTTTGA	0.61035	0.61344
cg0388534	RGMB	TCF-4E [T	1052	1058	6.302385	GGCAAA	0.61035	0.61344
cg0836780	RGMB	c-Ets-1 [T	741	747	6.295602	ATGGAA	0.48828	0.48798
cg1245001	RGMB	c-Ets-1 [T	1465	1471	6.295602	TTTCCAT	0.48828	0.48798
cg0836780	RGMB	c-Jun [T00	239	245	6.293948	AGGGTC	0.61035	0.60769
cg0836780	RGMB	GR-alpha [	18	22	6.263098	TGAGG	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	73	77	6.263098	TGAGG	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	229	233	6.263098	TAAGG	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	467	471	6.263098	TGAGG	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	614	618	6.263098	CCTTA	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	956	960	6.263098	CCTCA	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	1119	1123	6.263098	TAAGG	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	1185	1189	6.263098	CCTTA	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	1197	1201	6.263098	CCTCA	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	1247	1251	6.263098	CCTCA	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	1330	1334	6.263098	TGAGG	3.90625	3.91061
cg0836780	RGMB	GR-alpha [	1885	1889	6.263098	CCTTA	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	48	52	6.263098	CCTCA	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	211	215	6.263098	TAAGG	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	277	281	6.263098	CCTTA	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	289	293	6.263098	CCTCA	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	339	343	6.263098	CCTCA	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	422	426	6.263098	TGAGG	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	977	981	6.263098	CCTTA	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	1119	1123	6.263098	TGAGG	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	1137	1141	6.263098	TGAGG	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	1253	1257	6.263098	TGAGG	3.90625	3.91061
cg1245001	RGMB	GR-alpha [	1792	1796	6.263098	TGAGG	3.90625	3.91061
cg0388534	RGMB	GR-alpha [	161	165	6.263098	CCTTA	3.90625	3.91061
cg0388534	RGMB	GR-alpha [	360	364	6.263098	CCTTA	3.90625	3.91061
cg0388534	RGMB	GR-alpha [	736	740	6.263098	CCTTA	3.90625	3.91061
cg0388534	RGMB	GR-alpha [	876	880	6.263098	CCTCA	3.90625	3.91061
cg0388534	RGMB	GR-alpha [	1089	1093	6.263098	TGAGG	3.90625	3.91061
cg0388534	RGMB	GR-alpha [	1217	1221	6.263098	CCTCA	3.90625	3.91061
cg0388534	RGMB	GR-alpha [	1604	1608	6.263098	CCTCA	3.90625	3.91061
cg1245001	RGMB	c-Myb [T0	1739	1746	6.259888	TGCAGT	0.30518	0.3056
cg0388534	RGMB	c-Myb [T0	1160	1167	6.259888	TAACTG	0.30518	0.3056
cg1245001	RGMB	C/EBPalp	1693	1699	6.245236	TGCAAT	0.97656	0.99

cg1245001	RGMB	NF-AT1 [	1461	1470	6.201624	TGCATT	0.03815	0.03846
cg0388534	RGMB	p53 [T006	233	239	6.188498	GACGCC	0.61035	0.594
cg083678	RGMB	c-Ets-1 [T	648	654	6.167515	GTGGAA	0.36621	0.36731
cg0388534	RGMB	c-Ets-1 [T	326	332	6.167515	GTGGAA	0.36621	0.36731
cg0388534	RGMB	c-Ets-1 [T	1287	1293	6.167515	GTGGAA	0.36621	0.36731
cg0388534	RGMB	AP-1 [T00	224	232	6.13358	TGACTC	0.09155	0.09072
cg0388534	RGMB	NF-AT2 [	1869	1878	6.128234	GGAAAC	0.04196	0.04255
cg1245001	RGMB	c-Myb [T0	1568	1575	6.12608	GCAAGT	0.21362	0.21535
cg1245001	RGMB	p53 [T006	1637	1643	6.095267	TTGGCC	0.61035	0.594
cg083678	RGMB	GR-alpha	354	358	6.055408	CCTGA	3.90625	3.9065
cg083678	RGMB	GR-alpha	425	429	6.055408	TCAGG	3.90625	3.9065
cg083678	RGMB	GR-alpha	535	539	6.055408	TTAGG	3.90625	3.9065
cg083678	RGMB	GR-alpha	577	581	6.055408	TTAGG	3.90625	3.9065
cg083678	RGMB	GR-alpha	606	610	6.055408	CCTAA	3.90625	3.9065
cg083678	RGMB	GR-alpha	683	687	6.055408	TCAGG	3.90625	3.9065
cg083678	RGMB	GR-alpha	839	843	6.055408	CCTGA	3.90625	3.9065
cg083678	RGMB	GR-alpha	1576	1580	6.055408	CCTGA	3.90625	3.9065
cg083678	RGMB	GR-alpha	1977	1981	6.055408	TTAGG	3.90625	3.9065
cg1245001	RGMB	GR-alpha	668	672	6.055408	CCTGA	3.90625	3.9065
cg1245001	RGMB	GR-alpha	1069	1073	6.055408	TTAGG	3.90625	3.9065
cg1245001	RGMB	GR-alpha	1135	1139	6.055408	CCTGA	3.90625	3.9065
cg1245001	RGMB	GR-alpha	1160	1164	6.055408	CCTGA	3.90625	3.9065
cg1245001	RGMB	GR-alpha	1744	1748	6.055408	TTAGG	3.90625	3.9065
cg0388534	RGMB	GR-alpha	106	110	6.055408	TTAGG	3.90625	3.9065
cg0388534	RGMB	GR-alpha	806	810	6.055408	TTAGG	3.90625	3.9065
cg0388534	RGMB	GR-alpha	954	958	6.055408	CCTAA	3.90625	3.9065
cg0388534	RGMB	GR-alpha	1444	1448	6.055408	TCAGG	3.90625	3.9065
cg0388534	RGMB	GR-alpha	1472	1476	6.055408	CCTGA	3.90625	3.9065
cg083678	RGMB	c-Myb [T0	1314	1321	6.04018	AAACTG	0.21362	0.21535
cg1245001	RGMB	c-Myb [T0	406	413	6.04018	AAACTG	0.21362	0.21535
cg083678	RGMB	C/EBPalp	986	992	5.996794	AACAAT	0.97656	0.99
cg1245001	RGMB	C/EBPalp	78	84	5.996794	AACAAT	0.97656	0.99
cg0388534	RGMB	RXR-alph	1554	1560	5.937582	GGGTGA	0.73242	0.72249
cg0388534	RGMB	RXR-alph	1734	1740	5.937582	GGGTAA	0.73242	0.72249
cg083678	RGMB	GCF [T00	1986	1994	5.917256	GCGCTG	0.64087	0.6219
cg1245001	RGMB	GCF [T00	1078	1086	5.917256	GCGCTG	0.64087	0.6219
cg0388534	RGMB	HOXD9 [	585	594	5.898575	AATAAT	0.05722	0.0598
cg0388534	RGMB	HOXD10	585	594	5.898575	AATAAT	0.05722	0.0598
cg083678	RGMB	STAT4 [T	292	297	5.882353	CCTTCC	0.48828	0.48408
cg1245001	RGMB	STAT4 [T	1396	1401	5.882353	GGAAGG	0.48828	0.48408
cg1245001	RGMB	STAT4 [T	1796	1801	5.882353	GGAAGG	0.48828	0.48408
cg0388534	RGMB	STAT4 [T	1447	1452	5.882353	GGAAGG	0.48828	0.48408
cg0388534	RGMB	STAT4 [T	1521	1526	5.882353	CCTTCC	0.48828	0.48408
cg0388534	RGMB	STAT4 [T	1885	1890	5.882353	GGAAGG	0.48828	0.48408
cg0388534	RGMB	STAT4 [T	1901	1906	5.882353	GGAAGG	0.48828	0.48408
cg0388534	RGMB	C/EBPalp	825	831	5.850545	GGCAAT	0.97656	0.99
cg0388534	RGMB	E2F-1 [T0	1434	1441	5.846171	CTTGCC	0.18311	0.18044
cg0388534	RGMB	HNF-1C [	358	366	5.821046	ATCCTT	0.14496	0.14811

cg0388534	RGMB	c-Ets-1 [T	1522	1528	5.814485	CTTCCC	0.36621	0.36731
cg0388534	RGMB	AR [T000	1958	1966	5.811663	GGACAG	0.24414	0.24229
cg0388534	RGMB	c-Jun [T00	316	322	5.783074	AAAGTC	0.36621	0.37082
cg0388534	RGMB	c-Jun [T00	638	644	5.783074	AAAGTC	0.36621	0.37082
cg1245001	RGMB	NF-AT1 [	1435	1443	5.77403	TTTCTTT	0.06866	0.06922
cg0836780	RGMB	NF-AT2 [	1969	1978	5.75046	GGAAAG	0.04196	0.04255
cg1245001	RGMB	NF-AT2 [	1061	1070	5.75046	GGAAAG	0.04196	0.04255
cg0836780	RGMB	p53 [T006	1837	1843	5.720243	TTAGCC	0.61035	0.59991
cg1245001	RGMB	p53 [T006	929	935	5.720243	TTAGCC	0.61035	0.59991
cg0836780	RGMB	HNF-1C [	1042	1050	5.695506	GTTAAA	0.07629	0.07817
cg0836780	RGMB	HNF-1C [	1307	1315	5.695506	GTTAAA	0.07629	0.07817
cg1245001	RGMB	HNF-1C [	134	142	5.695506	GTTAAA	0.07629	0.07817
cg1245001	RGMB	HNF-1C [	399	407	5.695506	GTTAAA	0.07629	0.07817
cg0388534	RGMB	ENKTF-1	1716	1723	5.687009	CAGGGC	0.73242	0.7249
cg0836780	RGMB	c-Ets-1 [T	89	95	5.686398	AGGGAA	0.36621	0.3623
cg1245001	RGMB	c-Ets-1 [T	1794	1800	5.686398	AGGGAA	0.36621	0.3623
cg0388534	RGMB	c-Ets-1 [T	1762	1768	5.686398	AGGGAA	0.36621	0.3623
cg0836780	RGMB	T3R-beta1	1324	1332	5.591999	GAATGG	0.21362	0.21287
cg1245001	RGMB	T3R-beta1	416	424	5.591999	GAATGG	0.21362	0.21287
cg0836780	RGMB	c-Jun [T00	625	631	5.590308	AGTGTC	0.48828	0.48665
cg0388534	RGMB	c-Jun [T00	4	10	5.587335	TGACCT	0.48828	0.48665
cg0836780	RGMB	AP-2alpha	1702	1707	5.568965	GCCTAT	0.48828	0.4878
cg1245001	RGMB	AP-2alpha	794	799	5.568965	GCCTAT	0.48828	0.4878
cg1245001	RGMB	AP-2alpha	1559	1564	5.568965	ATAGGC	0.48828	0.4878
cg0388534	RGMB	AP-2alpha	792	797	5.568965	ATAGGC	0.48828	0.4878
cg1245001	RGMB	IRF-1 [T0	1465	1473	5.564062	TTTCCAT	0.22888	0.23087
cg1245001	RGMB	NFI/CTF [	1378	1385	5.558661	AGGTTT	0.54932	0.55038
cg0388534	RGMB	NFI/CTF [	695	702	5.558661	AGGCTT	0.54932	0.55038
cg0388534	RGMB	NFI/CTF [	1636	1643	5.558661	GTGATT	0.54932	0.55038
cg0836780	RGMB	c-Ets-1 [T	61	67	5.558311	CTTCCC	0.36621	0.3623
cg0388534	RGMB	c-Ets-1 [T	1899	1905	5.558311	GGGGAA	0.36621	0.3623
cg0388534	RGMB	T3R-beta1	1551	1559	5.553412	CGCGGG	0.21362	0.21287
cg0836780	RGMB	Pax-5 [T0	1984	1990	5.544826	GGGCGC	0.73242	0.72046
cg0836780	RGMB	TFIID [T0	521	527	5.544826	TTTAAC	0.73242	0.75085
cg0836780	RGMB	TFIID [T0	576	582	5.544826	TTTAGG	0.73242	0.75085
cg0836780	RGMB	TFIID [T0	668	674	5.544826	TGTTAA	0.73242	0.75085
cg0836780	RGMB	TFIID [T0	891	897	5.544826	TTTAGA	0.73242	0.75085
cg0836780	RGMB	TFIID [T0	1041	1047	5.544826	TGTTAA	0.73242	0.75085
cg0836780	RGMB	TFIID [T0	1306	1312	5.544826	TGTTAA	0.73242	0.75085
cg1245001	RGMB	Pax-5 [T0	1076	1082	5.544826	GGGCGC	0.73242	0.72046
cg1245001	RGMB	TFIID [T0	133	139	5.544826	TGTTAA	0.73242	0.75085
cg1245001	RGMB	TFIID [T0	398	404	5.544826	TGTTAA	0.73242	0.75085
cg1245001	RGMB	TFIID [T0	1188	1194	5.544826	TACTAA	0.73242	0.75085
cg0388534	RGMB	Pax-5 [T0	824	830	5.544826	GGGCAA	0.73242	0.72046
cg0388534	RGMB	Pax-5 [T0	1063	1069	5.544826	GGGCGG	0.73242	0.72046
cg0388534	RGMB	Pax-5 [T0	1576	1582	5.544826	ACCGCC	0.73242	0.72046
cg0388534	RGMB	TFIID [T0	1592	1598	5.544826	TTTACC	0.73242	0.75085
cg0836780	RGMB	p53 [T006	979	985	5.508538	TCAGCC	0.61035	0.59991

cg1245001	RGMB	p53 [T006	71	77	5.508538	TCAGCC(	0.61035	0.59991
cg0836780	RGMB	NF-AT2 [T	452	461	5.474728	GGAAAA	0.01144	0.01156
cg0836780	RGMB	NF-AT2 [T	743	752	5.474728	GGAAAT	0.01144	0.01156
cg0388534	RGMB	HNF-1A [	440	447	5.466509	GTTAAG	0.24414	0.2469
cg0388534	RGMB	C/EBPalph	893	899	5.455853	CATTGA	0.73242	0.74391
cg0836780	RGMB	HOXD9 [T	1253	1262	5.453039	TTCTTTT	0.04578	0.04743
cg0836780	RGMB	HOXD10 [	1253	1262	5.453039	TTCTTTT	0.04578	0.04743
cg1245001	RGMB	HOXD9 [T	345	354	5.453039	TTCTTTT	0.04578	0.04743
cg1245001	RGMB	HOXD10 [	345	354	5.453039	TTCTTTT	0.04578	0.04743
cg1245001	RGMB	c-Ets-1 [T(	1578	1584	5.430224	CGGGAA	0.36621	0.3623
cg0836780	RGMB	USF1 [T0(	1291	1300	5.418177	CACGTG	0.04578	0.04535
cg1245001	RGMB	USF1 [T0(	383	392	5.418177	CACGTG	0.04578	0.04535
cg0836780	RGMB	HNF-1B [	1402	1410	5.394512	TCAGTA	0.03052	0.03111
cg1245001	RGMB	HNF-1B [	494	502	5.394512	TCAGTA	0.03052	0.03111
cg0388534	RGMB	C/EBPalph	101	107	5.38654	AATTGT	0.73242	0.74391
cg0836780	RGMB	NF-1 [T00	980	987	5.377909	CAGCCC	0.24414	0.24258
cg1245001	RGMB	NF-1 [T00	72	79	5.377909	CAGCCC	0.24414	0.24258
cg0836780	RGMB	NF-AT1 [T	743	751	5.354841	GGAAAT	0.03815	0.03856
cg0836780	RGMB	IRF-1 [T0(	792	800	5.351774	TTTCCCA	0.22888	0.23087
cg1245001	RGMB	IRF-1 [T0(	1880	1888	5.351774	TTTCCCA	0.22888	0.23087
cg0836780	RGMB	HNF-1C [	518	526	5.345227	CTTTTTA	0.07629	0.07817
cg1245001	RGMB	MEF-2A [	1960	1970	5.321562	AGTGAA	0.02003	0.02072
cg0836780	RGMB	IRF-1 [T0(	289	297	5.309227	TTTCCTT	0.22888	0.23087
cg0388534	RGMB	IRF-1 [T0(	1901	1909	5.309227	GGAAGG	0.22888	0.23087
cg0836780	RGMB	HOXD9 [T	553	562	5.275652	AATAAA	0.04578	0.04743
cg0836780	RGMB	HOXD10 [	553	562	5.275652	AATAAA	0.04578	0.04743
cg1245001	RGMB	RXR-alpha	1387	1393	5.271235	GGGTTG(	0.61035	0.6044
cg0388534	RGMB	RXR-alpha	1028	1034	5.271235	GCAACC(	0.61035	0.6044
cg0388534	RGMB	RXR-alpha	1891	1897	5.271235	GGGTAG	0.61035	0.6044
cg0388534	RGMB	NF-AT2 [T	250	259	5.231211	GGAAAA	0.03815	0.03879
cg0836780	RGMB	HNF-1C [	1730	1738	5.214027	GTTATA	0.04578	0.04693
cg1245001	RGMB	HNF-1C [	822	830	5.214027	GTTATA	0.04578	0.04693
cg0388534	RGMB	GR [T050	459	465	5.207533	GTCTTTC	0.24414	0.24606
cg0388534	RGMB	c-Fos [T00	220	229	5.119614	GCAATG	0.02289	0.02308
cg0836780	RGMB	NF-AT2 [T	787	796	5.113619	TATTGTT	0.03815	0.03879
cg0836780	RGMB	AP-2alpha	865	870	5.100982	AAAGGC	0.97656	0.97567
cg1245001	RGMB	AP-2alpha	1906	1911	5.100982	GCCTTT	0.97656	0.97567
cg0388534	RGMB	AP-2alpha	1049	1054	5.100982	AAAGGC	0.97656	0.97567
cg0388534	RGMB	AP-2alpha	1055	1060	5.100982	AAAGGC	0.97656	0.97567
cg0388534	RGMB	AP-2alpha	1802	1807	5.100982	AAAGGC	0.97656	0.97567
cg0836780	RGMB	RXR-alpha	1201	1207	5.089356	AGCACC(	0.48828	0.484
cg1245001	RGMB	RXR-alpha	293	299	5.089356	AGCACC(	0.48828	0.484
cg0388534	RGMB	RXR-alpha	261	267	5.089356	AGCACC(	0.48828	0.484
cg0388534	RGMB	SRY [T00	1195	1203	5.086565	CTTTGTA	0.06104	0.06209
cg0836780	RGMB	GR-beta [T	162	166	5.042296	AATCC	3.90625	3.95351
cg0836780	RGMB	GR-beta [T	351	355	5.042296	AATCC	3.90625	3.95351
cg0836780	RGMB	GR-beta [T	716	720	5.042296	AATAC	3.90625	3.95351
cg0836780	RGMB	GR-beta [T	760	764	5.042296	GGATT	3.90625	3.95351

cg0836780	RGMB	GR-beta [T	1036	1040	5.042296	AATCC	3.90625	3.95351
cg0836780	RGMB	GR-beta [T	1243	1247	5.042296	AATAC	3.90625	3.95351
cg0836780	RGMB	GR-beta [T	1419	1423	5.042296	AATAC	3.90625	3.95351
cg1245001	RGMB	GR-beta [T	128	132	5.042296	AATCC	3.90625	3.95351
cg1245001	RGMB	GR-beta [T	335	339	5.042296	AATAC	3.90625	3.95351
cg1245001	RGMB	GR-beta [T	511	515	5.042296	AATAC	3.90625	3.95351
cg1245001	RGMB	GR-beta [T	1098	1102	5.042296	AATCC	3.90625	3.95351
cg1245001	RGMB	GR-beta [T	1195	1199	5.042296	AATAC	3.90625	3.95351
cg1245001	RGMB	GR-beta [T	1232	1236	5.042296	AATCC	3.90625	3.95351
cg1245001	RGMB	GR-beta [T	1877	1881	5.042296	GGATT	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	214	218	5.042296	GGATT	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	473	477	5.042296	AATAC	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	489	493	5.042296	GTATT	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	588	592	5.042296	AATAC	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	678	682	5.042296	GTATT	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	701	705	5.042296	GGATT	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	1016	1020	5.042296	GGATT	3.90625	3.95351
cg0388534	RGMB	GR-beta [T	1272	1276	5.042296	AATCC	3.90625	3.95351
cg0836780	RGMB	c-Ets-1 [T	1878	1884	5.038739	TTGGAA	0.48828	0.49031
cg1245001	RGMB	c-Ets-1 [T	970	976	5.038739	TTGGAA	0.48828	0.49031
cg0388534	RGMB	Sp1 [T007	1062	1071	5.025839	AGGGCG	0.06485	0.06365
cg0836780	RGMB	NFI/CTF [	86	93	5.021086	CCAAGG	0.24414	0.24103
cg0836780	RGMB	NFI/CTF [	770	777	5.021086	CCCCTTC	0.24414	0.24103
cg0388534	RGMB	HNF-1A [	359	366	4.972635	TCCTTA	0.36621	0.37179
cg1245001	RGMB	c-Ets-1 [T	1773	1779	4.910652	ATGGAA	0.48828	0.49031
cg0836780	RGMB	XBP-1 [T	867	872	4.894955	AGGCAT	0.97656	0.96979
cg0836780	RGMB	XBP-1 [T	1175	1180	4.894955	ATGCCT	0.97656	0.96979
cg1245001	RGMB	XBP-1 [T	267	272	4.894955	ATGCCT	0.97656	0.96979
cg0388534	RGMB	XBP-1 [T	794	799	4.894955	AGGCAT	0.97656	0.96979
cg0836780	RGMB	AP-2alpha	1977	1982	4.890408	TTAGGC	0.97656	0.97567
cg1245001	RGMB	AP-2alpha	1069	1074	4.890408	TTAGGC	0.97656	0.97567
cg0388534	RGMB	AP-2alpha	106	111	4.890408	TTAGGC	0.97656	0.97567
cg0388534	RGMB	c-Jun [T00	526	532	4.883696	TATGTC	0.61035	0.61057
cg0836780	RGMB	NF-1 [T00	82	89	4.880836	TGTTCC	0.24414	0.24398
cg0836780	RGMB	RXR-alpha	405	411	4.86724	CATACC	0.48828	0.484
cg0836780	RGMB	NF-Y [T0	825	832	4.867193	ATTGGA	0.36621	0.36847
cg0388534	RGMB	NF-Y [T0	1137	1144	4.867193	ATTGGA	0.36621	0.36847
cg0836780	RGMB	GCF [T00	53	61	4.846987	GGTCGG	0.27466	0.26486
cg0388534	RGMB	GCF [T00	1661	1669	4.846987	GCGCGG	0.27466	0.26486
cg0836780	RGMB	HNF-3alph	1091	1098	4.842999	TATTTA	0.09155	0.09582
cg0836780	RGMB	HNF-3alph	1538	1545	4.842999	TATTTTA	0.09155	0.09582
cg0836780	RGMB	HNF-3alph	1543	1550	4.842999	TATTTTA	0.09155	0.09582
cg1245001	RGMB	HNF-3alph	183	190	4.842999	TATTTA	0.09155	0.09582
cg1245001	RGMB	HNF-3alph	630	637	4.842999	TATTTTA	0.09155	0.09582
cg1245001	RGMB	HNF-3alph	635	642	4.842999	TATTTTA	0.09155	0.09582
cg1245001	RGMB	HNF-3alph	1485	1492	4.842999	TATTTTA	0.09155	0.09582
cg0388534	RGMB	HNF-3alph	1295	1302	4.842999	TTTAAA	0.09155	0.09582
cg0836780	RGMB	C/EBPalph	787	793	4.776286	TATTGT	0.97656	0.99332

cg0836780	RGMB	TFII-I [T0	743	748	4.756447	GGAAAT	2.92969	2.93695
cg0836780	RGMB	TFII-I [T0	760	765	4.756447	GGATTG	2.92969	2.93695
cg0836780	RGMB	TFII-I [T0	784	789	4.756447	GGATAT	2.92969	2.93695
cg0836780	RGMB	TFII-I [T0	828	833	4.756447	GGAATG	2.92969	2.93695
cg0836780	RGMB	TFII-I [T0	925	930	4.756447	GGAATG	2.92969	2.93695
cg0836780	RGMB	TFII-I [T0	1499	1504	4.756447	GGAATG	2.92969	2.93695
cg0836780	RGMB	TFII-I [T0	1750	1755	4.756447	GGATAT	2.92969	2.93695
cg0836780	RGMB	FOXP3 [T	24	29	4.756447	GTTGAC	2.92969	2.96063
cg1245001	RGMB	TFII-I [T0	17	22	4.756447	GGAATG	2.92969	2.93695
cg1245001	RGMB	TFII-I [T0	591	596	4.756447	GGAATG	2.92969	2.93695
cg1245001	RGMB	TFII-I [T0	842	847	4.756447	GGATAT	2.92969	2.93695
cg1245001	RGMB	TFII-I [T0	1464	1469	4.756447	ATTTCC	2.92969	2.93695
cg1245001	RGMB	TFII-I [T0	1747	1752	4.756447	GGAAAT	2.92969	2.93695
cg1245001	RGMB	TFII-I [T0	1862	1867	4.756447	ATATCC	2.92969	2.93695
cg1245001	RGMB	TFII-I [T0	1879	1884	4.756447	ATTTCC	2.92969	2.93695
cg1245001	RGMB	FOXP3 [T	1788	1793	4.756447	GTTTTG	2.92969	2.96063
cg1245001	RGMB	FOXP3 [T	1938	1943	4.756447	GTTTTG	2.92969	2.96063
cg0388534	RGMB	TFII-I [T0	284	289	4.756447	GGATAT	2.92969	2.93695
cg0388534	RGMB	TFII-I [T0	685	690	4.756447	GGATAT	2.92969	2.93695
cg0388534	RGMB	TFII-I [T0	931	936	4.756447	ATGTCC	2.92969	2.93695
cg0388534	RGMB	TFII-I [T0	1452	1457	4.756447	GGAAAT	2.92969	2.93695
cg0388534	RGMB	TFII-I [T0	1567	1572	4.756447	ATTTCC	2.92969	2.93695
cg0388534	RGMB	FOXP3 [T	176	181	4.756447	GTTTTT	2.92969	2.96063
cg0388534	RGMB	FOXP3 [T	784	789	4.756447	AAAAAC	2.92969	2.96063
cg0388534	RGMB	FOXP3 [T	940	945	4.756447	GTTGAT	2.92969	2.96063
cg0388534	RGMB	FOXP3 [T	1366	1371	4.756447	AAAAAC	2.92969	2.96063
cg0388534	RGMB	FOXP3 [T	1752	1757	4.756447	AAAAAC	2.92969	2.96063
cg0836780	RGMB	NF-kappa	57	67	4.738398	GGCGCT	0.03242	0.03169
cg0836780	RGMB	c-Ets-1 [T	293	299	4.654478	CTTCCA	0.85449	0.85764
cg0388534	RGMB	p53 [T006	1861	1867	4.645444	GGGCGC	0.24414	0.23584
cg0388534	RGMB	TCF-4 [T0	1797	1806	4.639022	AGGTCA	0.04196	0.04202
cg0388534	RGMB	c-Ets-2 [T	1900	1908	4.589988	GGGAAG	0.06866	0.06881
cg0388534	RGMB	C/EBPalph	1638	1644	4.560723	GATTGG	0.24414	0.24411
cg0836780	RGMB	c-Ets-1 [T	193	199	4.539113	TAGGAA	0.85449	0.85764
cg0388534	RGMB	c-Ets-1 [T	951	957	4.539113	ATTCCT	0.85449	0.85764
cg0836780	RGMB	T3R-beta1	1266	1274	4.481316	AACTGG	0.27466	0.27551
cg1245001	RGMB	T3R-beta1	358	366	4.481316	AACTGG	0.27466	0.27551
cg0836780	RGMB	T3R-beta1	967	975	4.462023	TCACCA	0.27466	0.27551
cg1245001	RGMB	T3R-beta1	59	67	4.462023	TCACCA	0.27466	0.27551
cg0836780	RGMB	HNF-1C [	598	606	4.459798	ATTAGT	0.07629	0.07843
cg0388534	RGMB	GATA-2 [	713	721	4.444445	GGATAG	0.24414	0.24541
cg0836780	RGMB	AP-2alpha	202	207	4.438035	GCCTAG	0.97656	0.96979
cg0836780	RGMB	RXR-alph	1104	1110	4.423008	GGGTTG	0.24414	0.24292
cg1245001	RGMB	RXR-alph	196	202	4.423008	GGGTTG	0.24414	0.24292
cg0836780	RGMB	AP-2alpha	1884	1889	4.422424	GCCTTA	0.97656	0.96979
cg1245001	RGMB	AP-2alpha	976	981	4.422424	GCCTTA	0.97656	0.96979
cg0836780	RGMB	USF1 [T0	1287	1296	4.414822	TTCACA	0.06866	0.06835
cg1245001	RGMB	USF1 [T0	379	388	4.414822	TTCACA	0.06866	0.06835

cg0836780	RGMB	STAT4 [T	60	65	4.411765	GCTTCC	1.95312	1.94235
cg0836780	RGMB	STAT4 [T	828	833	4.411765	GGAATG	1.95312	1.94235
cg0836780	RGMB	STAT4 [T	925	930	4.411765	GGAATG	1.95312	1.94235
cg0836780	RGMB	STAT4 [T	1499	1504	4.411765	GGAATG	1.95312	1.94235
cg0836780	RGMB	STAT4 [T	1880	1885	4.411765	GGAAGC	1.95312	1.94235
cg1245001	RGMB	STAT4 [T	17	22	4.411765	GGAATG	1.95312	1.94235
cg1245001	RGMB	STAT4 [T	591	596	4.411765	GGAATG	1.95312	1.94235
cg1245001	RGMB	STAT4 [T	972	977	4.411765	GGAAGC	1.95312	1.94235
cg1245001	RGMB	STAT4 [T	1775	1780	4.411765	GGAAGA	1.95312	1.94235
cg0388534	RGMB	STAT4 [T	1617	1622	4.411765	GGAACG	1.95312	1.94235
cg0388534	RGMB	STAT4 [T	1685	1690	4.411765	GCTTCC	1.95312	1.94235
cg0388534	RGMB	STAT4 [T	1764	1769	4.411765	GGAAGA	1.95312	1.94235
cg0388534	RGMB	p53 [T006	1718	1724	4.33696	GGGCCA	0.24414	0.23584
cg0836780	RGMB	HOXD9 [T	1537	1546	4.321431	TTATTT	0.03433	0.03596
cg0836780	RGMB	HOXD9 [T	1542	1551	4.321431	TTATTT	0.03433	0.03596
cg0836780	RGMB	HOXD10 [	1537	1546	4.321431	TTATTT	0.03433	0.03596
cg0836780	RGMB	HOXD10 [	1542	1551	4.321431	TTATTT	0.03433	0.03596
cg1245001	RGMB	HOXD9 [T	629	638	4.321431	TTATTT	0.03433	0.03596
cg1245001	RGMB	HOXD9 [T	634	643	4.321431	TTATTT	0.03433	0.03596
cg1245001	RGMB	HOXD10 [	629	638	4.321431	TTATTT	0.03433	0.03596
cg1245001	RGMB	HOXD10 [	634	643	4.321431	TTATTT	0.03433	0.03596
cg0388534	RGMB	HOXD9 [T	90	99	4.321431	AATAAA	0.03433	0.03596
cg0388534	RGMB	HOXD10 [	90	99	4.321431	AATAAA	0.03433	0.03596
cg0836780	RGMB	PEA3 [T0	579	587	4.30818	AGGATG	0.13733	0.13791
cg0388534	RGMB	C/EBPalph	87	93	4.235345	AGCAAT	0.48828	0.49358
cg0388534	RGMB	C/EBPalph	149	155	4.235345	AGCAAT	0.48828	0.49358
cg0388534	RGMB	C/EBPalph	242	248	4.235345	TATTGA	0.48828	0.49358
cg0388534	RGMB	C/EBPalph	353	359	4.235345	TATTGA	0.48828	0.49358
cg0388534	RGMB	C/EBPalph	392	398	4.235345	ATCAAT	0.48828	0.49358
cg0836780	RGMB	GR-beta [T	130	134	4.201913	CTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	148	152	4.201913	AATCG	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	182	186	4.201913	CTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	396	400	4.201913	TTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	423	427	4.201913	AATCA	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	510	514	4.201913	AATAG	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	553	557	4.201913	AATAA	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	566	570	4.201913	AATAG	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	583	587	4.201913	TGATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	622	626	4.201913	AATAG	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1000	1004	4.201913	CGATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1031	1035	4.201913	CGATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1090	1094	4.201913	CTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1258	1262	4.201913	TTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1272	1276	4.201913	TGATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1345	1349	4.201913	TGATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1456	1460	4.201913	AATAG	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1537	1541	4.201913	TTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1542	1546	4.201913	TTATT	7.8125	7.94607

cg0836780	RGMB	GR-beta [T	1547	1551	4.201913	TTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1580	1584	4.201913	AATAG	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1822	1826	4.201913	AATCG	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1833	1837	4.201913	CTATT	7.8125	7.94607
cg0836780	RGMB	GR-beta [T	1921	1925	4.201913	TGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	92	96	4.201913	CGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	123	127	4.201913	CGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	182	186	4.201913	CTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	350	354	4.201913	TTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	364	368	4.201913	TGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	437	441	4.201913	TGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	548	552	4.201913	AATAG	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	629	633	4.201913	TTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	634	638	4.201913	TTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	639	643	4.201913	TTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	672	676	4.201913	AATAG	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	914	918	4.201913	AATCG	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	925	929	4.201913	CTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1013	1017	4.201913	TGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1264	1268	4.201913	AATCG	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1495	1499	4.201913	CTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1503	1507	4.201913	AATAA	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1558	1562	4.201913	AATAG	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1649	1653	4.201913	TTATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1673	1677	4.201913	TGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1696	1700	4.201913	AATAG	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1750	1754	4.201913	AATAA	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1837	1841	4.201913	TGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1947	1951	4.201913	TGATT	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1967	1971	4.201913	AATAG	7.8125	7.94607
cg1245001	RGMB	GR-beta [T	1979	1983	4.201913	TTATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	20	24	4.201913	AATAG	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	90	94	4.201913	AATAA	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	152	156	4.201913	AATAA	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	241	245	4.201913	CTATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	308	312	4.201913	AATCA	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	352	356	4.201913	TTATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	366	370	4.201913	CTATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	395	399	4.201913	AATAA	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	484	488	4.201913	AATCA	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	499	503	4.201913	TGATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	585	589	4.201913	AATAA	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	666	670	4.201913	CTATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	669	673	4.201913	TTATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	844	848	4.201913	AATAA	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	896	900	4.201913	TGATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	1000	1004	4.201913	CGATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	1299	1303	4.201913	AATAA	7.8125	7.94607

cg0388534	RGMB	GR-beta [T	1342	1346	4.201913	AATCG	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	1637	1641	4.201913	TGATT	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	1772	1776	4.201913	AATCG	7.8125	7.94607
cg0388534	RGMB	GR-beta [T	1879	1883	4.201913	AATCG	7.8125	7.94607
cg0836780	RGMB	c-Ets-1 [T	1573	1579	4.154851	ATTCCT	0.24414	0.24526
cg1245001	RGMB	c-Ets-1 [T	665	671	4.154851	ATTCCT	0.24414	0.24526
cg0836780	RGMB	NF-1 [T00	1447	1454	4.135372	TGACCC	0.24414	0.24154
cg0836780	RGMB	NF-1 [T00	1816	1823	4.135372	TGACCC	0.24414	0.24154
cg1245001	RGMB	NF-1 [T00	539	546	4.135372	TGACCC	0.24414	0.24154
cg1245001	RGMB	NF-1 [T00	908	915	4.135372	TGACCC	0.24414	0.24154
cg0388534	RGMB	c-Jun [T00	224	230	4.1298	TGACTC	0.24414	0.24526
cg1245001	RGMB	c-Ets-2 [T	1391	1399	4.091811	TGCAAG	0.16022	0.16243
cg1245001	RGMB	PXR-1:RX	1271	1278	4.090374	TGAACC	0.12207	0.12119
cg0836780	RGMB	IRF-1 [T0	535	543	4.035054	TTAGGG	0.1297	0.13087
cg0388534	RGMB	NF-AT1 [T	1869	1877	4.033119	GGAAAC	0.07629	0.07734
cg0836780	RGMB	C/EBPalph	628	634	4.019783	GTCAAT	0.48828	0.49358
cg1245001	RGMB	RXR-alpha	1175	1181	4.019014	GAAACC	0.97656	0.9671
cg1245001	RGMB	RXR-alpha	1210	1216	4.019014	GGGTGT	0.97656	0.9671
cg0388534	RGMB	RXR-alpha	331	337	4.019014	AAGACC	0.97656	0.9671
cg0836780	RGMB	c-Ets-2 [T	248	256	4.017001	TTCCTTT	0.16022	0.16243
cg1245001	RGMB	c-Ets-2 [T	1368	1376	4.017001	GGAAAG	0.16022	0.16243
cg0836780	RGMB	Pax-5 [T0	1097	1103	4.007279	AATGCC	1.09863	1.07975
cg0836780	RGMB	TFIID [T0	140	146	4.007279	TTTTAA	1.09863	1.13456
cg0836780	RGMB	TFIID [T0	397	403	4.007279	TATTAA	1.09863	1.13456
cg0836780	RGMB	TFIID [T0	552	558	4.007279	TAATAA	1.09863	1.13456
cg0836780	RGMB	TFIID [T0	1257	1263	4.007279	TTTATTA	1.09863	1.13456
cg0836780	RGMB	TFIID [T0	1261	1267	4.007279	TTATAA	1.09863	1.13456
cg0836780	RGMB	TFIID [T0	1731	1737	4.007279	TTATAA	1.09863	1.13456
cg1245001	RGMB	Pax-5 [T0	189	195	4.007279	AATGCC	1.09863	1.07975
cg1245001	RGMB	TFIID [T0	349	355	4.007279	TTTATTA	1.09863	1.13456
cg1245001	RGMB	TFIID [T0	353	359	4.007279	TTATAA	1.09863	1.13456
cg1245001	RGMB	TFIID [T0	823	829	4.007279	TTATAA	1.09863	1.13456
cg1245001	RGMB	TFIID [T0	1488	1494	4.007279	TTTATG	1.09863	1.13456
cg1245001	RGMB	TFIID [T0	1508	1514	4.007279	TTATAA	1.09863	1.13456
cg1245001	RGMB	TFIID [T0	1676	1682	4.007279	TTTTAA	1.09863	1.13456
cg1245001	RGMB	TFIID [T0	1833	1839	4.007279	TTTATG	1.09863	1.13456
cg1245001	RGMB	TFIID [T0	1858	1864	4.007279	TTTAAT	1.09863	1.13456
cg0388534	RGMB	TFIID [T0	112	118	4.007279	TTATAA	1.09863	1.13456
cg0388534	RGMB	TFIID [T0	136	142	4.007279	TTTACA	1.09863	1.13456
cg0388534	RGMB	TFIID [T0	509	515	4.007279	TTTAAG	1.09863	1.13456
cg0388534	RGMB	TFIID [T0	568	574	4.007279	TAGTAA	1.09863	1.13456
cg0388534	RGMB	TFIID [T0	1019	1025	4.007279	TTTTAA	1.09863	1.13456
cg0388534	RGMB	TFIID [T0	1239	1245	4.007279	TCATAA	1.09863	1.13456
cg1245001	RGMB	USF2 [T0	1129	1138	4.003951	AGATCA	0.01144	0.01129
cg0388534	RGMB	MAZ [T00	289	301	3.986869	TAGGGG	0.00587	0.00576
cg1245001	RGMB	c-Myb [T0	1580	1587	3.973336	GGAAGT	0.09155	0.09154
cg0388534	RGMB	c-Myb [T0	624	631	3.973336	TAACTT	0.09155	0.09154
cg0836780	RGMB	AP-2alpha	69	74	3.970052	GCCTTG	0.97656	0.96469

cg0836780	RGMB	AP-2alpha	1798	1803	3.970052	CAAGGC	0.97656	0.96469
cg1245001	RGMB	AP-2alpha	890	895	3.970052	CAAGGC	0.97656	0.96469
cg1245001	RGMB	AP-2alpha	1872	1877	3.970052	GCCTTG	0.97656	0.96469
cg0388534	RGMB	AP-2alpha	1085	1090	3.970052	GCCTTG	0.97656	0.96469
cg0836780	RGMB	p53 [T006	855	861	3.961937	CTAGCC	0.73242	0.71379
cg0836780	RGMB	MEF-2A [	696	706	3.898698	TGCGAA	0.00429	0.0044
cg0388534	RGMB	c-Ets-1 [T	22	28	3.846637	TAGGAA	0.24414	0.24526
cg0836780	RGMB	c-Jun [T00	1776	1782	3.807346	TTAGTC	0.24414	0.24526
cg1245001	RGMB	c-Jun [T00	868	874	3.807346	TTAGTC	0.24414	0.24526
cg0836780	RGMB	NFI/CTF [	1491	1498	3.793671	GCCCTT	0.18311	0.18109
cg1245001	RGMB	NFI/CTF [	583	590	3.793671	GCCCTT	0.18311	0.18109
cg0836780	RGMB	GR [T050	209	215	3.763516	CAAAGA	0.73242	0.74251
cg0836780	RGMB	GR [T050	848	854	3.763516	TTCTTTG	0.73242	0.74251
cg0836780	RGMB	GR [T050	1073	1079	3.763516	TTCTTTG	0.73242	0.74251
cg0836780	RGMB	GR [T050	1146	1152	3.763516	CTCTTT	0.73242	0.74251
cg1245001	RGMB	GR [T050	165	171	3.763516	TTCTTTG	0.73242	0.74251
cg1245001	RGMB	GR [T050	238	244	3.763516	CTCTTT	0.73242	0.74251
cg1245001	RGMB	GR [T050	1787	1793	3.763516	AGTTTT	0.73242	0.74251
cg1245001	RGMB	GR [T050	1937	1943	3.763516	TGTTTT	0.73242	0.74251
cg0388534	RGMB	GR [T050	1193	1199	3.763516	TTCTTTG	0.73242	0.74251
cg1245001	RGMB	p53 [T006	1851	1857	3.750231	CAAGCC	0.73242	0.71379
cg0388534	RGMB	p53 [T006	1526	1532	3.750231	CCAGCC	0.73242	0.71379
cg0836780	RGMB	AP-2alpha	43	48	3.743866	GCCTTC	0.48828	0.48238
cg0836780	RGMB	AP-2alpha	111	116	3.743866	GCCTTC	0.48828	0.48238
cg0836780	RGMB	AP-2alpha	1627	1632	3.743866	GCCTTC	0.48828	0.48238
cg0836780	RGMB	AP-2alpha	1870	1875	3.743866	GAAGGC	0.48828	0.48238
cg1245001	RGMB	AP-2alpha	719	724	3.743866	GCCTTC	0.48828	0.48238
cg1245001	RGMB	AP-2alpha	962	967	3.743866	GAAGGC	0.48828	0.48238
cg1245001	RGMB	AP-2alpha	1797	1802	3.743866	GAAGGC	0.48828	0.48238
cg0836780	RGMB	TBP [T007	1258	1267	3.743085	TTATTA	0.03052	0.03162
cg1245001	RGMB	TBP [T007	350	359	3.743085	TTATTA	0.03052	0.03162
cg0388534	RGMB	TBP [T007	414	423	3.743085	TTTATA	0.03052	0.03162
cg0836780	RGMB	NF-Y [T0	1586	1593	3.732121	GATCCA	0.48828	0.48904
cg0836780	RGMB	NF-Y [T0	1817	1824	3.732121	GACCCA	0.48828	0.48904
cg1245001	RGMB	NF-Y [T0	678	685	3.732121	GATCCA	0.48828	0.48904
cg1245001	RGMB	NF-Y [T0	909	916	3.732121	GACCCA	0.48828	0.48904
cg0388534	RGMB	p53 [T006	824	830	3.728319	GGGCAA	0.73242	0.7189
cg0388534	RGMB	PEA3 [T0	1005	1013	3.710864	TGGATG	0.09155	0.09258
cg0836780	RGMB	IRF-1 [T0	247	255	3.692688	TTTCCTT	0.06866	0.06927
cg1245001	RGMB	IRF-1 [T0	1369	1377	3.692688	GAAAGG	0.06866	0.06927
cg0836780	RGMB	MEF-2A [	183	193	3.681692	TATTTTT	0.00191	0.00199
cg0836780	RGMB	C/EBPalp	1649	1655	3.555778	GATTGT	0.24414	0.24752
cg1245001	RGMB	C/EBPalp	741	747	3.555778	GATTGT	0.24414	0.24752
cg1245001	RGMB	E2F-1 [T0	1577	1584	3.55167	GCGGGA	0.15259	0.14974
cg0836780	RGMB	c-Ets-2 [T	290	298	3.518824	TTCCTT	0.18311	0.18304
cg1245001	RGMB	c-Ets-2 [T	1440	1448	3.518824	TTCCTT	0.18311	0.18304
cg0836780	RGMB	p53 [T006	1097	1103	3.516613	AATGCC	0.73242	0.7189
cg1245001	RGMB	p53 [T006	189	195	3.516613	AATGCC	0.73242	0.7189

cg0836780	RGMB	HNF-3alp	183	190	3.500065	TATTTTT	0.27466	0.28532
cg0836780	RGMB	HNF-3alp	387	394	3.500065	AATTTT	0.27466	0.28532
cg0836780	RGMB	HNF-3alp	618	625	3.500065	AGAAAA	0.27466	0.28532
cg0836780	RGMB	HNF-3alp	1548	1555	3.500065	TATTTTT	0.27466	0.28532
cg1245001	RGMB	HNF-3alp	640	647	3.500065	TATTTTT	0.27466	0.28532
cg1245001	RGMB	HNF-3alp	1650	1657	3.500065	TATTTTC	0.27466	0.28532
cg1245001	RGMB	HNF-3alp	1973	1980	3.500065	TGAAAA	0.27466	0.28532
cg0388534	RGMB	HNF-3alp	47	54	3.500065	TGAAAA	0.27466	0.28532
cg0388534	RGMB	c-Myb [T0	0	7	3.469384	CAACTG	0.12207	0.12203
cg1245001	RGMB	VDR [T00	1267	1275	3.462841	CGCTTG	0.21362	0.21341
cg0388534	RGMB	NF-AT1 [	327	336	3.445347	TGGAAA	0.07629	0.07722
cg0388534	RGMB	GCF [T00	1931	1939	3.409768	GCGCAG	0.03052	0.02982
cg0836780	RGMB	NF-AT1 [	452	460	3.407861	GGAAAA	0.03052	0.03089
cg1245001	RGMB	NF-AT1 [	1373	1381	3.407861	GGAAAA	0.03052	0.03089
cg0836780	RGMB	RXR-alph	240	246	3.392904	GGGTCA	1.09863	1.08572
cg0836780	RGMB	RXR-alph	1123	1129	3.392904	GGAACC	1.09863	1.08572
cg1245001	RGMB	RXR-alph	215	221	3.392904	GGAACC	1.09863	1.08572
cg0388534	RGMB	RXR-alph	730	736	3.392904	TTTACC	1.09863	1.08572
cg0388534	RGMB	RXR-alph	982	988	3.392904	GGGTAC	1.09863	1.08572
cg0388534	RGMB	Elk-1 [T00	1443	1451	3.381796	TTCAGG	0.04578	0.04588
cg0388534	RGMB	p53 [T006	1985	1991	3.375208	GGGCGG	0.73242	0.7189
cg0388534	RGMB	T3R-beta1	852	860	3.370634	AGCTGG	0.27466	0.2755
cg0836780	RGMB	GR-beta [	631	635	3.361531	AATCT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	679	683	3.361531	ATATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	703	707	3.361531	AATAT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	786	790	3.361531	ATATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	975	979	3.361531	AGATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1069	1073	3.361531	AGATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1284	1288	3.361531	AGATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1443	1447	3.361531	AATCT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1464	1468	3.361531	AATCT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1591	1595	3.361531	AATAT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1648	1652	3.361531	AGATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1752	1756	3.361531	ATATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [	1928	1932	3.361531	AGATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	67	71	3.361531	AGATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	161	165	3.361531	AGATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	376	380	3.361531	AGATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	535	539	3.361531	AATCT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	556	560	3.361531	AATCT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	683	687	3.361531	AATAT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	740	744	3.361531	AGATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	844	848	3.361531	ATATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	1020	1024	3.361531	AGATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	1420	1424	3.361531	AATCT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	1484	1488	3.361531	ATATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	1532	1536	3.361531	AGATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [	1645	1649	3.361531	ATATT	3.90625	3.99611

cg1245001	RGMB	GR-beta [T	1861	1865	3.361531	AATAT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	117	121	3.361531	AATCT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	254	258	3.361531	AATCT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	432	436	3.361531	AATCT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	706	710	3.361531	ATATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	922	926	3.361531	AATAT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	963	967	3.361531	AGATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1103	1107	3.361531	AGATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1142	1146	3.361531	AATCT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1302	1306	3.361531	AATCT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1565	1569	3.361531	AGATT	3.90625	3.99611
cg0388534	RGMB	PR B [T00	101	107	3.29756	AATTGTT	0.24414	0.25122
cg0388534	RGMB	PR A [T01	101	107	3.29756	AATTGTT	0.24414	0.25122
cg0388534	RGMB	c-Ets-2 [T0	1215	1223	3.2883	TTCCTCA	0.18311	0.18304
cg0388534	RGMB	c-Ets-2 [T0	1864	1872	3.2883	CGCGAG	0.18311	0.18304
cg0388534	RGMB	c-Ets-1 [T0	1883	1889	3.231072	GCGGAA	0.24414	0.23981
cg0388534	RGMB	AP-2alpha	1187	1192	3.229049	GCCTCT	0.48828	0.48238
cg0388534	RGMB	NF-AT2 [T	1289	1298	3.201983	GGAAAA	0.03433	0.03494
cg0388534	RGMB	CTF [T001	1635	1646	3.193907	TGTGATT	0.00572	0.00569
cg0836780	RGMB	RXR-alpha	1760	1766	3.170788	GGGTGTA	0.24414	0.24522
cg1245001	RGMB	RXR-alpha	852	858	3.170788	GGGTGTA	0.24414	0.24522
cg0388534	RGMB	RXR-alpha	1367	1373	3.170788	AAAACC	0.24414	0.24522
cg0836780	RGMB	TCF-4E [T	494	500	3.151193	CTTTGCA	0.24414	0.24672
cg0836780	RGMB	TCF-4E [T	1148	1154	3.151193	CTTTGCA	0.24414	0.24672
cg1245001	RGMB	TCF-4E [T	240	246	3.151193	CTTTGCA	0.24414	0.24672
cg0388534	RGMB	SRY [T00	1814	1822	3.088221	CTTTGTA	0.06104	0.06203
cg0836780	RGMB	TCF-4 [T0	1074	1083	3.085213	TCTTTGA	0.03433	0.0351
cg1245001	RGMB	TCF-4 [T0	166	175	3.085213	TCTTTGA	0.03433	0.0351
cg0388534	RGMB	Sp1 [T007	1574	1583	3.079852	ACACCG	0.03433	0.03306
cg1245001	RGMB	TFIID [T0	1889	1895	3.075094	TGCAAA	0.12207	0.12409
cg0836780	RGMB	E2F-1 [T0	1696	1703	3.059334	TTTACCC	0.03052	0.03049
cg1245001	RGMB	E2F-1 [T0	788	795	3.059334	TTTACCC	0.03052	0.03049
cg0836780	RGMB	c-Jun [T00	1447	1453	3.049104	TGACCCA	0.24414	0.24403
cg0836780	RGMB	c-Jun [T00	1816	1822	3.049104	TGACCCA	0.24414	0.24403
cg1245001	RGMB	c-Jun [T00	539	545	3.049104	TGACCCA	0.24414	0.24403
cg1245001	RGMB	c-Jun [T00	908	914	3.049104	TGACCCA	0.24414	0.24403
cg1245001	RGMB	p53 [T006	1328	1334	3.024997	GGGCAA	0.48828	0.47786
cg1245001	RGMB	Elk-1 [T00	1392	1400	2.987643	GCAAGG	0.07629	0.07656
cg1245001	RGMB	c-Ets-2 [T0	1363	1371	2.945838	AAAAAG	0.06104	0.06231
cg0836780	RGMB	STAT4 [T	82	87	2.941176	TGTTCC	2.92969	2.929
cg0836780	RGMB	STAT4 [T	91	96	2.941176	GGAAGT	2.92969	2.929
cg0836780	RGMB	STAT4 [T	1123	1128	2.941176	GGAACC	2.92969	2.929
cg0836780	RGMB	STAT4 [T	1969	1974	2.941176	GGAAAG	2.92969	2.929
cg1245001	RGMB	STAT4 [T	215	220	2.941176	GGAACC	2.92969	2.929
cg1245001	RGMB	STAT4 [T	1061	1066	2.941176	GGAAAG	2.92969	2.929
cg1245001	RGMB	STAT4 [T	1368	1373	2.941176	GGAAAG	2.92969	2.929
cg1245001	RGMB	STAT4 [T	1418	1423	2.941176	GGAATC	2.92969	2.929
cg1245001	RGMB	STAT4 [T	1438	1443	2.941176	CTTTCC	2.92969	2.929

cg1245001	RGMB	STAT4 [T	1452	1457	2.941176	GGTTCC	2.92969	2.929
cg1245001	RGMB	STAT4 [T	1580	1585	2.941176	GGAAGT	2.92969	2.929
cg0388534	RGMB	STAT4 [T	24	29	2.941176	GGAACC	2.92969	2.929
cg0388534	RGMB	STAT4 [T	278	283	2.941176	GGAACA	2.92969	2.929
cg0388534	RGMB	STAT4 [T	328	333	2.941176	GGAAAG	2.92969	2.929
cg0388534	RGMB	STAT4 [T	626	631	2.941176	ACTTCC	2.92969	2.929
cg0388534	RGMB	STAT4 [T	920	925	2.941176	GGAATA	2.92969	2.929
cg0388534	RGMB	STAT4 [T	1047	1052	2.941176	GGAAAG	2.92969	2.929
cg0388534	RGMB	STAT4 [T	1140	1145	2.941176	GGAATC	2.92969	2.929
cg0388534	RGMB	STAT4 [T	1624	1629	2.941176	GGTTCC	2.92969	2.929
cg0388534	RGMB	STAT4 [T	1905	1910	2.941176	GGAAAG	2.92969	2.929
cg0388534	RGMB	STAT1bet	1567	1576	2.898434	ATTTCC	0.0515	0.05191
cg1245001	RGMB	IRF-1 [T0	1439	1447	2.890712	TTTCCTT	0.07629	0.07756
cg1245001	RGMB	NF-1 [T00	1637	1644	2.813149	TTGGCC	0.24414	0.24101
cg0836780	RGMB	PR B [T00	787	793	2.80933	TATTGT	0.73242	0.74818
cg0836780	RGMB	PR B [T00	986	992	2.80933	AACAAT	0.73242	0.74818
cg0836780	RGMB	PR B [T00	1649	1655	2.80933	GATTGT	0.73242	0.74818
cg0836780	RGMB	PR A [T01	787	793	2.80933	TATTGT	0.73242	0.74818
cg0836780	RGMB	PR A [T01	986	992	2.80933	AACAAT	0.73242	0.74818
cg0836780	RGMB	PR A [T01	1649	1655	2.80933	GATTGT	0.73242	0.74818
cg1245001	RGMB	PR B [T00	78	84	2.80933	AACAAT	0.73242	0.74818
cg1245001	RGMB	PR B [T00	741	747	2.80933	GATTGT	0.73242	0.74818
cg1245001	RGMB	PR A [T01	78	84	2.80933	AACAAT	0.73242	0.74818
cg1245001	RGMB	PR A [T01	741	747	2.80933	GATTGT	0.73242	0.74818
cg0836780	RGMB	TBP [T00	1728	1737	2.807313	TCGTTA	0.12207	0.12635
cg1245001	RGMB	TBP [T00	820	829	2.807313	TCGTTA	0.12207	0.12635
cg1245001	RGMB	TBP [T00	1505	1514	2.807313	TAATTA	0.12207	0.12635
cg0836780	RGMB	NF-AT1 [	742	751	2.756277	TGGAAA	0.05913	0.05995
cg0388534	RGMB	NF-AT1 [	1564	1573	2.756277	CAGATT	0.05913	0.05995
cg0388534	RGMB	RXR-alph	421	427	2.726556	GGGTCG	0.85449	0.84796
cg0388534	RGMB	c-Ets-2 [T	628	636	2.715313	TTCCTC	0.07629	0.07593
cg0836780	RGMB	MEF-2A [	1449	1459	2.660781	ACCCAA	0.00572	0.00593
cg1245001	RGMB	MEF-2A [	541	551	2.660781	ACCCAA	0.00572	0.00593
cg0836780	RGMB	NF-AT1 [	1969	1977	2.619709	GGAAAG	0.09155	0.0926
cg1245001	RGMB	NF-AT1 [	1061	1069	2.619709	GGAAAG	0.09155	0.0926
cg0836780	RGMB	NF-AT1 [	788	796	2.595974	ATTGTT	0.09155	0.0926
cg1245001	RGMB	PXR-1:RX	1145	1152	2.577808	GGAGTT	0.12207	0.12266
cg0836780	RGMB	AP-2alpha	73	78	2.550491	TGAGGC	0.48828	0.48266
cg0836780	RGMB	AP-2alpha	1196	1201	2.550491	GCCTCA	0.48828	0.48266
cg1245001	RGMB	AP-2alpha	288	293	2.550491	GCCTCA	0.48828	0.48266
cg1245001	RGMB	AP-2alpha	1119	1124	2.550491	TGAGGC	0.48828	0.48266
cg0836780	RGMB	RXR-alph	1901	1907	2.544678	AGAACC	0.85449	0.84796
cg1245001	RGMB	RXR-alph	993	999	2.544678	AGAACC	0.85449	0.84796
cg0836780	RGMB	c-Jun [T00	963	969	2.538231	TAAGTC	0.48828	0.48929
cg1245001	RGMB	c-Jun [T00	55	61	2.538231	TAAGTC	0.48828	0.48929
cg0388534	RGMB	c-Jun [T00	739	745	2.538231	TAAGTC	0.48828	0.48929
cg0836780	RGMB	PXR-1:RX	356	363	2.454225	TGAACT	0.12207	0.12266
cg0388534	RGMB	NF-AT1 [	250	258	2.449764	GGAAAA	0.09155	0.0926

cg0388534	RGMB	IRF-1 [T0	1448	1456	2.418514	GAAGGG	0.02289	0.02311
cg1245001	RGMB	Ik-1 [T027	1100	1112	2.374299	TCCCAG	0.00063	0.00061
cg0836780	RGMB	C/EBPalph	746	752	2.371703	AATTGT	0.48828	0.49114
cg0388534	RGMB	NF-Y [T0	1639	1646	2.355069	ATTGGC	0.21362	0.21485
cg0388534	RGMB	VDR [T00	70	78	2.308561	CGGCTG	0.10681	0.10609
cg0388534	RGMB	COUP-TF	1793	1805	2.273345	GGAGAG	0.00089	0.00088
cg0836780	RGMB	GATA-2 [	1116	1124	2.222222	AGATAA	0.22888	0.23091
cg0836780	RGMB	GATA-2 [	1184	1192	2.222222	TCCTTAT	0.22888	0.23091
cg1245001	RGMB	GATA-2 [	208	216	2.222222	AGATAA	0.22888	0.23091
cg1245001	RGMB	GATA-2 [	276	284	2.222222	TCCTTAT	0.22888	0.23091
cg1245001	RGMB	T3R-beta1	1132	1140	2.221365	TCACCT	0.15259	0.15262
cg0836780	RGMB	GATA-1 [	783	788	2.176375	TGGATA	3.90625	3.92756
cg0836780	RGMB	GATA-1 [	1749	1754	2.176375	TGGATA	3.90625	3.92756
cg1245001	RGMB	GATA-1 [	841	846	2.176375	TGGATA	3.90625	3.92756
cg0388534	RGMB	GATA-1 [	283	288	2.176375	AGGATA	3.90625	3.92756
cg0388534	RGMB	GATA-1 [	684	689	2.176375	TGGATA	3.90625	3.92756
cg0388534	RGMB	GATA-1 [	712	717	2.176375	TGGATA	3.90625	3.92756
cg0388534	RGMB	GATA-1 [	883	888	2.176375	TATCCT	3.90625	3.92756
cg0388534	RGMB	c-Ets-2 [T	61	69	2.142327	TTCCTCT	0.16785	0.16856
cg0388534	RGMB	AP-2alpha	1477	1482	2.098119	GCCTCG	0.97656	0.95407
cg0388534	RGMB	AP-2alpha	1917	1922	2.098119	CGAGGC	0.97656	0.95407
cg0388534	RGMB	NF-AT2 [	174	183	2.029228	AAGTTT	0.01526	0.0156
cg0836780	RGMB	LEF-1 [T0	850	857	2.004405	CTTTGCT	0.18311	0.18582
cg0388534	RGMB	LEF-1 [T0	461	468	2.004405	CTTTGTT	0.18311	0.18582
cg1245001	RGMB	GATA-1 [	1863	1868	2.001358	TATCCC	3.90625	3.92756
cg0836780	RGMB	NF-AT1 [	650	658	1.970716	GGAAAA	0.06866	0.07012
cg0388534	RGMB	NF-AT1 [	1289	1297	1.970716	GGAAAA	0.06866	0.07012
cg0388534	RGMB	p53 [T006	870	876	1.970013	TTTGCC	0.36621	0.36261
cg0388534	RGMB	p53 [T006	1412	1418	1.970013	TTTGCC	0.36621	0.36261
cg0388534	RGMB	TCF-4 [T0	476	485	1.934085	ACTTTG	0.04196	0.04299
cg1245001	RGMB	GATA-1 [	1527	1532	1.896347	CGGATA	3.90625	3.92756
cg1245001	RGMB	GATA-1 [	1601	1606	1.896347	TATCCG	3.90625	3.92756
cg0388534	RGMB	GATA-1 [	1127	1132	1.896347	CCGATA	3.90625	3.92756
cg0388534	RGMB	PR B [T00	76	82	1.892895	AACACT	0.12207	0.12429
cg0388534	RGMB	PR A [T01	76	82	1.892895	AACACT	0.12207	0.12429
cg0836780	RGMB	RXR-alpha	22	28	1.87833	GGGTTG	0.12207	0.12194
cg0836780	RGMB	AP-2alpha	1686	1691	1.871933	GGAGGC	0.97656	0.95407
cg1245001	RGMB	AP-2alpha	778	783	1.871933	GGAGGC	0.97656	0.95407
cg1245001	RGMB	AP-2alpha	1247	1252	1.871933	GGAGGC	0.97656	0.95407
cg1245001	RGMB	AP-2alpha	1279	1284	1.871933	GGAGGC	0.97656	0.95407
cg0388534	RGMB	TBP [T00	109	118	1.871542	GGCTTA	0.18311	0.18942
cg0388534	RGMB	C/EBPalph	877	883	1.830762	CTCAAT	0.48828	0.49438
cg1245001	RGMB	TFII-I [T0	1317	1322	1.824994	CTCTCC	0.48828	0.48408
cg0388534	RGMB	TFII-I [T0	1429	1434	1.824994	CTCTCC	0.48828	0.48408
cg0388534	RGMB	TFII-I [T0	1793	1798	1.824994	GGAGAG	0.48828	0.48408
cg0388534	RGMB	TFII-I [T0	1936	1941	1.824994	GGAGAG	0.48828	0.48408
cg0388534	RGMB	TFII-I [T0	1992	1997	1.824994	GGAGAG	0.48828	0.48408
cg0388534	RGMB	FOXP3 [T	138	143	1.824994	TACAAC	0.48828	0.49451

cg1245001	RGMB	c-Ets-1 [T	1745	1751	1.769212	TAGGAA	0.12207	0.12414
cg0388534	RGMB	c-Ets-1 [T	248	254	1.769212	TAGGAA	0.12207	0.12414
cg0388534	RGMB	C/EBPalph	707	713	1.761449	TATTGT	0.48828	0.49438
cg0388534	RGMB	PXR-1:RX	533	540	1.759733	TGAACT	0.06104	0.06168
cg0836780	RGMB	p53 [T006	1488	1494	1.758307	TCTGCC	0.36621	0.36261
cg1245001	RGMB	p53 [T006	580	586	1.758307	TCTGCC	0.36621	0.36261
cg1245001	RGMB	p53 [T006	1125	1131	1.758307	GGGCAG	0.36621	0.36261
cg0836780	RGMB	RXR-alpha	1446	1452	1.696452	CTGACC	0.48828	0.48222
cg0836780	RGMB	RXR-alpha	1815	1821	1.696452	CTGACC	0.48828	0.48222
cg1245001	RGMB	RXR-alpha	538	544	1.696452	CTGACC	0.48828	0.48222
cg1245001	RGMB	RXR-alpha	907	913	1.696452	CTGACC	0.48828	0.48222
cg0388534	RGMB	RXR-alpha	1226	1232	1.696452	CGGACC	0.48828	0.48222
cg0388534	RGMB	TCF-4 [T0	379	388	1.687438	GCTTTG	0.04578	0.04635
cg0836780	RGMB	GR-beta [T	196	200	1.680765	GAATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	213	217	1.680765	GAATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	224	228	1.680765	AATGC	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	272	276	1.680765	GCATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	498	502	1.680765	GCATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	823	827	1.680765	GAATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	919	923	1.680765	GAATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1097	1101	1.680765	AATGC	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1230	1234	1.680765	AATTC	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1387	1391	1.680765	AATGC	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1485	1489	1.680765	AATTC	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1572	1576	1.680765	AATTC	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1664	1668	1.680765	GCATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1675	1679	1.680765	GCATT	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1736	1740	1.680765	AATTC	3.90625	3.94936
cg0836780	RGMB	GR-beta [T	1811	1815	1.680765	AATGC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	11	15	1.680765	GAATT	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	189	193	1.680765	AATGC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	322	326	1.680765	AATTC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	479	483	1.680765	AATGC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	577	581	1.680765	AATTC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	664	668	1.680765	AATTC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	756	760	1.680765	GCATT	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	767	771	1.680765	GCATT	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	828	832	1.680765	AATTC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	903	907	1.680765	AATGC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	1426	1430	1.680765	AATTC	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	1462	1466	1.680765	GCATT	3.90625	3.94936
cg1245001	RGMB	GR-beta [T	1691	1695	1.680765	AATGC	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	56	60	1.680765	GCATT	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	100	104	1.680765	GAATT	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	426	430	1.680765	GAATT	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	603	607	1.680765	GCATT	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	828	832	1.680765	AATTC	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	950	954	1.680765	AATTC	3.90625	3.94936

cg0388534	RGMB	GR-beta [T	1267	1271	1.680765	GAATT	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	1496	1500	1.680765	GAATT	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	1497	1501	1.680765	AATTC	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	1786	1790	1.680765	AATTC	3.90625	3.94936
cg0388534	RGMB	GR-beta [T	1971	1975	1.680765	GAATT	3.90625	3.94936
cg0836780	RGMB	NF-AT2 [T	650	659	1.659787	GGAAAA	0.01717	0.01761
cg0388534	RGMB	c-Ets-2 [T	1687	1695	1.64415	TTCCTCC	0.04578	0.04579
cg0836780	RGMB	c-Ets-1 [T	247	253	1.641124	TTTCCTT	0.36621	0.36952
cg0836780	RGMB	c-Ets-1 [T	289	295	1.641124	TTTCCTT	0.36621	0.36952
cg1245001	RGMB	c-Ets-1 [T	1366	1372	1.641124	AAGGAA	0.36621	0.36952
cg1245001	RGMB	c-Ets-1 [T	1371	1377	1.641124	AAGGAA	0.36621	0.36952
cg1245001	RGMB	c-Ets-1 [T	1439	1445	1.641124	TTTCCTT	0.36621	0.36952
cg0388534	RGMB	c-Ets-1 [T	1903	1909	1.641124	AAGGAA	0.36621	0.36952
cg0836780	RGMB	C/EBPbeta	86	89	1.639871	CCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	372	375	1.639871	CCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	720	723	1.639871	CCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	774	777	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	782	785	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	826	829	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	879	882	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	923	926	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	984	987	1.639871	CCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1020	1023	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1451	1454	1.639871	CCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1495	1498	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1589	1592	1.639871	CCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1633	1636	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1672	1675	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1820	1823	1.639871	CCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1878	1881	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1891	1894	1.639871	CCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	15	18	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	76	79	1.639871	CCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	112	115	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	543	546	1.639871	CCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	587	590	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	681	684	1.639871	CCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	725	728	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	764	767	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	912	915	1.639871	CCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	970	973	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	983	986	1.639871	CCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1110	1113	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1142	1145	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1165	1168	1.639871	CCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1382	1385	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1637	1640	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1875	1878	1.639871	TTGG	15.625	15.72563

cg1245001	RGMB	C/EBPbeta	1911	1914	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1925	1928	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1941	1944	1.639871	TTGG	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1993	1996	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	336	339	1.639871	CCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	341	344	1.639871	CCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	436	439	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	470	473	1.639871	CCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	635	638	1.639871	CCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	699	702	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	822	825	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	993	996	1.639871	CCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1004	1007	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1043	1046	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1138	1141	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1181	1184	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1571	1574	1.639871	CCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1640	1643	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1692	1695	1.639871	CCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1758	1761	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1859	1862	1.639871	TTGG	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1947	1950	1.639871	TTGG	15.625	15.72563
cg0836780	RGMB	IRF-1 [T0	1965	1973	1.616539	AGAGGG	0.04578	0.04655
cg1245001	RGMB	IRF-1 [T0	1057	1065	1.616539	AGAGGG	0.04578	0.04655
cg0836780	RGMB	XBP-1 [T	241	246	1.583727	GGTCAT	0.97656	0.98146
cg1245001	RGMB	XBP-1 [T	1594	1599	1.583727	TGTCAT	0.97656	0.98146
cg1245001	RGMB	XBP-1 [T	1733	1738	1.583727	TGTCAT	0.97656	0.98146
cg0388534	RGMB	XBP-1 [T	528	533	1.583727	TGTCAT	0.97656	0.98146
cg0388534	RGMB	XBP-1 [T	617	622	1.583727	TGTCAT	0.97656	0.98146
cg0388534	RGMB	XBP-1 [T	1092	1097	1.583727	GGTCAT	0.97656	0.98146
cg0836780	RGMB	Pax-5 [T0	855	861	1.537547	CTAGCC	0.73242	0.71311
cg0836780	RGMB	TFIID [T0	649	655	1.537547	TGGAAA	0.73242	0.75096
cg0836780	RGMB	TFIID [T0	1352	1358	1.537547	TTCAAA	0.73242	0.75096
cg1245001	RGMB	TFIID [T0	444	450	1.537547	TTCAAA	0.73242	0.75096
cg1245001	RGMB	TFIID [T0	1197	1203	1.537547	TACAAA	0.73242	0.75096
cg1245001	RGMB	TFIID [T0	1714	1720	1.537547	TTTTTCA	0.73242	0.75096
cg1245001	RGMB	TFIID [T0	1909	1915	1.537547	TTTTGG	0.73242	0.75096
cg1245001	RGMB	TFIID [T0	1962	1968	1.537547	TGAAAA	0.73242	0.75096
cg0388534	RGMB	Pax-5 [T0	1718	1724	1.537547	GGGCCA	0.73242	0.71311
cg0388534	RGMB	Pax-5 [T0	1861	1867	1.537547	GGGCGC	0.73242	0.71311
cg0388534	RGMB	Pax-5 [T0	1985	1991	1.537547	GGGCGG	0.73242	0.71311
cg0388534	RGMB	TFIID [T0	135	141	1.537547	TTTTAC	0.73242	0.75096
cg0388534	RGMB	TFIID [T0	830	836	1.537547	TTCAAA	0.73242	0.75096
cg0388534	RGMB	TFIID [T0	1288	1294	1.537547	TGGAAA	0.73242	0.75096
cg0388534	RGMB	TFIID [T0	1318	1324	1.537547	TGAAAA	0.73242	0.75096
cg0388534	RGMB	TFIID [T0	1672	1678	1.537547	TGTAAA	0.73242	0.75096
cg0836780	RGMB	IRF-1 [T0	739	747	1.529008	AAATGG	0.04578	0.04655
cg0388534	RGMB	c-Ets-1 [T	60	66	1.513038	TTTCCTC	0.36621	0.36952

cg0388534	RGMB	c-Ets-1 [T(	179	185	1.513038	TTTCCTC	0.36621	0.36952
cg0388534	RGMB	c-Ets-1 [T(	1214	1220	1.513038	TTTCCTC	0.36621	0.36952
cg0388534	RGMB	c-Ets-1 [T(	1867	1873	1.513038	GAGGAA	0.36621	0.36952
cg0836780	RGMB	RXR-alpha	1377	1383	1.474336	TAGACC(	0.48828	0.48222
cg1245001	RGMB	RXR-alpha	469	475	1.474336	TAGACC(	0.48828	0.48222
cg0836780	RGMB	STAT4 [T(	195	200	1.470588	GGAATT	1.95312	1.96333
cg0836780	RGMB	STAT4 [T(	246	251	1.470588	TTTTCC	1.95312	1.96333
cg0836780	RGMB	STAT4 [T(	288	293	1.470588	TTTTCC	1.95312	1.96333
cg0836780	RGMB	STAT4 [T(	452	457	1.470588	GGAAAA	1.95312	1.96333
cg0836780	RGMB	STAT4 [T(	539	544	1.470588	GGAAAA	1.95312	1.96333
cg0836780	RGMB	STAT4 [T(	650	655	1.470588	GGAAAA	1.95312	1.96333
cg0836780	RGMB	STAT4 [T(	791	796	1.470588	GTTTCC	1.95312	1.96333
cg0836780	RGMB	STAT4 [T(	1572	1577	1.470588	AATTCC	1.95312	1.96333
cg1245001	RGMB	STAT4 [T(	664	669	1.470588	AATTCC	1.95312	1.96333
cg1245001	RGMB	STAT4 [T(	1373	1378	1.470588	GGAAAA	1.95312	1.96333
cg1245001	RGMB	STAT4 [T(	1426	1431	1.470588	AATTCC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	59	64	1.470588	TTTTCC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	178	183	1.470588	TTTTCC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	194	199	1.470588	AGTTCC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	250	255	1.470588	GGAAAA	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	950	955	1.470588	AATTCC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	1213	1218	1.470588	TTTTCC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	1289	1294	1.470588	GGAAAA	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	1497	1502	1.470588	AATTCC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	1869	1874	1.470588	GGAAAC	1.95312	1.96333
cg0388534	RGMB	STAT4 [T(	1964	1969	1.470588	GGAACT	1.95312	1.96333
cg0836780	RGMB	PR B [T00	687	693	1.404665	GAGTGT	0.36621	0.37023
cg0836780	RGMB	PR A [T01	687	693	1.404665	GAGTGT	0.36621	0.37023
cg0836780	RGMB	NF-AT1 [	649	658	1.378139	TGGAAA	0.01907	0.0194
cg0388534	RGMB	NF-AT1 [	1288	1297	1.378139	TGGAAA	0.01907	0.0194
cg0836780	RGMB	C/EBPbeta	25	28	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	72	75	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	234	237	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	259	262	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	595	598	1.366559	TCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	629	632	1.366559	TCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	662	665	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	915	918	1.366559	TCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1064	1067	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1077	1080	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1322	1325	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1353	1356	1.366559	TCAA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1645	1648	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1680	1683	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1920	1923	1.366559	TTGA	15.625	15.72563
cg0836780	RGMB	C/EBPbeta	1925	1928	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	7	10	1.366559	TCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	156	159	1.366559	TTGA	15.625	15.72563

cg1245001	RGMB	C/EBPbeta	169	172	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	414	417	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	445	448	1.366559	TCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	737	740	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	772	775	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1012	1015	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1017	1020	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1150	1153	1.366559	TCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1270	1273	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1352	1355	1.366559	TCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1481	1484	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1499	1502	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1725	1728	1.366559	TCAA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1791	1794	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1946	1949	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1951	1954	1.366559	TTGA	15.625	15.72563
cg1245001	RGMB	C/EBPbeta	1983	1986	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	15	18	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	130	133	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	244	247	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	355	358	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	369	372	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	382	385	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	393	396	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	479	482	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	498	501	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	831	834	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	878	881	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	895	898	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	941	944	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1071	1074	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1088	1091	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1100	1103	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1265	1268	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1406	1409	1.366559	TTGA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1459	1462	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1606	1609	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1789	1792	1.366559	TCAA	15.625	15.72563
cg0388534	RGMB	C/EBPbeta	1800	1803	1.366559	TCAA	15.625	15.72563
cg083678	RGMB	AP-2alpha	1709	1714	1.357116	ACAGGC	0.48828	0.48203
cg1245001	RGMB	AP-2alpha	801	806	1.357116	ACAGGC	0.48828	0.48203
cg1245001	RGMB	AP-2alpha	1092	1097	1.357116	GCCTGT	0.48828	0.48203
cg1245001	RGMB	AP-2alpha	1226	1231	1.357116	GCCTGT	0.48828	0.48203
cg0388534	RGMB	AP-2alpha	693	698	1.357116	ACAGGC	0.48828	0.48203
cg0388534	RGMB	Sp1 [T007	1984	1993	1.28618	CGGGCG	0.03242	0.03129
cg0388534	RGMB	c-Myb [T0	1506	1513	1.285398	GGCAGT	0.06104	0.06064
cg1245001	RGMB	IRF-1 [T0	1364	1372	1.274173	AAAAGG	0.04578	0.04655
cg0388534	RGMB	C/EBPalp	367	373	1.220508	TATTGA	0.24414	0.247

cg0388534	RGMB	HNF-1A [	199	206	1.213286	CGTTTA	0.48828	0.49664
cg1245001	RGMB	PEA3 [T0	1804	1812	1.194633	CCACAT	0.06866	0.06895
cg0388534	RGMB	GATA-2 [	603	611	1.111111	GCATTA	0.09155	0.09208
cg0388534	RGMB	c-Ets-2 [T	180	188	1.071163	TTCCTCT	0.06104	0.06166
cg1245001	RGMB	HNF-1A [	1898	1905	1.069403	GCTTTA	0.48828	0.49664
cg0836780	RGMB	GATA-1 [	1188	1193	1.038567	TATCAT	1.95312	1.98662
cg1245001	RGMB	GATA-1 [	280	285	1.038567	TATCAT	1.95312	1.98662
cg1245001	RGMB	GATA-1 [	1481	1486	1.038567	TTGATA	1.95312	1.98662
cg0388534	RGMB	GATA-1 [	244	249	1.038567	TTGATA	1.95312	1.98662
cg0388534	RGMB	GATA-1 [	941	946	1.038567	TTGATA	1.95312	1.98662
cg0388534	RGMB	GATA-1 [	1069	1074	1.038567	TATCAA	1.95312	1.98662
cg0388534	RGMB	GATA-1 [	1146	1151	1.038567	TATCAT	1.95312	1.98662
cg0388534	RGMB	SRY [T00	461	469	0.999172	CTTTGTT	0.06104	0.06205
cg1245001	RGMB	TBP [T007	1536	1545	0.935771	TTTATA	0.12207	0.12628
cg0836780	RGMB	GATA-1 [	123	128	0.863549	GTGATA	1.95312	1.98662
cg0836780	RGMB	GR-beta [	106	110	0.840383	AATGA	7.8125	7.94706
cg0836780	RGMB	GR-beta [	243	247	0.840383	TCATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	386	390	0.840383	TAATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	444	448	0.840383	AATGG	7.8125	7.94706
cg0836780	RGMB	GR-beta [	477	481	0.840383	TAATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	532	536	0.840383	CAATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	533	537	0.840383	AATTA	7.8125	7.94706
cg0836780	RGMB	GR-beta [	596	600	0.840383	CAATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	597	601	0.840383	AATTA	7.8125	7.94706
cg0836780	RGMB	GR-beta [	740	744	0.840383	AATGG	7.8125	7.94706
cg0836780	RGMB	GR-beta [	746	750	0.840383	AATTG	7.8125	7.94706
cg0836780	RGMB	GR-beta [	824	828	0.840383	AATTG	7.8125	7.94706
cg0836780	RGMB	GR-beta [	958	962	0.840383	TCATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	970	974	0.840383	CCATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1229	1233	0.840383	TAATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1249	1253	0.840383	TCATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1325	1329	0.840383	AATGG	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1349	1353	0.840383	TCATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1358	1362	0.840383	AATGA	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1366	1370	0.840383	AATGA	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1484	1488	0.840383	TAATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1501	1505	0.840383	AATGA	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1571	1575	0.840383	CAATT	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1774	1778	0.840383	AATTA	7.8125	7.94706
cg0836780	RGMB	GR-beta [	1780	1784	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [	50	54	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [	62	66	0.840383	CCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [	321	325	0.840383	TAATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [	341	345	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [	417	421	0.840383	AATGG	7.8125	7.94706
cg1245001	RGMB	GR-beta [	441	445	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [	450	454	0.840383	AATGA	7.8125	7.94706
cg1245001	RGMB	GR-beta [	458	462	0.840383	AATGA	7.8125	7.94706

cg1245001	RGMB	GR-beta [T	576	580	0.840383	TAATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	593	597	0.840383	AATGA	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	663	667	0.840383	CAATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	866	870	0.840383	AATTA	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	872	876	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1202	1206	0.840383	AATTA	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1449	1453	0.840383	AATGG	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1505	1509	0.840383	TAATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1506	1510	0.840383	AATTA	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1596	1600	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1623	1627	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1735	1739	0.840383	TCATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1818	1822	0.840383	AATGA	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1894	1898	0.840383	AATGG	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1930	1934	0.840383	TAATT	7.8125	7.94706
cg1245001	RGMB	GR-beta [T	1977	1981	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	51	55	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	101	105	0.840383	AATTG	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	222	226	0.840383	AATGA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	350	354	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	427	431	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	544	548	0.840383	TAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	545	549	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	557	561	0.840383	TAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	558	562	0.840383	AATTG	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	642	646	0.840383	TCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	768	772	0.840383	AATGA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	803	807	0.840383	TCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	827	831	0.840383	CAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	879	883	0.840383	CAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	880	884	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	892	896	0.840383	CCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	904	908	0.840383	TCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	956	960	0.840383	TAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	957	961	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1024	1028	0.840383	AATGG	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1094	1098	0.840383	TCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1136	1140	0.840383	AATTG	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1204	1208	0.840383	CAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1205	1209	0.840383	AATTG	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1262	1266	0.840383	CCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1268	1272	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1352	1356	0.840383	TAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1353	1357	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1381	1385	0.840383	TCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1385	1389	0.840383	TAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1386	1390	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1737	1741	0.840383	TAATT	7.8125	7.94706

cg0388534	RGMB	GR-beta [T	1738	1742	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1743	1747	0.840383	AATTA	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1785	1789	0.840383	TAATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1850	1854	0.840383	CCATT	7.8125	7.94706
cg0388534	RGMB	GR-beta [T	1972	1976	0.840383	AATTA	7.8125	7.94706
cg0836780	RGMB	HNF-1A [	669	676	0.781639	GTTAAA	0.48828	0.49664
cg0388534	RGMB	GATA-1 [	924	929	0.758539	TATCAG	1.95312	1.98662
cg1245001	RGMB	AP-2alpha	1159	1164	0.678558	GCCTGA	0.48828	0.48199
cg0836780	RGMB	PEA3 [T0	1637	1645	0.597316	CTACAT	0.04578	0.04629
cg1245001	RGMB	PEA3 [T0	729	737	0.597316	CTACAT	0.04578	0.04629
cg0836780	RGMB	C/EBPalph	761	767	0.540941	GATTGT	0.24414	0.24507
cg0836780	RGMB	C/EBPalph	1273	1279	0.540941	GATTGT	0.24414	0.24507
cg0836780	RGMB	C/EBPalph	1819	1825	0.540941	CCCAAT	0.24414	0.24507
cg1245001	RGMB	C/EBPalph	365	371	0.540941	GATTGT	0.24414	0.24507
cg1245001	RGMB	C/EBPalph	911	917	0.540941	CCCAAT	0.24414	0.24507
cg0388534	RGMB	PR B [T00	191	197	0.48823	AACAGT	0.12207	0.12407
cg0388534	RGMB	PR A [T01	191	197	0.48823	AACAGT	0.12207	0.12407
cg0388534	RGMB	NF-AT1 [	175	183	0.479048	AGTTTT	0.02289	0.02328
cg0836780	RGMB	HNF-1A [	1042	1049	0.287765	GTTAAA	0.24414	0.24974
cg0836780	RGMB	HNF-1A [	1307	1314	0.287765	GTTAAA	0.24414	0.24974
cg1245001	RGMB	HNF-1A [	134	141	0.287765	GTTAAA	0.24414	0.24974
cg1245001	RGMB	HNF-1A [	399	406	0.287765	GTTAAA	0.24414	0.24974
cg0836780	RGMB	GATA-1 [	276	281	0.280028	TAGATA	0.97656	0.99875
cg0836780	RGMB	GATA-1 [	674	679	0.280028	AAGATA	0.97656	0.99875
cg0836780	RGMB	GATA-1 [	943	948	0.280028	TATCTT	0.97656	0.99875
cg1245001	RGMB	GATA-1 [	35	40	0.280028	TATCTT	0.97656	0.99875
cg0388534	RGMB	GATA-1 [	540	545	0.280028	TATCTA	0.97656	0.99875
cg0388534	RGMB	GATA-1 [	564	569	0.280028	AAGATA	0.97656	0.99875
cg0388534	RGMB	GATA-1 [	607	612	0.280028	TATCTA	0.97656	0.99875
cg0388534	RGMB	GATA-1 [	1107	1112	0.280028	TAGATA	0.97656	0.99875
cg1245001	RGMB	c-Ets-1 [T	1394	1400	0.256174	AAGGAA	0.24414	0.24569
cg0836780	RGMB	AP-2alpha	1177	1182	0.226186	GCCTGG	0.97656	0.95305
cg0836780	RGMB	AP-2alpha	1746	1751	0.226186	GCCTGG	0.97656	0.95305
cg1245001	RGMB	AP-2alpha	269	274	0.226186	GCCTGG	0.97656	0.95305
cg1245001	RGMB	AP-2alpha	838	843	0.226186	GCCTGG	0.97656	0.95305
cg1245001	RGMB	AP-2alpha	1324	1329	0.226186	GCCTGG	0.97656	0.95305
cg0388534	RGMB	AP-2alpha	650	655	0.226186	CCAGGC	0.97656	0.95305
cg0836780	RGMB	GR-alpha [	237	241	0.207689	AAAGG	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	250	254	0.207689	CCTTT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	301	305	0.207689	CCTTT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	865	869	0.207689	AAAGG	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	886	890	0.207689	AAAGG	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1060	1064	0.207689	CCTTT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1525	1529	0.207689	CCTTT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1565	1569	0.207689	CCTCT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1842	1846	0.207689	CCTCT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1965	1969	0.207689	AGAGG	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1971	1975	0.207689	AAAGG	7.8125	7.81264

cg1245001	RGMB	GR-alpha [	152	156	0.207689	CCTTT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	617	621	0.207689	CCTTT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	657	661	0.207689	CCTCT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	934	938	0.207689	CCTCT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1057	1061	0.207689	AGAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1063	1067	0.207689	AAAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1365	1369	0.207689	AAAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1370	1374	0.207689	AAAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1376	1380	0.207689	AAAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1407	1411	0.207689	AAAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1754	1758	0.207689	AGAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1856	1860	0.207689	CCTTT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1867	1871	0.207689	CCTTT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1907	1911	0.207689	CCTTT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	63	67	0.207689	CCTCT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	144	148	0.207689	AGAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	182	186	0.207689	CCTCT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	238	242	0.207689	CCTCT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	721	725	0.207689	AAAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1049	1053	0.207689	AAAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1055	1059	0.207689	AAAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1188	1192	0.207689	CCTCT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1244	1248	0.207689	AAAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1428	1432	0.207689	CCTCT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1647	1651	0.207689	AAAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1795	1799	0.207689	AGAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1802	1806	0.207689	AAAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1813	1817	0.207689	CCTTT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1895	1899	0.207689	AGAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1907	1911	0.207689	AAAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1940	1944	0.207689	AGAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1994	1998	0.207689	AGAGG	7.8125	7.81264
cg1245001	RGMB	HNF-1A [	1928	1935	0.143882	GTTAAT	0.24414	0.25261
cg0388534	RGMB	Elk-1 [T00	1686	1694	0.134348	CTTCCT	0.06104	0.06047
cg0388534	RGMB	c-Ets-1 [T	627	633	0.128087	CTTCCT	0.24414	0.2429
cg0388534	RGMB	c-Ets-1 [T	1686	1692	0.128087	CTTCCT	0.24414	0.2429
cg0836780	RGMB	GR-alpha [	129	133	0	CCTAT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	311	315	0	CCTGT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	807	811	0	ATAGG	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	814	818	0	CCTGT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1039	1043	0	CCTGT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1683	1687	0	ACAGG	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1703	1707	0	CCTAT	7.8125	7.81264
cg0836780	RGMB	GR-alpha [	1709	1713	0	ACAGG	7.8125	7.81264
cg0836780	RGMB	AP-2alpha	99	104	0	GCCTGC	0.97656	0.95305
cg0836780	RGMB	XBP-1 [T	1778	1783	0	AGTCAT	0.97656	0.98127
cg0836780	RGMB	TFII-I [T0	1969	1974	0	GGAAAG	1.46484	1.45997
cg0836780	RGMB	STAT4 [T	743	748	0	GGAAAT	0.48828	0.49387

cg0836780	RGMB	YY1 [T00	36	39	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	119	122	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	404	407	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	413	416	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	445	448	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	712	715	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	741	744	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	796	799	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	805	808	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	970	973	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1008	1011	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1156	1159	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1207	1210	0	CCAT	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1211	1214	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1326	1329	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1594	1597	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1624	1627	0	ATGG	7.8125	7.81711
cg0836780	RGMB	YY1 [T00	1853	1856	0	CCAT	7.8125	7.81711
cg0836780	RGMB	ER-alpha [	241	245	0	GGTCA	1.95312	1.9404
cg0836780	RGMB	ER-alpha [	1447	1451	0	TGACC	1.95312	1.9404
cg0836780	RGMB	ER-alpha [	1816	1820	0	TGACC	1.95312	1.9404
cg0836780	RGMB	GATA-1 [	29	34	0	CAGATA	0.97656	0.98738
cg0836780	RGMB	GATA-1 [	1115	1120	0	CAGATA	0.97656	0.98738
cg0836780	RGMB	GATA-1 [	1438	1443	0	CAGATA	0.97656	0.98738
cg0836780	RGMB	C/EBPbeta	103	106	0	GCAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	200	203	0	TTGC	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	208	211	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	265	268	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	307	310	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	332	335	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	486	489	0	TTGC	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	496	499	0	TTGC	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	531	534	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	693	696	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	748	751	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	763	766	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	789	792	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	802	805	0	TTGC	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	852	855	0	TTGC	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	987	990	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1012	1015	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1017	1020	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1107	1110	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1131	1134	0	GCAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1150	1153	0	TTGC	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1275	1278	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1384	1387	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1532	1535	0	TTGC	15.625	15.71349

cg0836780	RGMB	C/EBPbeta	1560	1563	0	GCAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1570	1573	0	GCAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1605	1608	0	TTGC	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1651	1654	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1667	1670	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1713	1716	0	GCAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1725	1728	0	TTGT	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1771	1774	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1797	1800	0	ACAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1896	1899	0	GCAA	15.625	15.71349
cg0836780	RGMB	C/EBPbeta	1932	1935	0	TTGT	15.625	15.71349
cg0836780	RGMB	NFI/CTF [	1820	1827	0	CCAATC	0.18311	0.18147
cg0836780	RGMB	TFIID [T0	139	145	0	TTTTTAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	141	147	0	TTTAAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	142	148	0	TTAAAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	143	149	0	TAAAAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	188	194	0	TTTTCTA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	218	224	0	TTTTTTA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	219	225	0	TTTTTAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	519	525	0	TTTTTAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	555	561	0	TAAAAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	617	623	0	TAGAAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	893	899	0	TAGAAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	1353	1359	0	TCAAAA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	1552	1558	0	TTTTTTA	1.09863	1.13474
cg0836780	RGMB	TFIID [T0	1553	1559	0	TTTTTAA	1.09863	1.13474
cg0836780	RGMB	FOXP3 [T	331	336	0	CACAAC	1.46484	1.47315
cg0836780	RGMB	FOXP3 [T	1011	1016	0	GACAAC	1.46484	1.47315
cg0836780	RGMB	FOXP3 [T	1106	1111	0	GTTGTT	1.46484	1.47315
cg0836780	RGMB	FOXP3 [T	1724	1729	0	GTTGTC	1.46484	1.47315
cg0836780	RGMB	GR-beta [T	197	201	0	AATTT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	214	218	0	AATTT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	387	391	0	AATTT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	456	460	0	AATGT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	478	482	0	AATTT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	653	657	0	AAATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	654	658	0	AATTT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	724	728	0	AATGT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	745	749	0	AAATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	830	834	0	AATGT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	920	924	0	AATTT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	927	931	0	AATGT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	989	993	0	AATGT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	1219	1223	0	ACATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	1735	1739	0	AAATT	3.90625	3.99611
cg0836780	RGMB	GR-beta [T	1773	1777	0	AAATT	3.90625	3.99611
cg0836780	RGMB	GR [T050	303	309	0	TTTTTTG	0.36621	0.37562
cg0836780	RGMB	GR [T050	1354	1360	0	CAAAAA	0.36621	0.37562

cg0836780	RGMB	GR [T050	1452	1458	0	CAAAAA	0.36621	0.37562
cg0836780	RGMB	HNF-3alph	1415	1422	0	TGAAAA	0.09155	0.09511
cg0836780	RGMB	TCF-4E [T	850	856	0	CTTTGCT	0.12207	0.12262
cg0836780	RGMB	HNF-1A [	519	526	0	TTTTTAA	0.24414	0.25261
cg0836780	RGMB	IRF-2 [T01	1224	1229	0	TCACTT	0.48828	0.49387
cg0836780	RGMB	c-Myc [T0	1291	1296	0	CACGTG	0.48828	0.48199
cg1245001	RGMB	GR-alpha [	131	135	0	CCTGT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	775	779	0	ACAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	795	799	0	CCTAT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	801	805	0	ACAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1093	1097	0	CCTGT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1180	1184	0	CCTGT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1227	1231	0	CCTGT	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1559	1563	0	ATAGG	7.8125	7.81264
cg1245001	RGMB	GR-alpha [	1767	1771	0	CCTGT	7.8125	7.81264
cg1245001	RGMB	XBP-1 [T0	870	875	0	AGTCAT	0.97656	0.98127
cg1245001	RGMB	XBP-1 [T0	1491	1496	0	ATGACT	0.97656	0.98127
cg1245001	RGMB	Pax-5 [T0	1851	1857	0	CAAGCC	1.09863	1.06846
cg1245001	RGMB	TFII-I [T0	1061	1066	0	GGAAAG	1.46484	1.45997
cg1245001	RGMB	TFII-I [T0	1368	1373	0	GGAAAG	1.46484	1.45997
cg1245001	RGMB	TFII-I [T0	1438	1443	0	CTTTCC	1.46484	1.45997
cg1245001	RGMB	TFII-I [T0	1528	1533	0	GGATAG	1.46484	1.45997
cg1245001	RGMB	STAT4 [T	1464	1469	0	ATTTCC	0.48828	0.49387
cg1245001	RGMB	STAT4 [T	1747	1752	0	GGAAAT	0.48828	0.49387
cg1245001	RGMB	STAT4 [T	1879	1884	0	ATTTCC	0.48828	0.49387
cg1245001	RGMB	YY1 [T00	62	65	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	100	103	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	248	251	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	299	302	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	303	306	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	418	421	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	686	689	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	716	719	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	945	948	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1170	1173	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1450	1453	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1456	1459	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1468	1471	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1544	1547	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1643	1646	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1722	1725	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1773	1776	0	ATGG	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1884	1887	0	CCAT	7.8125	7.81711
cg1245001	RGMB	YY1 [T00	1895	1898	0	ATGG	7.8125	7.81711
cg1245001	RGMB	ER-alpha [	539	543	0	TGACC	1.95312	1.9404
cg1245001	RGMB	ER-alpha [	908	912	0	TGACC	1.95312	1.9404
cg1245001	RGMB	ER-alpha [	1162	1166	0	TGACC	1.95312	1.9404
cg1245001	RGMB	ER-alpha [	1764	1768	0	TGACC	1.95312	1.9404

cg1245001	RGMB	GATA-1 [	207	212	0	CAGATA	0.97656	0.98738
cg1245001	RGMB	GATA-1 [	530	535	0	CAGATA	0.97656	0.98738
cg1245001	RGMB	GATA-1 [	1669	1674	0	TATCTG	0.97656	0.98738
cg1245001	RGMB	C/EBPbeta	79	82	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	104	107	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	109	112	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	199	202	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	223	226	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	242	245	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	367	370	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	476	479	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	624	627	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	652	655	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	662	665	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	697	700	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	743	746	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	759	762	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	805	808	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	817	820	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	863	866	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	889	892	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	988	991	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1024	1027	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1198	1201	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1290	1293	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1330	1333	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1333	1336	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1339	1342	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1390	1393	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1392	1395	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1555	1558	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1568	1571	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1588	1591	0	TTGT	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1657	1660	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1694	1697	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1738	1741	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1781	1784	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1784	1787	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1850	1853	0	ACAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1870	1873	0	TTGC	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1890	1893	0	GCAA	15.625	15.71349
cg1245001	RGMB	C/EBPbeta	1917	1920	0	TTGT	15.625	15.71349
cg1245001	RGMB	NFI/CTF [	912	919	0	CCAATC	0.18311	0.18147
cg1245001	RGMB	TFIID [T0	445	451	0	TCAAAA	1.09863	1.13474
cg1245001	RGMB	TFIID [T0	644	650	0	TTTTTTA	1.09863	1.13474
cg1245001	RGMB	TFIID [T0	645	651	0	TTTTTAA	1.09863	1.13474
cg1245001	RGMB	TFIID [T0	1352	1358	0	TCAAAA	1.09863	1.13474
cg1245001	RGMB	TFIID [T0	1535	1541	0	TTTTATA	1.09863	1.13474

cg1245001	RGMB	TFIID [T0	1677	1683	0	TTTAAA/	1.09863	1.13474
cg1245001	RGMB	FOXP3 [T	103	108	0	GACAAC	1.46484	1.47315
cg1245001	RGMB	FOXP3 [T	198	203	0	GTTGTT	1.46484	1.47315
cg1245001	RGMB	FOXP3 [T	816	821	0	GTTGTC	1.46484	1.47315
cg1245001	RGMB	FOXP3 [T	1780	1785	0	AACAAC	1.46484	1.47315
cg1245001	RGMB	FOXP3 [T	1916	1921	0	GTTGTT	1.46484	1.47315
cg1245001	RGMB	GR-beta [T	12	16	0	AATTT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	19	23	0	AATGT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	81	85	0	AATGT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	311	315	0	ACATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	827	831	0	AAATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	865	869	0	AAATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	1201	1205	0	AAATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	1425	1429	0	AAATT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	1931	1935	0	AATTT	3.90625	3.99611
cg1245001	RGMB	GR-beta [T	1976	1980	0	AAATT	3.90625	3.99611
cg1245001	RGMB	PR B [T00	1471	1477	0	TACTGTT	0.36621	0.36944
cg1245001	RGMB	PR A [T01	1471	1477	0	TACTGTT	0.36621	0.36944
cg1245001	RGMB	GR [T050	446	452	0	CAAAAA	0.36621	0.37562
cg1245001	RGMB	GR [T050	544	550	0	CAAAAA	0.36621	0.37562
cg1245001	RGMB	GR [T050	1353	1359	0	CAAAAA	0.36621	0.37562
cg1245001	RGMB	HNF-3alph	507	514	0	TGAAAA	0.09155	0.09511
cg1245001	RGMB	HNF-3alph	1191	1198	0	TAAAAA	0.09155	0.09511
cg1245001	RGMB	IRF-2 [T01	316	321	0	TCACTT	0.48828	0.49387
cg1245001	RGMB	c-Myc [T0	383	388	0	CACGTG	0.48828	0.48199
cg0388534	RGMB	GR-alpha [	7	11	0	CCTAT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	21	25	0	ATAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	247	251	0	ATAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	281	285	0	ACAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	288	292	0	ATAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	417	421	0	ATAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	693	697	0	ACAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	792	796	0	ATAGG	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1033	1037	0	CCTGT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1535	1539	0	CCTAT	7.8125	7.81264
cg0388534	RGMB	GR-alpha [	1960	1964	0	ACAGG	7.8125	7.81264
cg0388534	RGMB	AP-2alpha	1681	1686	0	GCCTGC	0.97656	0.95305
cg0388534	RGMB	XBP-1 [T0	223	228	0	ATGACT	0.97656	0.98127
cg0388534	RGMB	XBP-1 [T0	640	645	0	AGTCAT	0.97656	0.98127
cg0388534	RGMB	XBP-1 [T0	741	746	0	AGTCAT	0.97656	0.98127
cg0388534	RGMB	RXR-alpha	438	444	0	GGGTTA/	0.24414	0.2444
cg0388534	RGMB	Pax-5 [T0	1526	1532	0	CCAGCC	1.09863	1.06846
cg0388534	RGMB	Pax-5 [T0	1724	1730	0	GGGCAG	1.09863	1.06846
cg0388534	RGMB	p53 [T006	1724	1730	0	GGGCAG	0.36621	0.35912
cg0388534	RGMB	TFII-I [T0	328	333	0	GGAAAG	1.46484	1.45997
cg0388534	RGMB	TFII-I [T0	713	718	0	GGATAG	1.46484	1.45997
cg0388534	RGMB	TFII-I [T0	1047	1052	0	GGAAAG	1.46484	1.45997
cg0388534	RGMB	TFII-I [T0	1905	1910	0	GGAAAG	1.46484	1.45997

cg0388534	RGMB	TFII-I [T0	1958	1963	0	GGACAG	1.46484	1.45997
cg0388534	RGMB	STAT4 [T	1452	1457	0	GGAAAT	0.48828	0.49387
cg0388534	RGMB	STAT4 [T	1567	1572	0	ATTTCC	0.48828	0.49387
cg0388534	RGMB	c-Ets-1 [T	1445	1451	0	CAGGAA	0.24414	0.2429
cg0388534	RGMB	YY1 [T00	276	279	0	ATGG	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	683	686	0	ATGG	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	892	895	0	CCAT	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	1025	1028	0	ATGG	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	1231	1234	0	CCAT	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	1262	1265	0	CCAT	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	1531	1534	0	CCAT	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	1850	1853	0	CCAT	7.8125	7.81711
cg0388534	RGMB	YY1 [T00	1956	1959	0	ATGG	7.8125	7.81711
cg0388534	RGMB	Elk-1 [T00	627	635	0	CTTCCTC	0.06104	0.06047
cg0388534	RGMB	ER-alpha [	4	8	0	TGACC	1.95312	1.9404
cg0388534	RGMB	ER-alpha [	1092	1096	0	GGTCA	1.95312	1.9404
cg0388534	RGMB	ER-alpha [	1798	1802	0	GGTCA	1.95312	1.9404
cg0388534	RGMB	GATA-1 [	789	794	0	CAGATA	0.97656	0.98738
cg0388534	RGMB	GATA-1 [	1537	1542	0	TATCTG	0.97656	0.98738
cg0388534	RGMB	C/EBPbeta	33	36	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	44	47	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	88	91	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	103	106	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	127	130	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	139	142	0	ACAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	150	153	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	218	221	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	220	223	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	463	466	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	560	563	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	562	565	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	578	581	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	654	657	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	709	712	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	758	761	0	ACAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	826	829	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	871	874	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	990	993	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1028	1031	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1053	1056	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1133	1136	0	ACAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1197	1200	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1203	1206	0	ACAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1207	1210	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1285	1288	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1315	1318	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1333	1336	0	GCAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1336	1339	0	ACAA	15.625	15.71349

cg0388534	RGMB	C/EBPbeta	1339	1342	0	ACAA	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1413	1416	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1435	1438	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1588	1591	0	TTGC	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1816	1819	0	TTGT	15.625	15.71349
cg0388534	RGMB	C/EBPbeta	1840	1843	0	TTGC	15.625	15.71349
cg0388534	RGMB	TFIID [T0	15	21	0	TTGAAA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	303	309	0	TAAAAA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	413	419	0	TTTTATA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	479	485	0	TTGAAA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	506	512	0	TTTTTTA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	507	513	0	TTTTTAA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	609	615	0	TCTAAA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	1745	1751	0	TTAAAA	1.09863	1.13474
cg0388534	RGMB	TFIID [T0	1746	1752	0	TAAAAA	1.09863	1.13474
cg0388534	RGMB	FOXP3 [T	1335	1340	0	AACAAC	1.46484	1.47315
cg0388534	RGMB	GR-beta [T	50	54	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	132	136	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	133	137	0	AATTT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	349	353	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	453	457	0	AATGT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	572	576	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	573	577	0	AATTT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	615	619	0	AATGT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	835	839	0	AATGT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	949	953	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1135	1139	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1281	1285	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1282	1286	0	AATTT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1292	1296	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1293	1297	0	AATTT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1311	1315	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1312	1316	0	AATTT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1455	1459	0	AATGT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1559	1563	0	ACATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1742	1746	0	AAATT	3.90625	3.99611
cg0388534	RGMB	GR-beta [T	1781	1785	0	ACATT	3.90625	3.99611
cg0388534	RGMB	PR B [T00	1872	1878	0	AACAGT	0.36621	0.36944
cg0388534	RGMB	PR A [T01	1872	1878	0	AACAGT	0.36621	0.36944
cg0388534	RGMB	GR [T050	574	580	0	ATTTTTC	0.36621	0.37562
cg0388534	RGMB	HNF-3alph	16	23	0	TGAAAA	0.09155	0.09511
cg0388534	RGMB	IRF-2 [T01	96	101	0	AAGTGA	0.48828	0.49387
cg0388534	RGMB	IRF-2 [T01	399	404	0	AAGTGA	0.48828	0.49387
cg0388534	RGMB	IRF-2 [T01	847	852	0	AAGTGA	0.48828	0.49387
cg0388534	RGMB	IRF-2 [T01	1219	1224	0	TCACTT	0.48828	0.49387
cg0388534	RGMB	IRF-2 [T01	1252	1257	0	AAGTGA	0.48828	0.49387
cg1719341	RLIM	c-Ets-1 [T	554	560	9.969337	ATTCCC	0.24414	0.2459
cg1719341	RLIM	XBP-1 [T	168	173	9.789909	CGCCAT	1.95312	1.95208

cg1719341	RLIM	XBP-1 [T0	729	734	9.789909	AGCCAT	1.95312	1.95208
cg1719341	RLIM	XBP-1 [T0	971	976	9.789909	CGCCAT	1.95312	1.95208
cg1719341	RLIM	XBP-1 [T0	1072	1077	9.789909	AGACAT	1.95312	1.95208
cg1719341	RLIM	NF-kappa	1805	1816	9.729343	TGGGAA	0.01776	0.01758
cg1719341	RLIM	c-Myb [T0	1122	1129	9.729271	ATCAGT	0.36621	0.37054
cg1719341	RLIM	ELF-1 [T0	328	340	9.604198	CGAGAG	0.00417	0.00423
cg1719341	RLIM	NF-AT1 [	174	182	9.557905	GGAAAA	0.16785	0.1682
cg1719341	RLIM	Pax-5 [T0	39	45	9.552105	GGGCGC	1.46484	1.43083
cg1719341	RLIM	Pax-5 [T0	907	913	9.552105	GGGCGG	1.46484	1.43083
cg1719341	RLIM	Pax-5 [T0	938	944	9.552105	GACGCC	1.46484	1.43083
cg1719341	RLIM	Pax-5 [T0	1318	1324	9.552105	GGGCGG	1.46484	1.43083
cg1719341	RLIM	Pax-5 [T0	1416	1422	9.552105	GGGCGC	1.46484	1.43083
cg1719341	RLIM	TFIID [T0	84	90	9.552105	TTTGGA	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	151	157	9.552105	TTTCCC	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	153	159	9.552105	TCCCAA	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	543	549	9.552105	TTTCTCA	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	916	922	9.552105	TTTGGA	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	1027	1033	9.552105	TTTCCC	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	1302	1308	9.552105	TTTGGG	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	1390	1396	9.552105	TACGAA	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	1776	1782	9.552105	TTCGAA	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	1805	1811	9.552105	TGGGAA	1.46484	1.48472
cg1719341	RLIM	TFIID [T0	1966	1972	9.552105	TTTCCC	1.46484	1.48472
cg1719341	RLIM	TFII-I [T0	150	155	9.512894	TTTTCC	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	174	179	9.512894	GGAAAA	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	350	355	9.512894	CCTTCC	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	765	770	9.512894	GGAAAC	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	883	888	9.512894	GGACGG	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	919	924	9.512894	GGAAAA	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1581	1586	9.512894	AAATCC	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1616	1621	9.512894	GGACAA	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1688	1693	9.512894	GGAAGG	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1716	1721	9.512894	GGACAA	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1807	1812	9.512894	GGAAAA	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1826	1831	9.512894	GGATTT	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1931	1936	9.512894	GGAAAA	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1959	1964	9.512894	TTTTCC	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1965	1970	9.512894	TTTTCC	7.32422	7.29728
cg1719341	RLIM	TFII-I [T0	1982	1987	9.512894	TTTTCC	7.32422	7.29728
cg1719341	RLIM	FOXP3 [T	107	112	9.512894	GTTGCC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	205	210	9.512894	GAGAAC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	427	432	9.512894	AGCAAC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	495	500	9.512894	GAGAAC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	601	606	9.512894	GTTGGT	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	718	723	9.512894	GTTGCT	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	933	938	9.512894	GTTATG	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	1001	1006	9.512894	GTTCTG	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	1194	1199	9.512894	GCCAAC	7.32422	7.35678

cg1719341	RLIM	FOXP3 [T	1357	1362	9.512894	GCCAAC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	1589	1594	9.512894	GTTCTC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	1747	1752	9.512894	GATAAC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	1816	1821	9.512894	GATAAC	7.32422	7.35678
cg1719341	RLIM	FOXP3 [T	1822	1827	9.512894	GTTGGG	7.32422	7.35678
cg1719341	RLIM	TCF-4E [T	1752	1758	9.453578	CTTTGA	0.48828	0.49215
cg1719341	RLIM	c-Jun [T00	1916	1922	9.397655	ATTGTC	0.73242	0.73031
cg1719341	RLIM	c-Ets-1 [T	1014	1020	9.276861	TGGGAA	0.36621	0.36441
cg1719341	RLIM	E2F-1 [T0	966	973	9.261732	TCCTCC	0.15259	0.14917
cg1719341	RLIM	MEF-2A [	1381	1391	9.220261	TACTAA	0.07343	0.07563
cg1719341	RLIM	NF-AT1 [	1023	1031	9.18189	TCGCTTT	0.22888	0.22959
cg1719341	RLIM	PPAR-alph	29	39	9.158357	CGGCCC	0.0515	0.04986
cg1719341	RLIM	c-Ets-1 [T	1886	1892	9.148774	AGGGAA	0.85449	0.85523
cg1719341	RLIM	c-Myb [T0	1943	1950	9.110773	CCAAGT	0.39673	0.40028
cg1719341	RLIM	COUP-TF	183	195	9.093379	GGGGAG	0.01878	0.01865
cg1719341	RLIM	NFI/CTF [	1195	1202	9.042931	CCAACT	0.48828	0.48804
cg1719341	RLIM	NF-AT1 [	87	95	9.042733	GGAAAT	0.22888	0.22959
cg1719341	RLIM	NF-AT1 [	1229	1237	9.042733	GGAAAT	0.22888	0.22959
cg1719341	RLIM	E2F-1 [T0	181	188	9.028527	GCGGGG	0.27466	0.26875
cg1719341	RLIM	c-Jun [T00	1202	1208	9.013496	CATGTC	0.61035	0.61059
cg1719341	RLIM	LEF-1 [T0	1301	1308	8.973041	CTTTGG	0.54932	0.55326
cg1719341	RLIM	GR [T050	1579	1585	8.971049	CAAAAT	0.61035	0.61632
cg1719341	RLIM	c-Ets-2 [T	284	292	8.912323	TTCCTAA	0.27466	0.27495
cg1719341	RLIM	c-Ets-2 [T	1224	1232	8.912323	GCTTAG	0.27466	0.27495
cg1719341	RLIM	ETF [T002	957	967	8.876947	GCCCCA	0.02384	0.02303
cg1719341	RLIM	c-Myb [T0	1889	1896	8.872587	GAACTC	0.39673	0.40028
cg1719341	RLIM	PR B [T00	929	935	8.827054	AGCTGT	0.36621	0.36944
cg1719341	RLIM	PR B [T00	1572	1578	8.827054	AACAGA	0.36621	0.36944
cg1719341	RLIM	PR A [T01	929	935	8.827054	AGCTGT	0.36621	0.36944
cg1719341	RLIM	PR A [T01	1572	1578	8.827054	AACAGA	0.36621	0.36944
cg1719341	RLIM	NFI/CTF [	119	126	8.814757	TCACTT	0.48828	0.48804
cg1719341	RLIM	NF-1 [T00	151	158	8.790071	TTTCCC	0.24414	0.24467
cg1719341	RLIM	NF-1 [T00	1303	1310	8.790071	TTGGGA	0.24414	0.24467
cg1719341	RLIM	NF-1 [T00	1966	1973	8.790071	TTTCCC	0.24414	0.24467
cg1719341	RLIM	E2F-1 [T0	627	634	8.76494	TGCTCC	0.27466	0.26875
cg1719341	RLIM	XBP-1 [T	1651	1656	8.75604	TATCAT	2.92969	2.9674
cg1719341	RLIM	NF-AT1 [	147	155	8.532897	CCCTTTT	0.10681	0.10725
cg1719341	RLIM	NF-AT1 [	919	927	8.532897	GGAAAA	0.10681	0.10725
cg1719341	RLIM	NF-AT1 [	1962	1970	8.532897	TCCTTTT	0.10681	0.10725
cg1719341	RLIM	IRF-1 [T0	83	91	8.497322	TTTTGG	0.20599	0.20664
cg1719341	RLIM	IRF-1 [T0	915	923	8.497322	GTTTGG	0.20599	0.20664
cg1719341	RLIM	LEF-1 [T0	357	364	8.457856	CTTCAA	0.15259	0.15214
cg1719341	RLIM	LEF-1 [T0	1752	1759	8.457856	CTTTGA	0.15259	0.15214
cg1719341	RLIM	PR B [T00	208	214	8.338824	AACAGA	1.09863	1.10009
cg1719341	RLIM	PR B [T00	781	787	8.338824	AACAGG	1.09863	1.10009
cg1719341	RLIM	PR B [T00	1261	1267	8.338824	AACAGG	1.09863	1.10009
cg1719341	RLIM	PR B [T00	1977	1983	8.338824	TTCTGTT	1.09863	1.10009
cg1719341	RLIM	PR A [T01	208	214	8.338824	AACAGA	1.09863	1.10009

cg1719341	RLIM	PR A [T01	781	787	8.338824	AACAGG	1.09863	1.10009
cg1719341	RLIM	PR A [T01	1261	1267	8.338824	AACAGG	1.09863	1.10009
cg1719341	RLIM	PR A [T01	1977	1983	8.338824	TTCTGTT	1.09863	1.10009
cg1719341	RLIM	ATF3 [T01	1048	1055	8.313799	GGACGT	0.27466	0.27431
cg1719341	RLIM	PU.1 [T02	328	340	8.291334	CGAGAG	0.00918	0.00926
cg1719341	RLIM	GR-alpha [	65	69	8.281568	GAAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	185	189	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	199	203	8.281568	CCTCC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	273	277	8.281568	CCTCC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	297	301	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	347	351	8.281568	CCTCC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	350	354	8.281568	CCTTC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	356	360	8.281568	CCTTC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	446	450	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	621	625	8.281568	CGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	636	640	8.281568	CCTCC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	663	667	8.281568	CCTCC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	853	857	8.281568	CCTCG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	871	875	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	874	878	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	877	881	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	901	905	8.281568	CAAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	964	968	8.281568	CCTCC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	967	971	8.281568	CCTCC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1020	1024	8.281568	CCTTC	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1045	1049	8.281568	GAAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1441	1445	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1472	1476	8.281568	GGAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1532	1536	8.281568	CAAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1672	1676	8.281568	CAAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1685	1689	8.281568	CAAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1689	1693	8.281568	GAAGG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1708	1712	8.281568	CCTTG	7.8125	7.72956
cg1719341	RLIM	GR-alpha [	1849	1853	8.281568	GAAGG	7.8125	7.72956
cg1719341	RLIM	c-Jun [T00	186	192	8.242207	GAGGTC	0.48828	0.49076
cg1719341	RLIM	c-Jun [T00	1331	1337	8.242207	GAGGTC	0.48828	0.49076
cg1719341	RLIM	ENKTF-1	165	172	8.19852	GCCCGC	0.73242	0.71737
cg1719341	RLIM	ENKTF-1	319	326	8.19852	CGCGGC	0.73242	0.71737
cg1719341	RLIM	ENKTF-1	394	401	8.19852	TGGCAG	0.73242	0.71737
cg1719341	RLIM	ENKTF-1	986	993	8.19852	TGGCGA	0.73242	0.71737
cg1719341	RLIM	ENKTF-1	1353	1360	8.19852	CCTGGC	0.73242	0.71737
cg1719341	RLIM	ENKTF-1	1412	1419	8.19852	TGGCGG	0.73242	0.71737
cg1719341	RLIM	ENKTF-1	1499	1506	8.19852	TCTCGC	0.73242	0.71737
cg1719341	RLIM	ENKTF-1	1891	1898	8.19852	ACTCGC	0.73242	0.71737
cg1719341	RLIM	NF-1 [T00	252	259	8.191058	GAGGCC	0.24414	0.24409
cg1719341	RLIM	NF-1 [T00	1240	1247	8.191058	TAGACC	0.24414	0.24409
cg1719341	RLIM	AhR [T01	1280	1290	8.184723	CTCACG	0.04864	0.04833
cg1719341	RLIM	SRY [T00	356	364	8.174786	CCTTCA	0.15259	0.15383

cg1719341	RLIM	RBP-Jkapp	553	564	8.111183	GATTCC	0.00596	0.00597
cg1719341	RLIM	VDR [T00	1149	1157	8.079962	GTTCAA	0.24414	0.24712
cg1719341	RLIM	GR-alpha [	34	38	8.073878	CCAGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	59	63	8.073878	CCTGC	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	303	307	8.073878	CCTGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	436	440	8.073878	CCTGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	573	577	8.073878	CTAGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	640	644	8.073878	CCTGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	705	709	8.073878	CCTGC	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	1162	1166	8.073878	CCTGC	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	1353	1357	8.073878	CCTGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	1451	1455	8.073878	GCAGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	1469	1473	8.073878	CCAGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	1518	1522	8.073878	CCTGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	1612	1616	8.073878	CCAGG	7.8125	7.72238
cg1719341	RLIM	GR-alpha [	1712	1716	8.073878	GTAGG	7.8125	7.72238
cg1719341	RLIM	Pax-5 [T0	28	34	8.014558	GCGGCC	2.19727	2.14502
cg1719341	RLIM	Pax-5 [T0	68	74	8.014558	GGGCTC	2.19727	2.14502
cg1719341	RLIM	Pax-5 [T0	126	132	8.014558	GGGCAG	2.19727	2.14502
cg1719341	RLIM	Pax-5 [T0	306	312	8.014558	GGGCTG	2.19727	2.14502
cg1719341	RLIM	Pax-5 [T0	415	421	8.014558	GGAGCC	2.19727	2.14502
cg1719341	RLIM	Pax-5 [T0	813	819	8.014558	GCAGCC	2.19727	2.14502
cg1719341	RLIM	TFIID [T0	85	91	8.014558	TTGGAA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	283	289	8.014558	TTTCCTA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	490	496	8.014558	TTTGAG	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	917	923	8.014558	TTGGAA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1035	1041	8.014558	TTTGAA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1078	1084	8.014558	TTTCAG	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1227	1233	8.014558	TAGGAA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1251	1257	8.014558	TAAGAA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1542	1548	8.014558	TCTCAA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1626	1632	8.014558	TTAGAA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1829	1835	8.014558	TTTGTA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1856	1862	8.014558	TTTCTTA	2.19727	2.24348
cg1719341	RLIM	TFIID [T0	1983	1989	8.014558	TTTCCA	2.19727	2.24348
cg1719341	RLIM	C/EBPalph	665	671	8.006685	TCCAAT	0.24414	0.24674
cg1719341	RLIM	C/EBPalph	1214	1220	8.006685	CATTGT	0.24414	0.24674
cg1719341	RLIM	IRF-1 [T0	283	291	7.896985	TTTCCTA	0.25177	0.25263
cg1719341	RLIM	IRF-1 [T0	1225	1233	7.896985	CTTAGG	0.25177	0.25263
cg1719341	RLIM	p53 [T006	483	489	7.853573	GGGCCA	0.48828	0.47377
cg1719341	RLIM	p53 [T006	415	421	7.833758	GGAGCC	0.48828	0.47377
cg1719341	RLIM	RXR-alpha	339	345	7.815913	ACTACC	0.24414	0.24104
cg1719341	RLIM	AR [T000	1716	1724	7.804321	GGACAA	0.19836	0.19634
cg1719341	RLIM	T3R-beta1	1518	1526	7.774776	CCTGGG	0.27466	0.27236
cg1719341	RLIM	c-Ets-2 [T	760	768	7.76635	CGACAG	0.32043	0.32298
cg1719341	RLIM	NF-AT1 [	925	933	7.744746	GGAAAG	0.19836	0.19941
cg1719341	RLIM	c-Myb [T0	1921	1928	7.739476	CACAGT	0.42725	0.43114
cg1719341	RLIM	p53 [T006	96	102	7.641867	AAGGCC	0.73242	0.7186

cg1719341	RLIM	RBP-Jkapp	1010	1021	7.593528	ATTGTG	0.02337	0.02342
cg1719341	RLIM	NFI/CTF [	101	108	7.587343	CCAAGA	0.36621	0.36674
cg1719341	RLIM	NFI/CTF [	1986	1993	7.587343	CCAATA	0.36621	0.36674
cg1719341	RLIM	ATF [T00	1048	1059	7.582678	GGACGT	0.02575	0.02573
cg1719341	RLIM	EBF [T05	8	18	7.555934	TCCTCA	0.01144	0.01125
cg1719341	RLIM	c-Jun [T00	19	25	7.538568	GATGTC	0.48828	0.48775
cg1719341	RLIM	c-Jun [T00	1049	1055	7.538568	GACGTC	0.48828	0.48775
cg1719341	RLIM	c-Jun [T00	1113	1119	7.538568	TGACAT	0.48828	0.48775
cg1719341	RLIM	GR [T050	73	79	7.527031	CAAAAT	1.83105	1.86007
cg1719341	RLIM	GR [T050	487	493	7.527031	CATTTC	1.83105	1.86007
cg1719341	RLIM	GR [T050	974	980	7.527031	CATTTC	1.83105	1.86007
cg1719341	RLIM	GR [T050	1032	1038	7.527031	CATTTC	1.83105	1.86007
cg1719341	RLIM	GR [T050	1245	1251	7.527031	CAAAAT	1.83105	1.86007
cg1719341	RLIM	GR [T050	1637	1643	7.527031	CAAACA	1.83105	1.86007
cg1719341	RLIM	p53 [T006	39	45	7.458735	GGGCGC	0.73242	0.7186
cg1719341	RLIM	p53 [T006	1416	1422	7.458735	GGGCGC	0.73242	0.7186
cg1719341	RLIM	AR [T000	1695	1703	7.406474	GGACAG	0.25177	0.25079
cg1719341	RLIM	E2F-1 [T0	501	508	7.336545	GCGGCA	0.45776	0.44878
cg1719341	RLIM	E2F-1 [T0	794	801	7.336545	GATGCC	0.45776	0.44878
cg1719341	RLIM	c-Ets-1 [T	151	157	7.199436	TTTCCC	0.73242	0.73099
cg1719341	RLIM	c-Ets-1 [T	1027	1033	7.199436	TTTCCC	0.73242	0.73099
cg1719341	RLIM	c-Ets-1 [T	1805	1811	7.199436	TGGGAA	0.73242	0.73099
cg1719341	RLIM	c-Ets-1 [T	1966	1972	7.199436	TTTCCC	0.73242	0.73099
cg1719341	RLIM	XBP-1 [T	77	82	7.172312	ATGAGG	2.92969	2.97018
cg1719341	RLIM	XBP-1 [T	538	543	7.172312	CATCAT	2.92969	2.97018
cg1719341	RLIM	XBP-1 [T	669	674	7.172312	ATGAGT	2.92969	2.97018
cg1719341	RLIM	XBP-1 [T	792	797	7.172312	ATGATG	2.92969	2.97018
cg1719341	RLIM	c-Myb [T0	1145	1152	7.127234	ACCAGT	0.18311	0.18399
cg1719341	RLIM	c-Jun [T00	1061	1067	7.096776	TGACTG	0.73242	0.73173
cg1719341	RLIM	NF-AT1 [	1956	1964	7.095752	TTCTTTT	0.15259	0.1548
cg1719341	RLIM	NF-AT1 [	1979	1987	7.095752	CTGTTTT	0.15259	0.1548
cg1719341	RLIM	HNF-1B [	1656	1664	7.037014	TGTTAG	0.07629	0.07762
cg1719341	RLIM	NF-AT2 [	1931	1940	7.008591	GGAAAA	0.04578	0.04634
cg1719341	RLIM	C/EBPalph	1915	1921	7.00174	CATTGT	0.73242	0.74337
cg1719341	RLIM	HNF-3alph	72	79	7.000129	TCAAAA	0.82397	0.84946
cg1719341	RLIM	HNF-3alph	487	494	7.000129	CATTTC	0.82397	0.84946
cg1719341	RLIM	HNF-3alph	974	981	7.000129	CATTTC	0.82397	0.84946
cg1719341	RLIM	HNF-3alph	1032	1039	7.000129	CATTTC	0.82397	0.84946
cg1719341	RLIM	HNF-3alph	1075	1082	7.000129	CATTTC	0.82397	0.84946
cg1719341	RLIM	HNF-3alph	1578	1585	7.000129	TCAAAA	0.82397	0.84946
cg1719341	RLIM	HNF-3alph	1623	1630	7.000129	AATTTA	0.82397	0.84946
cg1719341	RLIM	IRF-1 [T0	151	159	6.968314	TTTCCC	0.1297	0.13036
cg1719341	RLIM	IRF-1 [T0	1803	1811	6.968314	GGTGGG	0.1297	0.13036
cg1719341	RLIM	NF-1 [T00	602	609	6.948522	TTGGTT	0.48828	0.4856
cg1719341	RLIM	ENKTF-1	462	469	6.942764	CTCTGC	1.46484	1.44228
cg1719341	RLIM	p53 [T006	28	34	6.938545	GCGGCC	1.09863	1.07125
cg1719341	RLIM	AhR:Arnt	1402	1411	6.928166	CCGGGC	0.0515	0.04974
cg1719341	RLIM	VDR [T00	1460	1468	6.925682	TAGCTG	0.42725	0.43062

cg1719341	RLIM	p53 [T006	1785	1791	6.891821	GGGCGG	1.09863	1.07125
cg1719341	RLIM	IRF-1 [T0	1983	1991	6.880783	TTTCCA	0.1297	0.13036
cg1719341	RLIM	c-Jun [T00	1524	1530	6.787369	TGACAG	0.73242	0.73173
cg1719341	RLIM	C/EBPalp	1985	1991	6.786177	TCCAAT	0.73242	0.74337
cg1719341	RLIM	NFI/CTF [	752	759	6.786076	CCAAGC	0.73242	0.73214
cg1719341	RLIM	NFI/CTF [	913	920	6.786076	CGGTTT	0.73242	0.73214
cg1719341	RLIM	p53 [T006	68	74	6.778774	GGGCTC	1.09863	1.07125
cg1719341	RLIM	ATF3 [T01	1113	1120	6.744803	TGACAT	0.27466	0.27656
cg1719341	RLIM	NF-1 [T00	1354	1361	6.722386	CTGGCC	0.24414	0.24147
cg1719341	RLIM	T3R-beta1	1361	1369	6.702681	ACATGG	0.21362	0.21147
cg1719341	RLIM	T3R-beta1	1785	1793	6.702681	GGGCGG	0.21362	0.21147
cg1719341	RLIM	c-Ets-2 [T	780	788	6.695187	CAACAG	0.09155	0.09289
cg1719341	RLIM	TFII-I [T0	820	825	6.581441	CACTCC	0.97656	0.97366
cg1719341	RLIM	TFII-I [T0	1909	1914	6.581441	CACTCC	0.97656	0.97366
cg1719341	RLIM	FOXP3 [T	577	582	6.581441	GTTTTA	0.97656	0.99397
cg1719341	RLIM	FOXP3 [T	1167	1172	6.581441	GTTTTA	0.97656	0.99397
cg1719341	RLIM	FOXP3 [T	1173	1178	6.581441	TTCAAC	0.97656	0.99397
cg1719341	RLIM	RXR-alph	54	60	6.563693	AATACC	0.24414	0.2434
cg1719341	RLIM	p53 [T006	306	312	6.563521	GGGCTG	0.48828	0.47541
cg1719341	RLIM	p53 [T006	813	819	6.563521	GCAGCC	0.48828	0.47541
cg1719341	RLIM	XBP-1 [T	1668	1673	6.478682	ATGCCA	0.97656	0.97062
cg1719341	RLIM	XBP-1 [T	1905	1910	6.478682	ATGCCA	0.97656	0.97062
cg1719341	RLIM	XBP-1 [T	1994	1999	6.478682	ATGCCA	0.97656	0.97062
cg1719341	RLIM	c-Jun [T00	473	479	6.475265	CGCGTC	0.61035	0.60769
cg1719341	RLIM	c-Ets-1 [T	85	91	6.423689	TTGGAA	0.48828	0.48798
cg1719341	RLIM	c-Ets-1 [T	917	923	6.423689	TTGGAA	0.48828	0.48798
cg1719341	RLIM	c-Ets-1 [T	1983	1989	6.423689	TTTCCA	0.48828	0.48798
cg1719341	RLIM	TCF-4E [	358	364	6.302385	TTCAAA	0.61035	0.61344
cg1719341	RLIM	c-Ets-1 [T	172	178	6.295602	ATGGAA	0.48828	0.48798
cg1719341	RLIM	c-Jun [T00	582	588	6.293948	AGGGTC	0.61035	0.60769
cg1719341	RLIM	GR-alpha [	1	5	6.263098	CCTCA	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	9	13	6.263098	CCTCA	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	78	82	6.263098	TGAGG	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	251	255	6.263098	TGAGG	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	288	292	6.263098	TAAGG	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	1330	1334	6.263098	TGAGG	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	1447	1451	6.263098	TGAGG	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	1755	1759	6.263098	TGAGG	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	1884	1888	6.263098	TGAGG	3.90625	3.91061
cg1719341	RLIM	GR-alpha [	1937	1941	6.263098	CCTTA	3.90625	3.91061
cg1719341	RLIM	TCF-4 [T0	1751	1760	6.262917	ACTTTG	0.04959	0.05016
cg1719341	RLIM	IRF-1 [T0	761	769	6.206911	GACAGG	0.16785	0.16909
cg1719341	RLIM	p53 [T006	907	913	6.188498	GGGCGG	0.61035	0.594
cg1719341	RLIM	p53 [T006	938	944	6.188498	GACGCC	0.61035	0.594
cg1719341	RLIM	CTF [T001	834	845	6.088964	TAGCCA	0.00858	0.00853
cg1719341	RLIM	GR-alpha [	11	15	6.055408	TCAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	44	48	6.055408	CCTAA	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	132	136	6.055408	CCTGA	3.90625	3.9065

cg1719341	RLIM	GR-alpha [	190	194	6.055408	TCAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	224	228	6.055408	CCTGA	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	249	253	6.055408	CCTGA	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	286	290	6.055408	CCTAA	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	580	584	6.055408	TTAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	586	590	6.055408	TCAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	723	727	6.055408	TCAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	1111	1115	6.055408	CCTGA	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	1226	1230	6.055408	TTAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	1328	1332	6.055408	CCTGA	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	1335	1339	6.055408	TCAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	1860	1864	6.055408	TTAGG	3.90625	3.9065
cg1719341	RLIM	GR-alpha [	1873	1877	6.055408	CCTGA	3.90625	3.9065
cg1719341	RLIM	C/EBPalph	744	750	5.996794	CATTGT	0.97656	0.99
cg1719341	RLIM	RXR-alpha	1521	1527	5.937582	GGGTGA	0.73242	0.72249
cg1719341	RLIM	GCF [T00	448	456	5.917256	AGGCGG	0.64087	0.6219
cg1719341	RLIM	STAT4 [T	350	355	5.882353	CCTTCC	0.48828	0.48408
cg1719341	RLIM	STAT4 [T	1688	1693	5.882353	GGAAGG	0.48828	0.48408
cg1719341	RLIM	ELF-1 [T0	780	792	5.849516	CAACAG	0.00751	0.00755
cg1719341	RLIM	E2F-1 [T0	897	904	5.846171	GCGGCA	0.18311	0.18044
cg1719341	RLIM	c-Ets-1 [T	1304	1310	5.814485	TGGGAA	0.36621	0.36731
cg1719341	RLIM	STAT1bet	83	92	5.796867	TTTTGG	0.1545	0.1557
cg1719341	RLIM	C/EBPalph	1617	1623	5.781231	GACAAT	0.97656	0.99
cg1719341	RLIM	HNF-1C [	1843	1851	5.695506	GTTAAA	0.07629	0.07817
cg1719341	RLIM	ENKTF-1	1190	1197	5.687009	CAGTGC	0.73242	0.7249
cg1719341	RLIM	c-Ets-1 [T	13	19	5.686398	AGGGAA	0.36621	0.3623
cg1719341	RLIM	c-Ets-1 [T	144	150	5.686398	CTTCCC	0.36621	0.3623
cg1719341	RLIM	c-Ets-1 [T	192	198	5.686398	AGGGAA	0.36621	0.3623
cg1719341	RLIM	AP-2alpha	828	833	5.568965	GCCTAT	0.48828	0.4878
cg1719341	RLIM	C/EBPalph	1792	1798	5.565669	GATTGT	0.73242	0.74391
cg1719341	RLIM	NFI/CTF [	155	162	5.558661	CCAAAC	0.54932	0.55038
cg1719341	RLIM	NFI/CTF [	161	168	5.558661	CCAAGC	0.54932	0.55038
cg1719341	RLIM	NFI/CTF [	837	844	5.558661	CCAATC	0.54932	0.55038
cg1719341	RLIM	c-Ets-1 [T	351	357	5.558311	CTTCCC	0.36621	0.3623
cg1719341	RLIM	c-Ets-1 [T	738	744	5.558311	CTTCCC	0.36621	0.3623
cg1719341	RLIM	Pax-5 [T0	483	489	5.544826	GGGCCA	0.73242	0.72046
cg1719341	RLIM	Pax-5 [T0	1785	1791	5.544826	GGGCGG	0.73242	0.72046
cg1719341	RLIM	TFIID [T0	1381	1387	5.544826	TACTAA	0.73242	0.75085
cg1719341	RLIM	TFIID [T0	1625	1631	5.544826	TTTAGA	0.73242	0.75085
cg1719341	RLIM	TFIID [T0	1662	1668	5.544826	TGATAA	0.73242	0.75085
cg1719341	RLIM	C/EBPalph	47	53	5.38654	AATTGG	0.73242	0.74391
cg1719341	RLIM	RAR-beta	1366	1375	5.333686	GTGAAA	0.15259	0.15189
cg1719341	RLIM	HOXD9 [	1165	1174	5.275652	GCGTTT	0.04578	0.04743
cg1719341	RLIM	HOXD10 [	1165	1174	5.275652	GCGTTT	0.04578	0.04743
cg1719341	RLIM	RXR-alph	959	965	5.271235	CCCACC	0.61035	0.6044
cg1719341	RLIM	RXR-alph	1106	1112	5.271235	TCTACC	0.61035	0.6044
cg1719341	RLIM	RXR-alph	1802	1808	5.271235	GGGTGG	0.61035	0.6044
cg1719341	RLIM	IRF-1 [T0	170	178	5.21856	CCATGG	0.1297	0.1302

cg1719341	RLIM	GR [T050	81	87	5.207533	GGTTTTC	0.24414	0.24606
cg1719341	RLIM	c-Ets-2 [T	1683	1691	5.162974	ATCAAG	0.13733	0.13828
cg1719341	RLIM	c-Myb [T0	1585	1592	5.137438	CCCAGT	0.30518	0.30568
cg1719341	RLIM	p53 [T006	1318	1324	5.133514	GGGCGG	0.48828	0.47747
cg1719341	RLIM	AP-2alpha	95	100	5.100982	AAAGGC	0.97656	0.97567
cg1719341	RLIM	AP-2alpha	859	864	5.100982	AAAGGC	0.97656	0.97567
cg1719341	RLIM	AP-2alpha	1853	1858	5.100982	GCCTTT	0.97656	0.97567
cg1719341	RLIM	NF-Y [T0	663	670	5.094053	CCTCCA	0.36621	0.36847
cg1719341	RLIM	GR-beta [	54	58	5.042296	AATAC	3.90625	3.95351
cg1719341	RLIM	GR-beta [	552	556	5.042296	GGATT	3.90625	3.95351
cg1719341	RLIM	GR-beta [	839	843	5.042296	AATCC	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1134	1138	5.042296	AATCC	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1181	1185	5.042296	GTATT	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1291	1295	5.042296	AATCC	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1388	1392	5.042296	AATAC	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1582	1586	5.042296	AATCC	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1645	1649	5.042296	AATAC	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1724	1728	5.042296	GGATT	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1773	1777	5.042296	GTATT	3.90625	3.95351
cg1719341	RLIM	GR-beta [	1826	1830	5.042296	GGATT	3.90625	3.95351
cg1719341	RLIM	E2F-1 [T0	868	875	5.042045	GCGGGA	0.18311	0.17901
cg1719341	RLIM	PU.1 [T02	780	792	5.031024	CAACAG	0.00191	0.00191
cg1719341	RLIM	C/EBPalph	1481	1487	5.024728	GATTGC	0.97656	0.99332
cg1719341	RLIM	c-Jun [T00	244	250	5.000337	TGACGC	0.61035	0.61057
cg1719341	RLIM	c-Jun [T00	937	943	5.000337	TGACGC	0.61035	0.61057
cg1719341	RLIM	c-Myb [T0	1196	1203	4.974489	CAACTG	0.30518	0.30568
cg1719341	RLIM	XBP-1 [T	795	800	4.894955	ATGCCG	0.97656	0.96979
cg1719341	RLIM	XBP-1 [T	1757	1762	4.894955	AGGCAT	0.97656	0.96979
cg1719341	RLIM	XBP-1 [T	1870	1875	4.894955	ATGCCT	0.97656	0.96979
cg1719341	RLIM	AP-2alpha	43	48	4.890408	GCCTAA	0.97656	0.97567
cg1719341	RLIM	NF-1 [T00	1191	1198	4.880836	AGTGCC	0.24414	0.24398
cg1719341	RLIM	RXR-alpha	683	689	4.86724	GAGACC	0.48828	0.484
cg1719341	RLIM	GCF [T00	318	326	4.846987	GCGCGG	0.27466	0.26486
cg1719341	RLIM	GCF [T00	453	461	4.846987	GCGCTG	0.27466	0.26486
cg1719341	RLIM	NF-AT1 [	918	927	4.823485	TGGAAA	0.07629	0.07704
cg1719341	RLIM	TFII-I [T0	87	92	4.756447	GGAAAT	2.92969	2.93695
cg1719341	RLIM	TFII-I [T0	282	287	4.756447	ATTTCC	2.92969	2.93695
cg1719341	RLIM	TFII-I [T0	838	843	4.756447	CAATCC	2.92969	2.93695
cg1719341	RLIM	TFII-I [T0	1133	1138	4.756447	CAATCC	2.92969	2.93695
cg1719341	RLIM	TFII-I [T0	1229	1234	4.756447	GGAAAT	2.92969	2.93695
cg1719341	RLIM	FOXP3 [T	82	87	4.756447	GTTTTG	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	175	180	4.756447	GAAAAC	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	257	262	4.756447	CAAAAC	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	265	270	4.756447	AAAAAC	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	383	388	4.756447	CTCAAC	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	680	685	4.756447	GTTGAG	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	1038	1043	4.756447	GAAAAC	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	1258	1263	4.756447	GAAAAC	2.92969	2.96063

cg1719341	RLIM	FOXP3 [T	1569	1574	4.756447	GAAAAC	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	1932	1937	4.756447	GAAAAC	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	1947	1952	4.756447	GTTTTT	2.92969	2.96063
cg1719341	RLIM	FOXP3 [T	1981	1986	4.756447	GTTTTC	2.92969	2.96063
cg1719341	RLIM	VDR [T00	1126	1134	4.617121	GTTCAC	0.37384	0.37445
cg1719341	RLIM	C/EBPalp	836	842	4.560723	GCCAAT	0.24414	0.24411
cg1719341	RLIM	IRF-1 [T0	1966	1974	4.549799	TTTCCC	0.05341	0.05405
cg1719341	RLIM	USF2 [T0	1322	1331	4.528187	GGATCA	0.06866	0.06782
cg1719341	RLIM	NF-AT2 [	1807	1816	4.460114	GGAAAA	0.04196	0.04255
cg1719341	RLIM	GATA-2 [	1815	1823	4.444445	TGATAA	0.24414	0.24541
cg1719341	RLIM	AP-2alpha	288	293	4.422424	TAAGGC	0.97656	0.96979
cg1719341	RLIM	STAT4 [T	15	20	4.411765	GGAAGA	1.95312	1.94235
cg1719341	RLIM	STAT4 [T	194	199	4.411765	GGAAGC	1.95312	1.94235
cg1719341	RLIM	STAT4 [T	522	527	4.411765	TCTTCC	1.95312	1.94235
cg1719341	RLIM	STAT4 [T	737	742	4.411765	TCTTCC	1.95312	1.94235
cg1719341	RLIM	STAT4 [T	1306	1311	4.411765	GGAAGC	1.95312	1.94235
cg1719341	RLIM	p53 [T006	1609	1615	4.33696	GGGCCA	0.24414	0.23584
cg1719341	RLIM	Sp1 [T007	1317	1326	4.333247	CGGGCG	0.08583	0.08339
cg1719341	RLIM	RAR-beta	154	163	4.307573	CCCAAA	0.14496	0.1447
cg1719341	RLIM	c-Ets-1 [T0	850	856	4.282938	ATTCCT	0.85449	0.85764
cg1719341	RLIM	RXR-alph	1938	1944	4.24113	CTTACC	0.97656	0.9671
cg1719341	RLIM	GR-beta [	134	138	4.201913	TGATT	7.8125	7.94607
cg1719341	RLIM	GR-beta [	280	284	4.201913	CGATT	7.8125	7.94607
cg1719341	RLIM	GR-beta [	830	834	4.201913	CTATT	7.8125	7.94607
cg1719341	RLIM	GR-beta [	848	852	4.201913	CGATT	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1170	1174	4.201913	TTATT	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1238	1242	4.201913	AATAG	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1436	1440	4.201913	AATCG	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1458	1462	4.201913	AATAG	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1620	1624	4.201913	AATAA	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1634	1638	4.201913	AATCA	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1682	1686	4.201913	AATCA	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1791	1795	4.201913	TGATT	7.8125	7.94607
cg1719341	RLIM	GR-beta [	1988	1992	4.201913	AATAG	7.8125	7.94607
cg1719341	RLIM	NF-Y [T0	1967	1974	4.186615	TTCCCA	0.18311	0.1853
cg1719341	RLIM	NF-Y [T0	1983	1990	4.186615	TTTCCA	0.18311	0.1853
cg1719341	RLIM	NF-1 [T00	123	130	4.135372	TTGGGG	0.24414	0.24154
cg1719341	RLIM	NF-AT1 [	86	95	4.134416	TGGAAA	0.08392	0.08485
cg1719341	RLIM	NF-AT1 [	1979	1988	4.134416	CTGTTTT	0.08392	0.08485
cg1719341	RLIM	HNF-1B [	1842	1850	4.127556	AGTTAA	0.01526	0.0157
cg1719341	RLIM	p53 [T006	300	306	4.125254	GGGCCT	0.73242	0.71379
cg1719341	RLIM	p53 [T006	433	439	4.125254	GGGCCT	0.73242	0.71379
cg1719341	RLIM	p53 [T006	954	960	4.125254	CAGGCC	0.73242	0.71379
cg1719341	RLIM	RXR-alph	1368	1374	4.019014	GAAACC	0.97656	0.9671
cg1719341	RLIM	Pax-5 [T0	96	102	4.007279	AAGGCC	1.09863	1.07975
cg1719341	RLIM	Pax-5 [T0	772	778	4.007279	ACTGCC	1.09863	1.07975
cg1719341	RLIM	Pax-5 [T0	1838	1844	4.007279	GGGCAG	1.09863	1.07975
cg1719341	RLIM	TFIID [T0	1794	1800	4.007279	TTGTAA	1.09863	1.13456

cg1719341	RLIM	TFIID [T0	1830	1836	4.007279	TTGTAA	1.09863	1.13456
cg1719341	RLIM	AP-2alpha	901	906	3.970052	CAAGGC	0.97656	0.96469
cg1719341	RLIM	AP-2alpha	1532	1537	3.970052	CAAGGC	0.97656	0.96469
cg1719341	RLIM	p53 [T006	694	700	3.961937	CTAGCC	0.73242	0.71379
cg1719341	RLIM	Sp1 [T007	1784	1793	3.893616	AGGGCG	0.08965	0.08686
cg1719341	RLIM	GR [T050	257	263	3.763516	CAAAAC	0.73242	0.74251
cg1719341	RLIM	GR [T050	360	366	3.763516	CAAAGA	0.73242	0.74251
cg1719341	RLIM	p53 [T006	162	168	3.750231	CAAGCC	0.73242	0.71379
cg1719341	RLIM	p53 [T006	655	661	3.750231	CAAGCC	0.73242	0.71379
cg1719341	RLIM	AP-2alpha	1849	1854	3.743866	GAAGGC	0.48828	0.48238
cg1719341	RLIM	TBP [T00	1602	1611	3.743085	TTTATA	0.03052	0.03162
cg1719341	RLIM	c-Ets-1 [T	1705	1711	3.71855	GTTCCT	0.61035	0.60765
cg1719341	RLIM	IRF-1 [T0	1927	1935	3.692688	TAAAGG	0.06866	0.06927
cg1719341	RLIM	p53 [T006	772	778	3.516613	ACTGCC	0.73242	0.7189
cg1719341	RLIM	p53 [T006	1838	1844	3.516613	GGGCAG	0.73242	0.7189
cg1719341	RLIM	HNF-3alp	1182	1189	3.500065	TATTTA	0.27466	0.28532
cg1719341	RLIM	Sp1 [T007	906	915	3.440764	CGGGCG	0.07439	0.07186
cg1719341	RLIM	PXR-1:RX	1464	1471	3.395883	TGAACC	0.12207	0.12271
cg1719341	RLIM	p53 [T006	1404	1410	3.375208	GGGCGT	0.73242	0.7189
cg1719341	RLIM	GR-beta [	90	94	3.361531	AATCT	3.90625	3.99611
cg1719341	RLIM	GR-beta [	238	242	3.361531	AGATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [	1099	1103	3.361531	ATATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [	1426	1430	3.361531	AATCT	3.90625	3.99611
cg1719341	RLIM	GR-beta [	1480	1484	3.361531	AGATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [	1811	1815	3.361531	AATCT	3.90625	3.99611
cg1719341	RLIM	GR-beta [	1953	1957	3.361531	AGATT	3.90625	3.99611
cg1719341	RLIM	GATA-2 [	731	739	3.333333	CCATTA	0.30518	0.30786
cg1719341	RLIM	AP-2alpha	460	465	3.229049	GCCTCT	0.48828	0.48238
cg1719341	RLIM	AP-2alpha	690	695	3.229049	GCCTCT	0.48828	0.48238
cg1719341	RLIM	Elk-1 [T00	1684	1692	3.121991	TCAAGG	0.07629	0.07656
cg1719341	RLIM	c-Ets-2 [T	1706	1714	3.020647	TTCCTTC	0.06104	0.06231
cg1719341	RLIM	c-Ets-2 [T	920	928	2.945838	GAAAAG	0.06104	0.06231
cg1719341	RLIM	c-Ets-2 [T	1926	1934	2.945838	TTAAAG	0.06104	0.06231
cg1719341	RLIM	c-Ets-2 [T	1961	1969	2.945838	TTCCTTT	0.06104	0.06231
cg1719341	RLIM	STAT4 [T	143	148	2.941176	ACTTCC	2.92969	2.929
cg1719341	RLIM	STAT4 [T	333	338	2.941176	GGAAGT	2.92969	2.929
cg1719341	RLIM	STAT4 [T	553	558	2.941176	GATTCC	2.92969	2.929
cg1719341	RLIM	STAT4 [T	785	790	2.941176	GGAAGT	2.92969	2.929
cg1719341	RLIM	STAT4 [T	849	854	2.941176	GATTCC	2.92969	2.929
cg1719341	RLIM	STAT4 [T	925	930	2.941176	GGAAAG	2.92969	2.929
cg1719341	RLIM	STAT4 [T	1016	1021	2.941176	GGAACC	2.92969	2.929
cg1719341	RLIM	STAT4 [T	1026	1031	2.941176	CTTTCC	2.92969	2.929
cg1719341	RLIM	IRF-1 [T0	1027	1035	2.93326	TTTCCC	0.07629	0.07756
cg1719341	RLIM	p53 [T006	126	132	2.813291	GGGCAG	0.48828	0.47786
cg1719341	RLIM	NF-1 [T00	97	104	2.813149	AGGCCC	0.24414	0.24101
cg1719341	RLIM	PR B [T00	744	750	2.80933	CATTGT	0.73242	0.74818
cg1719341	RLIM	PR A [T01	744	750	2.80933	CATTGT	0.73242	0.74818
cg1719341	RLIM	NFI/CTF [	598	605	2.683003	TCGGTT	0.06104	0.06008

cg1719341	RLIM	c-Myb [T0	267	274	2.570796	AAACTG(	0.06104	0.06117
cg1719341	RLIM	AP-2alpha	0	5	2.550491	GCCTCA	0.48828	0.48266
cg1719341	RLIM	AP-2alpha	251	256	2.550491	TGAGGC	0.48828	0.48266
cg1719341	RLIM	AP-2alpha	1447	1452	2.550491	TGAGGC	0.48828	0.48266
cg1719341	RLIM	AP-2alpha	1755	1760	2.550491	TGAGGC	0.48828	0.48266
cg1719341	RLIM	TCF-4 [T0	356	365	2.548903	CCTTCA/	0.03433	0.03506
cg1719341	RLIM	AR [T000-	1616	1624	2.519152	GGACAA	0.11444	0.11507
cg1719341	RLIM	RelA [T00	1804	1814	2.485523	GTGGGA.	0.00572	0.00574
cg1719341	RLIM	NF-AT1 [	1807	1815	2.449764	GGAAAA	0.09155	0.0926
cg1719341	RLIM	NF-AT1 [	1931	1939	2.449764	GGAAAA	0.09155	0.0926
cg1719341	RLIM	Ik-1 [T027	1293	1305	2.374299	TCCCAG(	0.00063	0.00061
cg1719341	RLIM	HNF-1C [	1657	1665	2.372238	GTTAGT(	0.04578	0.04709
cg1719341	RLIM	C/EBPalpl	981	987	2.371703	AATTGT(	0.48828	0.49114
cg1719341	RLIM	C/EBPalpl	1009	1015	2.371703	AATTGT(	0.48828	0.49114
cg1719341	RLIM	C/EBPalpl	1969	1975	2.371703	CCCAAT	0.48828	0.49114
cg1719341	RLIM	Elk-1 [T00	781	789	2.299314	AACAGG	0.09155	0.09114
cg1719341	RLIM	T3R-beta1	1325	1333	2.221365	TCACCT(	0.15259	0.15262
cg1719341	RLIM	c-Ets-2 [T(	851	859	2.217136	TTCCTCC	0.16785	0.16856
cg1719341	RLIM	Elk-1 [T00	329	337	2.164966	GAGAGG	0.05341	0.05317
cg1719341	RLIM	Elk-1 [T00	523	531	2.164966	CTTCCTC	0.05341	0.05317
cg1719341	RLIM	RAR-beta	1462	1471	2.144554	GCTGAA(	0.07629	0.07625
cg1719341	RLIM	c-Ets-2 [T(	328	336	2.142327	CGAGAG	0.16785	0.16856
cg1719341	RLIM	c-Ets-2 [T(	524	532	2.142327	TTCCTCT	0.16785	0.16856
cg1719341	RLIM	AP-2alpha	621	626	2.098119	CGAGGC	0.97656	0.95407
cg1719341	RLIM	NF-AT1 [	173	182	2.067208	TGGAAA.	0.03815	0.03874
cg1719341	RLIM	AP-2alpha	198	203	1.871933	GCCTCC	0.97656	0.95407
cg1719341	RLIM	AP-2alpha	272	277	1.871933	GCCTCC	0.97656	0.95407
cg1719341	RLIM	AP-2alpha	446	451	1.871933	GGAGGC	0.97656	0.95407
cg1719341	RLIM	AP-2alpha	662	667	1.871933	GCCTCC	0.97656	0.95407
cg1719341	RLIM	AP-2alpha	1441	1446	1.871933	GGAGGC	0.97656	0.95407
cg1719341	RLIM	AP-2alpha	1472	1477	1.871933	GGAGGC	0.97656	0.95407
cg1719341	RLIM	C/EBPalpl	1881	1887	1.830762	AATTGA(	0.48828	0.49438
cg1719341	RLIM	c-Ets-1 [T(	283	289	1.769212	TTTCCTA	0.12207	0.12414
cg1719341	RLIM	c-Ets-1 [T(	1227	1233	1.769212	TAGGAA.	0.12207	0.12414
cg1719341	RLIM	RXR-alpha	440	446	1.696452	GGGTCC(	0.48828	0.48222
cg1719341	RLIM	RXR-alpha	583	589	1.696452	GGGTCA(	0.48828	0.48222
cg1719341	RLIM	GR-beta [	980	984	1.680765	GAATT	3.90625	3.94936
cg1719341	RLIM	GR-beta [	1008	1012	1.680765	GAATT	3.90625	3.94936
cg1719341	RLIM	GR-beta [	1667	1671	1.680765	AATGC	3.90625	3.94936
cg1719341	RLIM	GR-beta [	1759	1763	1.680765	GCATT	3.90625	3.94936
cg1719341	RLIM	GR-beta [	1869	1873	1.680765	AATGC	3.90625	3.94936
cg1719341	RLIM	GR-beta [	1880	1884	1.680765	GAATT	3.90625	3.94936
cg1719341	RLIM	c-Ets-1 [T(	923	929	1.641124	AAGGAA	0.36621	0.36952
cg1719341	RLIM	c-Ets-1 [T(	1929	1935	1.641124	AAGGAA	0.36621	0.36952
cg1719341	RLIM	c-Ets-1 [T(	1960	1966	1.641124	TTTCCTT	0.36621	0.36952
cg1719341	RLIM	C/EBPbeta	49	52	1.639871	TTGG	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	85	88	1.639871	TTGG	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	101	104	1.639871	CCAA	15.625	15.72563

cg1719341	RLIM	C/EBPbeta	123	126	1.639871	TTGG	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	155	158	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	161	164	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	256	259	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	558	561	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	602	605	1.639871	TTGG	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	666	669	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	752	755	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	837	840	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	917	920	1.639871	TTGG	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1195	1198	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1244	1247	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1303	1306	1.639871	TTGG	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1358	1361	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1671	1674	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1823	1826	1.639871	TTGG	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1943	1946	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1970	1973	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1986	1989	1.639871	CCAA	15.625	15.72563
cg1719341	RLIM	ATF-2 [T0	1047	1056	1.621338	AGGACG	0.01526	0.01516
cg1719341	RLIM	XBP-1 [T	21	26	1.583727	TGTCAT	0.97656	0.98146
cg1719341	RLIM	EBF [T05	31	41	1.581175	GCCCCA	0.00381	0.00363
cg1719341	RLIM	Pax-5 [T0	694	700	1.537547	CTAGCC	0.73242	0.71311
cg1719341	RLIM	Pax-5 [T0	1404	1410	1.537547	GGGCGT	0.73242	0.71311
cg1719341	RLIM	Pax-5 [T0	1609	1615	1.537547	GGGCCA	0.73242	0.71311
cg1719341	RLIM	TFIID [T0	83	89	1.537547	TTTTGG	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	173	179	1.537547	TGGAAA	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	918	924	1.537547	TGGAAA	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	976	982	1.537547	TTTTGA	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	1034	1040	1.537547	TTTTGA	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	1150	1156	1.537547	TTCAAA	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	1795	1801	1.537547	TGTAAA	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	1831	1837	1.537547	TGTAAA	0.73242	0.75096
cg1719341	RLIM	TFIID [T0	1982	1988	1.537547	TTTTCCA	0.73242	0.75096
cg1719341	RLIM	NF-Y [T0	48	55	1.51343	ATTGGT	0.18311	0.18459
cg1719341	RLIM	RXR-alpha	156	162	1.474336	CAAACC	0.48828	0.48222
cg1719341	RLIM	STAT4 [T	150	155	1.470588	TTTTCC	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	174	179	1.470588	GGAAAA	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	765	770	1.470588	GGAAAC	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	919	924	1.470588	GGAAAA	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	1704	1709	1.470588	AGTTCC	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	1807	1812	1.470588	GGAAAA	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	1888	1893	1.470588	GGAACT	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	1931	1936	1.470588	GGAAAA	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	1959	1964	1.470588	TTTTCC	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	1965	1970	1.470588	TTTTCC	1.95312	1.96333
cg1719341	RLIM	STAT4 [T	1982	1987	1.470588	TTTTCC	1.95312	1.96333
cg1719341	RLIM	NF-Y [T0	834	841	1.447632	TAGCCA	0.18311	0.18459

cg1719341	RLIM	GR [T050	264	270	1.444018	CAAAAA	0.12207	0.1245
cg1719341	RLIM	c-Ets-1 [T0	763	769	1.384951	CAGGAA	0.36621	0.36952
cg1719341	RLIM	C/EBPbeta	72	75	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	263	266	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	359	362	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	384	387	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	491	494	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	654	657	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	681	684	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	978	981	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1036	1039	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1068	1071	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1151	1154	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1174	1177	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1206	1209	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1544	1547	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1578	1581	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1595	1598	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1636	1639	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1684	1687	1.366559	TCAA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1754	1757	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	C/EBPbeta	1883	1886	1.366559	TTGA	15.625	15.72563
cg1719341	RLIM	AP-2alpha	366	371	1.357116	GCCTGT	0.48828	0.48203
cg1719341	RLIM	AP-2alpha	953	958	1.357116	ACAGGC	0.48828	0.48203
cg1719341	RLIM	AP-2alpha	1262	1267	1.357116	ACAGGC	0.48828	0.48203
cg1719341	RLIM	AP-2alpha	1285	1290	1.357116	GCCTGT	0.48828	0.48203
cg1719341	RLIM	AP-2alpha	1420	1425	1.357116	GCCTGT	0.48828	0.48203
cg1719341	RLIM	HNF-3alph	1234	1241	1.342935	TTAAAA	0.03052	0.03194
cg1719341	RLIM	c-Myb [T0	1839	1846	1.285398	GGCAGT	0.06104	0.06064
cg1719341	RLIM	IRF-1 [T0	921	929	1.274173	AAAAGG	0.04578	0.04655
cg1719341	RLIM	IRF-1 [T0	1960	1968	1.274173	TTTCCTT	0.04578	0.04655
cg1719341	RLIM	ENKTF-1	968	975	1.255756	CTCCGC	0.24414	0.23904
cg1719341	RLIM	HNF-1A [	1759	1766	1.069403	GCATTA	0.48828	0.49664
cg1719341	RLIM	HNF-1A [	1925	1932	1.069403	GTTAAA	0.48828	0.49664
cg1719341	RLIM	GATA-1 [	1651	1656	1.038567	TATCAT	1.95312	1.98662
cg1719341	RLIM	CREB [T0	1047	1055	0.989089	AGGACG	0.05341	0.05293
cg1719341	RLIM	PXR-1:RX	1146	1153	0.941658	CCAGTT	0.12207	0.12266
cg1719341	RLIM	GATA-1 [	1096	1101	0.863549	GTGATA	1.95312	1.98662
cg1719341	RLIM	GATA-1 [	1661	1666	0.863549	GTGATA	1.95312	1.98662
cg1719341	RLIM	GR-beta [T	46	50	0.840383	TAATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	47	51	0.840383	AATTG	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	76	80	0.840383	AATGA	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	392	396	0.840383	AATGG	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	486	490	0.840383	CCATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	540	544	0.840383	TCATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	668	672	0.840383	AATGA	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	731	735	0.840383	CCATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	743	747	0.840383	CCATT	7.8125	7.94706

cg1719341	RLIM	GR-beta [T	973	977	0.840383	CCATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	981	985	0.840383	AATTG	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1009	1013	0.840383	AATTG	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1031	1035	0.840383	CCATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1213	1217	0.840383	CCATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1232	1236	0.840383	AATTA	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1248	1252	0.840383	AATTA	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1396	1400	0.840383	AATTA	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1622	1626	0.840383	TAATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1881	1885	0.840383	AATTG	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1914	1918	0.840383	CCATT	7.8125	7.94706
cg1719341	RLIM	GR-beta [T	1971	1975	0.840383	CAATT	7.8125	7.94706
cg1719341	RLIM	GATA-1 [	1745	1750	0.758539	CTGATA	1.95312	1.98662
cg1719341	RLIM	GATA-1 [	1814	1819	0.758539	CTGATA	1.95312	1.98662
cg1719341	RLIM	AP-2alpha	131	136	0.678558	GCCTGA	0.48828	0.48199
cg1719341	RLIM	AP-2alpha	223	228	0.678558	GCCTGA	0.48828	0.48199
cg1719341	RLIM	AP-2alpha	248	253	0.678558	GCCTGA	0.48828	0.48199
cg1719341	RLIM	AP-2alpha	723	728	0.678558	TCAGGC	0.48828	0.48199
cg1719341	RLIM	AP-2alpha	1872	1877	0.678558	GCCTGA	0.48828	0.48199
cg1719341	RLIM	C/EBPalph	1131	1137	0.540941	CACAAT	0.24414	0.24507
cg1719341	RLIM	HNF-1A [	1843	1850	0.287765	GTTAAA	0.24414	0.24974
cg1719341	RLIM	GATA-1 [	735	740	0.280028	TATCTT	0.97656	0.99875
cg1719341	RLIM	c-Ets-1 [T	1686	1692	0.256174	AAGGAA	0.24414	0.24569
cg1719341	RLIM	AP-2alpha	302	307	0.226186	GCCTGG	0.97656	0.95305
cg1719341	RLIM	AP-2alpha	435	440	0.226186	GCCTGG	0.97656	0.95305
cg1719341	RLIM	AP-2alpha	1352	1357	0.226186	GCCTGG	0.97656	0.95305
cg1719341	RLIM	AP-2alpha	1517	1522	0.226186	GCCTGG	0.97656	0.95305
cg1719341	RLIM	GR-alpha [	95	99	0.207689	AAAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	148	152	0.207689	CCTTT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	330	334	0.207689	AGAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	461	465	0.207689	CCTCT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	526	530	0.207689	CCTCT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	691	695	0.207689	CCTCT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	859	863	0.207689	AAAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	922	926	0.207689	AAAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1782	1786	0.207689	AAAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1799	1803	0.207689	AAAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1835	1839	0.207689	AAAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1854	1858	0.207689	CCTTT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1928	1932	0.207689	AAAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1963	1967	0.207689	CCTTT	7.8125	7.81264
cg1719341	RLIM	c-Ets-1 [T	331	337	0.128087	GAGGAA	0.24414	0.2429
cg1719341	RLIM	c-Ets-1 [T	523	529	0.128087	CTTCCTC	0.24414	0.2429
cg1719341	RLIM	PXR-1:RX	1123	1130	0.123583	TCAGTT	0.12207	0.12407
cg1719341	RLIM	GR-alpha [	367	371	0	CCTGT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	549	553	0	ACAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	762	766	0	ACAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	782	786	0	ACAGG	7.8125	7.81264

cg1719341	RLIM	GR-alpha [	829	833	0	CCTAT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	953	957	0	ACAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1262	1266	0	ACAGG	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1286	1290	0	CCTGT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1421	1425	0	CCTGT	7.8125	7.81264
cg1719341	RLIM	GR-alpha [	1605	1609	0	ATAGG	7.8125	7.81264
cg1719341	RLIM	AP-2alpha	704	709	0	GCCTGC	0.97656	0.95305
cg1719341	RLIM	AP-2alpha	1161	1166	0	GCCTGC	0.97656	0.95305
cg1719341	RLIM	XBP-1 [T	936	941	0	ATGACG	0.97656	0.98127
cg1719341	RLIM	RXR-alpha	1464	1470	0	TGAACC	0.24414	0.2444
cg1719341	RLIM	Pax-5 [T0	162	168	0	CAAGCC	1.09863	1.06846
cg1719341	RLIM	Pax-5 [T0	300	306	0	GGGCCT	1.09863	1.06846
cg1719341	RLIM	Pax-5 [T0	433	439	0	GGGCCT	1.09863	1.06846
cg1719341	RLIM	Pax-5 [T0	655	661	0	CAAGCC	1.09863	1.06846
cg1719341	RLIM	Pax-5 [T0	954	960	0	CAGGCC	1.09863	1.06846
cg1719341	RLIM	ENKTF-1	406	413	0	CTACGC	0.12207	0.1201
cg1719341	RLIM	TFII-I [T0	925	930	0	GGAAAG	1.46484	1.45997
cg1719341	RLIM	TFII-I [T0	1026	1031	0	CTTTCC	1.46484	1.45997
cg1719341	RLIM	TFII-I [T0	1695	1700	0	GGACAG	1.46484	1.45997
cg1719341	RLIM	STAT4 [T	87	92	0	GGAAAT	0.48828	0.49387
cg1719341	RLIM	STAT4 [T	282	287	0	ATTTCC	0.48828	0.49387
cg1719341	RLIM	STAT4 [T	1229	1234	0	GGAAAT	0.48828	0.49387
cg1719341	RLIM	c-Ets-1 [T	783	789	0	CAGGAA	0.24414	0.2429
cg1719341	RLIM	YY1 [T00	170	173	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	172	175	0	ATGG	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	393	396	0	ATGG	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	486	489	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	731	734	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	743	746	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	946	949	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	973	976	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	1031	1034	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	1213	1216	0	CCAT	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	1363	1366	0	ATGG	7.8125	7.81711
cg1719341	RLIM	YY1 [T00	1914	1917	0	CCAT	7.8125	7.81711
cg1719341	RLIM	GCF [T00	697	705	0	GCCCAG	0.09155	0.08765
cg1719341	RLIM	ER-alpha [	188	192	0	GGTCA	1.95312	1.9404
cg1719341	RLIM	ER-alpha [	584	588	0	GGTCA	1.95312	1.9404
cg1719341	RLIM	ER-alpha [	1333	1337	0	GGTCA	1.95312	1.9404
cg1719341	RLIM	C/EBPbeta	108	111	0	TTGC	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	428	431	0	GCAA	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	719	722	0	TTGC	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	746	749	0	TTGT	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	779	782	0	ACAA	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	900	903	0	GCAA	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	983	986	0	TTGT	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	997	1000	0	TTGC	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1011	1014	0	TTGT	15.625	15.71349

cg1719341	RLIM	C/EBPbeta	1132	1135	0	ACAA	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1216	1219	0	TTGT	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1483	1486	0	TTGC	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1531	1534	0	GCAA	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1618	1621	0	ACAA	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1710	1713	0	TTGT	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1718	1721	0	ACAA	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1794	1797	0	TTGT	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1830	1833	0	TTGT	15.625	15.71349
cg1719341	RLIM	C/EBPbeta	1917	1920	0	TTGT	15.625	15.71349
cg1719341	RLIM	TFIID [T0	137	143	0	TTTTTTA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	263	269	0	TCAAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	855	861	0	TCGAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	1036	1042	0	TTGAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	1151	1157	0	TCAAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	1544	1550	0	TCAAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	1627	1633	0	TAGAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	1736	1742	0	TTTAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	1777	1783	0	TCGAAA	1.09863	1.13474
cg1719341	RLIM	TFIID [T0	1949	1955	0	TTTTAGA	1.09863	1.13474
cg1719341	RLIM	FOXP3 [T	778	783	0	CACAAC	1.46484	1.47315
cg1719341	RLIM	GR-beta [T	993	997	0	AAATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	994	998	0	AATTT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	1074	1078	0	ACATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	1093	1097	0	AATGT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	1231	1235	0	AAATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	1247	1251	0	AAATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	1395	1399	0	AAATT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	1623	1627	0	AATTT	3.90625	3.99611
cg1719341	RLIM	GR-beta [T	1972	1976	0	AATTT	3.90625	3.99611
cg1719341	RLIM	GR [T050	1152	1158	0	CAAAAA	0.36621	0.37562
cg1719341	RLIM	GR [T050	1545	1551	0	CAAAAA	0.36621	0.37562
cg1719341	RLIM	HNF-3alph	1384	1391	0	TAAAAA	0.09155	0.09511
cg1719341	RLIM	IRF-2 [T01	119	124	0	TCACTT	0.48828	0.49387
cg1719341	RLIM	IRF-2 [T01	566	571	0	TCACTT	0.48828	0.49387
cg1719341	RLIM	IRF-2 [T01	787	792	0	AAGTGA	0.48828	0.49387
cg2244321	RNF213	c-Ets-1 [T	1766	1772	9.969337	ATTCCC	0.24414	0.2459
cg2244321	RNF213	PEA3 [T0	1719	1727	9.937959	TGGATG	0.18311	0.18304
cg2244321	RNF213	c-Myb [T0	1124	1131	9.815171	GAACTT	0.36621	0.3712
cg2244321	RNF213	XBP-1 [T	252	257	9.789909	ATGGCG	1.95312	1.95208
cg2244321	RNF213	XBP-1 [T	1254	1259	9.789909	ATGTCT	1.95312	1.95208
cg2244321	RNF213	PR B [T00	143	149	9.743489	AACACA	1.09863	1.10292
cg2244321	RNF213	PR B [T00	237	243	9.743489	AACACA	1.09863	1.10292
cg2244321	RNF213	PR B [T00	1540	1546	9.743489	CTGTGT	1.09863	1.10292
cg2244321	RNF213	PR B [T00	1856	1862	9.743489	GCGTGT	1.09863	1.10292
cg2244321	RNF213	PR B [T00	1928	1934	9.743489	AACACA	1.09863	1.10292
cg2244321	RNF213	PR A [T01	143	149	9.743489	AACACA	1.09863	1.10292
cg2244321	RNF213	PR A [T01	237	243	9.743489	AACACA	1.09863	1.10292

cg2244321	RNF213	PR A [T01	1540	1546	9.743489	CTGTGT	1.09863	1.10292
cg2244321	RNF213	PR A [T01	1856	1862	9.743489	GCGTGT	1.09863	1.10292
cg2244321	RNF213	PR A [T01	1928	1934	9.743489	AACACA	1.09863	1.10292
cg2244321	RNF213	TFIID [T0	308	314	9.552105	TTTGGA	1.46484	1.48472
cg2244321	RNF213	TFIID [T0	612	618	9.552105	TTCCAA	1.46484	1.48472
cg2244321	RNF213	TFIID [T0	1023	1029	9.552105	TGGGAA	1.46484	1.48472
cg2244321	RNF213	TFIID [T0	1398	1404	9.552105	TGGCAA	1.46484	1.48472
cg2244321	RNF213	TFIID [T0	1519	1525	9.552105	TTTGGT	1.46484	1.48472
cg2244321	RNF213	TFIID [T0	1598	1604	9.552105	TCCCAA	1.46484	1.48472
cg2244321	RNF213	TFIID [T0	1653	1659	9.552105	TTTGGA	1.46484	1.48472
cg2244321	RNF213	NF-1 [T00	995	1002	9.535536	TTGGCC	0.73242	0.73053
cg2244321	RNF213	NF-1 [T00	1861	1868	9.535536	TTGGTC	0.73242	0.73053
cg2244321	RNF213	NF-AT1 [	1025	1033	9.521781	GGAAAT	0.16785	0.1682
cg2244321	RNF213	TFII-I [T0	49	54	9.512894	CCTTCC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	88	93	9.512894	GGACAC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	250	255	9.512894	GGATGG	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	319	324	9.512894	AAATCC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	610	615	9.512894	CCTTCC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	657	662	9.512894	AAATCC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	745	750	9.512894	GGACTT	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	761	766	9.512894	GGAAAA	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	843	848	9.512894	CCTTCC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1054	1059	9.512894	GGACTT	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1140	1145	9.512894	GGATGG	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1194	1199	9.512894	AAGTCC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1214	1219	9.512894	CCTTCC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1233	1238	9.512894	GGAAGG	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1690	1695	9.512894	GGATAC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1720	1725	9.512894	GGATGG	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1760	1765	9.512894	GGAAAC	7.32422	7.29728
cg2244321	RNF213	TFII-I [T0	1848	1853	9.512894	GGACCG	7.32422	7.29728
cg2244321	RNF213	FOXP3 [T	140	145	9.512894	AGCAAC	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	293	298	9.512894	GTTTAG	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	558	563	9.512894	GTTGGC	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	806	811	9.512894	GTTTAT	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	1104	1109	9.512894	AGCAAC	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	1225	1230	9.512894	GAGAAC	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	1238	1243	9.512894	GTTTAG	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	1289	1294	9.512894	ACCAAC	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	1622	1627	9.512894	ATAAAC	7.32422	7.35678
cg2244321	RNF213	FOXP3 [T	1860	1865	9.512894	GTTGGT	7.32422	7.35678
cg2244321	RNF213	Ik-1 [T027	476	488	9.497194	TGAGTA	0.02941	0.02907
cg2244321	RNF213	c-Jun [T00	1260	1266	9.442241	GCTGTC	0.73242	0.73031
cg2244321	RNF213	c-Jun [T00	1741	1747	9.442241	GCTGTC	0.73242	0.73031
cg2244321	RNF213	RelA [T00	1022	1032	9.429339	CTGGGA	0.02813	0.0279
cg2244321	RNF213	HNF-1B [	1693	1701	9.388842	TACTTA	0.09155	0.09374
cg2244321	RNF213	RBP-Jkap	1765	1776	9.256527	CATTCC	0.01884	0.01886
cg2244321	RNF213	MEF-2A [	529	539	9.220261	TATTTTT	0.07343	0.07563

cg2244321	RNF213	MEF-2A [	1649	1659	9.220261	TATTTTT	0.07343	0.07563
cg2244321	RNF213	NF-AT1 [	1886	1894	9.18189	GGAAAG	0.22888	0.22959
cg2244321	RNF213	PPAR-alp	1373	1383	9.158357	CCCTGG	0.0515	0.04986
cg2244321	RNF213	USF2 [T0	207	216	9.056375	CAGGTG	0.1545	0.15287
cg2244321	RNF213	c-Myb [T0	289	296	9.024874	CTCAGT	0.39673	0.40028
cg2244321	RNF213	LEF-1 [T0	1598	1605	8.973041	TCCCAA	0.54932	0.55326
cg2244321	RNF213	GR [T050	753	759	8.971049	GCTTTC	0.61035	0.61632
cg2244321	RNF213	GR [T050	1401	1407	8.971049	CAAAAT	0.61035	0.61632
cg2244321	RNF213	T3R-beta1	467	475	8.924046	TCACCC	0.2594	0.25766
cg2244321	RNF213	IRF-1 [T0	1756	1764	8.916359	GGGTGG	0.09155	0.09147
cg2244321	RNF213	IRF-1 [T0	1882	1890	8.916359	GTGTGG	0.09155	0.09147
cg2244321	RNF213	c-Ets-2 [T	1429	1437	8.912323	TTCCTGC	0.27466	0.27495
cg2244321	RNF213	p53 [T006	1210	1216	8.912104	GGGCCC	0.12207	0.11837
cg2244321	RNF213	T3R-beta1	1264	1272	8.904753	TCACCC	0.2594	0.25766
cg2244321	RNF213	c-Ets-1 [T	1279	1285	8.8926	CGGGAA	0.85449	0.85523
cg2244321	RNF213	RelA [T00	758	768	8.88775	TGGGGA	0.02432	0.0241
cg2244321	RNF213	HNF-4alp	1601	1613	8.87767	CAAAGT	0.01502	0.01524
cg2244321	RNF213	PR B [T00	1698	1704	8.827054	AACAGA	0.36621	0.36944
cg2244321	RNF213	PR A [T01	1698	1704	8.827054	AACAGA	0.36621	0.36944
cg2244321	RNF213	NF-1 [T00	1596	1603	8.790071	CCTCCC	0.24414	0.24467
cg2244321	RNF213	XBP-1 [T	592	597	8.75604	ATGATC	2.92969	2.9674
cg2244321	RNF213	XBP-1 [T	717	722	8.75604	ATGAAA	2.92969	2.9674
cg2244321	RNF213	XBP-1 [T	739	744	8.75604	ATGAAA	2.92969	2.9674
cg2244321	RNF213	XBP-1 [T	894	899	8.75604	GTTCAT	2.92969	2.9674
cg2244321	RNF213	XBP-1 [T	1091	1096	8.75604	GCTCAT	2.92969	2.9674
cg2244321	RNF213	XBP-1 [T	1812	1817	8.75604	ATGAGA	2.92969	2.9674
cg2244321	RNF213	NF-kappa	759	769	8.591618	GGGGAA	0.02146	0.02103
cg2244321	RNF213	c-Jun [T00	1949	1955	8.571705	CCAGTC	0.12207	0.12139
cg2244321	RNF213	PPAR-alp	197	207	8.384593	CAGGCC	0.02003	0.01963
cg2244321	RNF213	PPAR-alp	986	996	8.384593	GGCTGG	0.02003	0.01963
cg2244321	RNF213	HNF-3alp	1130	1137	8.343064	GTAAAA	0.27466	0.28528
cg2244321	RNF213	HNF-3alp	1667	1674	8.343064	GATTTA	0.27466	0.28528
cg2244321	RNF213	PR B [T00	1779	1785	8.338824	AACAGA	1.09863	1.10009
cg2244321	RNF213	PR A [T01	1779	1785	8.338824	AACAGA	1.09863	1.10009
cg2244321	RNF213	GR-alpha [	34	38	8.281568	CCTTC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	49	53	8.281568	CCTTC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	84	88	8.281568	CCTTG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	179	183	8.281568	CAAGG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	241	245	8.281568	CAAGG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	433	437	8.281568	CCTCC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	471	475	8.281568	CCTCC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	610	614	8.281568	CCTTC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	768	772	8.281568	CAAGG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	783	787	8.281568	CCTTG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	835	839	8.281568	CCTCC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	843	847	8.281568	CCTTC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	955	959	8.281568	CCTTC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	959	963	8.281568	CAAGG	7.8125	7.72956

cg2244321	RNF213	GR-alpha [	1120	1124	8.281568	GAAGG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1160	1164	8.281568	CGAGG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1169	1173	8.281568	GAAGG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1214	1218	8.281568	CCTTC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1234	1238	8.281568	GAAGG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1422	1426	8.281568	CCTTG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1447	1451	8.281568	CCTCG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1460	1464	8.281568	CCTCC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1596	1600	8.281568	CCTCC	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1639	1643	8.281568	CCTCG	7.8125	7.72956
cg2244321	RNF213	GR-alpha [	1709	1713	8.281568	GGAGG	7.8125	7.72956
cg2244321	RNF213	NF-kappa	1210	1221	8.276134	GGGCCC	0.01526	0.01499
cg2244321	RNF213	NF-AT1 [	971	979	8.236182	GCTCTT	0.1297	0.12988
cg2244321	RNF213	p53 [T006	213	219	8.208781	GGGGCC	0.48828	0.47377
cg2244321	RNF213	ENKTF-1	257	264	8.19852	GCTCGC	0.73242	0.71737
cg2244321	RNF213	ENKTF-1	560	567	8.19852	TGGCCA	0.73242	0.71737
cg2244321	RNF213	NF-1 [T00	174	181	8.191058	GAGCCC	0.24414	0.24409
cg2244321	RNF213	NF-1 [T00	606	613	8.191058	TTGGCC	0.24414	0.24409
cg2244321	RNF213	GR-alpha [	93	97	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	108	112	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	122	126	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	168	172	8.073878	GCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	196	200	8.073878	CCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	202	206	8.073878	CCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	206	210	8.073878	GCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	285	289	8.073878	CCTGC	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	442	446	8.073878	GCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	461	465	8.073878	CCTGC	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	498	502	8.073878	CCTGC	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	563	567	8.073878	CCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	581	585	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	649	653	8.073878	CCTGC	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	839	843	8.073878	CCTGC	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	871	875	8.073878	CCTGC	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	930	934	8.073878	CCTAG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	931	935	8.073878	CTAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	944	948	8.073878	GTAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	963	967	8.073878	GCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1012	1016	8.073878	CCTGC	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1021	1025	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1031	1035	8.073878	GCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1362	1366	8.073878	GCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1374	1378	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1382	1386	8.073878	CCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1431	1435	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1567	1571	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1607	1611	8.073878	GCAGG	7.8125	7.72238
cg2244321	RNF213	GR-alpha [	1634	1638	8.073878	CCTAG	7.8125	7.72238

cg2244321	RNF213	GR-alpha [	1792	1796	8.073878	CCTGG	7.8125	7.72238
cg2244321	RNF213	AR [T000	88	96	8.055836	GGACAC	0.19836	0.19634
cg2244321	RNF213	Pax-5 [T0	173	179	8.014558	GGAGCC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	184	190	8.014558	GGCTT	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	213	219	8.014558	GGGGCC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	280	286	8.014558	GAAGCC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	1002	1008	8.014558	TGAGCC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	1177	1183	8.014558	GGGCTC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	1209	1215	8.014558	TGGGCC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	1434	1440	8.014558	GGGCTC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	1570	1576	8.014558	GGGCTC	2.19727	2.14502
cg2244321	RNF213	Pax-5 [T0	1909	1915	8.014558	GGGCTC	2.19727	2.14502
cg2244321	RNF213	TFIID [T0	367	373	8.014558	TTTGAG	2.19727	2.24348
cg2244321	RNF213	TFIID [T0	709	715	8.014558	TATCAA	2.19727	2.24348
cg2244321	RNF213	TFIID [T0	1558	1564	8.014558	TCTCAA	2.19727	2.24348
cg2244321	RNF213	p53 [T006	173	179	7.833758	GGAGCC	0.48828	0.47377
cg2244321	RNF213	c-Myb [T0	418	425	7.739476	CTCAGT	0.42725	0.43114
cg2244321	RNF213	NFI/CTF [	753	760	7.587343	GCTTTT	0.36621	0.36674
cg2244321	RNF213	NFI/CTF [	1916	1923	7.587343	GCATTT	0.36621	0.36674
cg2244321	RNF213	NF-AT1 [	761	769	7.574801	GGAAAA	0.19836	0.19941
cg2244321	RNF213	GR [T050	615	621	7.527031	CAAAAT	1.83105	1.86007
cg2244321	RNF213	GR [T050	747	753	7.527031	ACTTTT	1.83105	1.86007
cg2244321	RNF213	GR [T050	1348	1354	7.527031	TTGTTT	1.83105	1.86007
cg2244321	RNF213	RAR-beta	1336	1345	7.47824	TGGGTT	0.24414	0.24343
cg2244321	RNF213	C/EBPalp	897	903	7.465744	CATTGA	0.48828	0.49653
cg2244321	RNF213	NF-kappa	1795	1805	7.452991	GGGGAT	0.04435	0.04347
cg2244321	RNF213	AR [T000	75	83	7.406474	CAGCTG	0.25177	0.25079
cg2244321	RNF213	IRF-1 [T0	757	765	7.387351	TTGGGG	0.14496	0.14449
cg2244321	RNF213	NF-kappa	1211	1221	7.313747	GGCCCT	0.04435	0.04347
cg2244321	RNF213	c-Ets-1 [T	1023	1029	7.199436	TGGGAA	0.73242	0.73099
cg2244321	RNF213	GCF [T00	1392	1400	7.186486	GCGCAG	0.45776	0.44706
cg2244321	RNF213	XBP-1 [T	776	781	7.172312	CTTCAT	2.92969	2.97018
cg2244321	RNF213	XBP-1 [T	1146	1151	7.172312	ATTCAT	2.92969	2.97018
cg2244321	RNF213	XBP-1 [T	1404	1409	7.172312	AATCAT	2.92969	2.97018
cg2244321	RNF213	p53 [T006	1209	1215	7.153797	TGGGCC	1.09863	1.07125
cg2244321	RNF213	Ik-1 [T027	615	627	7.122895	CAAAAT	0.01064	0.01049
cg2244321	RNF213	TFIID [T0	1239	1245	7.082373	TTTAGC	0.12207	0.12407
cg2244321	RNF213	HNF-3alp	1649	1656	7.000129	TATTTTT	0.82397	0.84946
cg2244321	RNF213	HNF-3alp	1677	1684	7.000129	TATAAA	0.82397	0.84946
cg2244321	RNF213	RXR-alpha	1629	1635	6.967687	ACCACC	0.36621	0.36214
cg2244321	RNF213	c-Ets-1 [T	759	765	6.943262	GGGGAA	0.73242	0.73099
cg2244321	RNF213	ENKTF-1	996	1003	6.942764	TGGCCG	1.46484	1.44228
cg2244321	RNF213	ENKTF-1	1057	1064	6.942764	CTTAGC	1.46484	1.44228
cg2244321	RNF213	AhR:Arnt	505	514	6.928166	CCACGC	0.0515	0.04974
cg2244321	RNF213	VDR [T00	231	239	6.925682	TGCCTG	0.42725	0.43062
cg2244321	RNF213	VDR [T00	894	902	6.925682	GTTCAT	0.42725	0.43062
cg2244321	RNF213	c-Jun [T00	1861	1867	6.856451	TTGGTC	0.73242	0.73173
cg2244321	RNF213	PEA3 [T0	1139	1147	6.824411	AGGATG	0.22888	0.22933

cg2244321	RNF213	c-Jun [T00	1662	1668	6.787369	TGACAG	0.73242	0.73173
cg2244321	RNF213	NFI/CTF [	393	400	6.786076	CCAAGC	0.73242	0.73214
cg2244321	RNF213	RXR-alph	1544	1550	6.785809	GTTACC	0.36621	0.36214
cg2244321	RNF213	ELF-1 [T0	1425	1437	6.784516	TGACTT	0.0056	0.00562
cg2244321	RNF213	p53 [T006	1002	1008	6.778774	TGAGCC	1.09863	1.07125
cg2244321	RNF213	p53 [T006	1177	1183	6.778774	GGGCTC	1.09863	1.07125
cg2244321	RNF213	p53 [T006	1434	1440	6.778774	GGGCTC	1.09863	1.07125
cg2244321	RNF213	p53 [T006	1570	1576	6.778774	GGGCTC	1.09863	1.07125
cg2244321	RNF213	p53 [T006	1909	1915	6.778774	GGGCTC	1.09863	1.07125
cg2244321	RNF213	NF-1 [T00	389	396	6.722386	TCGCCC	0.24414	0.24147
cg2244321	RNF213	NF-1 [T00	559	566	6.722386	TTGGCC	0.24414	0.24147
cg2244321	RNF213	T3R-beta1	551	559	6.702681	TCACCA	0.21362	0.21147
cg2244321	RNF213	IRF-1 [T0	975	983	6.699483	TTTCCT	0.19073	0.19127
cg2244321	RNF213	PXR-1:RX	235	242	6.668182	TGAACA	0.24414	0.24672
cg2244321	RNF213	PXR-1:RX	891	898	6.668182	TGTGTT	0.24414	0.24672
cg2244321	RNF213	PXR-1:RX	900	907	6.668182	TGAACG	0.24414	0.24672
cg2244321	RNF213	IRF-1 [T0	1021	1029	6.622811	CCTGGG	0.19073	0.19127
cg2244321	RNF213	TFII-I [T0	400	405	6.581441	GGAGTG	0.97656	0.97366
cg2244321	RNF213	TFII-I [T0	1008	1013	6.581441	CACTCC	0.97656	0.97366
cg2244321	RNF213	TFII-I [T0	1725	1730	6.581441	GGAGAT	0.97656	0.97366
cg2244321	RNF213	TFII-I [T0	1936	1941	6.581441	CACTCC	0.97656	0.97366
cg2244321	RNF213	FOXP3 [T	315	320	6.581441	GTTGAA	0.97656	0.99397
cg2244321	RNF213	FOXP3 [T	1925	1930	6.581441	TAAAAC	0.97656	0.99397
cg2244321	RNF213	RXR-alph	1894	1900	6.563693	GGGTGT	0.24414	0.2434
cg2244321	RNF213	p53 [T006	280	286	6.563521	GAAGCC	0.48828	0.47541
cg2244321	RNF213	PPAR-alp	1470	1480	6.51544	AGCTGG	0.03719	0.03639
cg2244321	RNF213	c-Jun [T00	1274	1280	6.475265	TGACAC	0.61035	0.60769
cg2244321	RNF213	RAR-beta	545	554	6.415195	GGGGTT	0.18311	0.183
cg2244321	RNF213	p53 [T006	388	394	6.400205	GTCGCC	0.48828	0.47541
cg2244321	RNF213	p53 [T006	826	832	6.400205	GGGCGA	0.48828	0.47541
cg2244321	RNF213	GR-alpha [	465	469	6.263098	CCTCA	3.90625	3.91061
cg2244321	RNF213	GR-alpha [	586	590	6.263098	CCTCA	3.90625	3.91061
cg2244321	RNF213	GR-alpha [	1069	1073	6.263098	TAAGG	3.90625	3.91061
cg2244321	RNF213	GR-alpha [	1358	1362	6.263098	TGAGG	3.90625	3.91061
cg2244321	RNF213	GR-alpha [	1454	1458	6.263098	CCTCA	3.90625	3.91061
cg2244321	RNF213	GR-alpha [	1687	1691	6.263098	TGAGG	3.90625	3.91061
cg2244321	RNF213	GR-alpha [	1706	1710	6.263098	TGAGG	3.90625	3.91061
cg2244321	RNF213	c-Ets-1 [T	1758	1764	6.167515	GTGGAA	0.36621	0.36731
cg2244321	RNF213	c-Ets-1 [T	1884	1890	6.167515	GTGGAA	0.36621	0.36731
cg2244321	RNF213	HNF-1C [	1301	1309	6.115467	ATGTAT	0.14496	0.14811
cg2244321	RNF213	GR-alpha [	233	237	6.055408	CCTGA	3.90625	3.9065
cg2244321	RNF213	GR-alpha [	323	327	6.055408	CCTGA	3.90625	3.9065
cg2244321	RNF213	GR-alpha [	474	478	6.055408	CCTGA	3.90625	3.9065
cg2244321	RNF213	GR-alpha [	661	665	6.055408	CCTGA	3.90625	3.9065
cg2244321	RNF213	GR-alpha [	681	685	6.055408	TTAGG	3.90625	3.9065
cg2244321	RNF213	GR-alpha [	723	727	6.055408	TTAGG	3.90625	3.9065
cg2244321	RNF213	GR-alpha [	1067	1071	6.055408	CCTAA	3.90625	3.9065
cg2244321	RNF213	GR-alpha [	1830	1834	6.055408	TTAGG	3.90625	3.9065

cg2244321	RNF213	GR-alpha [	1865	1869	6.055408	TCAGG	3.90625	3.9065
cg2244321	RNF213	RXR-alph	1263	1269	5.937582	GTCACC	0.73242	0.72249
cg2244321	RNF213	STAT4 [T	49	54	5.882353	CCTTCC	0.48828	0.48408
cg2244321	RNF213	STAT4 [T	610	615	5.882353	CCTTCC	0.48828	0.48408
cg2244321	RNF213	STAT4 [T	843	848	5.882353	CCTTCC	0.48828	0.48408
cg2244321	RNF213	STAT4 [T	1214	1219	5.882353	CCTTCC	0.48828	0.48408
cg2244321	RNF213	STAT4 [T	1233	1238	5.882353	GGAAGG	0.48828	0.48408
cg2244321	RNF213	HNF-1C [	1692	1700	5.821046	ATACTT	0.14496	0.14811
cg2244321	RNF213	RBP-Jkap	1019	1030	5.820496	CTCCTG	0.00572	0.00572
cg2244321	RNF213	STAT1bet	1021	1030	5.796867	CCTGGG	0.1545	0.1557
cg2244321	RNF213	c-Jun [T00	325	331	5.783074	TGACTT	0.36621	0.37082
cg2244321	RNF213	c-Jun [T00	663	669	5.783074	TGACTT	0.36621	0.37082
cg2244321	RNF213	VDR [T00	896	904	5.771401	TCATTG	0.42725	0.42999
cg2244321	RNF213	ENKTF-1	253	260	5.687009	TGGCGC	0.73242	0.7249
cg2244321	RNF213	EBF [T05	1371	1381	5.623365	CGCCCT	0.01907	0.0183
cg2244321	RNF213	T3R-beta1	119	127	5.591999	TCACCT	0.21362	0.21287
cg2244321	RNF213	AP-2alpha	1150	1155	5.568965	ATAGGC	0.48828	0.4878
cg2244321	RNF213	NFI/CTF [	991	998	5.558661	GGGCTT	0.54932	0.55038
cg2244321	RNF213	NFI/CTF [	1328	1335	5.558661	GGGTTT	0.54932	0.55038
cg2244321	RNF213	c-Ets-1 [T	844	850	5.558311	CTTCCC	0.36621	0.3623
cg2244321	RNF213	c-Ets-1 [T	1215	1221	5.558311	CTTCCC	0.36621	0.3623
cg2244321	RNF213	T3R-beta1	1944	1952	5.553412	TCACCC	0.21362	0.21287
cg2244321	RNF213	TFIID [T	533	539	5.544826	TTTAGT	0.73242	0.75085
cg2244321	RNF213	TFIID [T	680	686	5.544826	TTTAGG	0.73242	0.75085
cg2244321	RNF213	p53 [T006	184	190	5.508538	GGGCTT	0.61035	0.59991
cg2244321	RNF213	E2F-1 [T0	845	852	5.476857	TTCCCC	0.03052	0.02989
cg2244321	RNF213	p53 [T006	214	220	5.39549	GGGCCC	0.61035	0.59991
cg2244321	RNF213	C/EBPalp	1681	1687	5.38654	AATTGG	0.73242	0.74391
cg2244321	RNF213	Egr-3 [T0	1076	1088	5.282214	CAGTGT	0.00477	0.00478
cg2244321	RNF213	GR [T050	1338	1344	5.207533	GGTTTT	0.24414	0.24606
cg2244321	RNF213	AhR:Arnt	1480	1489	5.196125	ACAGGC	0.00572	0.00556
cg2244321	RNF213	c-Jun [T00	1425	1431	5.193102	TGACTT	0.61035	0.61057
cg2244321	RNF213	AP-2alpha	59	64	5.100982	GCCTTT	0.97656	0.97567
cg2244321	RNF213	USF2 [T0	116	125	5.052423	CACTCA	0.103	0.10178
cg2244321	RNF213	USF2 [T0	492	501	5.052423	CAGGCA	0.103	0.10178
cg2244321	RNF213	GR-beta [	320	324	5.042296	AATCC	3.90625	3.95351
cg2244321	RNF213	GR-beta [	486	490	5.042296	GGATT	3.90625	3.95351
cg2244321	RNF213	GR-beta [	528	532	5.042296	GTATT	3.90625	3.95351
cg2244321	RNF213	GR-beta [	625	629	5.042296	GGATT	3.90625	3.95351
cg2244321	RNF213	GR-beta [	658	662	5.042296	AATCC	3.90625	3.95351
cg2244321	RNF213	GR-beta [	687	691	5.042296	GTATT	3.90625	3.95351
cg2244321	RNF213	GR-beta [	1144	1148	5.042296	GGATT	3.90625	3.95351
cg2244321	RNF213	GR-beta [	1444	1448	5.042296	AATCC	3.90625	3.95351
cg2244321	RNF213	GR-beta [	1611	1615	5.042296	GGATT	3.90625	3.95351
cg2244321	RNF213	GR-beta [	1648	1652	5.042296	GTATT	3.90625	3.95351
cg2244321	RNF213	c-Ets-1 [T	309	315	5.038739	TTGGAA	0.48828	0.49031
cg2244321	RNF213	c-Ets-1 [T	611	617	5.038739	CTTCCA	0.48828	0.49031
cg2244321	RNF213	c-Ets-1 [T	1654	1660	5.038739	TTGGAA	0.48828	0.49031

cg2244321	RNF213	PXR-1:RX	444	451	5.032032	AGGGTT	0.12207	0.12266
cg2244321	RNF213	NFI/CTF [	82	89	5.021086	CCCCTT	0.24414	0.24103
cg2244321	RNF213	NFI/CTF [	178	185	5.021086	CCAAGG	0.24414	0.24103
cg2244321	RNF213	RAR-beta:	1177	1188	4.98533	GGGCTC	0.00966	0.00942
cg2244321	RNF213	c-Ets-1 [T	1231	1237	4.910652	ATGGAA	0.48828	0.49031
cg2244321	RNF213	XBP-1 [T	965	970	4.894955	AGGCAT	0.97656	0.96979
cg2244321	RNF213	XBP-1 [T	1618	1623	4.894955	AGGCAT	0.97656	0.96979
cg2244321	RNF213	RXR-alph	1365	1371	4.86724	GGGTCT	0.48828	0.484
cg2244321	RNF213	RXR-alph	1974	1980	4.86724	CATACC	0.48828	0.484
cg2244321	RNF213	RXR-alph	1989	1995	4.86724	CATACC	0.48828	0.484
cg2244321	RNF213	GCF [T00	851	859	4.846987	GCACCG	0.27466	0.26486
cg2244321	RNF213	C/EBPalp	1577	1583	4.845599	AGCAAT	0.97656	0.99332
cg2244321	RNF213	HNF-3alp	1511	1518	4.842999	TTAAAA	0.09155	0.09582
cg2244321	RNF213	HNF-1A [	101	108	4.828753	AACTTA	0.36621	0.37179
cg2244321	RNF213	HNF-1A [	1283	1290	4.828753	AACTTA	0.36621	0.37179
cg2244321	RNF213	HNF-1A [	1693	1700	4.828753	TACTTA	0.36621	0.37179
cg2244321	RNF213	p53 [T006	1833	1839	4.786849	GGGCAC	0.48828	0.47747
cg2244321	RNF213	c-Ets-1 [T	50	56	4.782565	CTTCCA	0.48828	0.49031
cg2244321	RNF213	c-Ets-1 [T	277	283	4.782565	GTGGAA	0.48828	0.49031
cg2244321	RNF213	TFII-I [T0	1025	1030	4.756447	GGAAAT	2.92969	2.93695
cg2244321	RNF213	TFII-I [T0	1443	1448	4.756447	CAATCC	2.92969	2.93695
cg2244321	RNF213	TFII-I [T0	1765	1770	4.756447	CATTCC	2.92969	2.93695
cg2244321	RNF213	FOXP3 [T	305	310	4.756447	GTTTTT	2.92969	2.96063
cg2244321	RNF213	FOXP3 [T	1339	1344	4.756447	GTTTTG	2.92969	2.96063
cg2244321	RNF213	FOXP3 [T	1344	1349	4.756447	GTTTTT	2.92969	2.96063
cg2244321	RNF213	FOXP3 [T	1354	1359	4.756447	GTTTTG	2.92969	2.96063
cg2244321	RNF213	FOXP3 [T	1643	1648	4.756447	GTTTTG	2.92969	2.96063
cg2244321	RNF213	FOXP3 [T	1660	1665	4.756447	GTTGAC	2.92969	2.96063
cg2244321	RNF213	FOXP3 [T	1744	1749	4.756447	GTCAAC	2.92969	2.96063
cg2244321	RNF213	Ik-1 [T027	1465	1477	4.748597	CGAGTA	0.00313	0.00308
cg2244321	RNF213	VDR [T00	422	430	4.617121	GTTCAC	0.37384	0.37445
cg2244321	RNF213	USF2 [T0	87	96	4.528187	TGGACA	0.06866	0.06782
cg2244321	RNF213	T3R-beta1	1681	1689	4.481316	AATTGG	0.27466	0.27551
cg2244321	RNF213	AP-2alpha	929	934	4.438035	GCCTAG	0.97656	0.96979
cg2244321	RNF213	RXR-alph	596	602	4.423008	TCCACC	0.24414	0.24292
cg2244321	RNF213	RXR-alph	1082	1088	4.423008	GGGTGG	0.24414	0.24292
cg2244321	RNF213	RXR-alph	1756	1762	4.423008	GGGTGG	0.24414	0.24292
cg2244321	RNF213	AP-2alpha	1069	1074	4.422424	TAAGGC	0.97656	0.96979
cg2244321	RNF213	STAT4 [T	279	284	4.411765	GGAAGC	1.95312	1.94235
cg2244321	RNF213	STAT4 [T	1765	1770	4.411765	CATTCC	1.95312	1.94235
cg2244321	RNF213	p53 [T006	38	44	4.33696	CTGGCC	0.24414	0.23584
cg2244321	RNF213	p53 [T006	193	199	4.33696	GGGCCA	0.24414	0.23584
cg2244321	RNF213	RXR-alph	1377	1383	4.24113	GGGTCC	0.97656	0.9671
cg2244321	RNF213	AP-2alpha	944	949	4.211849	GTAGGC	0.97656	0.96469
cg2244321	RNF213	GR-beta [	21	25	4.201913	TTATT	7.8125	7.94607
cg2244321	RNF213	GR-beta [	454	458	4.201913	CGATT	7.8125	7.94607
cg2244321	RNF213	GR-beta [	704	708	4.201913	AATAA	7.8125	7.94607
cg2244321	RNF213	GR-beta [	808	812	4.201913	TTATT	7.8125	7.94607

cg2244321	RNF213	GR-beta [	1101	1105	4.201913	AATAG	7.8125	7.94607
cg2244321	RNF213	GR-beta [	1134	1138	4.201913	AATAA	7.8125	7.94607
cg2244321	RNF213	GR-beta [	1404	1408	4.201913	AATCA	7.8125	7.94607
cg2244321	RNF213	NF-1 [T00	651	658	4.135372	TGCCCC	0.24414	0.24154
cg2244321	RNF213	NF-AT1 [	1759	1768	4.134416	TGGAAA	0.08392	0.08485
cg2244321	RNF213	p53 [T006	197	203	4.125254	CAGGCC	0.73242	0.71379
cg2244321	RNF213	RXR-alph	546	552	4.019014	GGGTTT	0.97656	0.9671
cg2244321	RNF213	RXR-alph	1495	1501	4.019014	CACACC	0.97656	0.9671
cg2244321	RNF213	RXR-alph	1532	1538	4.019014	GGGTCT	0.97656	0.9671
cg2244321	RNF213	RXR-alph	1880	1886	4.019014	GGGTGT	0.97656	0.9671
cg2244321	RNF213	RXR-alph	1958	1964	4.019014	CACACC	0.97656	0.9671
cg2244321	RNF213	Pax-5 [T0	1210	1216	4.007279	GGGCCC	1.09863	1.07975
cg2244321	RNF213	Pax-5 [T0	1833	1839	4.007279	GGGCAC	1.09863	1.07975
cg2244321	RNF213	TFIID [T	807	813	4.007279	TTTATTA	1.09863	1.13456
cg2244321	RNF213	TFIID [T	1128	1134	4.007279	TTGTAA	1.09863	1.13456
cg2244321	RNF213	TFIID [T	1509	1515	4.007279	TTTTAA	1.09863	1.13456
cg2244321	RNF213	TFIID [T	1669	1675	4.007279	TTTTAA	1.09863	1.13456
cg2244321	RNF213	TFIID [T	1734	1740	4.007279	TAGTAA	1.09863	1.13456
cg2244321	RNF213	AP-2alpha	959	964	3.970052	CAAGGC	0.97656	0.96469
cg2244321	RNF213	AP-2alpha	1421	1426	3.970052	GCCTTG	0.97656	0.96469
cg2244321	RNF213	NF-Y [T0	1497	1504	3.95898	CACCCA	0.18311	0.1853
cg2244321	RNF213	GR [T050	1353	1359	3.763516	TGTTTT	0.73242	0.74251
cg2244321	RNF213	GR [T050	1642	1648	3.763516	CGTTTT	0.73242	0.74251
cg2244321	RNF213	p53 [T006	865	871	3.750231	CCAGCC	0.73242	0.71379
cg2244321	RNF213	p53 [T006	985	991	3.750231	GGGCTG	0.73242	0.71379
cg2244321	RNF213	p53 [T006	991	997	3.750231	GGGCTT	0.73242	0.71379
cg2244321	RNF213	p53 [T006	1049	1055	3.750231	GGGCTG	0.73242	0.71379
cg2244321	RNF213	AP-2alpha	609	614	3.743866	GCCTTC	0.48828	0.48238
cg2244321	RNF213	AP-2alpha	842	847	3.743866	GCCTTC	0.48828	0.48238
cg2244321	RNF213	AP-2alpha	954	959	3.743866	GCCTTC	0.48828	0.48238
cg2244321	RNF213	AP-2alpha	1169	1174	3.743866	GAAGGC	0.48828	0.48238
cg2244321	RNF213	TBP [T00	1730	1739	3.743085	TTTATA	0.03052	0.03162
cg2244321	RNF213	c-Ets-1 [T	1121	1127	3.71855	AAGGAA	0.61035	0.60765
cg2244321	RNF213	p53 [T006	1369	1375	3.586914	CTCGCC	0.73242	0.7189
cg2244321	RNF213	RXR-alph	218	224	3.574782	CCGACC	1.09863	1.08572
cg2244321	RNF213	c-Ets-2 [T	1118	1126	3.518824	GAGAAG	0.18311	0.18304
cg2244321	RNF213	HNF-3alph	1506	1513	3.500065	AATTTT	0.27466	0.28532
cg2244321	RNF213	VDR [T00	447	455	3.462841	GTTCAA	0.21362	0.21341
cg2244321	RNF213	RXR-alph	466	472	3.392904	CTCACC	1.09863	1.08572
cg2244321	RNF213	RXR-alph	1922	1928	3.392904	GGGTAA	1.09863	1.08572
cg2244321	RNF213	RXR-alph	1943	1949	3.392904	CTCACC	1.09863	1.08572
cg2244321	RNF213	p53 [T006	506	512	3.375208	CACGCC	0.73242	0.7189
cg2244321	RNF213	p53 [T006	1586	1592	3.375208	CCCGCC	0.73242	0.7189
cg2244321	RNF213	GR-beta [	707	711	3.361531	AATAT	3.90625	3.99611
cg2244321	RNF213	GR-beta [	1666	1670	3.361531	AGATT	3.90625	3.99611
cg2244321	RNF213	GR-beta [	1727	1731	3.361531	AGATT	3.90625	3.99611
cg2244321	RNF213	USF1 [T0	259	268	3.289896	TCGCCA	0.0515	0.05082
cg2244321	RNF213	AP-2alpha	226	231	3.229049	GCCTCT	0.48828	0.48238

cg2244321	RNF213	AP-2alpha	1782	1787	3.229049	AGAGGC	0.48828	0.48238
cg2244321	RNF213	RAR-beta	1327	1336	3.226064	TGGGTT1	0.12207	0.12169
cg2244321	RNF213	RXR-alpha	270	276	3.170788	GGGTGT	0.24414	0.24522
cg2244321	RNF213	RXR-alpha	1337	1343	3.170788	GGGTTT1	0.24414	0.24522
cg2244321	RNF213	RXR-alpha	1868	1874	3.170788	GGGTGT	0.24414	0.24522
cg2244321	RNF213	Pax-5 [T0(	1369	1375	3.075094	CTCGCC(	0.12207	0.11895
cg2244321	RNF213	TFIID [T0	817	823	3.075094	TTTTGCA	0.12207	0.12409
cg2244321	RNF213	C/EBPalph	1441	1447	3.014837	AGCAAT	0.48828	0.4911
cg2244321	RNF213	STAT4 [T	311	316	2.941176	GGAAGT	2.92969	2.929
cg2244321	RNF213	STAT4 [T	974	979	2.941176	CTTTCC	2.92969	2.929
cg2244321	RNF213	STAT4 [T	1427	1432	2.941176	ACTTCC	2.92969	2.929
cg2244321	RNF213	STAT4 [T	1656	1661	2.941176	GGAAGT	2.92969	2.929
cg2244321	RNF213	STAT4 [T	1886	1891	2.941176	GGAAAG	2.92969	2.929
cg2244321	RNF213	PR B [T00	1763	1769	2.80933	AACATT(	0.73242	0.74818
cg2244321	RNF213	PR A [T01	1763	1769	2.80933	AACATT(	0.73242	0.74818
cg2244321	RNF213	NF-AT1 [T	1885	1894	2.756277	TGGAAA	0.05913	0.05995
cg2244321	RNF213	c-Myb [T0	311	318	2.687937	GGAAGT	0.06104	0.06117
cg2244321	RNF213	c-Myb [T0	1656	1663	2.687937	GGAAGT	0.06104	0.06117
cg2244321	RNF213	NF-AT1 [T	1760	1768	2.595974	GGAAAC	0.09155	0.0926
cg2244321	RNF213	AP-2alpha	464	469	2.550491	GCCTCA	0.48828	0.48266
cg2244321	RNF213	AP-2alpha	585	590	2.550491	GCCTCA	0.48828	0.48266
cg2244321	RNF213	AP-2alpha	1358	1363	2.550491	TGAGGC	0.48828	0.48266
cg2244321	RNF213	AP-2alpha	1453	1458	2.550491	GCCTCA	0.48828	0.48266
cg2244321	RNF213	ENKTF-1	1964	1971	2.511511	CCCCGC(	0.12207	0.11894
cg2244321	RNF213	C/EBPalph	1499	1505	2.371703	CCCAAT	0.48828	0.49114
cg2244321	RNF213	Elk-1 [T00	1428	1436	2.299314	CTTCCTC	0.09155	0.09114
cg2244321	RNF213	T3R-beta1	3	11	2.240658	TAGTGG	0.15259	0.15262
cg2244321	RNF213	GATA-1 [	1689	1694	2.176375	AGGATA	3.90625	3.92756
cg2244321	RNF213	RAR-beta	444	453	2.16302	AGGGTT(	0.07629	0.07625
cg2244321	RNF213	c-Ets-2 [T	976	984	2.142327	TTCCTCT	0.16785	0.16856
cg2244321	RNF213	AP-2alpha	1638	1643	2.098119	GCCTCG	0.97656	0.95407
cg2244321	RNF213	AP-2alpha	834	839	1.871933	GCCTCC	0.97656	0.95407
cg2244321	RNF213	AP-2alpha	1459	1464	1.871933	GCCTCC	0.97656	0.95407
cg2244321	RNF213	AP-2alpha	1595	1600	1.871933	GCCTCC	0.97656	0.95407
cg2244321	RNF213	TBP [T007	1673	1682	1.871542	AAACTA	0.18311	0.18942
cg2244321	RNF213	TFII-I [T0	1086	1091	1.824994	GGAGAG	0.48828	0.48408
cg2244321	RNF213	TFII-I [T0	1202	1207	1.824994	GGAGAG	0.48828	0.48408
cg2244321	RNF213	C/EBPalph	22	28	1.761449	TATTGT(	0.48828	0.49438
cg2244321	RNF213	C/EBPalph	1098	1104	1.761449	CACAAT	0.48828	0.49438
cg2244321	RNF213	GR-beta [T	10	14	1.680765	GAATT	3.90625	3.94936
cg2244321	RNF213	GR-beta [T	618	622	1.680765	AATGC	3.90625	3.94936
cg2244321	RNF213	GR-beta [T	677	681	1.680765	GCATT	3.90625	3.94936
cg2244321	RNF213	GR-beta [T	1028	1032	1.680765	AATGC	3.90625	3.94936
cg2244321	RNF213	GR-beta [T	1580	1584	1.680765	AATTC	3.90625	3.94936
cg2244321	RNF213	GR-beta [T	1916	1920	1.680765	GCATT	3.90625	3.94936
cg2244321	RNF213	USF1 [T0(	263	272	1.644948	CACGTG(	0.0248	0.0242
cg2244321	RNF213	C/EBPbeta	86	89	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	178	181	1.639871	CCAA	15.625	15.72563

cg2244321	RNF213	C/EBPbeta	248	251	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	309	312	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	393	396	1.639871	CCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	559	562	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	606	609	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	614	617	1.639871	CCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	655	658	1.639871	CCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	757	760	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	995	998	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1290	1293	1.639871	CCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1332	1335	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1500	1503	1.639871	CCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1520	1523	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1600	1603	1.639871	CCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1654	1657	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1683	1686	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1861	1864	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1920	1923	1.639871	TTGG	15.625	15.72563
cg2244321	RNF213	XBP-1 [T	886	891	1.583727	GGTCAT	0.97656	0.98146
cg2244321	RNF213	XBP-1 [T	1273	1278	1.583727	ATGACA	0.97656	0.98146
cg2244321	RNF213	NF-AT2 [	1760	1769	1.542196	GGAAAC	0.01717	0.01761
cg2244321	RNF213	Pax-5 [T0	29	35	1.537547	CTTGCC	0.73242	0.71311
cg2244321	RNF213	Pax-5 [T0	38	44	1.537547	CTGGCC	0.73242	0.71311
cg2244321	RNF213	Pax-5 [T0	193	199	1.537547	GGGCCA	0.73242	0.71311
cg2244321	RNF213	Pax-5 [T0	506	512	1.537547	CACGCC	0.73242	0.71311
cg2244321	RNF213	Pax-5 [T0	1586	1592	1.537547	CCCGCC	0.73242	0.71311
cg2244321	RNF213	TFIID [T0	307	313	1.537547	TTTTGG	0.73242	0.75096
cg2244321	RNF213	TFIID [T0	613	619	1.537547	TCCAAA	0.73242	0.75096
cg2244321	RNF213	TFIID [T0	1129	1135	1.537547	TGTAAA	0.73242	0.75096
cg2244321	RNF213	TFIID [T0	1644	1650	1.537547	TTTTGTA	0.73242	0.75096
cg2244321	RNF213	TFIID [T0	1652	1658	1.537547	TTTTGG	0.73242	0.75096
cg2244321	RNF213	NF-Y [T0	1682	1689	1.51343	ATTGGT	0.18311	0.18459
cg2244321	RNF213	c-Ets-1 [T	975	981	1.513038	TTTCCTC	0.36621	0.36952
cg2244321	RNF213	E2F-1 [T0	1583	1590	1.490375	TCTCCC	0.06104	0.06008
cg2244321	RNF213	RXR-alph	1328	1334	1.474336	GGGTTT	0.48828	0.48222
cg2244321	RNF213	STAT4 [T	761	766	1.470588	GGAAAA	1.95312	1.96333
cg2244321	RNF213	STAT4 [T	1123	1128	1.470588	GGAACT	1.95312	1.96333
cg2244321	RNF213	STAT4 [T	1281	1286	1.470588	GGAACT	1.95312	1.96333
cg2244321	RNF213	STAT4 [T	1760	1765	1.470588	GGAAAC	1.95312	1.96333
cg2244321	RNF213	Sp1 [T007	1584	1593	1.469012	CTCCCG	0.03242	0.03129
cg2244321	RNF213	GR [T050	305	311	1.444018	GTTTTT	0.12207	0.1245
cg2244321	RNF213	GR [T050	1344	1350	1.444018	GTTTTT	0.12207	0.1245
cg2244321	RNF213	C/EBPbeta	316	319	1.366559	TTGA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	368	371	1.366559	TTGA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	449	452	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	588	591	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	711	714	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	785	788	1.366559	TTGA	15.625	15.72563

cg2244321	RNF213	C/EBPbeta	899	902	1.366559	TTGA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	958	961	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1357	1360	1.366559	TTGA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1424	1427	1.366559	TTGA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1438	1441	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1560	1563	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1574	1577	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1661	1664	1.366559	TTGA	15.625	15.72563
cg2244321	RNF213	C/EBPbeta	1745	1748	1.366559	TCAA	15.625	15.72563
cg2244321	RNF213	AP-2alpha	146	151	1.357116	ACAGGC	0.48828	0.48203
cg2244321	RNF213	AP-2alpha	491	496	1.357116	ACAGGC	0.48828	0.48203
cg2244321	RNF213	AP-2alpha	1480	1485	1.357116	ACAGGC	0.48828	0.48203
cg2244321	RNF213	AP-2alpha	1616	1621	1.357116	ACAGGC	0.48828	0.48203
cg2244321	RNF213	PEA3 [T0	43	51	1.194633	CCACAT	0.06866	0.06895
cg2244321	RNF213	T3R-beta1	153	161	1.110682	TCACCA	0.07629	0.07585
cg2244321	RNF213	GATA-1 [	709	714	1.038567	TATCAA	1.95312	1.98662
cg2244321	RNF213	GR-beta [T	591	595	0.840383	AATGA	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	716	720	0.840383	AATGA	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	721	725	0.840383	AATTA	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	738	742	0.840383	AATGA	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	896	900	0.840383	TCATT	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1093	1097	0.840383	TCATT	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1272	1276	0.840383	AATGA	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1295	1299	0.840383	TAATT	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1296	1300	0.840383	AATTA	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1325	1329	0.840383	AATGG	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1501	1505	0.840383	CAATT	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1502	1506	0.840383	AATTA	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1505	1509	0.840383	TAATT	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1579	1583	0.840383	CAATT	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1681	1685	0.840383	AATTG	7.8125	7.94706
cg2244321	RNF213	GR-beta [T	1717	1721	0.840383	AATGG	7.8125	7.94706
cg2244321	RNF213	AP-2alpha	232	237	0.678558	GCCTGA	0.48828	0.48199
cg2244321	RNF213	AP-2alpha	196	201	0.226186	CCAGGC	0.97656	0.95305
cg2244321	RNF213	AP-2alpha	202	207	0.226186	CCAGGC	0.97656	0.95305
cg2244321	RNF213	AP-2alpha	563	568	0.226186	CCAGGC	0.97656	0.95305
cg2244321	RNF213	AP-2alpha	1382	1387	0.226186	CCAGGC	0.97656	0.95305
cg2244321	RNF213	p53 [T006	29	35	0.211706	CTTGCC	0.36621	0.35912
cg2244321	RNF213	GR-alpha [	60	64	0.207689	CCTTT	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	190	194	0.207689	AGAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	227	231	0.207689	CCTCT	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	742	746	0.207689	AAAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	823	827	0.207689	AGAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	978	982	0.207689	CCTCT	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	1137	1141	0.207689	AAAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	1204	1208	0.207689	AGAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	1782	1786	0.207689	AGAGG	7.8125	7.81264
cg2244321	RNF213	PXR-1:RX	419	426	0.123583	TCAGTT	0.12207	0.12407

cg2244321	RNF213	GR-alpha [	146	150	0	ACAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	491	495	0	ACAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	692	696	0	ACAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	1150	1154	0	ATAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	1480	1484	0	ACAGG	7.8125	7.81264
cg2244321	RNF213	GR-alpha [	1616	1620	0	ACAGG	7.8125	7.81264
cg2244321	RNF213	AP-2alpha	648	653	0	GCCTGC	0.97656	0.95305
cg2244321	RNF213	AP-2alpha	963	968	0	GCAGGC	0.97656	0.95305
cg2244321	RNF213	AP-2alpha	1031	1036	0	GCAGGC	0.97656	0.95305
cg2244321	RNF213	RXR-alpha	445	451	0	GGGTTC	0.24414	0.2444
cg2244321	RNF213	Pax-5 [T0	197	203	0	CAGGCC	1.09863	1.06846
cg2244321	RNF213	Pax-5 [T0	214	220	0	GGGCCC	1.09863	1.06846
cg2244321	RNF213	Pax-5 [T0	649	655	0	CCTGCC	1.09863	1.06846
cg2244321	RNF213	Pax-5 [T0	865	871	0	CCAGCC	1.09863	1.06846
cg2244321	RNF213	Pax-5 [T0	871	877	0	CCTGCC	1.09863	1.06846
cg2244321	RNF213	Pax-5 [T0	985	991	0	GGGCTG	1.09863	1.06846
cg2244321	RNF213	Pax-5 [T0	991	997	0	GGGCTT	1.09863	1.06846
cg2244321	RNF213	Pax-5 [T0	1049	1055	0	GGGCTG	1.09863	1.06846
cg2244321	RNF213	p53 [T006	649	655	0	CCTGCC	0.36621	0.35912
cg2244321	RNF213	p53 [T006	871	877	0	CCTGCC	0.36621	0.35912
cg2244321	RNF213	TFII-I [T0	78	83	0	CTGTCC	1.46484	1.45997
cg2244321	RNF213	TFII-I [T0	974	979	0	CTTTCC	1.46484	1.45997
cg2244321	RNF213	TFII-I [T0	1886	1891	0	GGAAAG	1.46484	1.45997
cg2244321	RNF213	STAT4 [T	1025	1030	0	GGAAAT	0.48828	0.49387
cg2244321	RNF213	c-Ets-1 [T	1428	1434	0	CTTCCTC	0.24414	0.2429
cg2244321	RNF213	YY1 [T00	252	255	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	554	557	0	CCAT	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	601	604	0	CCAT	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	876	879	0	CCAT	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	884	887	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1142	1145	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1155	1158	0	CCAT	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1231	1234	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1326	1329	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1529	1532	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1718	1721	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1722	1725	0	ATGG	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1905	1908	0	CCAT	7.8125	7.81711
cg2244321	RNF213	YY1 [T00	1907	1910	0	ATGG	7.8125	7.81711
cg2244321	RNF213	ER-alpha [	886	890	0	GGTCA	1.95312	1.9404
cg2244321	RNF213	ER-alpha [	1863	1867	0	GGTCA	1.95312	1.9404
cg2244321	RNF213	C/EBPbeta	24	27	0	TTGT	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	30	33	0	TTGC	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	57	60	0	TTGC	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	141	144	0	GCAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	240	243	0	ACAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	429	432	0	GCAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	524	527	0	TTGT	15.625	15.71349

cg2244321	RNF213	C/EBPbeta	751	754	0	TTGC	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	767	770	0	GCAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	799	802	0	TTGT	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	819	822	0	TTGC	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1099	1102	0	ACAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1105	1108	0	GCAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1108	1111	0	ACAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1128	1131	0	TTGT	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1342	1345	0	TTGT	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1348	1351	0	TTGT	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1352	1355	0	TTGT	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1400	1403	0	GCAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1442	1445	0	GCAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1537	1540	0	TTGC	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1578	1581	0	GCAA	15.625	15.71349
cg2244321	RNF213	C/EBPbeta	1646	1649	0	TTGT	15.625	15.71349
cg2244321	RNF213	TFIID [T0	365	371	0	TTTTTGA	1.09863	1.13474
cg2244321	RNF213	TFIID [T0	668	674	0	TTTTCTA	1.09863	1.13474
cg2244321	RNF213	TFIID [T0	711	717	0	TCAAAA	1.09863	1.13474
cg2244321	RNF213	TFIID [T0	1508	1514	0	TTTTTAA	1.09863	1.13474
cg2244321	RNF213	TFIID [T0	1510	1516	0	TTTAAA	1.09863	1.13474
cg2244321	RNF213	GR-beta [T	11	15	0	AATTT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	720	724	0	AAATT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	1113	1117	0	AATGT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	1300	1304	0	AATGT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	1506	1510	0	AATTT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	1514	1518	0	AAATT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	1515	1519	0	AATTT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	1680	1684	0	AAATT	3.90625	3.99611
cg2244321	RNF213	GR-beta [T	1764	1768	0	ACATT	3.90625	3.99611
cg2244321	RNF213	PR B [T00	1307	1313	0	AACAGT	0.36621	0.36944
cg2244321	RNF213	PR A [T01	1307	1313	0	AACAGT	0.36621	0.36944
cg2244321	RNF213	GR [T050	364	370	0	TTTTTTG	0.36621	0.37562
cg2244321	RNF213	GR [T050	520	526	0	TTTTTTG	0.36621	0.37562
cg2244321	RNF213	GR [T050	712	718	0	CAAAAA	0.36621	0.37562
cg2244321	RNF213	GR [T050	815	821	0	TTTTTTG	0.36621	0.37562
cg2244321	RNF213	GR [T050	1109	1115	0	CAAAAA	0.36621	0.37562
cg2244321	RNF213	GR [T050	1516	1522	0	ATTTTTC	0.36621	0.37562
cg2244321	RNF213	GR [T050	1650	1656	0	ATTTTTC	0.36621	0.37562
cg2244321	RNF213	HNF-3alph	529	536	0	TATTTTT	0.09155	0.09511
cg2244321	RNF213	c-Myc [T0	263	268	0	CACGTG	0.48828	0.48199
cg0357715	SSBP2	RAR-beta:	1846	1857	9.97066	TCAGGT	0.06974	0.07677
cg0357715	SSBP2	PEA3 [T0	1364	1372	9.937959	CTCCAT	0.18311	0.18382
cg0357715	SSBP2	STAT1bet	1092	1101	9.807397	AGAAGG	0.14877	0.14533
cg0357715	SSBP2	XBP-1 [T	536	541	9.789909	AGACAT	1.95312	1.94901
cg0357715	SSBP2	XBP-1 [T	762	767	9.789909	ATGTCT	1.95312	1.94901
cg0357715	SSBP2	XBP-1 [T	1908	1913	9.789909	ATGGCT	1.95312	1.94901
cg0357715	SSBP2	NF-AT2 [T	926	935	9.755755	GGAAAT	0.08774	0.08205

cg0357715	SSBP2	c-Myb [T0	969	976	9.729271	TAACTG	0.36621	0.34746
cg0357715	SSBP2	GATA-3 [	1520	1531	9.652214	TTCCCTA	0.01597	0.01535
cg0357715	SSBP2	HNF-1C [	573	581	9.601936	AAAAAT	0.19836	0.18179
cg0357715	SSBP2	TFIID [T0	53	59	9.552105	TTTCACA	1.46484	1.37777
cg0357715	SSBP2	TFIID [T0	105	111	9.552105	TGACAA	1.46484	1.37777
cg0357715	SSBP2	TFIID [T0	343	349	9.552105	TTTCTCA	1.46484	1.37777
cg0357715	SSBP2	TFIID [T0	387	393	9.552105	TGAGAA	1.46484	1.37777
cg0357715	SSBP2	TFIID [T0	798	804	9.552105	TTTCCCA	1.46484	1.37777
cg0357715	SSBP2	TFIID [T0	1408	1414	9.552105	TTTGGTA	1.46484	1.37777
cg0357715	SSBP2	Pax-5 [T0	1951	1957	9.552105	GTTGCC	1.46484	1.61918
cg0357715	SSBP2	FOXP3 [T	67	72	9.512894	GTTATT	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	129	134	9.512894	GTTATC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	169	174	9.512894	GTTGCT	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	265	270	9.512894	AAGAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	284	289	9.512894	GTTATT	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	467	472	9.512894	GATAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	551	556	9.512894	CATAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	576	581	9.512894	AATAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	634	639	9.512894	AGCAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	656	661	9.512894	GTAAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	840	845	9.512894	GTTTAG	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	938	943	9.512894	GTTGGT	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	1007	1012	9.512894	GTTCTG	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	1145	1150	9.512894	GTTCTT	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	1435	1440	9.512894	CATAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	1481	1486	9.512894	GTAAAC	7.32422	7.22156
cg0357715	SSBP2	FOXP3 [T	1951	1956	9.512894	GTTGCC	7.32422	7.22156
cg0357715	SSBP2	TFII-I [T0	466	471	9.512894	GGATAA	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	672	677	9.512894	GGATGG	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	683	688	9.512894	AAGTCC	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	1307	1312	9.512894	AAGTCC	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	1366	1371	9.512894	CCATCC	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	1518	1523	9.512894	GTTTCC	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	1559	1564	9.512894	AAATCC	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	1627	1632	9.512894	GGAAAC	7.32422	7.44385
cg0357715	SSBP2	TFII-I [T0	1835	1840	9.512894	CCTTCC	7.32422	7.44385
cg0357715	SSBP2	Ik-1 [T027	1854	1866	9.497194	TCCCAC	0.02941	0.03137
cg0357715	SSBP2	c-Jun [T00	1070	1076	9.397655	ATTGTCA	0.73242	0.7366
cg0357715	SSBP2	NFI/CTF [	1423	1430	9.352332	CCAAGG	0.54932	0.55369
cg0357715	SSBP2	AP-1 [T00	950	958	9.290522	TGACTG	0.09155	0.08441
cg0357715	SSBP2	STAT5A [	423	435	9.080962	CATTTC	0.02816	0.02551
cg0357715	SSBP2	c-Ets-1 [T	674	680	9.065503	ATGGAA	0.85449	0.84987
cg0357715	SSBP2	c-Myb [T0	1483	1490	9.024874	AAACTG	0.39673	0.37851
cg0357715	SSBP2	MEF-2A [	1220	1230	9.003254	AACATA	0.07343	0.06466
cg0357715	SSBP2	GR [T050	123	129	8.971049	GCTTTC	0.61035	0.5928
cg0357715	SSBP2	c-Ets-2 [T	1837	1845	8.912323	TTCCTGC	0.27466	0.27171
cg0357715	SSBP2	c-Jun [T00	1832	1838	8.832178	TGACCT	0.61035	0.60549
cg0357715	SSBP2	c-Jun [T00	182	188	8.807683	TGACAA	0.61035	0.60549

cg0357715	SSBP2	LEF-1 [T0	452	459	8.759086	CTTTGTC	0.54932	0.53171
cg0357715	SSBP2	XBP-1 [T	243	248	8.75604	TATCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	492	497	8.75604	ATGAAA	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1035	1040	8.75604	TTTCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1066	1071	8.75604	GCTCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1185	1190	8.75604	TATCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1207	1212	8.75604	TTTCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1212	1217	8.75604	TCTCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1252	1257	8.75604	ATGATA	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1335	1340	8.75604	GCTCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1432	1437	8.75604	GATCAT	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1549	1554	8.75604	ATGAGA	2.92969	2.75329
cg0357715	SSBP2	XBP-1 [T	1668	1673	8.75604	TCTCAT	2.92969	2.75329
cg0357715	SSBP2	NF-kappa	1660	1671	8.728454	TGGGAA	0.01526	0.0164
cg0357715	SSBP2	STAT1bet	1293	1302	8.695301	CCCTGG	0.22316	0.2175
cg0357715	SSBP2	HNF-1C [	766	774	8.618905	CTGTAT	0.04578	0.04325
cg0357715	SSBP2	c-Myb [T0	636	643	8.529773	CAACTT	0.30518	0.28602
cg0357715	SSBP2	c-Myb [T0	869	876	8.443873	TACAGT	0.30518	0.28602
cg0357715	SSBP2	AhR:Arnt	1894	1903	8.431005	ACACGC	0.07439	0.08553
cg0357715	SSBP2	POU2F2 (	246	256	8.346865	CATCTA	0.0515	0.04751
cg0357715	SSBP2	HNF-3alph	227	234	8.343064	TATTTA	0.27466	0.23078
cg0357715	SSBP2	HNF-3alph	649	656	8.343064	TTAAAA	0.27466	0.23078
cg0357715	SSBP2	HNF-3alph	722	729	8.343064	TATTTTA	0.27466	0.23078
cg0357715	SSBP2	PR B [T00	1159	1165	8.338824	AACAGA	1.09863	1.09384
cg0357715	SSBP2	PR B [T00	1635	1641	8.338824	AACAGA	1.09863	1.09384
cg0357715	SSBP2	PR B [T00	1768	1774	8.338824	AACAGG	1.09863	1.09384
cg0357715	SSBP2	PR A [T01	1159	1165	8.338824	AACAGA	1.09863	1.09384
cg0357715	SSBP2	PR A [T01	1635	1641	8.338824	AACAGA	1.09863	1.09384
cg0357715	SSBP2	PR A [T01	1768	1774	8.338824	AACAGG	1.09863	1.09384
cg0357715	SSBP2	GR-alpha [	378	382	8.281568	GAAGG	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	622	626	8.281568	GGAGG	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1014	1018	8.281568	GAAGG	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1093	1097	8.281568	GAAGG	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1359	1363	8.281568	CCTCC	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1363	1367	8.281568	CCTCC	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1424	1428	8.281568	CAAGG	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1490	1494	8.281568	GGAGG	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1835	1839	8.281568	CCTTC	7.8125	8.20394
cg0357715	SSBP2	GR-alpha [	1868	1872	8.281568	CCTCC	7.8125	8.20394
cg0357715	SSBP2	HOXD9 [	63	72	8.224939	GTATGT	0.08774	0.0777
cg0357715	SSBP2	HOXD10 [	63	72	8.224939	GTATGT	0.08774	0.0777
cg0357715	SSBP2	NF-1 [T00	139	146	8.191058	TTGGGC	0.24414	0.24485
cg0357715	SSBP2	NF-1 [T00	1419	1426	8.191058	TAGTCC	0.24414	0.24485
cg0357715	SSBP2	VDR [T00	616	624	8.079962	GTTCAG	0.24414	0.22992
cg0357715	SSBP2	GR-alpha [	93	97	8.073878	CCTGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	629	633	8.073878	GCAGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	688	692	8.073878	CCTAC	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	923	927	8.073878	GCAGG	7.8125	8.20289

cg0357715	SSBP2	GR-alpha [	1079	1083	8.073878	CTAGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1294	1298	8.073878	CCTGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1322	1326	8.073878	CCTGC	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1389	1393	8.073878	GCAGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1623	1627	8.073878	GTAGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1658	1662	8.073878	CCTGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1839	1843	8.073878	CCTGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1956	1960	8.073878	CCAGG	7.8125	8.20289
cg0357715	SSBP2	GR-alpha [	1974	1978	8.073878	CCTGG	7.8125	8.20289
cg0357715	SSBP2	TFIID [T0	21	27	8.014558	TCACAA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	126	132	8.014558	TTTGTTA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	345	351	8.014558	TCTCAA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	438	444	8.014558	TTTGAG	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	453	459	8.014558	TTTGTG	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	500	506	8.014558	TCTCAA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	542	548	8.014558	TTACAA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	904	910	8.014558	TCACAA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	1180	1186	8.014558	TTTCTTA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	1229	1235	8.014558	TAAGAA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	1763	1769	8.014558	TTTGAA	2.19727	1.99811
cg0357715	SSBP2	TFIID [T0	1965	1971	8.014558	TCTCAA	2.19727	1.99811
cg0357715	SSBP2	Pax-5 [T0	141	147	8.014558	GGGCTT	2.19727	2.42766
cg0357715	SSBP2	Pax-5 [T0	307	313	8.014558	GAGGCC	2.19727	2.42766
cg0357715	SSBP2	Pax-5 [T0	1017	1023	8.014558	GGGCTG	2.19727	2.42766
cg0357715	SSBP2	Pax-5 [T0	1842	1848	8.014558	GGGCTC	2.19727	2.42766
cg0357715	SSBP2	Pax-5 [T0	1977	1983	8.014558	GGGCTC	2.19727	2.42766
cg0357715	SSBP2	C/EBPalp	727	733	8.006685	TACAAT	0.24414	0.23098
cg0357715	SSBP2	HNF-1B [	66	74	7.862525	TGTTAT	0.06866	0.0616
cg0357715	SSBP2	NF-AT2 [	1297	1306	7.779688	GGAAAG	0.08965	0.08482
cg0357715	SSBP2	GATA-2 [	239	247	7.777778	TCTGTA	0.30518	0.29346
cg0357715	SSBP2	GATA-2 [	1253	1261	7.777778	TGATAC	0.30518	0.29346
cg0357715	SSBP2	c-Ets-2 [T	519	527	7.76635	TTCCTA	0.32043	0.30792
cg0357715	SSBP2	c-Myb [T0	383	390	7.739476	TAACTG	0.42725	0.40917
cg0357715	SSBP2	IRF-1 [T0	1293	1301	7.732782	CCCTGG	0.14496	0.14723
cg0357715	SSBP2	NF-AT1 [	1627	1635	7.72101	GGAAAC	0.19836	0.19379
cg0357715	SSBP2	NFI/CTF [	135	142	7.587343	ACTTTT	0.36621	0.36269
cg0357715	SSBP2	NFI/CTF [	885	892	7.587343	ACATTT	0.36621	0.36269
cg0357715	SSBP2	c-Jun [T00	707	713	7.538568	GATGTC	0.48828	0.48672
cg0357715	SSBP2	GR [T050	135	141	7.527031	ACTTTT	1.83105	1.71535
cg0357715	SSBP2	GR [T050	255	261	7.527031	CAAACA	1.83105	1.71535
cg0357715	SSBP2	GR [T050	348	354	7.527031	CAAATA	1.83105	1.71535
cg0357715	SSBP2	GR [T050	394	400	7.527031	TTGTTT	1.83105	1.71535
cg0357715	SSBP2	GR [T050	503	509	7.527031	CAAATA	1.83105	1.71535
cg0357715	SSBP2	GR [T050	609	615	7.527031	CAAAAT	1.83105	1.71535
cg0357715	SSBP2	GR [T050	826	832	7.527031	TTATTT	1.83105	1.71535
cg0357715	SSBP2	GR [T050	874	880	7.527031	TTGTTT	1.83105	1.71535
cg0357715	SSBP2	GR [T050	907	913	7.527031	CAAAAG	1.83105	1.71535
cg0357715	SSBP2	GR [T050	1756	1762	7.527031	TTGTTT	1.83105	1.71535

cg0357715	SSBP2	GR [T050	1760	1766	7.527031	TTGTTTC	1.83105	1.71535
cg0357715	SSBP2	HNF-1C [	964	972	7.498386	TTGTTTA	0.08392	0.07663
cg0357715	SSBP2	p53 [T006	223	229	7.47855	GGGCTA	0.73242	0.79826
cg0357715	SSBP2	c-Ets-2 [T	921	929	7.268173	GAGCAG	0.09155	0.08977
cg0357715	SSBP2	NF-AT1 [	794	802	7.211175	TCTCTTT	0.15259	0.14325
cg0357715	SSBP2	c-Ets-1 [T	798	804	7.199436	TTTCCCA	0.73242	0.73732
cg0357715	SSBP2	SRY [T00	1407	1415	7.175614	CTTTGGT	0.30518	0.29547
cg0357715	SSBP2	SRY [T00	1462	1470	7.175614	CTTTGCT	0.30518	0.29547
cg0357715	SSBP2	XBP-1 [T	144	149	7.172312	CTTCAT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	147	152	7.172312	CATCAT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	216	221	7.172312	ATGATT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	233	238	7.172312	ATGATT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	528	533	7.172312	ATGATT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	984	989	7.172312	ATGAAT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	1039	1044	7.172312	ATGAGG	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	1169	1174	7.172312	ATGAAT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	1338	1343	7.172312	CATCAT	2.92969	2.7512
cg0357715	SSBP2	XBP-1 [T	1450	1455	7.172312	ATGAGG	2.92969	2.7512
cg0357715	SSBP2	Ik-1 [T027	1873	1885	7.122895	CCAGTA	0.01064	0.01145
cg0357715	SSBP2	TFIID [T0	171	177	7.082373	TGCTAA	0.12207	0.11255
cg0357715	SSBP2	NF-AT1 [	926	934	7.072017	GGAAAT	0.15259	0.14325
cg0357715	SSBP2	c-Ets-1 [T	1519	1525	7.071349	TTTCCCT	0.73242	0.73732
cg0357715	SSBP2	c-Ets-1 [T	1625	1631	7.071349	AGGGAA	0.73242	0.73732
cg0357715	SSBP2	HNF-1C [	67	75	7.028835	GTTATTA	0.08392	0.07499
cg0357715	SSBP2	NFI/CTF [	935	942	7.014249	AAGGTT	0.73242	0.74795
cg0357715	SSBP2	C/EBPalph	1069	1075	7.00174	CATTGTC	0.73242	0.68282
cg0357715	SSBP2	HNF-3alph	694	701	7.000129	TATTTCT	0.82397	0.71909
cg0357715	SSBP2	HNF-3alph	827	834	7.000129	TATTTGC	0.82397	0.71909
cg0357715	SSBP2	HNF-3alph	990	997	7.000129	AATTTTC	0.82397	0.71909
cg0357715	SSBP2	HNF-3alph	1575	1582	7.000129	TATTTAT	0.82397	0.71909
cg0357715	SSBP2	HNF-3alph	1701	1708	7.000129	AATTTAT	0.82397	0.71909
cg0357715	SSBP2	IRF-1 [T0	798	806	6.968314	TTTCCCA	0.1297	0.12685
cg0357715	SSBP2	c-Ets-1 [T	1289	1295	6.943262	TTTCCCC	0.73242	0.73732
cg0357715	SSBP2	ENKTF-1	1894	1901	6.942764	ACACGC	1.46484	1.56616
cg0357715	SSBP2	p53 [T006	307	313	6.938545	GAGGCC	1.09863	1.22478
cg0357715	SSBP2	VDR [T00	835	843	6.925682	GTTCAG	0.42725	0.41
cg0357715	SSBP2	HNF-1B [	152	160	6.912308	TGTTAA	0.07629	0.07044
cg0357715	SSBP2	c-Jun [T00	1781	1787	6.787369	TCTGTCA	0.73242	0.73062
cg0357715	SSBP2	NFI/CTF [	940	947	6.786076	TGGTTTC	0.73242	0.74795
cg0357715	SSBP2	NFI/CTF [	1648	1655	6.786076	CCAAGC	0.73242	0.74795
cg0357715	SSBP2	p53 [T006	1842	1848	6.778774	GGGCTC	1.09863	1.22478
cg0357715	SSBP2	p53 [T006	1977	1983	6.778774	GGGCTC	1.09863	1.22478
cg0357715	SSBP2	POU2F2 (	273	283	6.735173	CGTTTA	0.04292	0.03779
cg0357715	SSBP2	T3R-beta1	1944	1952	6.702681	TCACCA	0.21362	0.2251
cg0357715	SSBP2	FOXP3 [T	402	407	6.581441	TTCAAC	0.97656	0.904
cg0357715	SSBP2	TFII-I [T0	862	867	6.581441	CACTCC	0.97656	0.9991
cg0357715	SSBP2	TFII-I [T0	1796	1801	6.581441	GGAGTG	0.97656	0.9991
cg0357715	SSBP2	p53 [T006	141	147	6.563521	GGGCTT	0.48828	0.54643

cg0357715	SSBP2	PPAR-alpl	1878	1888	6.51544	AGCTGG	0.03719	0.04058
cg0357715	SSBP2	XBP-1 [T	858	863	6.478682	ATGCCA	0.97656	0.99906
cg0357715	SSBP2	C/EBPalpl	742	748	6.460799	GTCAAT	0.48828	0.47407
cg0357715	SSBP2	c-Fos [T00	1737	1746	6.448203	TCTGTGA	0.04578	0.04485
cg0357715	SSBP2	RAR-beta	1938	1947	6.415195	GGGGTT	0.18311	0.1857
cg0357715	SSBP2	MEF-2A [	605	615	6.342474	AGCACA	0.02384	0.02083
cg0357715	SSBP2	TCF-4E [T	962	968	6.302385	CTTTGTT	0.61035	0.59686
cg0357715	SSBP2	TCF-4E [T	1407	1413	6.302385	CTTTGGT	0.61035	0.59686
cg0357715	SSBP2	PPAR-alpl	308	318	6.299891	AGGCCC	0.03719	0.04058
cg0357715	SSBP2	GR-alpha [	306	310	6.263098	TGAGG	3.90625	3.89624
cg0357715	SSBP2	GR-alpha [	568	572	6.263098	CCTTA	3.90625	3.89624
cg0357715	SSBP2	GR-alpha [	1040	1044	6.263098	TGAGG	3.90625	3.89624
cg0357715	SSBP2	GR-alpha [	1141	1145	6.263098	TAAGG	3.90625	3.89624
cg0357715	SSBP2	GR-alpha [	1451	1455	6.263098	TGAGG	3.90625	3.89624
cg0357715	SSBP2	GR-alpha [	1487	1491	6.263098	TGAGG	3.90625	3.89624
cg0357715	SSBP2	GR-alpha [	1563	1567	6.263098	CCTTA	3.90625	3.89624
cg0357715	SSBP2	GR-alpha [	1862	1866	6.263098	CCTCA	3.90625	3.89624
cg0357715	SSBP2	c-Myb [T0	280	287	6.259888	AGCAGT	0.30518	0.30272
cg0357715	SSBP2	c-Myb [T0	831	838	6.259888	TGCAGT	0.30518	0.30272
cg0357715	SSBP2	C/EBPalpl	286	292	6.245236	TATTGCA	0.97656	0.91422
cg0357715	SSBP2	C/EBPalpl	1579	1585	6.245236	TATTGAA	0.97656	0.91422
cg0357715	SSBP2	PEA3 [T0	671	679	6.227095	AGGATG	0.03815	0.03662
cg0357715	SSBP2	NF-AT1 [	1296	1305	6.201624	TGGAAA	0.03815	0.03661
cg0357715	SSBP2	SRY [T00	452	460	6.176442	CTTTGTC	0.15259	0.14742
cg0357715	SSBP2	c-Jun [T00	105	111	6.152811	TGACAA	0.36621	0.34478
cg0357715	SSBP2	RelA [T00	1659	1669	6.102071	CTGGGA	0.01097	0.01155
cg0357715	SSBP2	GR-alpha [	618	622	6.055408	TCAGG	3.90625	3.89835
cg0357715	SSBP2	GR-alpha [	842	846	6.055408	TTAGG	3.90625	3.89835
cg0357715	SSBP2	GR-alpha [	1498	1502	6.055408	CCTAA	3.90625	3.89835
cg0357715	SSBP2	GR-alpha [	1610	1614	6.055408	TTAGG	3.90625	3.89835
cg0357715	SSBP2	GR-alpha [	1789	1793	6.055408	TCAGG	3.90625	3.89835
cg0357715	SSBP2	GR-alpha [	1830	1834	6.055408	CCTGA	3.90625	3.89835
cg0357715	SSBP2	GR-alpha [	1846	1850	6.055408	TCAGG	3.90625	3.89835
cg0357715	SSBP2	c-Ets-1 [T	1295	1301	6.039428	CTGGAA	0.36621	0.36174
cg0357715	SSBP2	RXR-alpha	1342	1348	5.937582	ATTACC	0.73242	0.78318
cg0357715	SSBP2	STAT4 [T	1835	1840	5.882353	CCTTCC	0.48828	0.51201
cg0357715	SSBP2	C/EBPalpl	846	852	5.850545	GGCAAT	0.97656	0.91422
cg0357715	SSBP2	c-Ets-1 [T	1660	1666	5.814485	TGGGAA	0.36621	0.36174
cg0357715	SSBP2	STAT1bet	797	806	5.796867	CTTTCCC	0.1545	0.14881
cg0357715	SSBP2	STAT1bet	922	931	5.796867	AGCAGG	0.1545	0.14881
cg0357715	SSBP2	HNF-1B [	965	973	5.778578	TGTTTAA	0.09918	0.08736
cg0357715	SSBP2	NF-AT1 [	1096	1104	5.77403	GGAAAG	0.06866	0.06621
cg0357715	SSBP2	POU2F2 (	583	593	5.731804	TATATAA	0.06437	0.05879
cg0357715	SSBP2	ENKTF-1	1654	1661	5.687009	TGGCCC	0.73242	0.76357
cg0357715	SSBP2	NF-1 [T00	889	896	5.626299	TTGGAC	0.24414	0.25051
cg0357715	SSBP2	HNF-1A [	1260	1267	5.610392	GACTTA	0.24414	0.23087
cg0357715	SSBP2	NFI/CTF [	1536	1543	5.558661	GGGCTT	0.54932	0.55504
cg0357715	SSBP2	c-Ets-1 [T	1542	1548	5.558311	GGGGAA	0.36621	0.38732

cg0357715	SSBP2	AP-1 [T00	1741	1749	5.54906	TGACTC	0.09155	0.08822
cg0357715	SSBP2	TFIID [T0	152	158	5.544826	TGTTAA	0.73242	0.65314
cg0357715	SSBP2	TFIID [T0	1114	1120	5.544826	TTTAAC	0.73242	0.65314
cg0357715	SSBP2	TFIID [T0	1410	1416	5.544826	TGGTAA	0.73242	0.65314
cg0357715	SSBP2	Pax-5 [T0	223	229	5.544826	GGGCTA	0.73242	0.79
cg0357715	SSBP2	Pax-5 [T0	845	851	5.544826	GGGCAA	0.73242	0.79
cg0357715	SSBP2	p53 [T006	1017	1023	5.508538	GGGCTG	0.61035	0.65765
cg0357715	SSBP2	IRF-1 [T0	1289	1297	5.42531	TTTCCC	0.22888	0.21959
cg0357715	SSBP2	IRF-1 [T0	922	930	5.404935	AGCAGG	0.22888	0.21959
cg0357715	SSBP2	C/EBPalp	392	398	5.38654	AATTGT	0.73242	0.68229
cg0357715	SSBP2	C/EBPalp	1120	1126	5.38654	AACAAT	0.73242	0.68229
cg0357715	SSBP2	NF-1 [T00	221	228	5.377909	TTGGGC	0.24414	0.25051
cg0357715	SSBP2	HOXD9 [	35	44	5.275652	AATAAA	0.04578	0.03952
cg0357715	SSBP2	HOXD9 [	511	520	5.275652	CGATTT	0.04578	0.03952
cg0357715	SSBP2	HOXD9 [	929	938	5.275652	AATAAA	0.04578	0.03952
cg0357715	SSBP2	HOXD10 [	35	44	5.275652	AATAAA	0.04578	0.03952
cg0357715	SSBP2	HOXD10 [	511	520	5.275652	CGATTT	0.04578	0.03952
cg0357715	SSBP2	HOXD10 [	929	938	5.275652	AATAAA	0.04578	0.03952
cg0357715	SSBP2	RXR-alph	1825	1831	5.271235	GCAACC	0.61035	0.65415
cg0357715	SSBP2	GR [T050	545	551	5.207533	CAAAAC	0.24414	0.24013
cg0357715	SSBP2	GR [T050	1460	1466	5.207533	GTCTTC	0.24414	0.24013
cg0357715	SSBP2	c-Jun [T00	1510	1516	5.193102	TGACTT	0.61035	0.60573
cg0357715	SSBP2	c-Myb [T0	312	319	5.137438	CCCAGT	0.30518	0.30087
cg0357715	SSBP2	HNF-1A [	316	323	5.116518	GTTAAG	0.36621	0.34064
cg0357715	SSBP2	GR-beta [	365	369	5.042296	AATAC	3.90625	3.7093
cg0357715	SSBP2	GR-beta [	1105	1109	5.042296	AATCC	3.90625	3.7093
cg0357715	SSBP2	GR-beta [	1560	1564	5.042296	AATCC	3.90625	3.7093
cg0357715	SSBP2	GR-beta [	1574	1578	5.042296	GTATT	3.90625	3.7093
cg0357715	SSBP2	GR-beta [	1584	1588	5.042296	AATAC	3.90625	3.7093
cg0357715	SSBP2	GR-beta [	1617	1621	5.042296	AATAC	3.90625	3.7093
cg0357715	SSBP2	GR-beta [	1686	1690	5.042296	AATAC	3.90625	3.7093
cg0357715	SSBP2	GR-beta [	1921	1925	5.042296	GTATT	3.90625	3.7093
cg0357715	SSBP2	C/EBPalp	530	536	5.024728	GATTGC	0.97656	0.90302
cg0357715	SSBP2	NF-1 [T00	1152	1159	4.880836	TTGGTA	0.24414	0.24345
cg0357715	SSBP2	RXR-alph	1772	1778	4.86724	GGGTCT	0.48828	0.51407
cg0357715	SSBP2	HNF-3alp	1223	1230	4.842999	ATAAAA	0.09155	0.07438
cg0357715	SSBP2	HNF-3alp	1278	1285	4.842999	AATTTT	0.09155	0.07438
cg0357715	SSBP2	HNF-3alp	1281	1288	4.842999	TTTAAA	0.09155	0.07438
cg0357715	SSBP2	c-Myb [T0	469	476	4.840682	TAACTT	0.30518	0.30087
cg0357715	SSBP2	FOXP3 [T	38	43	4.756447	AAAAAC	2.92969	2.82
cg0357715	SSBP2	FOXP3 [T	340	345	4.756447	GTTTTT	2.92969	2.82
cg0357715	SSBP2	FOXP3 [T	545	550	4.756447	CAAAAC	2.92969	2.82
cg0357715	SSBP2	FOXP3 [T	1033	1038	4.756447	GTTTTC	2.92969	2.82
cg0357715	SSBP2	FOXP3 [T	1384	1389	4.756447	GTTTTG	2.92969	2.82
cg0357715	SSBP2	FOXP3 [T	1401	1406	4.756447	AAAAAC	2.92969	2.82
cg0357715	SSBP2	FOXP3 [T	1632	1637	4.756447	CAAAAC	2.92969	2.82
cg0357715	SSBP2	TFII-I [T0	731	736	4.756447	ATGTCC	2.92969	2.89715
cg0357715	SSBP2	TFII-I [T0	926	931	4.756447	GGAAAT	2.92969	2.89715

cg0357715	SSBP2	TFII-I [T0	1288	1293	4.756447	ATTTCC	2.92969	2.89715
cg0357715	SSBP2	TFII-I [T0	1348	1353	4.756447	CAGTCC	2.92969	2.89715
cg0357715	SSBP2	c-Ets-1 [T	518	524	4.539113	ATTCCT	0.85449	0.8381
cg0357715	SSBP2	USF2 [T0	1847	1856	4.528187	CAGGTG	0.06866	0.07203
cg0357715	SSBP2	T3R-beta1	92	100	4.462023	TCCTGG	0.27466	0.27245
cg0357715	SSBP2	T3R-beta1	565	573	4.462023	TCACCT	0.27466	0.27245
cg0357715	SSBP2	HNF-1C [	153	161	4.443787	GTTAAA	0.07629	0.06715
cg0357715	SSBP2	c-Jun [T00	950	956	4.441904	TGACTG	0.12207	0.11843
cg0357715	SSBP2	RXR-alph	184	190	4.423008	ACAACC	0.24414	0.25781
cg0357715	SSBP2	STAT4 [T	995	1000	4.411765	TCTTCC	1.95312	1.99838
cg0357715	SSBP2	STAT4 [T	1544	1549	4.411765	GGAAGA	1.95312	1.99838
cg0357715	SSBP2	STAT4 [T	1662	1667	4.411765	GGAAGC	1.95312	1.99838
cg0357715	SSBP2	c-Ets-1 [T	958	964	4.411026	ATTCCT	0.85449	0.8381
cg0357715	SSBP2	p53 [T006	1653	1659	4.33696	CTGGCC	0.24414	0.28373
cg0357715	SSBP2	C/EBPalp	200	206	4.235345	TATTGC	0.48828	0.46347
cg0357715	SSBP2	GR-beta [	35	39	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	68	72	4.201913	TTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	199	203	4.201913	TTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	217	221	4.201913	TGATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	226	230	4.201913	CTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	234	238	4.201913	TGATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	261	265	4.201913	AATCA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	285	289	4.201913	TTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	329	333	4.201913	TGATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	350	354	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	399	403	4.201913	TGATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	432	436	4.201913	CTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	457	461	4.201913	TGATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	505	509	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	511	515	4.201913	CGATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	516	520	4.201913	TTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	529	533	4.201913	TGATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	576	580	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	612	616	4.201913	AATAG	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	644	648	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	678	682	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	693	697	4.201913	TTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	826	830	4.201913	TTATT	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	881	885	4.201913	AATCA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	929	933	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	987	991	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	1227	1231	4.201913	AATAA	7.8125	7.23274
cg0357715	SSBP2	GR-beta [	1578	1582	4.201913	TTATT	7.8125	7.23274
cg0357715	SSBP2	EBF [T05	1655	1665	4.120419	GGCCCT	0.0248	0.02839
cg0357715	SSBP2	IRF-1 [T0	1623	1631	4.035054	GTAGGG	0.1297	0.12468
cg0357715	SSBP2	RXR-alph	1939	1945	4.019014	GGGTTT	0.97656	1.02803
cg0357715	SSBP2	c-Ets-2 [T	959	967	4.017001	TTCCTTT	0.16022	0.15061
cg0357715	SSBP2	TFIID [T0	69	75	4.007279	TATTAA	1.09863	0.94722

cg0357715	SSBP2	TFIID [T0	541	547	4.007279	TTTACA	1.09863	0.94722
cg0357715	SSBP2	TFIID [T0	725	731	4.007279	TTTACA	1.09863	0.94722
cg0357715	SSBP2	TFIID [T0	1280	1286	4.007279	TTTTAA	1.09863	0.94722
cg0357715	SSBP2	TFIID [T0	1397	1403	4.007279	TTGTAA	1.09863	0.94722
cg0357715	SSBP2	TFIID [T0	1479	1485	4.007279	TTGTAA	1.09863	0.94722
cg0357715	SSBP2	AP-2alpha	1424	1429	3.970052	CAAGGC	0.97656	1.02535
cg0357715	SSBP2	NFI/CTF [	1405	1412	3.793671	ACCTTT	0.18311	0.19063
cg0357715	SSBP2	GR [T050	1383	1389	3.763516	TGTTTC	0.73242	0.6946
cg0357715	SSBP2	GR [T050	1632	1638	3.763516	CAAAAC	0.73242	0.6946
cg0357715	SSBP2	p53 [T006	1536	1542	3.750231	GGGCTT	0.73242	0.82434
cg0357715	SSBP2	p53 [T006	845	851	3.728319	GGGCAA	0.73242	0.80362
cg0357715	SSBP2	HNF-3alp	72	79	3.500065	TAAAAA	0.27466	0.23175
cg0357715	SSBP2	HNF-3alp	352	359	3.500065	TAAAAA	0.27466	0.23175
cg0357715	SSBP2	HNF-3alp	361	368	3.500065	AAAAAA	0.27466	0.23175
cg0357715	SSBP2	HNF-3alp	433	440	3.500065	TATTTT	0.27466	0.23175
cg0357715	SSBP2	HNF-3alp	572	579	3.500065	AAAAAA	0.27466	0.23175
cg0357715	SSBP2	HNF-3alp	608	615	3.500065	ACAAAA	0.27466	0.23175
cg0357715	SSBP2	HNF-3alp	1922	1929	3.500065	TATTTT	0.27466	0.23175
cg0357715	SSBP2	VDR [T00	563	571	3.462841	GTTCAC	0.21362	0.21283
cg0357715	SSBP2	GR-beta [	14	18	3.361531	AATAT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	176	180	3.361531	AATAT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	295	299	3.361531	AATAT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	720	724	3.361531	AATAT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	721	725	3.361531	ATATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	855	859	3.361531	AATAT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	956	960	3.361531	AGATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	1110	1114	3.361531	ATATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	1285	1289	3.361531	AATAT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	1286	1290	3.361531	ATATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	1376	1380	3.361531	AGATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	1735	1739	3.361531	AATCT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	1748	1752	3.361531	AATCT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [	1987	1991	3.361531	AATCT	3.90625	3.51525
cg0357715	SSBP2	c-Ets-1 [T	996	1002	3.359159	CTTCCG	0.61035	0.61936
cg0357715	SSBP2	PR B [T00	392	398	3.29756	AATTGT	0.24414	0.21408
cg0357715	SSBP2	PR B [T00	1120	1126	3.29756	AACAAT	0.24414	0.21408
cg0357715	SSBP2	PR A [T01	392	398	3.29756	AATTGT	0.24414	0.21408
cg0357715	SSBP2	PR A [T01	1120	1126	3.29756	AACAAT	0.24414	0.21408
cg0357715	SSBP2	c-Jun [T00	1741	1747	3.244843	TGACTC	0.24414	0.2435
cg0357715	SSBP2	AP-2alpha	1331	1336	3.229049	AGAGGC	0.48828	0.5124
cg0357715	SSBP2	c-Fos [T00	1017	1026	3.154982	GGGCTG	0.06104	0.06233
cg0357715	SSBP2	TFIID [T0	1385	1391	3.075094	TTTTGC	0.12207	0.11309
cg0357715	SSBP2	c-Jun [T00	739	745	3.049104	TGGGTC	0.24414	0.2435
cg0357715	SSBP2	p53 [T006	1951	1957	3.024997	GTTGCC	0.48828	0.53227
cg0357715	SSBP2	C/EBPalp	1984	1990	3.014837	AGCAAT	0.48828	0.47526
cg0357715	SSBP2	STAT4 [T	517	522	2.941176	TATTCC	2.92969	2.92382
cg0357715	SSBP2	STAT4 [T	676	681	2.941176	GGAATA	2.92969	2.92382
cg0357715	SSBP2	STAT4 [T	797	802	2.941176	CTTTCC	2.92969	2.92382

cg0357715	SSBP2	STAT4 [T	957	962	2.941176	GATTCC	2.92969	2.92382
cg0357715	SSBP2	STAT4 [T	1096	1101	2.941176	GGAAAG	2.92969	2.92382
cg0357715	SSBP2	STAT4 [T	1297	1302	2.941176	GGAAAG	2.92969	2.92382
cg0357715	SSBP2	IRF-1 [T0	1092	1100	2.890712	AGAAGG	0.07629	0.07093
cg0357715	SSBP2	NF-AT1 [	1297	1305	2.619709	GGAAAG	0.09155	0.08666
cg0357715	SSBP2	AR [T000	728	736	2.593284	ACAATG	0.11444	0.11078
cg0357715	SSBP2	PXR-1:RX	832	839	2.577808	GCAGTT	0.12207	0.11843
cg0357715	SSBP2	AP-2alpha	306	311	2.550491	TGAGGC	0.48828	0.51216
cg0357715	SSBP2	RXR-alph	1324	1330	2.544678	TGCACC	0.85449	0.89683
cg0357715	SSBP2	RAR-beta:	1842	1853	2.492665	GGGCTC	0.00215	0.00241
cg0357715	SSBP2	c-Ets-2 [T	1091	1099	2.447661	TAGAAG	0.07629	0.07844
cg0357715	SSBP2	LEF-1 [T0	1462	1469	2.345041	CTTTGC	0.09155	0.09076
cg0357715	SSBP2	Elk-1 [T00	1836	1844	2.299314	CTTCCTC	0.09155	0.09306
cg0357715	SSBP2	T3R-beta1	1845	1853	2.221365	CTCAGG	0.15259	0.15303
cg0357715	SSBP2	LEF-1 [T0	1407	1414	2.21836	CTTTGG	0.18311	0.17215
cg0357715	SSBP2	GATA-1 [	465	470	2.176375	AGGATA	3.90625	3.79558
cg0357715	SSBP2	GATA-1 [	523	528	2.176375	TATCCA	3.90625	3.79558
cg0357715	SSBP2	GATA-1 [	1313	1318	2.176375	TATCCT	3.90625	3.79558
cg0357715	SSBP2	HOXD9 [	678	687	2.085829	AATAAA	0.00381	0.00327
cg0357715	SSBP2	HOXD10 [	678	687	2.085829	AATAAA	0.00381	0.00327
cg0357715	SSBP2	LEF-1 [T0	962	969	2.004405	CTTTGTT	0.18311	0.17215
cg0357715	SSBP2	SRY [T00	962	970	1.998343	CTTTGTT	0.03052	0.02861
cg0357715	SSBP2	NF-AT1 [	1285	1293	1.94698	AATATT	0.06866	0.0623
cg0357715	SSBP2	PR B [T00	336	342	1.892895	AAGTGT	0.12207	0.1127
cg0357715	SSBP2	PR B [T00	1605	1611	1.892895	AAGTGT	0.12207	0.1127
cg0357715	SSBP2	PR A [T01	336	342	1.892895	AAGTGT	0.12207	0.1127
cg0357715	SSBP2	PR A [T01	1605	1611	1.892895	AAGTGT	0.12207	0.1127
cg0357715	SSBP2	AP-2alpha	1358	1363	1.871933	GCCTCC	0.97656	1.07805
cg0357715	SSBP2	AP-2alpha	1490	1495	1.871933	GGAGGC	0.97656	1.07805
cg0357715	SSBP2	AP-2alpha	1867	1872	1.871933	GCCTCC	0.97656	1.07805
cg0357715	SSBP2	TBP [T00	581	590	1.871542	CTTATA	0.18311	0.15671
cg0357715	SSBP2	TBP [T00	1233	1242	1.871542	AAACTA	0.18311	0.15671
cg0357715	SSBP2	C/EBPalph	483	489	1.830762	CGCAAT	0.48828	0.46352
cg0357715	SSBP2	FOXP3 [T	1156	1161	1.824994	TACAAC	0.48828	0.46414
cg0357715	SSBP2	FOXP3 [T	1217	1222	1.824994	TACAAC	0.48828	0.46414
cg0357715	SSBP2	TFII-I [T0	916	921	1.824994	GGAGAG	0.48828	0.51201
cg0357715	SSBP2	TFII-I [T0	1317	1322	1.824994	CTCTCC	0.48828	0.51201
cg0357715	SSBP2	GR-beta [	110	114	1.680765	AATTC	3.90625	3.70067
cg0357715	SSBP2	GR-beta [	120	124	1.680765	AATGC	3.90625	3.70067
cg0357715	SSBP2	GR-beta [	849	853	1.680765	AATTC	3.90625	3.70067
cg0357715	SSBP2	GR-beta [	1123	1127	1.680765	AATTC	3.90625	3.70067
cg0357715	SSBP2	GR-beta [	1171	1175	1.680765	GAATT	3.90625	3.70067
cg0357715	SSBP2	GR-beta [	1172	1176	1.680765	AATTC	3.90625	3.70067
cg0357715	SSBP2	GR-beta [	1678	1682	1.680765	GCATT	3.90625	3.70067
cg0357715	SSBP2	GR-beta [	1714	1718	1.680765	GCATT	3.90625	3.70067
cg0357715	SSBP2	c-Ets-1 [T	1094	1100	1.641124	AAGGAA	0.36621	0.35197
cg0357715	SSBP2	C/EBPbeta	139	142	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	221	224	1.639871	TTGG	15.625	15.23827

cg0357715	SSBP2	C/EBPbeta	889	892	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	939	942	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	944	947	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1049	1052	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1152	1155	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1409	1412	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1423	1426	1.639871	CCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1540	1543	1.639871	TTGG	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1648	1651	1.639871	CCAA	15.625	15.23827
cg0357715	SSBP2	PXR-1:RX	613	620	1.63615	ATAGTT	0.06104	0.05484
cg0357715	SSBP2	IRF-1 [T0	1519	1527	1.616539	TTTCCC	0.04578	0.04268
cg0357715	SSBP2	XBP-1 [T	181	186	1.583727	ATGACA	0.97656	0.94995
cg0357715	SSBP2	XBP-1 [T	709	714	1.583727	TGTCAT	0.97656	0.94995
cg0357715	SSBP2	XBP-1 [T	1072	1077	1.583727	TGTCAT	0.97656	0.94995
cg0357715	SSBP2	TFIID [T0	543	549	1.537547	TACAAA	0.73242	0.65627
cg0357715	SSBP2	TFIID [T0	663	669	1.537547	TGAAAA	0.73242	0.65627
cg0357715	SSBP2	TFIID [T0	724	730	1.537547	TTTTACA	0.73242	0.65627
cg0357715	SSBP2	TFIID [T0	1398	1404	1.537547	TGTAAA	0.73242	0.65627
cg0357715	SSBP2	TFIID [T0	1917	1923	1.537547	TTTTGTA	0.73242	0.65627
cg0357715	SSBP2	TFIID [T0	1926	1932	1.537547	TTTTGTA	0.73242	0.65627
cg0357715	SSBP2	Pax-5 [T0	1653	1659	1.537547	CTGGCC	0.73242	0.83087
cg0357715	SSBP2	Pax-5 [T0	1726	1732	1.537547	CTTGCC	0.73242	0.83087
cg0357715	SSBP2	STAT4 [T	1518	1523	1.470588	GTTTCC	1.95312	1.90161
cg0357715	SSBP2	STAT4 [T	1627	1632	1.470588	GGAAAC	1.95312	1.90161
cg0357715	SSBP2	c-Ets-1 [T	924	930	1.384951	CAGGAA	0.36621	0.35197
cg0357715	SSBP2	C/EBPbeta	113	116	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	263	266	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	333	336	1.366559	TTGA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	347	350	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	398	401	1.366559	TTGA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	403	406	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	439	442	1.366559	TTGA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	502	505	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	743	746	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	878	881	1.366559	TTGA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1305	1308	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1509	1512	1.366559	TTGA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1581	1584	1.366559	TTGA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1764	1767	1.366559	TTGA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1967	1970	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	C/EBPbeta	1981	1984	1.366559	TCAA	15.625	15.23827
cg0357715	SSBP2	AP-2alpha	1888	1893	1.357116	ACAGGC	0.48828	0.51319
cg0357715	SSBP2	HNF-3alph	1111	1118	1.342935	TATTTA	0.03052	0.02477
cg0357715	SSBP2	HNF-3alph	1682	1689	1.342935	TTAAAA	0.03052	0.02477
cg0357715	SSBP2	GATA-2 [	1521	1529	1.111111	TCCCTA	0.09155	0.08894
cg0357715	SSBP2	GATA-1 [	243	248	1.038567	TATCAT	1.95312	1.80234
cg0357715	SSBP2	GATA-1 [	1185	1190	1.038567	TATCAT	1.95312	1.80234
cg0357715	SSBP2	GATA-1 [	1252	1257	1.038567	ATGATA	1.95312	1.80234

cg0357715	SSBP2	TBP [T007	1703	1712	0.935771	TTTATAC	0.12207	0.10448
cg0357715	SSBP2	GATA-1 [	131	136	0.863549	TATCAC	1.95312	1.80234
cg0357715	SSBP2	GATA-1 [	594	599	0.863549	GTGATA	1.95312	1.80234
cg0357715	SSBP2	GATA-1 [	715	720	0.863549	GTGATA	1.95312	1.80234
cg0357715	SSBP2	RXR-alph	740	746	0.848226	GGGTCA	0.48828	0.51313
cg0357715	SSBP2	RXR-alph	890	896	0.848226	TGGACC	0.48828	0.51313
cg0357715	SSBP2	GR-beta [	50	54	0.840383	CCATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	215	219	0.840383	AATGA	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	232	236	0.840383	AATGA	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	356	360	0.840383	AATTA	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	392	396	0.840383	AATTG	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	485	489	0.840383	CAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	491	495	0.840383	AATGA	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	646	650	0.840383	TAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	647	651	0.840383	AATTA	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	823	827	0.840383	TAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	824	828	0.840383	AATTA	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	848	852	0.840383	CAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	989	993	0.840383	TAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1054	1058	0.840383	AATGG	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1068	1072	0.840383	TCATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1122	1126	0.840383	CAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1177	1181	0.840383	TAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1251	1255	0.840383	AATGA	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1340	1344	0.840383	TCATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1670	1674	0.840383	TCATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1700	1704	0.840383	TAATT	7.8125	7.2174
cg0357715	SSBP2	GR-beta [	1913	1917	0.840383	TAATT	7.8125	7.2174
cg0357715	SSBP2	HNF-1A [	1614	1621	0.781639	GTTAAT	0.48828	0.45029
cg0357715	SSBP2	AP-2alpha	1789	1794	0.678558	TCAGGC	0.48828	0.51196
cg0357715	SSBP2	HNF-1A [	965	972	0.431647	TGTTTAA	0.24414	0.21942
cg0357715	SSBP2	AP-1 [T00	1021	1029	0.401835	TGACTC	0.09155	0.08806
cg0357715	SSBP2	HNF-1A [	153	160	0.287765	GTTAAA	0.24414	0.21942
cg0357715	SSBP2	AP-2alpha	1956	1961	0.226186	CCAGGC	0.97656	1.07867
cg0357715	SSBP2	p53 [T006	1726	1732	0.211706	CTTGCC	0.36621	0.40082
cg0357715	SSBP2	GR-alpha [	82	86	0.207689	CCTCT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	669	673	0.207689	AAAGG	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	911	915	0.207689	AGAGG	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	934	938	0.207689	AAAGG	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	961	965	0.207689	CCTTT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1316	1320	0.207689	CCTCT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1331	1335	0.207689	AGAGG	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1353	1357	0.207689	CCTCT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1406	1410	0.207689	CCTTT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1532	1536	0.207689	AAAGG	7.8125	7.79817
cg0357715	SSBP2	PXR-1:RX	560	567	0.123583	TGAGTT	0.12207	0.11255
cg0357715	SSBP2	GATA-1 [	1551	1556	0.105011	GAGATA	0.97656	0.92541
cg0357715	SSBP2	GR-beta [	57	61	0	ACATT	3.90625	3.51525

cg0357715	SSBP2	GR-beta [T	75	79	0	AAATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	76	80	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	109	113	0	AAATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	355	359	0	AAATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	391	395	0	AAATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	422	426	0	ACATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	486	490	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	538	542	0	ACATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	653	657	0	AATGT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	730	734	0	AATGT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	745	749	0	AATGT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	790	794	0	ACATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	885	889	0	ACATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	990	994	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	1178	1182	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	1277	1281	0	AAATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	1278	1282	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	1414	1418	0	AAATT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	1415	1419	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	1701	1705	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	GR-beta [T	1914	1918	0	AATTT	3.90625	3.51525
cg0357715	SSBP2	TFIID [T0	71	77	0	TTAAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	358	364	0	TTAAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	359	365	0	TAAAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	436	442	0	TTTTTGA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	570	576	0	TTAAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	571	577	0	TAAAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	1128	1134	0	TTTTAG	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	1237	1243	0	TATAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	1239	1245	0	TAAAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	1555	1561	0	TATAAA	1.09863	0.95175
cg0357715	SSBP2	TFIID [T0	1681	1687	0	TTTAAA	1.09863	0.95175
cg0357715	SSBP2	c-Jun [T00	1021	1027	0	TGACTC	0.12207	0.11843
cg0357715	SSBP2	GR-alpha [	463	467	0	ACAGG	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	521	525	0	CCTAT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	735	739	0	CCTGT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1311	1315	0	CCTAT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1503	1507	0	CCTGT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1523	1527	0	CCTAT	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1769	1773	0	ACAGG	7.8125	7.79817
cg0357715	SSBP2	GR-alpha [	1888	1892	0	ACAGG	7.8125	7.79817
cg0357715	SSBP2	FOXP3 [T	183	188	0	GACAAC	1.46484	1.44953
cg0357715	SSBP2	FOXP3 [T	873	878	0	GTTGTT	1.46484	1.44953
cg0357715	SSBP2	FOXP3 [T	1117	1122	0	AACAAC	1.46484	1.44953
cg0357715	SSBP2	FOXP3 [T	1641	1646	0	AACAAC	1.46484	1.44953
cg0357715	SSBP2	C/EBPbeta	23	26	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	107	110	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	117	120	0	GCAA	15.625	15.26275

cg0357715	SSBP2	C/EBPbeta	127	130	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	170	173	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	184	187	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	202	205	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	254	257	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	258	261	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	288	291	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	394	397	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	454	457	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	473	476	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	484	487	0	GCAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	532	535	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	544	547	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	608	611	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	635	638	0	GCAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	640	643	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	728	731	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	830	833	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	847	850	0	GCAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	874	877	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	906	909	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	964	967	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1071	1074	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1118	1121	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1121	1124	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1157	1160	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1200	1203	0	GCAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1218	1221	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1387	1390	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1397	1400	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1464	1467	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1479	1482	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1603	1606	0	GCAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1631	1634	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1642	1645	0	ACAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1727	1730	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1756	1759	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1760	1763	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1825	1828	0	GCAA	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1919	1922	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1928	1931	0	TTGT	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1952	1955	0	TTGC	15.625	15.26275
cg0357715	SSBP2	C/EBPbeta	1985	1988	0	GCAA	15.625	15.26275
cg0357715	SSBP2	YY1 [T00	50	53	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	207	210	0	ATGG	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	526	529	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	550	553	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	674	677	0	ATGG	7.8125	7.79459

cg0357715	SSBP2	YY1 [T00	1055	1058	0	ATGG	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1108	1111	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1366	1369	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1570	1573	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1731	1734	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1902	1905	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1908	1911	0	ATGG	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1936	1939	0	ATGG	7.8125	7.79459
cg0357715	SSBP2	YY1 [T00	1947	1950	0	CCAT	7.8125	7.79459
cg0357715	SSBP2	TFII-I [T0	522	527	0	CTATCC	1.46484	1.48598
cg0357715	SSBP2	TFII-I [T0	797	802	0	CTTTCC	1.46484	1.48598
cg0357715	SSBP2	TFII-I [T0	1096	1101	0	GGAAAG	1.46484	1.48598
cg0357715	SSBP2	TFII-I [T0	1297	1302	0	GGAAAG	1.46484	1.48598
cg0357715	SSBP2	TFII-I [T0	1312	1317	0	CTATCC	1.46484	1.48598
cg0357715	SSBP2	STAT4 [T	926	931	0	GGAAAT	0.48828	0.46235
cg0357715	SSBP2	STAT4 [T	1288	1293	0	ATTTCC	0.48828	0.46235
cg0357715	SSBP2	c-Ets-1 [T	1836	1842	0	CTTCCT	0.24414	0.24982
cg0357715	SSBP2	HOXD9 [	350	359	0	AATAAA	0.01144	0.00905
cg0357715	SSBP2	HOXD10 [	350	359	0	AATAAA	0.01144	0.00905
cg0357715	SSBP2	ER-alpha [	192	196	0	GGTCA	1.95312	1.99744
cg0357715	SSBP2	ER-alpha [	741	745	0	GGTCA	1.95312	1.99744
cg0357715	SSBP2	ER-alpha [	1832	1836	0	TGACC	1.95312	1.99744
cg0357715	SSBP2	TCF-4E [	1462	1468	0	CTTTGC	0.12207	0.11933
cg0357715	SSBP2	GR [T050	24	30	0	CAAAAA	0.36621	0.33174
cg0357715	SSBP2	GR [T050	435	441	0	TTTTTG	0.36621	0.33174
cg0357715	SSBP2	GR [T050	1752	1758	0	TTTTTG	0.36621	0.33174
cg0357715	SSBP2	GR [T050	1915	1921	0	ATTTTT	0.36621	0.33174
cg0357715	SSBP2	GR [T050	1924	1930	0	TTTTTG	0.36621	0.33174
cg0357715	SSBP2	TBP [T007	1551	1560	0	GAGATA	0.03052	0.02611
cg0357715	SSBP2	GATA-1 [	44	49	0	CAGATA	0.97656	0.92541
cg0357715	SSBP2	GATA-1 [	1525	1530	0	TATCTG	0.97656	0.92541
cg0357715	SSBP2	Pax-5 [T0	627	633	0	GGGCAG	1.09863	1.24633
cg0357715	SSBP2	Pax-5 [T0	1536	1542	0	GGGCTT	1.09863	1.24633
cg0357715	SSBP2	p53 [T006	627	633	0	GGGCAG	0.36621	0.40082
cg0357715	SSBP2	AP-2alpha	1389	1394	0	GCAGGC	0.97656	1.07867
cg0357715	SSBP2	NF-AT2 [	1284	1293	0	AAATAT	0.00763	0.00668
cg0357715	SSBP2	IRF-2 [T0	102	107	0	AAGTGA	0.48828	0.46235
cg0357715	SSBP2	IRF-2 [T0	133	138	0	TCACTT	0.48828	0.46235
cg0357715	SSBP2	IRF-2 [T0	194	199	0	TCACTT	0.48828	0.46235
cg0357715	SSBP2	HNF-1A [	1112	1119	0	ATTTTA	0.24414	0.20853
cg0726872	TMEM13	HNF-1B [	556	564	9.99573	GGTTAA	0.12207	0.12399
cg0726872	TMEM13	Elk-1 [T00	481	489	9.979803	CTTCCG	0.10681	0.10604
cg0726872	TMEM13	STAT1bet	1553	1562	9.807397	TGAGGG	0.14877	0.1495
cg0726872	TMEM13	XBP-1 [T0	370	375	9.789909	AGCCAT	1.95312	1.95208
cg0726872	TMEM13	XBP-1 [T0	905	910	9.789909	ATGTCT	1.95312	1.95208
cg0726872	TMEM13	PR B [T00	115	121	9.743489	CCGTGT	1.09863	1.10292
cg0726872	TMEM13	PR B [T00	679	685	9.743489	AACACC	1.09863	1.10292
cg0726872	TMEM13	PR A [T01	115	121	9.743489	CCGTGT	1.09863	1.10292

cg0726872	TMEM132	PR A [T01	679	685	9.743489	AACACC	1.09863	1.10292
cg0726872	TMEM132	RelA [T00	1496	1506	9.692457	GGGGGA	0.02813	0.0279
cg0726872	TMEM132	Pax-5 [T0	62	68	9.552105	TTAGCC	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	143	149	9.552105	GGGCGC	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	144	150	9.552105	GGCGCC	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	355	361	9.552105	GGGCGC	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	443	449	9.552105	GCCGCC	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	717	723	9.552105	GTGGCC	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	859	865	9.552105	GGGCGG	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	899	905	9.552105	GGGCGG	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	1188	1194	9.552105	TTGGCC	1.46484	1.43083
cg0726872	TMEM132	Pax-5 [T0	1630	1636	9.552105	GTAGCC	1.46484	1.43083
cg0726872	TMEM132	TFIID [T0	467	473	9.552105	TGTGAA	1.46484	1.48472
cg0726872	TMEM132	TFIID [T0	916	922	9.552105	TGAGAA	1.46484	1.48472
cg0726872	TMEM132	TFII-I [T0	86	91	9.512894	CCTTCC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	164	169	9.512894	GGACTT	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	346	351	9.512894	GGACGG	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	364	369	9.512894	GGACAC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	499	504	9.512894	CCTTCC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	572	577	9.512894	CCATCC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	801	806	9.512894	CGGTCC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	878	883	9.512894	GGAAGG	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1159	1164	9.512894	GGACGG	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1211	1216	9.512894	GTGTCC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1542	1547	9.512894	GGACCG	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1557	1562	9.512894	GGAAAA	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1769	1774	9.512894	GGAAGG	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1809	1814	9.512894	CGTTCC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1828	1833	9.512894	CCATCC	7.32422	7.29728
cg0726872	TMEM132	TFII-I [T0	1979	1984	9.512894	CCTTCC	7.32422	7.29728
cg0726872	TMEM132	FOXP3 [T	407	412	9.512894	GTTGCT	7.32422	7.35678
cg0726872	TMEM132	FOXP3 [T	563	568	9.512894	GTTGCC	7.32422	7.35678
cg0726872	TMEM132	c-Jun [T00	1010	1016	9.442241	TGACGG	0.73242	0.73031
cg0726872	TMEM132	EBF [T054	435	445	9.441272	CACCCT	0.06866	0.06676
cg0726872	TMEM132	NFI/CTF [	326	333	9.352332	GGCCTT	0.54932	0.54821
cg0726872	TMEM132	NFI/CTF [	452	459	9.352332	CCAATG	0.54932	0.54821
cg0726872	TMEM132	LEF-1 [T0	1987	1994	9.313676	CCCCAA	0.21362	0.2139
cg0726872	TMEM132	SRY [T009	1609	1617	9.264664	GGTGCA	0.12207	0.12265
cg0726872	TMEM132	c-Ets-1 [T	1562	1568	9.148774	AGGGAA	0.85449	0.85523
cg0726872	TMEM132	c-Ets-1 [T	1659	1665	9.148774	GTTCCCT	0.85449	0.85523
cg0726872	TMEM132	c-Ets-1 [T	1741	1747	9.148774	GTTCCCT	0.85449	0.85523
cg0726872	TMEM132	NF-kappaB	1562	1573	9.132273	AGGGAA	0.01872	0.01846
cg0726872	TMEM132	PXR-1:RX	677	684	9.122407	TGAACA	0.24414	0.2439
cg0726872	TMEM132	USF2 [T0	41	50	9.056375	CTCACA	0.1545	0.15287
cg0726872	TMEM132	USF2 [T0	873	882	9.056375	CAGGTG	0.1545	0.15287
cg0726872	TMEM132	USF2 [T0	1177	1186	9.056375	CACGCA	0.1545	0.15287
cg0726872	TMEM132	NF-AT1 [	672	680	9.042733	GGAAAT	0.22888	0.22959
cg0726872	TMEM132	PU.1 [T02	531	543	9.036131	CCACTT	0.00727	0.0073

cg0726872	TMEM132	E2F-1 [T0	1027	1034	9.028527	CTCCCC	0.27466	0.26875
cg0726872	TMEM132	c-Ets-1 [T	1810	1816	9.020687	GTTCCC	0.85449	0.85523
cg0726872	TMEM132	EBF [T054	704	714	8.948874	AACCCA	0.01526	0.01496
cg0726872	TMEM132	Elk-1 [T00	874	882	8.931691	AGGTGG	0.24414	0.24034
cg0726872	TMEM132	IRF-1 [T0	578	586	8.916359	TTTCCA	0.09155	0.09147
cg0726872	TMEM132	IRF-1 [T0	1793	1801	8.916359	TTTCCA	0.09155	0.09147
cg0726872	TMEM132	c-Ets-2 [T	667	675	8.912323	GCTCAG	0.27466	0.27495
cg0726872	TMEM132	p53 [T006	979	985	8.912104	GGGCCC	0.12207	0.11837
cg0726872	TMEM132	c-Jun [T00	1915	1921	8.832178	TGACCT	0.61035	0.61059
cg0726872	TMEM132	NFI/CTF [	805	812	8.814757	CCACTT	0.48828	0.48804
cg0726872	TMEM132	NFI/CTF [	892	899	8.814757	CCAAGA	0.48828	0.48804
cg0726872	TMEM132	c-Ets-1 [T	730	736	8.809329	CTGGAA	0.85449	0.85523
cg0726872	TMEM132	Elk-1 [T00	1495	1503	8.797343	GGGGGG	0.24414	0.24034
cg0726872	TMEM132	Elk-1 [T00	1980	1988	8.797343	CTTCCC	0.24414	0.24034
cg0726872	TMEM132	XBP-1 [T	18	23	8.75604	ATGAGC	2.92969	2.9674
cg0726872	TMEM132	XBP-1 [T	455	460	8.75604	ATGATC	2.92969	2.9674
cg0726872	TMEM132	XBP-1 [T	676	681	8.75604	ATGAAC	2.92969	2.9674
cg0726872	TMEM132	XBP-1 [T	1637	1642	8.75604	ATGAGC	2.92969	2.9674
cg0726872	TMEM132	STAT1bet	577	586	8.695301	CTTTCC	0.22316	0.22446
cg0726872	TMEM132	E2F [T002	329	338	8.608984	CTTGGC	0.03052	0.03019
cg0726872	TMEM132	RAR-beta	700	709	8.55975	CCAAAA	0.26703	0.26657
cg0726872	TMEM132	STAT5A [	460	472	8.552853	CGCTTT	0.00149	0.00152
cg0726872	TMEM132	NF-AT2 [	573	582	8.550786	CATCCT	0.04959	0.05001
cg0726872	TMEM132	NF-AT1 [	1557	1565	8.532897	GGAAAA	0.10681	0.10725
cg0726872	TMEM132	USF2 [T0	68	77	8.532138	CGCCCA	0.103	0.10183
cg0726872	TMEM132	USF2 [T0	1803	1812	8.532138	CAGGTG	0.103	0.10183
cg0726872	TMEM132	PR B [T00	403	409	8.338824	CCCTGT	1.09863	1.10009
cg0726872	TMEM132	PR B [T00	921	927	8.338824	AACAGG	1.09863	1.10009
cg0726872	TMEM132	PR A [T01	403	409	8.338824	CCCTGT	1.09863	1.10009
cg0726872	TMEM132	PR A [T01	921	927	8.338824	AACAGG	1.09863	1.10009
cg0726872	TMEM132	E2F-1 [T0	63	70	8.336446	TAGCCC	0.15259	0.14963
cg0726872	TMEM132	GR-alpha [	86	90	8.281568	CCTTC	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	131	135	8.281568	CAAGG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	190	194	8.281568	CCTCG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	254	258	8.281568	CCTCG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	274	278	8.281568	GGAGG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	294	298	8.281568	GAAGG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	305	309	8.281568	GGAGG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	328	332	8.281568	CCTTG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	420	424	8.281568	CCTTC	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	431	435	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	496	500	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	499	503	8.281568	CCTTC	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	528	532	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	588	592	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	609	613	8.281568	CCTTG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	684	688	8.281568	CCTCG	7.8125	7.72956
cg0726872	TMEM132	GR-alpha [	688	692	8.281568	GGAGG	7.8125	7.72956

cg0726872	TMEM13	GR-alpha [	750	754	8.281568	CCTTC	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	829	833	8.281568	CGAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	879	883	8.281568	GAAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1026	1030	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1132	1136	8.281568	CCTCG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1140	1144	8.281568	CCTTC	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1219	1223	8.281568	CCTCG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1267	1271	8.281568	GGAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1308	1312	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1355	1359	8.281568	GAAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1362	1366	8.281568	GGAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1516	1520	8.281568	GAAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1693	1697	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1702	1706	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1707	1711	8.281568	GGAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1770	1774	8.281568	GAAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1782	1786	8.281568	CCTCC	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1865	1869	8.281568	CAAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1918	1922	8.281568	CCTTG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1946	1950	8.281568	GGAGG	7.8125	7.72956
cg0726872	TMEM13	GR-alpha [	1979	1983	8.281568	CCTTC	7.8125	7.72956
cg0726872	TMEM13	c-Jun [T00	1947	1953	8.242207	GAGGTC	0.48828	0.49076
cg0726872	TMEM13	p53 [T006	211	217	8.208781	GGGCCC	0.48828	0.47377
cg0726872	TMEM13	p53 [T006	1365	1371	8.208781	GGGGCC	0.48828	0.47377
cg0726872	TMEM13	p53 [T006	1366	1372	8.208781	GGGCCC	0.48828	0.47377
cg0726872	TMEM13	ENKTF-1	128	135	8.19852	TGGCAA	0.73242	0.71737
cg0726872	TMEM13	ENKTF-1	331	338	8.19852	TGGCGA	0.73242	0.71737
cg0726872	TMEM13	ENKTF-1	447	454	8.19852	CCCAGC	0.73242	0.71737
cg0726872	TMEM13	AhR [T01	1175	1185	8.184723	CTCACG	0.04864	0.04833
cg0726872	TMEM13	p53 [T006	763	769	8.162057	AGCGCC	0.48828	0.47377
cg0726872	TMEM13	c-Jun [T00	599	605	8.128539	AATGTC	0.48828	0.49076
cg0726872	TMEM13	E2F-1 [T0	221	228	8.101379	GCTACC	0.30518	0.3
cg0726872	TMEM13	VDR [T00	673	681	8.079962	GAAATG	0.24414	0.24712
cg0726872	TMEM13	GR-alpha [	74	78	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	218	222	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	260	264	8.073878	GCAGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	282	286	8.073878	CCTGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	288	292	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	323	327	8.073878	GCAGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	359	363	8.073878	GCAGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	438	442	8.073878	CCTGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	504	508	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	707	711	8.073878	CCAGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	744	748	8.073878	CCAGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	770	774	8.073878	CCAGG	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	797	801	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	869	873	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM13	GR-alpha [	872	876	8.073878	GCAGG	7.8125	7.72238

cg0726872	TMEM132	GR-alpha [	983	987	8.073878	CCTGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	988	992	8.073878	GCAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1035	1039	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1038	1042	8.073878	GCAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1043	1047	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1102	1106	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1183	1187	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1334	1338	8.073878	CCAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1405	1409	8.073878	CCAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1440	1444	8.073878	CTAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1574	1578	8.073878	CCTAG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1575	1579	8.073878	CTAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1594	1598	8.073878	CCAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1642	1646	8.073878	CCTGC	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1832	1836	8.073878	CCTGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1841	1845	8.073878	GCAGG	7.8125	7.72238
cg0726872	TMEM132	GR-alpha [	1994	1998	8.073878	GCAGG	7.8125	7.72238
cg0726872	TMEM132	Pax-5 [T0	81	87	8.014558	TCTGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	210	216	8.014558	TGGGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	211	217	8.014558	GGGCCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	375	381	8.014558	TGGGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	376	382	8.014558	GGGCCA	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	423	429	8.014558	TCTGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	441	447	8.014558	GGGCCG	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	603	609	8.014558	TCAGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	693	699	8.014558	GGGCTC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	978	984	8.014558	TGGGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	996	1002	8.014558	GGGCCG	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1145	1151	8.014558	GCGGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1294	1300	8.014558	GGAGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1365	1371	8.014558	GGGGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1366	1372	8.014558	GGGCCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1408	1414	8.014558	GGAGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1500	1506	8.014558	GAAGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1519	1525	8.014558	GGGCTG	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1710	1716	8.014558	GGGCAG	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1712	1718	8.014558	GCAGCC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1904	1910	8.014558	GGGCAT	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1966	1972	8.014558	GGGCAC	2.19727	2.14502
cg0726872	TMEM132	Pax-5 [T0	1974	1980	8.014558	TCAGCC	2.19727	2.14502
cg0726872	TMEM132	TFIID [T0	391	397	8.014558	TCAGAA	2.19727	2.24348
cg0726872	TMEM132	TFIID [T0	914	920	8.014558	TTTGAG	2.19727	2.24348
cg0726872	TMEM132	ETF [T002	77	87	7.870358	GCCCTC	0.07153	0.06862
cg0726872	TMEM132	c-Ets-2 [T	535	543	7.84116	TTCCTA	0.32043	0.32298
cg0726872	TMEM132	p53 [T006	693	699	7.833758	GGGCTC	0.48828	0.47377
cg0726872	TMEM132	p53 [T006	1294	1300	7.833758	GGAGCC	0.48828	0.47377
cg0726872	TMEM132	p53 [T006	1408	1414	7.833758	GGAGCC	0.48828	0.47377
cg0726872	TMEM132	RXR-alph	22	28	7.815913	GCCACC	0.24414	0.24104

cg0726872	TMEM13	RXR-alph	1270	1276	7.815913	GGGTGG	0.24414	0.24104
cg0726872	TMEM13	RXR-alph	1481	1487	7.815913	GGGTGG	0.24414	0.24104
cg0726872	TMEM13	RXR-alph	1531	1537	7.815913	GGGTAG	0.24414	0.24104
cg0726872	TMEM13	T3R-beta1	819	827	7.813363	GAGCGG	0.27466	0.27236
cg0726872	TMEM13	NF-AT1 [	1789	1797	7.744746	CTCCTT	0.19836	0.19941
cg0726872	TMEM13	c-Jun [T00	1970	1976	7.686747	ACAGTC	0.48828	0.48775
cg0726872	TMEM13	p53 [T006	1771	1777	7.641867	AAGGCC	0.73242	0.7186
cg0726872	TMEM13	NF-kappa	788	798	7.632414	AGCGTC	0.04435	0.04347
cg0726872	TMEM13	ELF-1 [T0	531	543	7.608736	CCACTT	0.00846	0.00852
cg0726872	TMEM13	GR [T050	1373	1379	7.527031	CAAAAT	1.83105	1.86007
cg0726872	TMEM13	GR [T050	1990	1996	7.527031	CAAAGC	1.83105	1.86007
cg0726872	TMEM13	RAR-beta	1046	1055	7.47824	GCGGAA	0.24414	0.24343
cg0726872	TMEM13	IRF-1 [T0	668	676	7.477948	CTCAGG	0.14496	0.14449
cg0726872	TMEM13	p53 [T006	143	149	7.458735	GGGCGC	0.73242	0.7186
cg0726872	TMEM13	p53 [T006	144	150	7.458735	GGCGCC	0.73242	0.7186
cg0726872	TMEM13	PEA3 [T0	902	910	7.421728	CGGATG	0.34332	0.34161
cg0726872	TMEM13	LEF-1 [T0	1610	1617	7.396545	GTGCAA	0.21362	0.21302
cg0726872	TMEM13	PPAR-alph	2	12	7.370536	TGCTGG	0.04482	0.04393
cg0726872	TMEM13	E2F-1 [T0	480	487	7.336545	ACTTCC	0.45776	0.44878
cg0726872	TMEM13	p53 [T006	1674	1680	7.266844	GGGCTG	0.73242	0.7186
cg0726872	TMEM13	p53 [T006	1756	1762	7.266844	GGGCTG	0.73242	0.7186
cg0726872	TMEM13	HNF-1C [	557	565	7.229698	GTTAAT	0.08392	0.08606
cg0726872	TMEM13	XBP-1 [T	1071	1076	7.172312	ATGAGG	2.92969	2.97018
cg0726872	TMEM13	XBP-1 [T	1514	1519	7.172312	ATGAAG	2.92969	2.97018
cg0726872	TMEM13	p53 [T006	210	216	7.153797	TGGGCC	1.09863	1.07125
cg0726872	TMEM13	p53 [T006	375	381	7.153797	TGGGCC	1.09863	1.07125
cg0726872	TMEM13	p53 [T006	376	382	7.153797	GGGCCC	1.09863	1.07125
cg0726872	TMEM13	p53 [T006	978	984	7.153797	TGGGCC	1.09863	1.07125
cg0726872	TMEM13	p53 [T006	717	723	7.150251	GTGGCC	1.09863	1.07125
cg0726872	TMEM13	Ik-1 [T027	1721	1733	7.122895	GAGGGT	0.01064	0.01049
cg0726872	TMEM13	c-Ets-1 [T	1555	1561	7.071349	AGGGAA	0.73242	0.73099
cg0726872	TMEM13	ATF-2 [T0	542	551	7.05714	TCTACG	0.01907	0.01886
cg0726872	TMEM13	C/EBPalph	451	457	7.00174	GCCAAT	0.73242	0.74337
cg0726872	TMEM13	RXR-alph	249	255	6.967687	ACCACC	0.36621	0.36214
cg0726872	TMEM13	ENKTF-1	367	374	6.942764	CACAGC	1.46484	1.44228
cg0726872	TMEM13	ENKTF-1	1189	1196	6.942764	TGGCCC	1.46484	1.44228
cg0726872	TMEM13	ENKTF-1	1224	1231	6.942764	TGGCGC	1.46484	1.44228
cg0726872	TMEM13	ENKTF-1	1273	1280	6.942764	TGGCCG	1.46484	1.44228
cg0726872	TMEM13	ENKTF-1	1849	1856	6.942764	TGGCTG	1.46484	1.44228
cg0726872	TMEM13	p53 [T006	441	447	6.938545	GGGCCG	1.09863	1.07125
cg0726872	TMEM13	p53 [T006	996	1002	6.938545	GGGCCG	1.09863	1.07125
cg0726872	TMEM13	p53 [T006	1145	1151	6.938545	GCGGCC	1.09863	1.07125
cg0726872	TMEM13	NF-AT1 [	574	583	6.890694	ATCCTT	0.01907	0.01922
cg0726872	TMEM13	EBF [T05	1347	1357	6.87365	CCCCCT	0.03052	0.02964
cg0726872	TMEM13	E2F-1 [T0	1046	1053	6.839754	GCGGAA	0.30518	0.29782
cg0726872	TMEM13	PEA3 [T0	570	578	6.824411	GTCCAT	0.22888	0.22933
cg0726872	TMEM13	PEA3 [T0	1826	1834	6.824411	CTCCAT	0.22888	0.22933
cg0726872	TMEM13	c-Jun [T00	1855	1861	6.787369	TGACGG	0.73242	0.73173

cg0726872	TMEM132	NFI/CTF [	1184	1191	6.786076	CTGCTTC	0.73242	0.73214
cg0726872	TMEM132	RXR-alpha	277	283	6.785809	GGGTAC	0.36621	0.36214
cg0726872	TMEM132	p53 [T006	1630	1636	6.775228	GTAGCC	1.09863	1.07125
cg0726872	TMEM132	c-Myb [T0	1426	1433	6.719843	GGGAGT	0.30518	0.3056
cg0726872	TMEM132	c-Ets-1 [T	1046	1052	6.693449	GCGGAA	0.48828	0.48798
cg0726872	TMEM132	T3R-beta1	241	249	6.683388	TCACCG	0.21362	0.21147
cg0726872	TMEM132	AR [T000	1208	1216	6.603347	GACGTG	0.19836	0.19597
cg0726872	TMEM132	TFII-I [T0	848	853	6.581441	GGAGTG	0.97656	0.97366
cg0726872	TMEM132	TFII-I [T0	1390	1395	6.581441	GGAGTG	0.97656	0.97366
cg0726872	TMEM132	AR [T000	565	573	6.566205	TGCCTG	0.19836	0.19597
cg0726872	TMEM132	p53 [T006	1500	1506	6.563521	GAAGCC	0.48828	0.47541
cg0726872	TMEM132	p53 [T006	1712	1718	6.563521	GCAGCC	0.48828	0.47541
cg0726872	TMEM132	EBF [T05	794	804	6.491258	TCCCCTC	0.01907	0.01851
cg0726872	TMEM132	XBP-1 [T	1904	1909	6.478682	GGGCAT	0.97656	0.97062
cg0726872	TMEM132	p53 [T006	355	361	6.403751	GGGCGC	0.48828	0.47541
cg0726872	TMEM132	GR-alpha [	40	44	6.263098	CCTCA	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	101	105	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	312	316	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	508	512	6.263098	CCTCA	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	643	647	6.263098	CCTCA	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1072	1076	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1174	1178	6.263098	CCTCA	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1315	1319	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1492	1496	6.263098	TAAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1523	1527	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1553	1557	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1720	1724	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1800	1804	6.263098	CCTCA	3.90625	3.91061
cg0726872	TMEM132	GR-alpha [	1885	1889	6.263098	TGAGG	3.90625	3.91061
cg0726872	TMEM132	c-Myb [T0	413	420	6.259888	TGCAGT	0.30518	0.3056
cg0726872	TMEM132	NF-AT1 [	1789	1798	6.201624	CTCCTTT	0.03815	0.03846
cg0726872	TMEM132	p53 [T006	443	449	6.188498	GCCGCC	0.61035	0.594
cg0726872	TMEM132	p53 [T006	859	865	6.188498	GGGCGG	0.61035	0.594
cg0726872	TMEM132	c-Ets-1 [T	578	584	6.167515	TTTCCAC	0.36621	0.36731
cg0726872	TMEM132	c-Ets-1 [T	1793	1799	6.167515	TTTCCAC	0.36621	0.36731
cg0726872	TMEM132	p53 [T006	1188	1194	6.095267	TTGGCC	0.61035	0.594
cg0726872	TMEM132	GR-alpha [	310	314	6.055408	CCTGA	3.90625	3.9065
cg0726872	TMEM132	GR-alpha [	537	541	6.055408	CCTAA	3.90625	3.9065
cg0726872	TMEM132	GR-alpha [	651	655	6.055408	CCTAA	3.90625	3.9065
cg0726872	TMEM132	GR-alpha [	669	673	6.055408	TCAGG	3.90625	3.9065
cg0726872	TMEM132	GR-alpha [	885	889	6.055408	CCTGA	3.90625	3.9065
cg0726872	TMEM132	GR-alpha [	939	943	6.055408	TTAGG	3.90625	3.9065
cg0726872	TMEM132	GR-alpha [	1350	1354	6.055408	CCTGA	3.90625	3.9065
cg0726872	TMEM132	GR-alpha [	1802	1806	6.055408	TCAGG	3.90625	3.9065
cg0726872	TMEM132	RXR-alpha	1651	1657	5.937582	AGTACC	0.73242	0.72249
cg0726872	TMEM132	GCF [T00	1006	1014	5.917256	GCGCTG	0.64087	0.6219
cg0726872	TMEM132	GCF [T00	1079	1087	5.917256	GAGCGG	0.64087	0.6219
cg0726872	TMEM132	c-Fos [T00	335	344	5.891709	GAGTCA	0.09155	0.09126

cg0726872	TMEM132	STAT4 [T	86	91	5.882353	CCTTCC	0.48828	0.48408
cg0726872	TMEM132	STAT4 [T	499	504	5.882353	CCTTCC	0.48828	0.48408
cg0726872	TMEM132	STAT4 [T	878	883	5.882353	GGAAGG	0.48828	0.48408
cg0726872	TMEM132	STAT4 [T	1769	1774	5.882353	GGAAGG	0.48828	0.48408
cg0726872	TMEM132	STAT4 [T	1979	1984	5.882353	CCTTCC	0.48828	0.48408
cg0726872	TMEM132	AP-1 [T00	332	340	5.871862	GGCGAG	0.09155	0.09072
cg0726872	TMEM132	p53 [T006	62	68	5.720243	TTAGCC	0.61035	0.59991
cg0726872	TMEM132	RXR-alph	679	685	5.715466	AACACC	0.61035	0.6044
cg0726872	TMEM132	c-Jun [T00	387	393	5.703976	GGGTC	0.48828	0.48665
cg0726872	TMEM132	c-Jun [T00	887	893	5.703976	TGACCC	0.48828	0.48665
cg0726872	TMEM132	ENKTF-1	58	65	5.687009	TGGCTT	0.73242	0.7249
cg0726872	TMEM132	ENKTF-1	284	291	5.687009	TGGCCC	0.73242	0.7249
cg0726872	TMEM132	c-Ets-1 [T	500	506	5.686398	CTTCCC	0.36621	0.3623
cg0726872	TMEM132	AhR:Arnt	1231	1240	5.620669	ACACGC	0.0515	0.04981
cg0726872	TMEM132	AP-2alpha	1467	1472	5.568965	ATAGGC	0.48828	0.4878
cg0726872	TMEM132	NFI/CTF [	1457	1464	5.558661	GGGATT	0.54932	0.55038
cg0726872	TMEM132	NFI/CTF [	1583	1590	5.558661	GGGATT	0.54932	0.55038
cg0726872	TMEM132	c-Ets-1 [T	1497	1503	5.558311	GGGGAA	0.36621	0.3623
cg0726872	TMEM132	Pax-5 [T0	763	769	5.544826	AGCGCC	0.73242	0.72046
cg0726872	TMEM132	p53 [T006	603	609	5.508538	TCAGCC	0.61035	0.59991
cg0726872	TMEM132	p53 [T006	1519	1525	5.508538	GGGCTG	0.61035	0.59991
cg0726872	TMEM132	p53 [T006	1974	1980	5.508538	TCAGCC	0.61035	0.59991
cg0726872	TMEM132	c-Ets-1 [T	1980	1986	5.430224	CTTCCC	0.36621	0.3623
cg0726872	TMEM132	PPAR-alph	341	351	5.285833	CACTGG	0.03529	0.03451
cg0726872	TMEM132	RXR-alph	26	32	5.271235	CCCACC	0.61035	0.6044
cg0726872	TMEM132	RXR-alph	1149	1155	5.271235	CCCACC	0.61035	0.6044
cg0726872	TMEM132	RXR-alph	1385	1391	5.271235	GGGTGG	0.61035	0.6044
cg0726872	TMEM132	RXR-alph	1668	1674	5.271235	GGGTGG	0.61035	0.6044
cg0726872	TMEM132	RXR-alph	1750	1756	5.271235	GGGTGG	0.61035	0.6044
cg0726872	TMEM132	RXR-alph	1936	1942	5.271235	CCCACC	0.61035	0.6044
cg0726872	TMEM132	GR [T050	701	707	5.207533	CAAAAC	0.24414	0.24606
cg0726872	TMEM132	c-Jun [T00	478	484	5.193102	TGACTT	0.61035	0.61057
cg0726872	TMEM132	p53 [T006	899	905	5.133514	GGGCGG	0.48828	0.47747
cg0726872	TMEM132	EBF [T05	980	990	5.130966	GGCCCT	0.02289	0.02224
cg0726872	TMEM132	RXR-alph	523	529	5.089356	AGCACC	0.48828	0.484
cg0726872	TMEM132	RXR-alph	1723	1729	5.089356	GGGTGC	0.48828	0.484
cg0726872	TMEM132	RXR-alph	1733	1739	5.089356	AGCACC	0.48828	0.484
cg0726872	TMEM132	USF2 [T0	1096	1105	5.052423	CTGCCA	0.103	0.10178
cg0726872	TMEM132	GR-beta [	1458	1462	5.042296	GGATT	3.90625	3.95351
cg0726872	TMEM132	GR-beta [	1584	1588	5.042296	GGATT	3.90625	3.95351
cg0726872	TMEM132	Elk-1 [T00	534	542	5.027151	CTTCCT	0.03052	0.03091
cg0726872	TMEM132	c-Jun [T00	1301	1307	5.000337	GGTGTC	0.61035	0.61057
cg0726872	TMEM132	AR [T000	1674	1682	4.995624	GGGCTG	0.11444	0.11247
cg0726872	TMEM132	RAR-beta:	355	366	4.98533	GGGCGC	0.00966	0.00942
cg0726872	TMEM132	AP-1 [T00	1823	1831	4.955822	TGACTC	0.12207	0.12162
cg0726872	TMEM132	ATF3 [T0	543	550	4.941398	CTACGT	0.09155	0.09183
cg0726872	TMEM132	c-Ets-1 [T	87	93	4.910652	CTTCCA	0.48828	0.49031
cg0726872	TMEM132	c-Ets-1 [T	1767	1773	4.910652	ATGGAA	0.48828	0.49031

cg0726872	TMEM132	XBP-1 [T0	14	19	4.894955	AGGCAT	0.97656	0.96979
cg0726872	TMEM132	XBP-1 [T0	112	117	4.894955	ATGCCG	0.97656	0.96979
cg0726872	TMEM132	AR [T000	364	372	4.890444	GGACAC	0.11444	0.11247
cg0726872	TMEM132	AP-2alpha	650	655	4.890408	GCCTAA	0.97656	0.97567
cg0726872	TMEM132	c-Jun [T00	544	550	4.883696	TACGTC	0.61035	0.61057
cg0726872	TMEM132	RXR-alph	964	970	4.86724	GGGTCT	0.48828	0.484
cg0726872	TMEM132	NF-Y [T0	1586	1593	4.867193	ATTGGG	0.36621	0.36847
cg0726872	TMEM132	GCF [T00	182	190	4.846987	GCTCCG	0.27466	0.26486
cg0726872	TMEM132	GCF [T00	833	841	4.846987	GCACAG	0.27466	0.26486
cg0726872	TMEM132	GCF [T00	1001	1009	4.846987	GCTCAG	0.27466	0.26486
cg0726872	TMEM132	C/EBPalph	472	478	4.845599	AATTGC	0.97656	0.99332
cg0726872	TMEM132	p53 [T006	1928	1934	4.786849	GGGCAC	0.48828	0.47747
cg0726872	TMEM132	c-Ets-1 [T	876	882	4.782565	GTGGAA	0.48828	0.49031
cg0726872	TMEM132	TFII-I [T0	672	677	4.756447	GGAAAT	2.92969	2.93695
cg0726872	TMEM132	TFII-I [T0	1017	1022	4.756447	CAGTCC	2.92969	2.93695
cg0726872	TMEM132	TFII-I [T0	1458	1463	4.756447	GGATTG	2.92969	2.93695
cg0726872	TMEM132	TFII-I [T0	1584	1589	4.756447	GGATTG	2.92969	2.93695
cg0726872	TMEM132	FOXP3 [T	395	400	4.756447	AAAAAC	2.92969	2.96063
cg0726872	TMEM132	FOXP3 [T	701	706	4.756447	CAAAAC	2.92969	2.96063
cg0726872	TMEM132	c-Ets-1 [T	741	747	4.654478	CTTCCA	0.85449	0.85764
cg0726872	TMEM132	p53 [T006	1085	1091	4.645444	CGCGCC	0.24414	0.23584
cg0726872	TMEM132	COUP-TF	1944	1956	4.54669	GGGGAG	0.00358	0.00354
cg0726872	TMEM132	RXR-alph	433	439	4.423008	TCCACC	0.24414	0.24292
cg0726872	TMEM132	RXR-alph	1358	1364	4.423008	GGGTGG	0.24414	0.24292
cg0726872	TMEM132	RXR-alph	1795	1801	4.423008	TCCACC	0.24414	0.24292
cg0726872	TMEM132	STAT4 [T	315	320	4.411765	GGAAGC	1.95312	1.94235
cg0726872	TMEM132	STAT4 [T	740	745	4.411765	GCTTCC	1.95312	1.94235
cg0726872	TMEM132	STAT4 [T	1128	1133	4.411765	GCTTCC	1.95312	1.94235
cg0726872	TMEM132	STAT4 [T	1499	1504	4.411765	GGAAGC	1.95312	1.94235
cg0726872	TMEM132	STAT4 [T	1809	1814	4.411765	CGTTCC	1.95312	1.94235
cg0726872	TMEM132	p53 [T006	283	289	4.33696	CTGGCC	0.24414	0.23584
cg0726872	TMEM132	CREB [T0	542	550	4.299974	TCTACG	0.04578	0.04561
cg0726872	TMEM132	RXR-alph	638	644	4.24113	CGTACC	0.97656	0.9671
cg0726872	TMEM132	RXR-alph	773	779	4.24113	GGGTCC	0.97656	0.9671
cg0726872	TMEM132	GR-beta [	936	940	4.201913	TGATT	7.8125	7.94607
cg0726872	TMEM132	NF-Y [T0	1460	1467	4.186615	ATTGGG	0.18311	0.1853
cg0726872	TMEM132	NF-1 [T00	1985	1992	4.135372	CGCCCC	0.24414	0.24154
cg0726872	TMEM132	c-Jun [T00	334	340	4.1298	CGAGTC	0.24414	0.24526
cg0726872	TMEM132	p53 [T006	31	37	4.125254	CCGGCC	0.73242	0.71379
cg0726872	TMEM132	p53 [T006	745	751	4.125254	CAGGCC	0.73242	0.71379
cg0726872	TMEM132	p53 [T006	882	888	4.125254	GGGCCT	0.73242	0.71379
cg0726872	TMEM132	p53 [T006	1116	1122	4.125254	GGGCCG	0.73242	0.71379
cg0726872	TMEM132	p53 [T006	1288	1294	4.125254	GGGCCG	0.73242	0.71379
cg0726872	TMEM132	IRF-1 [T0	1553	1561	4.035054	TGAGGG	0.1297	0.13087
cg0726872	TMEM132	RXR-alph	1547	1553	4.019014	GGGTCT	0.97656	0.9671
cg0726872	TMEM132	Pax-5 [T0	399	405	4.007279	ACTGCC	1.09863	1.07975
cg0726872	TMEM132	Pax-5 [T0	979	985	4.007279	GGGCCC	1.09863	1.07975
cg0726872	TMEM132	Pax-5 [T0	1567	1573	4.007279	ACTGCC	1.09863	1.07975

cg0726872	TMEM132	Pax-5 [T0	1674	1680	4.007279	GGGCTG	1.09863	1.07975
cg0726872	TMEM132	Pax-5 [T0	1756	1762	4.007279	GGGCTG	1.09863	1.07975
cg0726872	TMEM132	Pax-5 [T0	1771	1777	4.007279	AAGGCC	1.09863	1.07975
cg0726872	TMEM132	Pax-5 [T0	1928	1934	4.007279	GGGCAC	1.09863	1.07975
cg0726872	TMEM132	Pax-5 [T0	1932	1938	4.007279	ACTGCC	1.09863	1.07975
cg0726872	TMEM132	AP-2alpha	327	332	3.970052	GCCTTG	0.97656	0.96469
cg0726872	TMEM132	EBF [T05	767	777	3.921887	CCCCCA	0.0248	0.02398
cg0726872	TMEM132	Sp1 [T007	441	450	3.783309	GGGCCG	0.08965	0.08686
cg0726872	TMEM132	GR [T050	1613	1619	3.763516	CAAAGA	0.73242	0.74251
cg0726872	TMEM132	p53 [T006	853	859	3.750231	GGGCTG	0.73242	0.71379
cg0726872	TMEM132	AP-2alpha	1770	1775	3.743866	GAAGGC	0.48828	0.48238
cg0726872	TMEM132	Sp1 [T007	898	907	3.720644	GGGGCG	0.07439	0.07186
cg0726872	TMEM132	c-Ets-1 [T	417	423	3.71855	GTTCCT	0.61035	0.60765
cg0726872	TMEM132	p53 [T006	1133	1139	3.586914	CTCGCC	0.73242	0.7189
cg0726872	TMEM132	E2F-1 [T0	1980	1987	3.55167	CTTCCC	0.15259	0.14974
cg0726872	TMEM132	c-Ets-2 [T	418	426	3.518824	TTCCTTC	0.18311	0.18304
cg0726872	TMEM132	p53 [T006	399	405	3.516613	ACTGCC	0.73242	0.7189
cg0726872	TMEM132	p53 [T006	1567	1573	3.516613	ACTGCC	0.73242	0.7189
cg0726872	TMEM132	p53 [T006	1932	1938	3.516613	ACTGCC	0.73242	0.7189
cg0726872	TMEM132	RXR-alph	154	160	3.392904	GGGTGC	1.09863	1.08572
cg0726872	TMEM132	RXR-alph	297	303	3.392904	GGGTGA	1.09863	1.08572
cg0726872	TMEM132	RXR-alph	1048	1054	3.392904	GGAACC	1.09863	1.08572
cg0726872	TMEM132	Sp1 [T007	858	867	3.383855	GGGGCG	0.07439	0.07186
cg0726872	TMEM132	Elk-1 [T00	311	319	3.381796	CTGAGG	0.04578	0.04588
cg0726872	TMEM132	p53 [T006	66	72	3.375208	CCCGCC	0.73242	0.7189
cg0726872	TMEM132	p53 [T006	1030	1036	3.375208	CCCGCC	0.73242	0.7189
cg0726872	TMEM132	p53 [T006	1232	1238	3.375208	CACGCC	0.73242	0.7189
cg0726872	TMEM132	p53 [T006	1983	1989	3.375208	CCCGCC	0.73242	0.7189
cg0726872	TMEM132	c-Fos [T00	1819	1828	3.366997	TGTCTG	0.05341	0.05347
cg0726872	TMEM132	GR-beta [	540	544	3.361531	AATCT	3.90625	3.99611
cg0726872	TMEM132	GR-beta [	734	738	3.361531	AATCT	3.90625	3.99611
cg0726872	TMEM132	PR B [T00	1375	1381	3.29756	AAATGT	0.24414	0.25122
cg0726872	TMEM132	PR A [T01	1375	1381	3.29756	AAATGT	0.24414	0.25122
cg0726872	TMEM132	c-Ets-2 [T	310	318	3.2883	CCTGAG	0.18311	0.18304
cg0726872	TMEM132	c-Ets-2 [T	1130	1138	3.2883	TTCCTCC	0.18311	0.18304
cg0726872	TMEM132	c-Ets-1 [T	481	487	3.231072	CTTCCG	0.24414	0.23981
cg0726872	TMEM132	AP-2alpha	726	731	3.229049	GCCTCT	0.48828	0.48238
cg0726872	TMEM132	AP-2alpha	1060	1065	3.229049	AGAGGC	0.48828	0.48238
cg0726872	TMEM132	AP-2alpha	1259	1264	3.229049	GCCTCT	0.48828	0.48238
cg0726872	TMEM132	RXR-alph	702	708	3.170788	AAAACC	0.24414	0.24522
cg0726872	TMEM132	TCF-4E [T	1611	1617	3.151193	TGCAAA	0.24414	0.24672
cg0726872	TMEM132	Pax-5 [T0	1133	1139	3.075094	CTCGCC	0.12207	0.11895
cg0726872	TMEM132	p53 [T006	1966	1972	3.028543	GGGCAC	0.48828	0.47786
cg0726872	TMEM132	STAT4 [T	480	485	2.941176	ACTTCC	2.92969	2.929
cg0726872	TMEM132	STAT4 [T	533	538	2.941176	ACTTCC	2.92969	2.929
cg0726872	TMEM132	STAT4 [T	577	582	2.941176	CTTTCC	2.92969	2.929
cg0726872	TMEM132	STAT4 [T	732	737	2.941176	GGAATC	2.92969	2.929
cg0726872	TMEM132	STAT4 [T	1048	1053	2.941176	GGAACC	2.92969	2.929

cg0726872	TMEM132	STAT4 [T	1658	1663	2.941176	GGTTCC	2.92969	2.929
cg0726872	TMEM132	STAT4 [T	1740	1745	2.941176	GGTTCC	2.92969	2.929
cg0726872	TMEM132	STAT4 [T	1792	1797	2.941176	CTTTCC	2.92969	2.929
cg0726872	TMEM132	p53 [T006	1710	1716	2.813291	GGGCAG	0.48828	0.47786
cg0726872	TMEM132	p53 [T006	1904	1910	2.813291	GGGCAT	0.48828	0.47786
cg0726872	TMEM132	NF-1 [T00	376	383	2.813149	GGGCCC	0.24414	0.24101
cg0726872	TMEM132	NF-1 [T00	1188	1195	2.813149	TTGGCC	0.24414	0.24101
cg0726872	TMEM132	AhR:Arnt	1235	1244	2.810335	GCCCGC	0.01717	0.01648
cg0726872	TMEM132	PR B [T00	559	565	2.80933	TAATGT	0.73242	0.74818
cg0726872	TMEM132	PR A [T01	559	565	2.80933	TAATGT	0.73242	0.74818
cg0726872	TMEM132	c-Jun [T00	1823	1829	2.654872	TGACTC	0.48828	0.48929
cg0726872	TMEM132	NF-AT1 [	574	582	2.619709	ATCCTT	0.09155	0.0926
cg0726872	TMEM132	c-Myb [T0	397	404	2.570796	AAACTG	0.06104	0.06117
cg0726872	TMEM132	AP-2alpha	39	44	2.550491	GCCTCA	0.48828	0.48266
cg0726872	TMEM132	AP-2alpha	101	106	2.550491	TGAGGC	0.48828	0.48266
cg0726872	TMEM132	AP-2alpha	507	512	2.550491	GCCTCA	0.48828	0.48266
cg0726872	TMEM132	AP-2alpha	1072	1077	2.550491	TGAGGC	0.48828	0.48266
cg0726872	TMEM132	AP-2alpha	1173	1178	2.550491	GCCTCA	0.48828	0.48266
cg0726872	TMEM132	RXR-alpha	1608	1614	2.544678	GGGTGC	0.85449	0.84796
cg0726872	TMEM132	RXR-alpha	1888	1894	2.544678	GGGTGC	0.85449	0.84796
cg0726872	TMEM132	C/EBPalph	1312	1318	2.441016	CATTGA	0.48828	0.49114
cg0726872	TMEM132	NF-Y [T0	449	456	2.355069	CAGCCA	0.21362	0.21485
cg0726872	TMEM132	c-Jun [T00	658	664	2.345465	TGACAC	0.48828	0.48929
cg0726872	TMEM132	GCF [T00	357	365	2.339499	GCGCAG	0.06104	0.05925
cg0726872	TMEM132	T3R-beta1	930	938	2.240658	TGCTGG	0.15259	0.15262
cg0726872	TMEM132	Sp1 [T007	64	73	2.203247	AGCCCG	0.03624	0.0349
cg0726872	TMEM132	GATA-1 [	233	238	2.176375	TATCGA	3.90625	3.92756
cg0726872	TMEM132	NF-kappa	691	701	2.17632	GGGGGC	0.00572	0.0055
cg0726872	TMEM132	Elk-1 [T00	1129	1137	2.164966	CTTCCT	0.05341	0.05317
cg0726872	TMEM132	AP-2alpha	189	194	2.098119	GCCTCG	0.97656	0.95407
cg0726872	TMEM132	AP-2alpha	829	834	2.098119	CGAGGC	0.97656	0.95407
cg0726872	TMEM132	GATA-1 [	1464	1469	2.001358	GGGATA	3.90625	3.92756
cg0726872	TMEM132	GATA-1 [	1624	1629	2.001358	GGGATA	3.90625	3.92756
cg0726872	TMEM132	AP-2alpha	305	310	1.871933	GGAGGC	0.97656	0.95407
cg0726872	TMEM132	AP-2alpha	1025	1030	1.871933	GCCTCC	0.97656	0.95407
cg0726872	TMEM132	TFII-I [T0	134	139	1.824994	GGAGAG	0.48828	0.48408
cg0726872	TMEM132	TFII-I [T0	350	355	1.824994	GGAGAG	0.48828	0.48408
cg0726872	TMEM132	TFII-I [T0	492	497	1.824994	CTCTCC	0.48828	0.48408
cg0726872	TMEM132	TFII-I [T0	711	716	1.824994	GGAGAG	0.48828	0.48408
cg0726872	TMEM132	TFII-I [T0	1337	1342	1.824994	GGAGAG	0.48828	0.48408
cg0726872	TMEM132	p53 [T006	81	87	1.758307	TCTGCC	0.36621	0.36261
cg0726872	TMEM132	p53 [T006	423	429	1.758307	TCTGCC	0.36621	0.36261
cg0726872	TMEM132	Sp1 [T007	1981	1990	1.706745	TTCCCG	0.03242	0.03129
cg0726872	TMEM132	RXR-alpha	388	394	1.696452	GGGTCA	0.48828	0.48222
cg0726872	TMEM132	RXR-alpha	886	892	1.696452	CTGACC	0.48828	0.48222
cg0726872	TMEM132	C/EBPbeta	330	333	1.639871	TTGG	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	380	383	1.639871	CCAA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	452	455	1.639871	CCAA	15.625	15.72563

cg0726872	TMEM132	C/EBPbeta	700	703	1.639871	CCAA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	809	812	1.639871	TTGG	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	892	895	1.639871	CCAA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1188	1191	1.639871	TTGG	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1372	1375	1.639871	CCAA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1461	1464	1.639871	TTGG	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1587	1590	1.639871	TTGG	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1989	1992	1.639871	CCAA	15.625	15.72563
cg0726872	TMEM132	XBP-1 [T0	657	662	1.583727	ATGACA	0.97656	0.98146
cg0726872	TMEM132	Pax-5 [T0	66	72	1.537547	CCCGCC	0.73242	0.71311
cg0726872	TMEM132	Pax-5 [T0	283	289	1.537547	CTGGCC	0.73242	0.71311
cg0726872	TMEM132	Pax-5 [T0	1030	1036	1.537547	CCCGCC	0.73242	0.71311
cg0726872	TMEM132	Pax-5 [T0	1085	1091	1.537547	CGCGCC	0.73242	0.71311
cg0726872	TMEM132	Pax-5 [T0	1232	1238	1.537547	CACGCC	0.73242	0.71311
cg0726872	TMEM132	Pax-5 [T0	1983	1989	1.537547	CCCGCC	0.73242	0.71311
cg0726872	TMEM132	RXR-alpha	1343	1349	1.474336	TAGACC	0.48828	0.48222
cg0726872	TMEM132	STAT4 [T	416	421	1.470588	AGTTCC	1.95312	1.96333
cg0726872	TMEM132	STAT4 [T	1557	1562	1.470588	GGAAAA	1.95312	1.96333
cg0726872	TMEM132	STAT4 [T	1564	1569	1.470588	GGAACT	1.95312	1.96333
cg0726872	TMEM132	NF-kappa	1497	1507	1.391281	GGGGAA	0.00525	0.00511
cg0726872	TMEM132	Sp1 [T007	1028	1037	1.388285	TCCCCG	0.03242	0.03129
cg0726872	TMEM132	c-Ets-1 [T	670	676	1.384951	CAGGAA	0.36621	0.36952
cg0726872	TMEM132	C/EBPbeta	611	614	1.366559	TTGA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	915	918	1.366559	TTGA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1314	1317	1.366559	TTGA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1552	1555	1.366559	TTGA	15.625	15.72563
cg0726872	TMEM132	C/EBPbeta	1920	1923	1.366559	TTGA	15.625	15.72563
cg0726872	TMEM132	AP-2alpha	12	17	1.357116	ACAGGC	0.48828	0.48203
cg0726872	TMEM132	AP-2alpha	105	110	1.357116	GCCTGT	0.48828	0.48203
cg0726872	TMEM132	AP-2alpha	566	571	1.357116	GCCTGT	0.48828	0.48203
cg0726872	TMEM132	c-Myb [T0	1565	1572	1.285398	GAACTG	0.06104	0.06064
cg0726872	TMEM132	ENKTF-1	174	181	1.255756	TGGCGC	0.24414	0.23904
cg0726872	TMEM132	ENKTF-1	1684	1691	1.255756	TGGCGA	0.24414	0.23904
cg0726872	TMEM132	T3R-beta1	1305	1313	1.129976	TCACCT	0.07629	0.07585
cg0726872	TMEM132	GCF [T00	176	184	1.070269	GCGCCG	0.18311	0.17647
cg0726872	TMEM132	GCF [T00	1845	1853	1.070269	GCGCTG	0.18311	0.17647
cg0726872	TMEM132	HIF-1 [T0	1959	1967	0.906247	ACGTGC	0.09918	0.0975
cg0726872	TMEM132	CTF [T001	449	460	0.895258	CAGCCA	0.00191	0.00192
cg0726872	TMEM132	RXR-alpha	1590	1596	0.848226	GGGTCC	0.48828	0.48333
cg0726872	TMEM132	GR-beta [T	454	458	0.840383	AATGA	7.8125	7.94706
cg0726872	TMEM132	GR-beta [T	472	476	0.840383	AATTG	7.8125	7.94706
cg0726872	TMEM132	GR-beta [T	675	679	0.840383	AATGA	7.8125	7.94706
cg0726872	TMEM132	GR-beta [T	1311	1315	0.840383	CCATT	7.8125	7.94706
cg0726872	TMEM132	GR-beta [T	1477	1481	0.840383	AATGG	7.8125	7.94706
cg0726872	TMEM132	AP-2alpha	309	314	0.678558	GCCTGA	0.48828	0.48199
cg0726872	TMEM132	AP-2alpha	884	889	0.678558	GCCTGA	0.48828	0.48199
cg0726872	TMEM132	C/EBPalph	1459	1465	0.540941	GATTGG	0.24414	0.24507
cg0726872	TMEM132	C/EBPalph	1585	1591	0.540941	GATTGG	0.24414	0.24507

cg0726872	TMEM132	c-Ets-1 [T	534	540	0.384261	CTTCCTA	0.24414	0.24569
cg0726872	TMEM132	HNF-1A [	557	564	0.287765	GTTAAT	0.24414	0.24974
cg0726872	TMEM132	AP-2alpha	744	749	0.226186	CCAGGC	0.97656	0.95305
cg0726872	TMEM132	GR-alpha [	79	83	0.207689	CCTCT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	352	356	0.207689	AGAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	491	495	0.207689	CCTCT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	576	580	0.207689	CCTTT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	713	717	0.207689	AGAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	727	731	0.207689	CCTCT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	895	899	0.207689	AGAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1060	1064	0.207689	AGAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1260	1264	0.207689	CCTCT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1505	1509	0.207689	CCTCT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1560	1564	0.207689	AAAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1621	1625	0.207689	AGAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1663	1667	0.207689	CCTCT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1745	1749	0.207689	CCTCT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1791	1795	0.207689	CCTTT	7.8125	7.81264
cg0726872	TMEM132	c-Ets-1 [T	313	319	0.128087	GAGGAA	0.24414	0.2429
cg0726872	TMEM132	c-Ets-1 [T	1129	1135	0.128087	CTTCCTC	0.24414	0.2429
cg0726872	TMEM132	GR-alpha [	12	16	0	ACAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	47	51	0	CCTGT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	92	96	0	ATAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	106	110	0	CCTGT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	404	408	0	CCTGT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	567	571	0	CCTGT	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	922	926	0	ACAGG	7.8125	7.81264
cg0726872	TMEM132	GR-alpha [	1467	1471	0	ATAGG	7.8125	7.81264
cg0726872	TMEM132	AP-2alpha	323	328	0	GCAGGC	0.97656	0.95305
cg0726872	TMEM132	AP-2alpha	868	873	0	GCCTGC	0.97656	0.95305
cg0726872	TMEM132	AP-2alpha	988	993	0	GCAGGC	0.97656	0.95305
cg0726872	TMEM132	AP-2alpha	1038	1043	0	GCAGGC	0.97656	0.95305
cg0726872	TMEM132	AP-2alpha	1042	1047	0	GCCTGC	0.97656	0.95305
cg0726872	TMEM132	AP-2alpha	1641	1646	0	GCCTGC	0.97656	0.95305
cg0726872	TMEM132	AP-2alpha	1841	1846	0	GCAGGC	0.97656	0.95305
cg0726872	TMEM132	Pax-5 [T0	31	37	0	CCGGCC	1.09863	1.06846
cg0726872	TMEM132	Pax-5 [T0	74	80	0	CCTGCC	1.09863	1.06846
cg0726872	TMEM132	Pax-5 [T0	745	751	0	CAGGCC	1.09863	1.06846
cg0726872	TMEM132	Pax-5 [T0	853	859	0	GGGCTG	1.09863	1.06846
cg0726872	TMEM132	Pax-5 [T0	882	888	0	GGGCCT	1.09863	1.06846
cg0726872	TMEM132	Pax-5 [T0	986	992	0	GGGCAG	1.09863	1.06846
cg0726872	TMEM132	Pax-5 [T0	1116	1122	0	GGGCCG	1.09863	1.06846
cg0726872	TMEM132	Pax-5 [T0	1288	1294	0	GGGCCG	1.09863	1.06846
cg0726872	TMEM132	p53 [T006	74	80	0	CCTGCC	0.36621	0.35912
cg0726872	TMEM132	p53 [T006	986	992	0	GGGCAG	0.36621	0.35912
cg0726872	TMEM132	ENKTF-1	836	843	0	CAGCGC	0.12207	0.1201
cg0726872	TMEM132	TFII-I [T0	568	573	0	CTGTCC	1.46484	1.45997
cg0726872	TMEM132	TFII-I [T0	577	582	0	CTTTCC	1.46484	1.45997

cg0726872	TMEM132	TFII-I [T0	1465	1470	0	GGATAG	1.46484	1.45997
cg0726872	TMEM132	TFII-I [T0	1625	1630	0	GGATAG	1.46484	1.45997
cg0726872	TMEM132	TFII-I [T0	1677	1682	0	CTGTCC	1.46484	1.45997
cg0726872	TMEM132	TFII-I [T0	1792	1797	0	CTTTCC	1.46484	1.45997
cg0726872	TMEM132	STAT4 [T	672	677	0	GGAAAT	0.48828	0.49387
cg0726872	TMEM132	YY1 [T00	90	93	0	CCAT	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	372	375	0	CCAT	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	374	377	0	ATGG	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	572	575	0	CCAT	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	1311	1314	0	CCAT	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	1478	1481	0	ATGG	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	1635	1638	0	CCAT	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	1767	1770	0	ATGG	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	1828	1831	0	CCAT	7.8125	7.81711
cg0726872	TMEM132	YY1 [T00	1902	1905	0	ATGG	7.8125	7.81711
cg0726872	TMEM132	ER-alpha [	202	206	0	TGACC	1.95312	1.9404
cg0726872	TMEM132	ER-alpha [	389	393	0	GGTCA	1.95312	1.9404
cg0726872	TMEM132	ER-alpha [	887	891	0	TGACC	1.95312	1.9404
cg0726872	TMEM132	ER-alpha [	1915	1919	0	TGACC	1.95312	1.9404
cg0726872	TMEM132	ER-alpha [	1949	1953	0	GGTCA	1.95312	1.9404
cg0726872	TMEM132	C/EBPbeta	130	133	0	GCAA	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	408	411	0	TTGC	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	412	415	0	TTGC	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	474	477	0	TTGC	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	564	567	0	TTGC	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	815	818	0	GCAA	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	1431	1434	0	TTGT	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	1612	1615	0	GCAA	15.625	15.71349
cg0726872	TMEM132	C/EBPbeta	1864	1867	0	ACAA	15.625	15.71349
cg0726872	TMEM132	FOXP3 [T	1430	1435	0	GTTGTG	1.46484	1.47315
cg0726872	TMEM132	GR-beta [T	471	475	0	AAATT	3.90625	3.99611
cg0726872	TMEM132	GR-beta [T	560	564	0	AATGT	3.90625	3.99611
cg0726872	TMEM132	GR-beta [T	599	603	0	AATGT	3.90625	3.99611
cg0726872	TMEM132	GR-beta [T	1376	1380	0	AATGT	3.90625	3.99611
cg0726872	TMEM132	IRF-2 [T0	510	515	0	TCACTT	0.48828	0.49387
cg1018009	TNIK	c-Ets-1 [T	242	248	9.969337	TGGGAA	0.24414	0.23698
cg1018009	TNIK	c-Ets-1 [T	492	498	9.969337	TGGGAA	0.24414	0.23698
cg1018009	TNIK	STAT5A [	1401	1413	9.952027	GTAAGA	0.01878	0.01703
cg1018009	TNIK	STAT1bet	1114	1123	9.807397	GTTTCC	0.14877	0.14533
cg1018009	TNIK	XBP-1 [T	231	236	9.789909	ATGGCG	1.95312	1.94901
cg1018009	TNIK	XBP-1 [T	296	301	9.789909	AGCCAT	1.95312	1.94901
cg1018009	TNIK	XBP-1 [T	968	973	9.789909	ATGTCT	1.95312	1.94901
cg1018009	TNIK	XBP-1 [T	1509	1514	9.789909	AGACAT	1.95312	1.94901
cg1018009	TNIK	PR B [T00	645	651	9.743489	AACACA	1.09863	1.0981
cg1018009	TNIK	PR B [T00	720	726	9.743489	AACACA	1.09863	1.0981
cg1018009	TNIK	PR A [T01	645	651	9.743489	AACACA	1.09863	1.0981
cg1018009	TNIK	PR A [T01	720	726	9.743489	AACACA	1.09863	1.0981
cg1018009	TNIK	LEF-1 [T0	390	397	9.72404	TGGCAA	0.21362	0.21229

cg1018009	TNIK	LEF-1 [T0	1383	1390	9.72404	CTTTGCC	0.21362	0.21229
cg1018009	TNIK	c-Ets-1 [T	747	753	9.713162	ATTCCCC	0.36621	0.37402
cg1018009	TNIK	NF-AT1 [T	1266	1274	9.691726	CTGGTTT	0.16785	0.16528
cg1018009	TNIK	EBF [T054	12	22	9.62688	CCCCCTC	0.06866	0.07687
cg1018009	TNIK	TFIID [T0	390	396	9.552105	TGGCAA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	460	466	9.552105	TGAGAA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	669	675	9.552105	TTTGGA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	777	783	9.552105	TGTGAA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	813	819	9.552105	TGAGAA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	1087	1093	9.552105	TCCCAA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	1384	1390	9.552105	TTTGCCA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	1831	1837	9.552105	TGAGAA	1.46484	1.37777
cg1018009	TNIK	TFIID [T0	1956	1962	9.552105	TTTCTCA	1.46484	1.37777
cg1018009	TNIK	Pax-5 [T0	444	450	9.552105	TTTGCCC	1.46484	1.61918
cg1018009	TNIK	Pax-5 [T0	548	554	9.552105	GGGCGG	1.46484	1.61918
cg1018009	TNIK	Pax-5 [T0	580	586	9.552105	TTAGCCC	1.46484	1.61918
cg1018009	TNIK	FOXP3 [T	130	135	9.512894	GTTCTG	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	187	192	9.512894	GAGAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	254	259	9.512894	CAGAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	268	273	9.512894	CAGAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	451	456	9.512894	GTTATC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	512	517	9.512894	CCCAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	621	626	9.512894	GAGAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	642	647	9.512894	AGCAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	771	776	9.512894	GTTCTT	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	835	840	9.512894	ACCAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	1017	1022	9.512894	ATAAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	1308	1313	9.512894	GAGAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	1451	1456	9.512894	GAGAAC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	1460	1465	9.512894	GTTATC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	1765	1770	9.512894	GTTATC	7.32422	7.22156
cg1018009	TNIK	FOXP3 [T	1923	1928	9.512894	GTTATG	7.32422	7.22156
cg1018009	TNIK	TFII-I [T0	27	32	9.512894	GGAAAA	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	43	48	9.512894	AATTCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	310	315	9.512894	TTTTCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	452	457	9.512894	TTATCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	568	573	9.512894	GGAATT	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	672	677	9.512894	GGAAAC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1095	1100	9.512894	AAATCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1114	1119	9.512894	GTTTCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1186	1191	9.512894	AAATCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1269	1274	9.512894	GTTTCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1293	1298	9.512894	GGAAGG	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1562	1567	9.512894	GGATAC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1578	1583	9.512894	TTTTCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1733	1738	9.512894	AATTCC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1867	1872	9.512894	GGAAAC	7.32422	7.44385
cg1018009	TNIK	TFII-I [T0	1881	1886	9.512894	TTTTCC	7.32422	7.44385

cg1018009	TNIK	TCF-4E [T	668	674	9.453578	CTTTGG	0.48828	0.46934
cg1018009	TNIK	TCF-4E [T	1813	1819	9.453578	CTCAAA	0.48828	0.46934
cg1018009	TNIK	c-Jun [T00	998	1004	9.442241	GCCGTC	0.73242	0.7366
cg1018009	TNIK	NFI/CTF [	666	673	9.352332	AGCTTT	0.54932	0.55369
cg1018009	TNIK	AP-1 [T00	1331	1339	9.3434	TGACTA	0.09155	0.08441
cg1018009	TNIK	c-Ets-1 [T	110	116	9.276861	GTTCCC	0.36621	0.37402
cg1018009	TNIK	AP-1 [T00	1927	1935	9.203282	TGACTA	0.24414	0.23028
cg1018009	TNIK	NF-AT1 [	848	856	9.18189	CCGCTT	0.22888	0.22581
cg1018009	TNIK	LEF-1 [T0	321	328	9.099721	CCACAA	0.54932	0.53171
cg1018009	TNIK	c-Ets-1 [T	44	50	9.065503	ATTCCA	0.85449	0.84987
cg1018009	TNIK	c-Ets-1 [T	949	955	9.065503	ATTCCA	0.85449	0.84987
cg1018009	TNIK	USF2 [T0	335	344	9.056375	CAGGTG	0.1545	0.16206
cg1018009	TNIK	NF-AT1 [	35	43	9.042733	GGAAAT	0.22888	0.22581
cg1018009	TNIK	c-Myb [T0	1984	1991	9.024874	CACAGT	0.39673	0.37851
cg1018009	TNIK	MEF-2A [	1036	1046	9.003254	AAAAAA	0.07343	0.06466
cg1018009	TNIK	LEF-1 [T0	668	675	8.973041	CTTTGG	0.54932	0.53171
cg1018009	TNIK	LEF-1 [T0	1087	1094	8.973041	TCCCAA	0.54932	0.53171
cg1018009	TNIK	GR [T050	1714	1720	8.971049	CAAACA	0.61035	0.5928
cg1018009	TNIK	T3R-beta1	92	100	8.924046	GTCGGG	0.2594	0.2685
cg1018009	TNIK	IRF-1 [T0	311	319	8.916359	TTTCCA	0.09155	0.09193
cg1018009	TNIK	c-Ets-2 [T	181	189	8.912323	TTCCTA	0.27466	0.27171
cg1018009	TNIK	GATA-2 [	1562	1570	8.888889	GGATAC	0.22888	0.22339
cg1018009	TNIK	PR B [T00	477	483	8.827054	ACCTGT	0.36621	0.35051
cg1018009	TNIK	PR A [T01	477	483	8.827054	ACCTGT	0.36621	0.35051
cg1018009	TNIK	NF-1 [T00	389	396	8.790071	TTGGCA	0.24414	0.24339
cg1018009	TNIK	LEF-1 [T0	774	781	8.759086	CTTTGT	0.54932	0.53171
cg1018009	TNIK	XBP-1 [T	407	412	8.75604	TCTCAT	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	652	657	8.75604	TTTCAT	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	656	661	8.75604	ATGAAA	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	730	735	8.75604	GTTCAT	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	812	817	8.75604	ATGAGA	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	1061	1066	8.75604	ATGAGC	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	1462	1467	8.75604	TATCAT	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	1690	1695	8.75604	TATCAT	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	1830	1835	8.75604	ATGAGA	2.92969	2.75329
cg1018009	TNIK	XBP-1 [T	1875	1880	8.75604	ATGAGC	2.92969	2.75329
cg1018009	TNIK	NF-AT1 [	1111	1119	8.746017	GTTGTT	0.10681	0.10494
cg1018009	TNIK	c-Myb [T0	424	431	8.728118	AAACTT	0.30518	0.28602
cg1018009	TNIK	STAT1bet	31	40	8.695301	AAGTGG	0.22316	0.2175
cg1018009	TNIK	STAT1bet	851	860	8.695301	CTTTCC	0.22316	0.2175
cg1018009	TNIK	LEF-1 [T0	1812	1819	8.457856	CCTCAA	0.15259	0.154
cg1018009	TNIK	RBP-Jkap	109	120	8.425028	AGTTCC	0.02074	0.02067
cg1018009	TNIK	RBP-Jkap	238	249	8.425028	TGCATG	0.02074	0.02067
cg1018009	TNIK	HNF-3alp	803	810	8.343064	CATTTA	0.27466	0.23078
cg1018009	TNIK	HNF-3alp	807	814	8.343064	TTAAAA	0.27466	0.23078
cg1018009	TNIK	HNF-3alp	1611	1618	8.343064	ATAAAA	0.27466	0.23078
cg1018009	TNIK	c-Ets-2 [T	563	571	8.339336	GGGCAG	0.13733	0.13927
cg1018009	TNIK	PR B [T00	103	109	8.338824	AACAGG	1.09863	1.09384

cg1018009	TNIK	PR B [T00	675	681	8.338824	AACAGC	1.09863	1.09384
cg1018009	TNIK	PR A [T01	103	109	8.338824	AACAGG	1.09863	1.09384
cg1018009	TNIK	PR A [T01	675	681	8.338824	AACAGC	1.09863	1.09384
cg1018009	TNIK	GR-alpha [	24	28	8.281568	CAAGG	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	279	283	8.281568	CGAGG	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	542	546	8.281568	GGAGG	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	557	561	8.281568	GGAGG	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	560	564	8.281568	GGAGG	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	827	831	8.281568	CCTTC	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	1022	1026	8.281568	CCTCC	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	1190	1194	8.281568	CCTCC	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	1294	1298	8.281568	GAAGG	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	1439	1443	8.281568	CCTTC	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	1447	1451	8.281568	CCTTG	7.8125	8.20394
cg1018009	TNIK	GR-alpha [	1973	1977	8.281568	GAAGG	7.8125	8.20394
cg1018009	TNIK	SRY [T00	320	328	8.174786	CCCACA	0.15259	0.14791
cg1018009	TNIK	IRF-1 [T0	668	676	8.151819	CTTTGG	0.25177	0.2462
cg1018009	TNIK	IRF-1 [T0	1882	1890	8.151819	TTTCCG	0.25177	0.2462
cg1018009	TNIK	c-Ets-1 [T	1708	1714	8.116854	CTGGAA	0.24414	0.2494
cg1018009	TNIK	GR-alpha [	1	5	8.073878	CCTGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	8	12	8.073878	CCTGC	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	55	59	8.073878	CCTGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	76	80	8.073878	CCAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	125	129	8.073878	CTAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	141	145	8.073878	CCTGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	170	174	8.073878	CCAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	183	187	8.073878	CCTAG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	305	309	8.073878	CCAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	553	557	8.073878	GCAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	565	569	8.073878	GCAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	737	741	8.073878	GTAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	855	859	8.073878	CCAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	995	999	8.073878	CCTGC	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	1025	1029	8.073878	CCTGC	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	1173	1177	8.073878	CCTAG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	1289	1293	8.073878	GCAGG	7.8125	8.20289
cg1018009	TNIK	GR-alpha [	1471	1475	8.073878	CCTGC	7.8125	8.20289
cg1018009	TNIK	TFIID [T0	531	537	8.014558	TCTGAA	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	618	624	8.014558	TTTGAG	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	670	676	8.014558	TTGGAA	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	775	781	8.014558	TTTGTG	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	1010	1016	8.014558	TTTCTTA	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	1073	1079	8.014558	TTGCAA	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	1203	1209	8.014558	TAGCAA	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	1633	1639	8.014558	TTTGATA	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	1762	1768	8.014558	TTTGTTA	2.19727	1.99811
cg1018009	TNIK	TFIID [T0	1882	1888	8.014558	TTTCCG	2.19727	1.99811
cg1018009	TNIK	Pax-5 [T0	136	142	8.014558	GAAGCC	2.19727	2.42766

cg1018009	TNIK	Pax-5 [T0	858	864	8.014558	GGGCAG	2.19727	2.42766
cg1018009	TNIK	c-Myb [T0	923	930	8.005241	GAACTC	0.21362	0.20997
cg1018009	TNIK	ETF [T002	556	566	7.870358	GGGAGG	0.07153	0.08737
cg1018009	TNIK	c-Ets-2 [T	168	176	7.84116	CACCAG	0.32043	0.30792
cg1018009	TNIK	NF-AT2 [	306	315	7.779688	CAGGTT	0.08965	0.08482
cg1018009	TNIK	c-Ets-2 [T	1271	1279	7.76635	TTCCTGT	0.32043	0.30792
cg1018009	TNIK	c-Ets-2 [T	1586	1594	7.76635	GGACAG	0.32043	0.30792
cg1018009	TNIK	IRF-1 [T0	852	860	7.732782	TTTCCAC	0.14496	0.14723
cg1018009	TNIK	c-Myb [T0	837	844	7.662426	CAACTT	0.42725	0.40917
cg1018009	TNIK	p53 [T006	824	830	7.641867	GGGCCT	0.73242	0.79826
cg1018009	TNIK	GR [T050	666	672	7.527031	AGCTTT	1.83105	1.71535
cg1018009	TNIK	GR [T050	1076	1082	7.527031	CAAATA	1.83105	1.71535
cg1018009	TNIK	GR [T050	1099	1105	7.527031	CCTTTTC	1.83105	1.71535
cg1018009	TNIK	GR [T050	1122	1128	7.527031	CAAAAT	1.83105	1.71535
cg1018009	TNIK	GR [T050	1206	1212	7.527031	CAAATA	1.83105	1.71535
cg1018009	TNIK	p53 [T006	1466	1472	7.47855	ATAGCC	0.73242	0.79826
cg1018009	TNIK	RAR-beta	127	136	7.47824	AGGGTT	0.24414	0.25121
cg1018009	TNIK	C/EBPalph	1003	1009	7.465744	CATTGC	0.48828	0.45033
cg1018009	TNIK	C/EBPalph	1500	1506	7.465744	TTCAAT	0.48828	0.45033
cg1018009	TNIK	E2F-1 [T0	550	557	7.336545	GCGGCA	0.45776	0.49661
cg1018009	TNIK	IRF-1 [T0	1863	1871	7.299819	GAGTGG	0.14496	0.14723
cg1018009	TNIK	p53 [T006	79	85	7.266844	GGGCTG	0.73242	0.79826
cg1018009	TNIK	SRY [T00	774	782	7.175614	CTTTGTC	0.30518	0.29547
cg1018009	TNIK	XBP-1 [T	384	389	7.172312	CTTCAT	2.92969	2.7512
cg1018009	TNIK	XBP-1 [T	526	531	7.172312	ATGAAT	2.92969	2.7512
cg1018009	TNIK	XBP-1 [T	586	591	7.172312	CCTCAT	2.92969	2.7512
cg1018009	TNIK	XBP-1 [T	904	909	7.172312	AATCAT	2.92969	2.7512
cg1018009	TNIK	XBP-1 [T	964	969	7.172312	CATCAT	2.92969	2.7512
cg1018009	TNIK	XBP-1 [T	1593	1598	7.172312	AATCAT	2.92969	2.7512
cg1018009	TNIK	XBP-1 [T	1603	1608	7.172312	CTTCAT	2.92969	2.7512
cg1018009	TNIK	XBP-1 [T	1607	1612	7.172312	ATTCAT	2.92969	2.7512
cg1018009	TNIK	c-Myb [T0	174	181	7.127234	GAACTG	0.18311	0.17765
cg1018009	TNIK	NF-AT1 [	27	35	7.095752	GGAAAA	0.15259	0.14325
cg1018009	TNIK	NF-AT1 [	1575	1583	7.095752	TTATTTT	0.15259	0.14325
cg1018009	TNIK	TFIID [T0	1031	1037	7.082373	TGCTAA	0.12207	0.11255
cg1018009	TNIK	c-Ets-1 [T	1115	1121	7.071349	TTTCCCT	0.73242	0.73732
cg1018009	TNIK	NF-AT2 [	1877	1886	7.008591	GAGCTT	0.04578	0.04306
cg1018009	TNIK	C/EBPalph	387	393	7.00174	CATTGG	0.73242	0.68282
cg1018009	TNIK	C/EBPalph	397	403	7.00174	GACAAT	0.73242	0.68282
cg1018009	TNIK	HNF-3alph	695	702	7.000129	CAAAAA	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	754	761	7.000129	AATTTTT	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	1074	1081	7.000129	TGCAAA	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	1159	1166	7.000129	CATTTTT	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	1354	1361	7.000129	AGAAAA	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	1421	1428	7.000129	AGAAAA	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	1572	1579	7.000129	TATTTAT	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	1576	1583	7.000129	TATTTC	0.82397	0.71909
cg1018009	TNIK	HNF-3alph	1628	1635	7.000129	AATTTTT	0.82397	0.71909

cg1018009	TNIK	HNF-3alp	1653	1660	7.000129	TATAAA	0.82397	0.71909
cg1018009	TNIK	HNF-3alp	1664	1671	7.000129	AATAAA	0.82397	0.71909
cg1018009	TNIK	HNF-3alp	1668	1675	7.000129	AATAAA	0.82397	0.71909
cg1018009	TNIK	GCF [T00	234	242	6.987525	GCGCTG	0.45776	0.50397
cg1018009	TNIK	TCF-4 [T0	1811	1820	6.961804	TCCTCA	0.01144	0.01106
cg1018009	TNIK	NF-1 [T00	19	26	6.948522	TGAACC	0.48828	0.50205
cg1018009	TNIK	NF-1 [T00	509	516	6.948522	AGACCC	0.48828	0.50205
cg1018009	TNIK	ENKTF-1	117	124	6.942764	CCATGC	1.46484	1.56616
cg1018009	TNIK	ENKTF-1	293	300	6.942764	CTCAGC	1.46484	1.56616
cg1018009	TNIK	ENKTF-1	390	397	6.942764	TGGCAA	1.46484	1.56616
cg1018009	TNIK	ENKTF-1	1383	1390	6.942764	CTTTGC	1.46484	1.56616
cg1018009	TNIK	VDR [T00	730	738	6.925682	GTTCAT	0.42725	0.41
cg1018009	TNIK	C/EBPalp	1125	1131	6.85549	AATTGC	0.73242	0.68282
cg1018009	TNIK	HOXD9 [	1181	1190	6.852796	AATACA	0.07629	0.06543
cg1018009	TNIK	HOXD10	1181	1190	6.852796	AATACA	0.07629	0.06543
cg1018009	TNIK	AR [T000	1586	1594	6.817719	GGACAG	0.23651	0.23986
cg1018009	TNIK	NFI/CTF [	487	494	6.786076	TTGCTT	0.73242	0.74795
cg1018009	TNIK	EBF [T05	455	465	6.76967	TCCCCT	0.03052	0.03432
cg1018009	TNIK	NF-1 [T00	986	993	6.722386	CTGGCC	0.24414	0.2565
cg1018009	TNIK	PXR-1:RX	727	734	6.668182	TCCGTT	0.24414	0.23169
cg1018009	TNIK	GATA-2 [	449	457	6.666667	CCGTTA	0.24414	0.2357
cg1018009	TNIK	FOXP3 [T	1434	1439	6.581441	TAAAAC	0.97656	0.904
cg1018009	TNIK	FOXP3 [T	1638	1643	6.581441	TAAAAC	0.97656	0.904
cg1018009	TNIK	TFII-I [T0	261	266	6.581441	ATCTCC	0.97656	0.9991
cg1018009	TNIK	TFII-I [T0	724	729	6.581441	CACTCC	0.97656	0.9991
cg1018009	TNIK	TFII-I [T0	1808	1813	6.581441	ATCTCC	0.97656	0.9991
cg1018009	TNIK	p53 [T006	136	142	6.563521	GAAGCC	0.48828	0.54643
cg1018009	TNIK	XBP-1 [T	119	124	6.478682	ATGCCA	0.97656	0.99906
cg1018009	TNIK	XBP-1 [T	1374	1379	6.478682	ATGCCA	0.97656	0.99906
cg1018009	TNIK	XBP-1 [T	1906	1911	6.478682	ATGCCA	0.97656	0.99906
cg1018009	TNIK	c-Ets-1 [T	670	676	6.423689	TTGGAA	0.48828	0.48842
cg1018009	TNIK	TCF-4E [	391	397	6.302385	GGCAAA	0.61035	0.59686
cg1018009	TNIK	TCF-4E [	1107	1113	6.302385	CTTTGTT	0.61035	0.59686
cg1018009	TNIK	TCF-4E [	1383	1389	6.302385	CTTTGC	0.61035	0.59686
cg1018009	TNIK	c-Ets-1 [T	1579	1585	6.295602	TTTCCA	0.48828	0.48842
cg1018009	TNIK	GR-alpha	66	70	6.263098	CCTTA	3.90625	3.89624
cg1018009	TNIK	GR-alpha	98	102	6.263098	TGAGG	3.90625	3.89624
cg1018009	TNIK	GR-alpha	195	199	6.263098	CCTCA	3.90625	3.89624
cg1018009	TNIK	GR-alpha	213	217	6.263098	TAAGG	3.90625	3.89624
cg1018009	TNIK	GR-alpha	265	269	6.263098	CCTCA	3.90625	3.89624
cg1018009	TNIK	GR-alpha	586	590	6.263098	CCTCA	3.90625	3.89624
cg1018009	TNIK	GR-alpha	943	947	6.263098	TGAGG	3.90625	3.89624
cg1018009	TNIK	GR-alpha	1119	1123	6.263098	CCTCA	3.90625	3.89624
cg1018009	TNIK	GR-alpha	1139	1143	6.263098	TAAGG	3.90625	3.89624
cg1018009	TNIK	GR-alpha	1260	1264	6.263098	TAAGG	3.90625	3.89624
cg1018009	TNIK	GR-alpha	1301	1305	6.263098	TAAGG	3.90625	3.89624
cg1018009	TNIK	GR-alpha	1546	1550	6.263098	CCTTA	3.90625	3.89624
cg1018009	TNIK	GR-alpha	1737	1741	6.263098	CCTCA	3.90625	3.89624

cg1018009	TNIK	GR-alpha [	1812	1816	6.263098	CCTCA	3.90625	3.89624
cg1018009	TNIK	c-Myb [T0	1801	1808	6.259888	TAACTG	0.30518	0.30272
cg1018009	TNIK	C/EBPalph	1071	1077	6.245236	TATTGC	0.97656	0.91422
cg1018009	TNIK	IRF-1 [T0	1270	1278	6.206911	TTTCCTC	0.16785	0.16217
cg1018009	TNIK	p53 [T006	548	554	6.188498	GGGCGG	0.61035	0.68483
cg1018009	TNIK	c-Ets-1 [T	33	39	6.167515	GTGGAA	0.36621	0.36174
cg1018009	TNIK	c-Ets-1 [T	311	317	6.167515	TTTCCA	0.36621	0.36174
cg1018009	TNIK	c-Ets-1 [T	1865	1871	6.167515	GTGGAA	0.36621	0.36174
cg1018009	TNIK	GR-alpha [	221	225	6.055408	TCAGG	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	334	338	6.055408	TCAGG	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	458	462	6.055408	CCTGA	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	690	694	6.055408	TTAGG	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	707	711	6.055408	CCTGA	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	1485	1489	6.055408	TTAGG	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	1749	1753	6.055408	TTAGG	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	1793	1797	6.055408	CCTGA	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	1902	1906	6.055408	CCTAA	3.90625	3.89835
cg1018009	TNIK	GR-alpha [	1946	1950	6.055408	TCAGG	3.90625	3.89835
cg1018009	TNIK	c-Ets-1 [T	852	858	6.039428	TTTCCA	0.36621	0.36174
cg1018009	TNIK	C/EBPalph	589	595	5.996794	CATTGT	0.97656	0.91422
cg1018009	TNIK	RXR-alpha	282	288	5.937582	GGGTAC	0.73242	0.78318
cg1018009	TNIK	GCF [T00	1327	1335	5.917256	GCGCTG	0.64087	0.72542
cg1018009	TNIK	STAT4 [T	1293	1298	5.882353	GGAAGG	0.48828	0.51201
cg1018009	TNIK	C/EBPalph	1937	1943	5.850545	AATTGA	0.97656	0.91422
cg1018009	TNIK	c-Ets-1 [T	143	149	5.814485	TGGGAA	0.36621	0.36174
cg1018009	TNIK	c-Jun [T00	1795	1801	5.783074	TGACTT	0.36621	0.34478
cg1018009	TNIK	NF-AT1 [	1440	1448	5.77403	CTTCTTT	0.06866	0.06621
cg1018009	TNIK	p53 [T006	580	586	5.720243	TTAGCC	0.61035	0.65765
cg1018009	TNIK	ENKTF-1	157	164	5.687009	TGGCAC	0.73242	0.76357
cg1018009	TNIK	ENKTF-1	1981	1988	5.687009	TGGCAC	0.73242	0.76357
cg1018009	TNIK	c-Ets-1 [T	1291	1297	5.686398	AGGGAA	0.36621	0.38732
cg1018009	TNIK	T3R-beta1	438	446	5.591999	TCACCA	0.21362	0.21789
cg1018009	TNIK	c-Jun [T00	1940	1946	5.590308	TGACAC	0.48828	0.49294
cg1018009	TNIK	NFI/CTF [	990	997	5.558661	CCAATC	0.54932	0.55504
cg1018009	TNIK	TFIID [T0	764	770	5.544826	TTTAGT	0.73242	0.65314
cg1018009	TNIK	TFIID [T0	879	885	5.544826	TGATAA	0.73242	0.65314
cg1018009	TNIK	TFIID [T0	919	925	5.544826	TTTAGA	0.73242	0.65314
cg1018009	TNIK	TFIID [T0	1282	1288	5.544826	TACTAA	0.73242	0.65314
cg1018009	TNIK	TFIID [T0	1635	1641	5.544826	TGATAA	0.73242	0.65314
cg1018009	TNIK	Pax-5 [T0	1466	1472	5.544826	ATAGCC	0.73242	0.79
cg1018009	TNIK	HNF-1A [	479	486	5.466509	CTGTTA	0.24414	0.23087
cg1018009	TNIK	C/EBPalph	1657	1663	5.38654	AATTGT	0.73242	0.68229
cg1018009	TNIK	C/EBPalph	1676	1682	5.38654	AATTGT	0.73242	0.68229
cg1018009	TNIK	RAR-beta	432	441	5.333686	TGGGTT	0.15259	0.15813
cg1018009	TNIK	RAR-beta	739	748	5.333686	AGGGTT	0.15259	0.15813
cg1018009	TNIK	MEF-2A [	692	702	5.321562	AGGCAA	0.02003	0.01733
cg1018009	TNIK	IRF-1 [T0	1444	1452	5.309227	TTTCCTT	0.22888	0.21959
cg1018009	TNIK	RXR-alpha	1697	1703	5.271235	TCTACC	0.61035	0.65415

cg1018009	TNIK	IRF-1 [T0(	1579	1587	5.21856	TTTCCAT	0.1297	0.12724
cg1018009	TNIK	GR [T050'	393	399	5.207533	CAAAGA	0.24414	0.24013
cg1018009	TNIK	c-Jun [T00	217	223	5.193102	GAAGTC.	0.61035	0.60573
cg1018009	TNIK	c-Jun [T00	974	980	5.193102	TGACTT(	0.61035	0.60573
cg1018009	TNIK	c-Ets-2 [T(	22	30	5.162974	ACCAAG	0.13733	0.13279
cg1018009	TNIK	c-Ets-2 [T(	1445	1453	5.162974	TTCCTTC	0.13733	0.13279
cg1018009	TNIK	AP-2alpha	1105	1110	5.100982	GCCTTT	0.97656	0.97517
cg1018009	TNIK	USF2 [T0(	472	481	5.052423	GCATCA(	0.103	0.10797
cg1018009	TNIK	GR-beta [T	246	250	5.042296	AATAC	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	992	996	5.042296	AATCC	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	1096	1100	5.042296	AATCC	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	1181	1185	5.042296	AATAC	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	1187	1191	5.042296	AATCC	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	1213	1217	5.042296	GTATT	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	1218	1222	5.042296	AATAC	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	1492	1496	5.042296	AATAC	3.90625	3.7093
cg1018009	TNIK	GR-beta [T	1744	1748	5.042296	AATAC	3.90625	3.7093
cg1018009	TNIK	IRF-1 [T0(	23	31	4.963725	CCAAGG.	0.1297	0.12724
cg1018009	TNIK	XBP-1 [T(	945	950	4.894955	AGGCAT	0.97656	0.99839
cg1018009	TNIK	AP-2alpha	690	695	4.890408	TTAGGC	0.97656	0.97517
cg1018009	TNIK	AP-2alpha	1749	1754	4.890408	TTAGGC	0.97656	0.97517
cg1018009	TNIK	IRF-1 [T0(	31	39	4.881305	AAGTGG.	0.1297	0.12724
cg1018009	TNIK	NF-1 [T00	1085	1092	4.880836	AGTCCC.	0.24414	0.24345
cg1018009	TNIK	c-Ets-1 [T(	1882	1888	4.872197	TTTCCGA	0.48828	0.48026
cg1018009	TNIK	C/EBPalpł	1064	1070	4.845599	AGCAAT'	0.97656	0.90302
cg1018009	TNIK	HNF-3alpł	1554	1561	4.842999	TATTTAA	0.09155	0.07438
cg1018009	TNIK	c-Myb [T0	483	490	4.840682	TAACTT(	0.30518	0.30087
cg1018009	TNIK	HNF-1A ['	481	488	4.828753	GTTAAC'	0.36621	0.34064
cg1018009	TNIK	NF-AT1 [T	1866	1875	4.823485	TGGAAA	0.07629	0.07281
cg1018009	TNIK	p53 [T006'	894	900	4.786849	GGGCAC'	0.48828	0.53921
cg1018009	TNIK	C/EBPalpł	1919	1925	4.776286	TATTGTT	0.97656	0.90302
cg1018009	TNIK	FOXP3 [T	309	314	4.756447	GTTTTC	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	422	427	4.756447	CAAAAC	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	831	836	4.756447	CTCAAC	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	866	871	4.756447	CAAAAC	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	885	890	4.756447	ATCAAC	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	1645	1650	4.756447	GTTTTC	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	1680	1685	4.756447	GTTGAT	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	1820	1825	4.756447	AAAAAC	2.92969	2.82
cg1018009	TNIK	FOXP3 [T	1954	1959	4.756447	GTTTTC	2.92969	2.82
cg1018009	TNIK	TFII-I [T0	35	40	4.756447	GGAAAT	2.92969	2.89715
cg1018009	TNIK	TFII-I [T0	494	499	4.756447	GGAATG	2.92969	2.89715
cg1018009	TNIK	TFII-I [T0	685	690	4.756447	GGATAT	2.92969	2.89715
cg1018009	TNIK	TFII-I [T0	785	790	4.756447	ATGTCC	2.92969	2.89715
cg1018009	TNIK	TFII-I [T0	910	915	4.756447	CAGTCC	2.92969	2.89715
cg1018009	TNIK	TFII-I [T0	948	953	4.756447	CATTCC	2.92969	2.89715
cg1018009	TNIK	TFII-I [T0	991	996	4.756447	CAATCC	2.92969	2.89715
cg1018009	TNIK	TFII-I [T0	1084	1089	4.756447	CAGTCC	2.92969	2.89715

cg1018009	TNIK	TFII-I [T0	1949	1954	4.756447	GGACTG	2.92969	2.89715
cg1018009	TNIK	HNF-1A [	361	368	4.684871	GTTAAG	0.12207	0.10966
cg1018009	TNIK	HNF-1A [	593	600	4.684871	GTTAAG	0.12207	0.10966
cg1018009	TNIK	HNF-1C [	1661	1669	4.656597	GTTAAT	0.07629	0.06715
cg1018009	TNIK	c-Ets-1 [T	56	62	4.654478	CTGGAA	0.85449	0.8381
cg1018009	TNIK	c-Ets-1 [T	133	139	4.654478	CTGGAA	0.85449	0.8381
cg1018009	TNIK	c-Ets-1 [T	302	308	4.654478	CTTCCA	0.85449	0.8381
cg1018009	TNIK	C/EBPalph	989	995	4.560723	GCCAAT	0.24414	0.24373
cg1018009	TNIK	T3R-beta1	475	483	4.481316	TCACCT	0.27466	0.27245
cg1018009	TNIK	HNF-1B [	1660	1668	4.435774	TGTTAA	0.05341	0.04718
cg1018009	TNIK	RXR-alpha	316	322	4.423008	ACAACC	0.24414	0.25781
cg1018009	TNIK	AP-2alpha	1545	1550	4.422424	GCCTTA	0.97656	0.99839
cg1018009	TNIK	STAT4 [T	58	63	4.411765	GGAAGA	1.95312	1.99838
cg1018009	TNIK	STAT4 [T	135	140	4.411765	GGAAGC	1.95312	1.99838
cg1018009	TNIK	STAT4 [T	145	150	4.411765	GGAAGC	1.95312	1.99838
cg1018009	TNIK	STAT4 [T	301	306	4.411765	TCTTCC	1.95312	1.99838
cg1018009	TNIK	STAT4 [T	494	499	4.411765	GGAATG	1.95312	1.99838
cg1018009	TNIK	STAT4 [T	948	953	4.411765	CATTCC	1.95312	1.99838
cg1018009	TNIK	STAT4 [T	1348	1353	4.411765	GGAAGC	1.95312	1.99838
cg1018009	TNIK	HOXD9 [	1043	1052	4.321431	AATAAA	0.03433	0.02831
cg1018009	TNIK	HOXD9 [	1050	1059	4.321431	AATAAA	0.03433	0.02831
cg1018009	TNIK	HOXD10 [	1043	1052	4.321431	AATAAA	0.03433	0.02831
cg1018009	TNIK	HOXD10 [	1050	1059	4.321431	AATAAA	0.03433	0.02831
cg1018009	TNIK	c-Ets-1 [T	1734	1740	4.282938	ATTCCT	0.85449	0.8381
cg1018009	TNIK	C/EBPalph	1178	1184	4.235345	AGCAAT	0.48828	0.46347
cg1018009	TNIK	C/EBPalph	1741	1747	4.235345	AGCAAT	0.48828	0.46347
cg1018009	TNIK	Elk-1 [T00	212	220	4.204473	ATAAGG	0.09155	0.08816
cg1018009	TNIK	GR-beta [	200	204	4.201913	AATCA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	663	667	4.201913	AATAG	7.8125	7.23274
cg1018009	TNIK	GR-beta [	711	715	4.201913	AATAG	7.8125	7.23274
cg1018009	TNIK	GR-beta [	745	749	4.201913	CTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	884	888	4.201913	AATCA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	904	908	4.201913	AATCA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1016	1020	4.201913	AATAA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1043	1047	4.201913	AATAA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1050	1054	4.201913	AATAA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1055	1059	4.201913	AATCA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1070	1074	4.201913	TTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1078	1082	4.201913	AATAG	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1134	1138	4.201913	TTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1164	1168	4.201913	TTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1226	1230	4.201913	AATAA	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1361	1365	4.201913	TTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1427	1431	4.201913	TTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1553	1557	4.201913	TTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1571	1575	4.201913	CTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1575	1579	4.201913	TTATT	7.8125	7.23274
cg1018009	TNIK	GR-beta [	1593	1597	4.201913	AATCA	7.8125	7.23274

cg1018009	TNIK	GR-beta [T	1664	1668	4.201913	AATAA	7.8125	7.23274
cg1018009	TNIK	GR-beta [T	1668	1672	4.201913	AATAA	7.8125	7.23274
cg1018009	TNIK	GR-beta [T	1672	1676	4.201913	AATAA	7.8125	7.23274
cg1018009	TNIK	NF-Y [T0	749	756	4.186615	TCCCCA	0.18311	0.17499
cg1018009	TNIK	c-Ets-1 [T	566	572	4.154851	CAGGAA	0.24414	0.23719
cg1018009	TNIK	c-Ets-1 [T	1589	1595	4.154851	CAGGAA	0.24414	0.23719
cg1018009	TNIK	NF-AT1 [T	34	43	4.134416	TGGAAA	0.08392	0.07965
cg1018009	TNIK	NF-AT1 [T	307	316	4.134416	AGGTTT	0.08392	0.07965
cg1018009	TNIK	NF-AT1 [T	848	857	4.134416	CCGCTT	0.08392	0.07965
cg1018009	TNIK	NF-AT1 [T	1575	1584	4.134416	TTATTT	0.08392	0.07965
cg1018009	TNIK	p53 [T006	1143	1149	4.125254	GGGCCT	0.73242	0.82434
cg1018009	TNIK	c-Ets-2 [T	211	219	4.091811	CATAAG	0.16022	0.15061
cg1018009	TNIK	IRF-1 [T0	1115	1123	4.035054	TTTCCCT	0.1297	0.12468
cg1018009	TNIK	RXR-alph	340	346	4.019014	GGGTAT	0.97656	1.02803
cg1018009	TNIK	RXR-alph	433	439	4.019014	GGGTTT	0.97656	1.02803
cg1018009	TNIK	RXR-alph	843	849	4.019014	CACACC	0.97656	1.02803
cg1018009	TNIK	c-Ets-2 [T	1343	1351	4.017001	AGAAAG	0.16022	0.15061
cg1018009	TNIK	EBF [T05	138	148	4.016439	AGCCCT	0.0248	0.02839
cg1018009	TNIK	STAT1bet	1443	1452	4.01053	CTTTCCT	0.03433	0.03308
cg1018009	TNIK	TFIID [T0	805	811	4.007279	TTTTAA	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1015	1021	4.007279	TAATAA	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1163	1169	4.007279	TTTATTA	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1431	1437	4.007279	TTTTAA	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1476	1482	4.007279	TTTAAG	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1609	1615	4.007279	TCATAA	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1651	1657	4.007279	TTTATA	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1652	1658	4.007279	TTATAA	1.09863	0.94722
cg1018009	TNIK	TFIID [T0	1663	1669	4.007279	TAATAA	1.09863	0.94722
cg1018009	TNIK	Pax-5 [T0	79	85	4.007279	GGGCTG	1.09863	1.18533
cg1018009	TNIK	Pax-5 [T0	824	830	4.007279	GGGCCT	1.09863	1.18533
cg1018009	TNIK	Pax-5 [T0	894	900	4.007279	GGGCAC	1.09863	1.18533
cg1018009	TNIK	c-Ets-1 [T	180	186	3.846637	GTTCCT	0.24414	0.23719
cg1018009	TNIK	c-Jun [T00	1331	1337	3.807346	TGACTA	0.24414	0.23729
cg1018009	TNIK	c-Jun [T00	1927	1933	3.807346	TGACTA	0.24414	0.23729
cg1018009	TNIK	GR [T050	422	428	3.763516	CAAAAC	0.73242	0.6946
cg1018009	TNIK	GR [T050	772	778	3.763516	TTCTTTG	0.73242	0.6946
cg1018009	TNIK	GR [T050	866	872	3.763516	CAAAAC	0.73242	0.6946
cg1018009	TNIK	GR [T050	1090	1096	3.763516	CAAAGA	0.73242	0.6946
cg1018009	TNIK	GR [T050	1815	1821	3.763516	CAAAGA	0.73242	0.6946
cg1018009	TNIK	AP-2alpha	826	831	3.743866	GCCTTC	0.48828	0.5124
cg1018009	TNIK	AP-2alpha	1973	1978	3.743866	GAAGGC	0.48828	0.5124
cg1018009	TNIK	Sp1 [T007	547	556	3.623596	GGGGCG	0.07439	0.08783
cg1018009	TNIK	AR [T000	782	790	3.59934	AAAATG	0.06866	0.06629
cg1018009	TNIK	c-Ets-1 [T	99	105	3.590463	GAGGAA	0.61035	0.61936
cg1018009	TNIK	C/EBPalph	257	263	3.555778	AACAAT	0.24414	0.23261
cg1018009	TNIK	HNF-3alph	659	666	3.500065	AAAAAA	0.27466	0.23175
cg1018009	TNIK	HNF-3alph	1039	1046	3.500065	AAAAAA	0.27466	0.23175
cg1018009	TNIK	HNF-3alph	1046	1053	3.500065	AAAAAA	0.27466	0.23175

cg1018009	TNIK	HNF-3alp	1121	1128	3.500065	TCAAAA	0.27466	0.23175
cg1018009	TNIK	VDR [T00	15	23	3.462841	CCTGTG	0.21362	0.21283
cg1018009	TNIK	c-Ets-1 [T	171	177	3.462376	CAGGAA	0.61035	0.61936
cg1018009	TNIK	NF-AT1 [	671	680	3.445347	TGGAAA	0.07629	0.07204
cg1018009	TNIK	RXR-alph	95	101	3.392904	GGGTGA	1.09863	1.1653
cg1018009	TNIK	RXR-alph	352	358	3.392904	GGGTTA	1.09863	1.1653
cg1018009	TNIK	GR-beta [	38	42	3.361531	AATCT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	260	264	3.361531	AATCT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	529	533	3.361531	AATCT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	597	601	3.361531	AGATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	687	691	3.361531	ATATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	699	703	3.361531	AATAT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	818	822	3.361531	AATCT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	1208	1212	3.361531	AATAT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	1278	1282	3.361531	AGATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	1482	1486	3.361531	ATATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	1527	1531	3.361531	AATAT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	1528	1532	3.361531	ATATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	1777	1781	3.361531	AATAT	3.90625	3.51525
cg1018009	TNIK	GR-beta [	1918	1922	3.361531	ATATT	3.90625	3.51525
cg1018009	TNIK	T3R-beta1	1960	1968	3.351341	TCACCT	0.27466	0.27326
cg1018009	TNIK	GATA-2 [	1682	1690	3.333333	TGATAA	0.30518	0.29349
cg1018009	TNIK	PR B [T00	1657	1663	3.29756	AATTGT	0.24414	0.21408
cg1018009	TNIK	PR B [T00	1676	1682	3.29756	AATTGT	0.24414	0.21408
cg1018009	TNIK	PR A [T01	1657	1663	3.29756	AATTGT	0.24414	0.21408
cg1018009	TNIK	PR A [T01	1676	1682	3.29756	AATTGT	0.24414	0.21408
cg1018009	TNIK	c-Ets-2 [T	96	104	3.2883	GGTGAG	0.18311	0.18314
cg1018009	TNIK	c-Ets-2 [T	1735	1743	3.2883	TTCCTC	0.18311	0.18314
cg1018009	TNIK	PXR-1:RX	19	26	3.2723	TGAACC	0.12207	0.11883
cg1018009	TNIK	Elk-1 [T00	1344	1352	2.987643	GAAAGG	0.07629	0.07518
cg1018009	TNIK	STAT4 [T	101	106	2.941176	GGAACA	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	179	184	2.941176	GGTTCC	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	216	221	2.941176	GGAAGT	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	244	249	2.941176	GGAATA	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	746	751	2.941176	TATTCC	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	851	856	2.941176	CTTTCC	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	1443	1448	2.941176	CTTTCC	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	1591	1596	2.941176	GGAATC	2.92969	2.92382
cg1018009	TNIK	STAT4 [T	1710	1715	2.941176	GGAACA	2.92969	2.92382
cg1018009	TNIK	p53 [T006	858	864	2.813291	GGGCAG	0.48828	0.53227
cg1018009	TNIK	PR B [T00	257	263	2.80933	AACAAT	0.73242	0.66711
cg1018009	TNIK	PR B [T00	589	595	2.80933	CATTGT	0.73242	0.66711
cg1018009	TNIK	PR B [T00	1919	1925	2.80933	TATTGT	0.73242	0.66711
cg1018009	TNIK	PR A [T01	257	263	2.80933	AACAAT	0.73242	0.66711
cg1018009	TNIK	PR A [T01	589	595	2.80933	CATTGT	0.73242	0.66711
cg1018009	TNIK	PR A [T01	1919	1925	2.80933	TATTGT	0.73242	0.66711
cg1018009	TNIK	TBP [T00	1649	1658	2.807313	TCTTTAT	0.12207	0.10444
cg1018009	TNIK	NFI/CTF [	513	520	2.683003	CCAACC	0.06104	0.06609

cg1018009	TNIK	NF-Y [T0	388	395	2.582704	ATTGGC	0.21362	0.20842
cg1018009	TNIK	AP-2alpha	194	199	2.550491	GCCTCA	0.48828	0.51216
cg1018009	TNIK	AP-2alpha	943	948	2.550491	TGAGGC	0.48828	0.51216
cg1018009	TNIK	RXR-alpha	128	134	2.544678	GGGTTC	0.85449	0.89683
cg1018009	TNIK	RXR-alpha	740	746	2.544678	GGGTTC	0.85449	0.89683
cg1018009	TNIK	NF-AT1 [	307	315	2.449764	AGGTTT	0.09155	0.08666
cg1018009	TNIK	NF-AT1 [	1878	1886	2.449764	AGCTTT	0.09155	0.08666
cg1018009	TNIK	C/EBPalp	627	633	2.441016	CATTGA	0.48828	0.47439
cg1018009	TNIK	C/EBPalp	953	959	2.441016	CATTGA	0.48828	0.47439
cg1018009	TNIK	C/EBPalp	647	653	2.371703	CACAAT	0.48828	0.47439
cg1018009	TNIK	C/EBPalp	751	757	2.371703	CCCAAT	0.48828	0.47439
cg1018009	TNIK	LEF-1 [T0	1107	1114	2.345041	CTTTGTT	0.09155	0.09076
cg1018009	TNIK	RXR-alpha	508	514	2.322562	CAGACC	0.85449	0.89683
cg1018009	TNIK	GATA-1 [	684	689	2.176375	TGGATA	3.90625	3.79558
cg1018009	TNIK	GATA-1 [	1561	1566	2.176375	AGGATA	3.90625	3.79558
cg1018009	TNIK	GATA-1 [	453	458	2.001358	TATCCC	3.90625	3.79558
cg1018009	TNIK	p53 [T006	444	450	1.970013	TTTGCCC	0.36621	0.38097
cg1018009	TNIK	TFII-I [T0	86	91	1.824994	GGAGAG	0.48828	0.51201
cg1018009	TNIK	TFII-I [T0	1412	1417	1.824994	GGAGAG	0.48828	0.51201
cg1018009	TNIK	GR-beta [	43	47	1.680765	AATTC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	496	500	1.680765	AATGC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	502	506	1.680765	AATTC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	569	573	1.680765	GAATT	3.90625	3.70067
cg1018009	TNIK	GR-beta [	633	637	1.680765	GCATT	3.90625	3.70067
cg1018009	TNIK	GR-beta [	802	806	1.680765	GCATT	3.90625	3.70067
cg1018009	TNIK	GR-beta [	947	951	1.680765	GCATT	3.90625	3.70067
cg1018009	TNIK	GR-beta [	960	964	1.680765	AATGC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	1007	1011	1.680765	GCATT	3.90625	3.70067
cg1018009	TNIK	GR-beta [	1233	1237	1.680765	AATTC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	1503	1507	1.680765	AATGC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	1615	1619	1.680765	AATTC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	1733	1737	1.680765	AATTC	3.90625	3.70067
cg1018009	TNIK	GR-beta [	1759	1763	1.680765	GAATT	3.90625	3.70067
cg1018009	TNIK	GR-beta [	1905	1909	1.680765	AATGC	3.90625	3.70067
cg1018009	TNIK	c-Ets-1 [T	25	31	1.641124	AAGGAA	0.36621	0.35197
cg1018009	TNIK	c-Ets-1 [T	1444	1450	1.641124	TTTCCTT	0.36621	0.35197
cg1018009	TNIK	C/EBPbeta	23	26	1.639871	CCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	349	352	1.639871	TTGG	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	389	392	1.639871	TTGG	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	491	494	1.639871	TTGG	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	513	516	1.639871	CCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	670	673	1.639871	TTGG	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	752	755	1.639871	CCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	836	839	1.639871	CCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	990	993	1.639871	CCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1089	1092	1.639871	CCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1377	1380	1.639871	CCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1702	1705	1.639871	CCAA	15.625	15.23827

cg1018009	TNIK	TFIID [T0	310	316	1.537547	TTTTCCA	0.73242	0.65627
cg1018009	TNIK	TFIID [T0	657	663	1.537547	TGAAAA	0.73242	0.65627
cg1018009	TNIK	TFIID [T0	779	785	1.537547	TGAAAA	0.73242	0.65627
cg1018009	TNIK	TFIID [T0	1152	1158	1.537547	TTTTACA	0.73242	0.65627
cg1018009	TNIK	TFIID [T0	1497	1503	1.537547	TTTTTCA	0.73242	0.65627
cg1018009	TNIK	TFIID [T0	1578	1584	1.537547	TTTTCCA	0.73242	0.65627
cg1018009	TNIK	STAT4 [T	27	32	1.470588	GGAAAA	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	43	48	1.470588	AATTCC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	109	114	1.470588	AGTTCC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	173	178	1.470588	GGAACT	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	310	315	1.470588	TTTTCC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	568	573	1.470588	GGAATT	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	672	677	1.470588	GGAAAC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	1114	1119	1.470588	GTTTCC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	1269	1274	1.470588	GTTTCC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	1578	1583	1.470588	TTTTCC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	1733	1738	1.470588	AATTCC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	1867	1872	1.470588	GGAAAC	1.95312	1.90161
cg1018009	TNIK	STAT4 [T	1881	1886	1.470588	TTTTCC	1.95312	1.90161
cg1018009	TNIK	c-Ets-1 [T	1270	1276	1.384951	TTTCCTC	0.36621	0.35197
cg1018009	TNIK	C/EBPbeta	197	200	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	619	622	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	629	632	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	832	835	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	865	868	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	886	889	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	955	958	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	973	976	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1057	1060	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1121	1124	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1251	1254	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1449	1452	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1501	1504	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1618	1621	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1634	1637	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1681	1684	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1814	1817	1.366559	TCAA	15.625	15.23827
cg1018009	TNIK	C/EBPbeta	1939	1942	1.366559	TTGA	15.625	15.23827
cg1018009	TNIK	AP-2alpha	1145	1150	1.357116	GCCTGT	0.48828	0.51319
cg1018009	TNIK	c-Myb [T0	189	196	1.285398	GAACTG	0.06104	0.06236
cg1018009	TNIK	POU2F1 [	494	504	1.177831	GGAATG	0.01383	0.01245
cg1018009	TNIK	NF-Y [T0	987	994	1.069274	TGGCCA	0.12207	0.11765
cg1018009	TNIK	GATA-1 [	1462	1467	1.038567	TATCAT	1.95312	1.80234
cg1018009	TNIK	GATA-1 [	1634	1639	1.038567	TTGATA	1.95312	1.80234
cg1018009	TNIK	GATA-1 [	1681	1686	1.038567	TTGATA	1.95312	1.80234
cg1018009	TNIK	GATA-1 [	1690	1695	1.038567	TATCAT	1.95312	1.80234
cg1018009	TNIK	SRY [T00	1107	1115	0.999172	CTTTGTT	0.06104	0.0571
cg1018009	TNIK	HOXD9 [	1159	1168	0.954221	CATTTTT	0.01526	0.01263

cg1018009	TNIK	HOXD10 [	1159	1168	0.954221	CATTTTT	0.01526	0.01263
cg1018009	TNIK	TBP [T007	1651	1660	0.935771	TTTATAA	0.12207	0.10448
cg1018009	TNIK	HNF-1A [	1934	1941	0.925521	GTTAATT	0.48828	0.45029
cg1018009	TNIK	RXR-alpha	1518	1524	0.848226	TGGACCC	0.48828	0.51313
cg1018009	TNIK	GR-beta [T	42	46	0.840383	TAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	345	349	0.840383	TAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	386	390	0.840383	TCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	400	404	0.840383	AATGG	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	441	445	0.840383	CCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	588	592	0.840383	TCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	626	630	0.840383	CCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	649	653	0.840383	CAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	753	757	0.840383	CAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	761	765	0.840383	TAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	811	815	0.840383	AATGA	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	873	877	0.840383	AATTA	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	952	956	0.840383	CCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1002	1006	0.840383	TCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1060	1064	0.840383	AATGA	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1066	1070	0.840383	CAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1125	1129	0.840383	AATTG	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1232	1236	0.840383	TAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1254	1258	0.840383	AATTA	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1409	1413	0.840383	AATGG	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1425	1429	0.840383	AATTA	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1551	1555	0.840383	AATTA	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1605	1609	0.840383	TCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1627	1631	0.840383	TAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1657	1661	0.840383	AATTG	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1676	1680	0.840383	AATTG	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1692	1696	0.840383	TCATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1936	1940	0.840383	TAATT	7.8125	7.2174
cg1018009	TNIK	GR-beta [T	1937	1941	0.840383	AATTG	7.8125	7.2174
cg1018009	TNIK	GATA-1 [	878	883	0.758539	CTGATA	1.95312	1.80234
cg1018009	TNIK	GATA-1 [	1623	1628	0.758539	CTGATA	1.95312	1.80234
cg1018009	TNIK	GATA-1 [	1767	1772	0.758539	TATCAG	1.95312	1.80234
cg1018009	TNIK	AP-2alpha	221	226	0.678558	TCAGGC	0.48828	0.51196
cg1018009	TNIK	AP-2alpha	706	711	0.678558	GCCTGA	0.48828	0.51196
cg1018009	TNIK	AP-2alpha	1792	1797	0.678558	GCCTGA	0.48828	0.51196
cg1018009	TNIK	PR B [T00	1641	1647	0.48823	AACTGTT	0.12207	0.11255
cg1018009	TNIK	PR A [T01	1641	1647	0.48823	AACTGTT	0.12207	0.11255
cg1018009	TNIK	HNF-1A [	1797	1804	0.287765	ACTTTAA	0.24414	0.21942
cg1018009	TNIK	GATA-1 [	412	417	0.280028	TATCTA	0.97656	0.8795
cg1018009	TNIK	GATA-1 [	1479	1484	0.280028	AAGATA	0.97656	0.8795
cg1018009	TNIK	c-Ets-1 [T	214	220	0.256174	AAGGAA	0.24414	0.23743
cg1018009	TNIK	c-Ets-1 [T	1346	1352	0.256174	AAGGAA	0.24414	0.23743
cg1018009	TNIK	AP-2alpha	54	59	0.226186	GCCTGG	0.97656	1.07867
cg1018009	TNIK	GR-alpha [	88	92	0.207689	AGAGG	7.8125	7.79817

cg1018009	TNIK	GR-alpha [	325	329	0.207689	AAAGG	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	789	793	0.207689	CCTCT	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1099	1103	0.207689	CCTTT	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1106	1110	0.207689	CCTTT	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1345	1349	0.207689	AAAGG	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1559	1563	0.207689	AAAGG	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1848	1852	0.207689	AGAGG	7.8125	7.79817
cg1018009	TNIK	GR-beta [T	346	350	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	501	505	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	570	574	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	615	619	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	616	620	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	650	654	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	754	758	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	762	766	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	784	788	0	AATGT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	872	876	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1067	1071	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1124	1128	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1131	1135	0	ACATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1158	1162	0	ACATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1253	1257	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1357	1361	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1358	1362	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1424	1428	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1540	1544	0	AATGT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1550	1554	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1614	1618	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1628	1632	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1656	1660	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1675	1679	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1686	1690	0	AATGT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1732	1736	0	AAATT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1760	1764	0	AATTT	3.90625	3.51525
cg1018009	TNIK	GR-beta [T	1993	1997	0	AATGT	3.90625	3.51525
cg1018009	TNIK	XBP-1 [T0	1000	1005	0	CGTCAT	0.97656	0.94838
cg1018009	TNIK	XBP-1 [T0	1926	1931	0	ATGACT	0.97656	0.94838
cg1018009	TNIK	ENKTF-1	232	239	0	TGGCGC	0.12207	0.13179
cg1018009	TNIK	TFIID [T0	756	762	0	TTTTTTA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	757	763	0	TTTTTAA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	806	812	0	TTTAAA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	1034	1040	0	TAAAAA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	1045	1051	0	TAAAAA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	1430	1436	0	TTTTTAA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	1432	1438	0	TTTAAA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	1498	1504	0	TTTTCAA	1.09863	0.95175
cg1018009	TNIK	TFIID [T0	1631	1637	0	TTTTTGA	1.09863	0.95175
cg1018009	TNIK	GR-alpha [	15	19	0	CCTGT	7.8125	7.79817

cg1018009	TNIK	GR-alpha [	70	74	0	ACAGG	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	104	108	0	ACAGG	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	478	482	0	CCTGT	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	523	527	0	CCTAT	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1146	1150	0	CCTGT	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1273	1277	0	CCTGT	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1513	1517	0	ATAGG	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1588	1592	0	ACAGG	7.8125	7.79817
cg1018009	TNIK	GR-alpha [	1963	1967	0	CCTAT	7.8125	7.79817
cg1018009	TNIK	FOXP3 [T	315	320	0	CACAAC	1.46484	1.44953
cg1018009	TNIK	FOXP3 [T	1111	1116	0	GTTGTT	1.46484	1.44953
cg1018009	TNIK	PR B [T00	1950	1956	0	GACTGTT	0.36621	0.35051
cg1018009	TNIK	PR A [T01	1950	1956	0	GACTGTT	0.36621	0.35051
cg1018009	TNIK	HNF-3alph	1428	1435	0	TATTTTT	0.09155	0.07727
cg1018009	TNIK	C/EBPbeta	249	252	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	258	261	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	316	319	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	323	326	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	359	362	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	392	395	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	398	401	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	421	424	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	445	448	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	487	490	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	499	502	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	573	576	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	591	594	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	643	646	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	648	651	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	694	697	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	776	779	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	870	873	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1005	1008	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1065	1068	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1073	1076	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1075	1078	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1103	1106	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1109	1112	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1112	1115	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1127	1130	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1179	1182	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1184	1187	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1195	1198	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1205	1208	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1243	1246	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1385	1388	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1506	1509	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1534	1537	0	GCAA	15.625	15.26275

cg1018009	TNIK	C/EBPbeta	1659	1662	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1678	1681	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1713	1716	0	ACAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1742	1745	0	GCAA	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1763	1766	0	TTGT	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1790	1793	0	TTGC	15.625	15.26275
cg1018009	TNIK	C/EBPbeta	1921	1924	0	TTGT	15.625	15.26275
cg1018009	TNIK	YY1 [T00	47	50	0	CCAT	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	117	120	0	CCAT	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	231	234	0	ATGG	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	241	244	0	ATGG	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	298	301	0	CCAT	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	367	370	0	ATGG	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	401	404	0	ATGG	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	441	444	0	CCAT	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	626	629	0	CCAT	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	891	894	0	ATGG	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	934	937	0	ATGG	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	952	955	0	CCAT	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	1410	1413	0	ATGG	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	1582	1585	0	CCAT	7.8125	7.79459
cg1018009	TNIK	YY1 [T00	1584	1587	0	ATGG	7.8125	7.79459
cg1018009	TNIK	TFII-I [T0	851	856	0	CTTTCC	1.46484	1.48598
cg1018009	TNIK	TFII-I [T0	1443	1448	0	CTTTCC	1.46484	1.48598
cg1018009	TNIK	TFII-I [T0	1586	1591	0	GGACAG	1.46484	1.48598
cg1018009	TNIK	STAT4 [T	35	40	0	GGAAAT	0.48828	0.46235
cg1018009	TNIK	ER-alpha [	936	940	0	GGTCA	1.95312	1.99744
cg1018009	TNIK	GR [T050	695	701	0	CAAAAA	0.36621	0.33174
cg1018009	TNIK	GR [T050	1630	1636	0	TTTTTTG	0.36621	0.33174
cg1018009	TNIK	Pax-5 [T0	8	14	0	CCTGCC	1.09863	1.24633
cg1018009	TNIK	Pax-5 [T0	563	569	0	GGGCAG	1.09863	1.24633
cg1018009	TNIK	Pax-5 [T0	1143	1149	0	GGGCCT	1.09863	1.24633
cg1018009	TNIK	p53 [T006	8	14	0	CCTGCC	0.36621	0.40082
cg1018009	TNIK	p53 [T006	563	569	0	GGGCAG	0.36621	0.40082
cg1018009	TNIK	HNF-1A [	1661	1668	0	GTTAAT	0.24414	0.20853
cg2325954	TPRG1	HOXD9 [	1053	1062	9.979471	AATATT	0.2327	0.24089
cg2325954	TPRG1	HOXD10 [	1053	1062	9.979471	AATATT	0.2327	0.24089
cg2325954	TPRG1	STAT5A [	1063	1075	9.952027	ATTTTTC	0.01878	0.01918
cg2325954	TPRG1	c-Myb [T0	1415	1422	9.815171	TCAAGT	0.36621	0.3712
cg2325954	TPRG1	HOXD9 [	1867	1876	9.802084	AATATT	0.2327	0.24089
cg2325954	TPRG1	HOXD10 [	1867	1876	9.802084	AATATT	0.2327	0.24089
cg2325954	TPRG1	XBP-1 [T0	153	158	9.789909	ATGGCG	1.95312	1.95208
cg2325954	TPRG1	XBP-1 [T0	240	245	9.789909	ATGTCT	1.95312	1.95208
cg2325954	TPRG1	XBP-1 [T0	338	343	9.789909	ATGTCT	1.95312	1.95208
cg2325954	TPRG1	XBP-1 [T0	387	392	9.789909	AGACAT	1.95312	1.95208
cg2325954	TPRG1	XBP-1 [T0	1125	1130	9.789909	AGCCAT	1.95312	1.95208
cg2325954	TPRG1	XBP-1 [T0	1521	1526	9.789909	AGCCAT	1.95312	1.95208
cg2325954	TPRG1	XBP-1 [T0	1790	1795	9.789909	ATGTCT	1.95312	1.95208

cg2325954	TPRG1	XBP-1 [T	1854	1859	9.789909	AGCCAT	1.95312	1.95208
cg2325954	TPRG1	XBP-1 [T	1933	1938	9.789909	AGCCAT	1.95312	1.95208
cg2325954	TPRG1	NF-1 [T00	393	400	9.761671	TTGGAG	0.24414	0.24405
cg2325954	TPRG1	NF-1 [T00	812	819	9.761671	TTGGTT	0.24414	0.24405
cg2325954	TPRG1	PR B [T00	1307	1313	9.743489	AACACA	1.09863	1.10292
cg2325954	TPRG1	PR B [T00	1612	1618	9.743489	GGGTGT	1.09863	1.10292
cg2325954	TPRG1	PR A [T01	1307	1313	9.743489	AACACA	1.09863	1.10292
cg2325954	TPRG1	PR A [T01	1612	1618	9.743489	GGGTGT	1.09863	1.10292
cg2325954	TPRG1	LEF-1 [T0	1099	1106	9.72404	CTTTGT	0.21362	0.2139
cg2325954	TPRG1	NF-AT1 [	198	206	9.691726	GGAAAC	0.16785	0.1682
cg2325954	TPRG1	HNF-1C [	1060	1068	9.601936	GTTATT	0.19836	0.20229
cg2325954	TPRG1	HNF-1C [	873	881	9.576203	GTTAAC	0.19836	0.20229
cg2325954	TPRG1	TFIID [T0	246	252	9.552105	TTTCAC	1.46484	1.48472
cg2325954	TPRG1	TFIID [T0	848	854	9.552105	TGAGAA	1.46484	1.48472
cg2325954	TPRG1	TFIID [T0	1100	1106	9.552105	TTTGTC	1.46484	1.48472
cg2325954	TPRG1	TFIID [T0	1375	1381	9.552105	TGTCAA	1.46484	1.48472
cg2325954	TPRG1	TFIID [T0	1804	1810	9.552105	TTTGAC	1.46484	1.48472
cg2325954	TPRG1	TFII-I [T0	23	28	9.512894	GGAAAA	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	84	89	9.512894	TTTTCC	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	198	203	9.512894	GGAAAC	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	406	411	9.512894	GGAACG	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	615	620	9.512894	AAATCC	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	670	675	9.512894	CCTTCC	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	841	846	9.512894	GGATAA	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	1082	1087	9.512894	GGAATT	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	1116	1121	9.512894	CGTTCC	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	1384	1389	9.512894	TTATCC	7.32422	7.29728
cg2325954	TPRG1	TFII-I [T0	1683	1688	9.512894	GGATAC	7.32422	7.29728
cg2325954	TPRG1	FOXP3 [T	483	488	9.512894	GTTCTG	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	576	581	9.512894	AATAAC	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	589	594	9.512894	CCCAAC	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	680	685	9.512894	GTTGCT	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	842	847	9.512894	GATAAC	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	865	870	9.512894	GTTGCT	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	936	941	9.512894	GTTTAT	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	968	973	9.512894	GTTGCC	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	1060	1065	9.512894	GTTATT	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	1213	1218	9.512894	CATAAC	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	1290	1295	9.512894	ACCAAC	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	1368	1373	9.512894	GTTGCT	7.32422	7.35678
cg2325954	TPRG1	FOXP3 [T	1393	1398	9.512894	GTTTAT	7.32422	7.35678
cg2325954	TPRG1	c-Jun [T00	377	383	9.442241	GCTGTC	0.73242	0.73031
cg2325954	TPRG1	MAZ [T00	1672	1684	9.294691	TCTAGG	0.01425	0.014
cg2325954	TPRG1	c-Ets-1 [T	404	410	9.276861	TGGGAA	0.36621	0.36441
cg2325954	TPRG1	HNF-1C [	626	634	9.225924	CTTCTTA	0.12207	0.12495
cg2325954	TPRG1	LEF-1 [T0	1515	1522	9.099721	CTGCAA	0.54932	0.55326
cg2325954	TPRG1	c-Ets-1 [T	1080	1086	9.065503	ATGGAA	0.85449	0.85523
cg2325954	TPRG1	NF-AT1 [	983	991	9.042733	TTCATT	0.22888	0.22959

cg2325954	TPRG1	NF-AT1 [T	1717	1725	9.042733	CACATT	0.22888	0.22959
cg2325954	TPRG1	GR [T050	412	418	8.971049	GTATTTC	0.61035	0.61632
cg2325954	TPRG1	GR [T050	808	814	8.971049	GTGTTTC	0.61035	0.61632
cg2325954	TPRG1	GR [T050	1135	1141	8.971049	CAAATA	0.61035	0.61632
cg2325954	TPRG1	GR [T050	1518	1524	8.971049	CAAAGC	0.61035	0.61632
cg2325954	TPRG1	GR [T050	1760	1766	8.971049	GTGTTTC	0.61035	0.61632
cg2325954	TPRG1	c-Ets-1 [T	993	999	8.937416	GTGGAA	0.85449	0.85523
cg2325954	TPRG1	Elk-1 [T00	913	921	8.931691	CGGTGG	0.24414	0.24034
cg2325954	TPRG1	c-Ets-2 [T	672	680	8.912323	TTCCTGC	0.27466	0.27495
cg2325954	TPRG1	GATA-2 [	475	483	8.888889	AGATAC	0.22888	0.22993
cg2325954	TPRG1	XBP-1 [T	168	173	8.75604	ATGAGC	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	732	737	8.75604	GCTCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	821	826	8.75604	TTTCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1272	1277	8.75604	GTTCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1334	1339	8.75604	GTTCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1350	1355	8.75604	TTTCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1399	1404	8.75604	TCTCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1445	1450	8.75604	ATGATA	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1565	1570	8.75604	GATCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1630	1635	8.75604	ATGAGA	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1707	1712	8.75604	TATCAT	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1874	1879	8.75604	ATGATA	2.92969	2.9674
cg2325954	TPRG1	XBP-1 [T	1949	1954	8.75604	ATGATA	2.92969	2.9674
cg2325954	TPRG1	STAT1bet	1720	1729	8.695301	ATTTCCT	0.22316	0.22446
cg2325954	TPRG1	MAZ [T00	518	530	8.497316	ATTAGG	0.00525	0.00516
cg2325954	TPRG1	ATF [T00	895	906	8.419848	TACATG	0.07725	0.07717
cg2325954	TPRG1	HNF-3alph	773	780	8.343064	AATTTA	0.27466	0.28528
cg2325954	TPRG1	HNF-3alph	1827	1834	8.343064	TTAAAA	0.27466	0.28528
cg2325954	TPRG1	PR B [T00	285	291	8.338824	AACAGC	1.09863	1.10009
cg2325954	TPRG1	PR B [T00	632	638	8.338824	AACAGC	1.09863	1.10009
cg2325954	TPRG1	PR B [T00	1216	1222	8.338824	AACAGC	1.09863	1.10009
cg2325954	TPRG1	PR A [T01	285	291	8.338824	AACAGC	1.09863	1.10009
cg2325954	TPRG1	PR A [T01	632	638	8.338824	AACAGC	1.09863	1.10009
cg2325954	TPRG1	PR A [T01	1216	1222	8.338824	AACAGC	1.09863	1.10009
cg2325954	TPRG1	ATF3 [T0	899	906	8.313799	TGACGT	0.27466	0.27431
cg2325954	TPRG1	ATF3 [T0	1372	1379	8.313799	CTATGT	0.27466	0.27431
cg2325954	TPRG1	PXR-1:RX	181	188	8.304332	AGTGTT	0.12207	0.12266
cg2325954	TPRG1	GR-alpha [	13	17	8.281568	CAAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	118	122	8.281568	CCTCC	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	176	180	8.281568	GGAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	306	310	8.281568	CCTTC	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	349	353	8.281568	CCTCC	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	419	423	8.281568	CCTCG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	523	527	8.281568	GGAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	653	657	8.281568	CCTCC	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	670	674	8.281568	CCTTC	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	687	691	8.281568	CCTCC	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	829	833	8.281568	CCTTG	7.8125	7.72956

cg2325954	TPRG1	GR-alpha [	858	862	8.281568	CAAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	905	909	8.281568	CCTCG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	1045	1049	8.281568	GAAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	1120	1124	8.281568	CCTCC	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	1436	1440	8.281568	GAAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	1658	1662	8.281568	CAAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	1677	1681	8.281568	GGAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	1920	1924	8.281568	GGAGG	7.8125	7.72956
cg2325954	TPRG1	GR-alpha [	1939	1943	8.281568	GGAGG	7.8125	7.72956
cg2325954	TPRG1	c-Jun [T00	948	954	8.242207	TGACCT	0.48828	0.49076
cg2325954	TPRG1	c-Jun [T00	1007	1013	8.242207	TGACCT	0.48828	0.49076
cg2325954	TPRG1	p53 [T006	1661	1667	8.208781	GGGGCC	0.48828	0.47377
cg2325954	TPRG1	p53 [T006	1662	1668	8.208781	GGGCCC	0.48828	0.47377
cg2325954	TPRG1	ENKTF-1	962	969	8.19852	TGGCGA	0.73242	0.71737
cg2325954	TPRG1	PXR-1:RX	230	237	8.180749	TGAACA	0.12207	0.12407
cg2325954	TPRG1	c-Ets-1 [T	1021	1027	8.116854	CTGGAA	0.24414	0.2425
cg2325954	TPRG1	VDR [T00	1334	1342	8.079962	GTTCAT	0.24414	0.24712
cg2325954	TPRG1	GR-alpha [	65	69	8.073878	GCAGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	103	107	8.073878	CCTAC	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	121	125	8.073878	CCTGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	141	145	8.073878	GCAGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	321	325	8.073878	CCAGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	352	356	8.073878	CCTGC	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	472	476	8.073878	CCTAG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	506	510	8.073878	CCTGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	619	623	8.073878	CCTGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	674	678	8.073878	CCTGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	921	925	8.073878	GCAGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1020	1024	8.073878	CCTGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1260	1264	8.073878	CCTAC	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1388	1392	8.073878	CCTAG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1389	1393	8.073878	CTAGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1599	1603	8.073878	CCTAC	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1673	1677	8.073878	CTAGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1885	1889	8.073878	GTAGG	7.8125	7.72238
cg2325954	TPRG1	GR-alpha [	1962	1966	8.073878	CCTGC	7.8125	7.72238
cg2325954	TPRG1	Pax-5 [T0	112	118	8.014558	TGTGCC	2.19727	2.14502
cg2325954	TPRG1	Pax-5 [T0	361	367	8.014558	TGTGCC	2.19727	2.14502
cg2325954	TPRG1	Pax-5 [T0	528	534	8.014558	GGGCAT	2.19727	2.14502
cg2325954	TPRG1	Pax-5 [T0	1661	1667	8.014558	GGGGCC	2.19727	2.14502
cg2325954	TPRG1	Pax-5 [T0	1662	1668	8.014558	GGGCCC	2.19727	2.14502
cg2325954	TPRG1	TFIID [T0	430	436	8.014558	TTTCTA	2.19727	2.24348
cg2325954	TPRG1	TFIID [T0	768	774	8.014558	TTACAA	2.19727	2.24348
cg2325954	TPRG1	TFIID [T0	821	827	8.014558	TTTCATA	2.19727	2.24348
cg2325954	TPRG1	TFIID [T0	1323	1329	8.014558	TTTCAG	2.19727	2.24348
cg2325954	TPRG1	TFIID [T0	1431	1437	8.014558	TTTCTGA	2.19727	2.24348
cg2325954	TPRG1	TFIID [T0	1485	1491	8.014558	TCAGAA	2.19727	2.24348
cg2325954	TPRG1	TFIID [T0	1721	1727	8.014558	TTTCCTA	2.19727	2.24348

cg2325954	TPRG1	TFIID [T0	1768	1774	8.014558	TTTCAG	2.19727	2.24348
cg2325954	TPRG1	TFIID [T0	1833	1839	8.014558	TCACAA	2.19727	2.24348
cg2325954	TPRG1	MEF-2A [	1062	1072	7.982343	TATTTTT	0.04005	0.04149
cg2325954	TPRG1	c-Ets-2 [T	1018	1026	7.84116	TTCCTGC	0.32043	0.32298
cg2325954	TPRG1	GATA-2 [	743	751	7.777778	TCTATAT	0.30518	0.30758
cg2325954	TPRG1	GATA-2 [	1703	1711	7.777778	ACAATA	0.30518	0.30758
cg2325954	TPRG1	c-Ets-2 [T	988	996	7.76635	TTCCTGT	0.32043	0.32298
cg2325954	TPRG1	c-Myb [T0	551	558	7.739476	TAACTG	0.42725	0.43114
cg2325954	TPRG1	c-Myb [T0	844	851	7.739476	TAACTG	0.42725	0.43114
cg2325954	TPRG1	c-Myb [T0	869	876	7.739476	CTCAGT	0.42725	0.43114
cg2325954	TPRG1	IRF-1 [T0	194	202	7.732782	CGCTGG	0.14496	0.14449
cg2325954	TPRG1	NFI/CTF [	389	396	7.587343	ACATTT	0.36621	0.36674
cg2325954	TPRG1	c-Myb [T0	964	971	7.587189	GCGAGT	0.42725	0.43114
cg2325954	TPRG1	c-Jun [T00	899	905	7.538568	TGACGT	0.48828	0.48775
cg2325954	TPRG1	GR [T050	283	289	7.527031	CAAACA	1.83105	1.86007
cg2325954	TPRG1	GR [T050	356	362	7.527031	CCTTTT	1.83105	1.86007
cg2325954	TPRG1	GR [T050	1131	1137	7.527031	CAAACA	1.83105	1.86007
cg2325954	TPRG1	GR [T050	1221	1227	7.527031	CATTTT	1.83105	1.86007
cg2325954	TPRG1	GR [T050	1470	1476	7.527031	CAAAAT	1.83105	1.86007
cg2325954	TPRG1	GR [T050	1836	1842	7.527031	CAAATA	1.83105	1.86007
cg2325954	TPRG1	C/EBPalph	752	758	7.465744	TGCAAT	0.48828	0.49653
cg2325954	TPRG1	C/EBPalph	1577	1583	7.465744	TTCAAT	0.48828	0.49653
cg2325954	TPRG1	IRF-1 [T0	19	27	7.387351	TTGGGG	0.14496	0.14449
cg2325954	TPRG1	NF-kappa	1681	1691	7.340726	GGGGAT	0.04435	0.04347
cg2325954	TPRG1	E2F-1 [T0	646	653	7.336545	AATGCC	0.45776	0.44878
cg2325954	TPRG1	p53 [T006	633	639	7.266844	ACAGCC	0.73242	0.7186
cg2325954	TPRG1	SRY [T00	1099	1107	7.175614	CTTTGT	0.30518	0.30739
cg2325954	TPRG1	XBP-1 [T	735	740	7.172312	CATCAT	2.92969	2.97018
cg2325954	TPRG1	XBP-1 [T	940	945	7.172312	ATTCAT	2.92969	2.97018
cg2325954	TPRG1	XBP-1 [T	982	987	7.172312	CTTCAT	2.92969	2.97018
cg2325954	TPRG1	XBP-1 [T	1002	1007	7.172312	CTTCAT	2.92969	2.97018
cg2325954	TPRG1	XBP-1 [T	1168	1173	7.172312	ATGAAG	2.92969	2.97018
cg2325954	TPRG1	XBP-1 [T	1204	1209	7.172312	AATCAT	2.92969	2.97018
cg2325954	TPRG1	XBP-1 [T	1568	1573	7.172312	CATCAT	2.92969	2.97018
cg2325954	TPRG1	XBP-1 [T	1857	1862	7.172312	CATCAT	2.92969	2.97018
cg2325954	TPRG1	NF-AT1 [	23	31	7.095752	GGAAAA	0.15259	0.1548
cg2325954	TPRG1	TFIID [T0	1359	1365	7.082373	TTTAGC	0.12207	0.12407
cg2325954	TPRG1	NF-AT2 [	80	89	7.008591	GAGGTT	0.04578	0.04634
cg2325954	TPRG1	HNF-3alph	428	435	7.000129	TATTTCT	0.82397	0.84946
cg2325954	TPRG1	HNF-3alph	1062	1069	7.000129	TATTTTT	0.82397	0.84946
cg2325954	TPRG1	HNF-3alph	1547	1554	7.000129	ACTAAA	0.82397	0.84946
cg2325954	TPRG1	HNF-3alph	1586	1593	7.000129	TATTTAT	0.82397	0.84946
cg2325954	TPRG1	HNF-3alph	1590	1597	7.000129	TATTTAT	0.82397	0.84946
cg2325954	TPRG1	c-Ets-1 [T	21	27	6.943262	GGGGAA	0.73242	0.73099
cg2325954	TPRG1	ENKTF-1	453	460	6.942764	TGGCGT	1.46484	1.44228
cg2325954	TPRG1	ENKTF-1	557	564	6.942764	TGGCTG	1.46484	1.44228
cg2325954	TPRG1	c-Jun [T00	1466	1472	6.856451	TGACCA	0.73242	0.73173
cg2325954	TPRG1	PEA3 [T0	1946	1954	6.824411	TGGATG	0.22888	0.22933

cg2325954	TPRG1	c-Jun [T00	1531	1537	6.787369	TGACAG	0.73242	0.73173
cg2325954	TPRG1	C/EBPalph	1842	1848	6.786177	TCCAAT	0.73242	0.74337
cg2325954	TPRG1	c-Ets-2 [T	1722	1730	6.769996	TTCCTA	0.03052	0.03102
cg2325954	TPRG1	NF-1 [T00	1150	1157	6.722386	TTGGCC	0.24414	0.24147
cg2325954	TPRG1	c-Myb [T0	861	868	6.719843	GGTAGT	0.30518	0.3056
cg2325954	TPRG1	c-Myb [T0	1991	1998	6.719843	GGGAGT	0.30518	0.3056
cg2325954	TPRG1	PXR-1:RX	1331	1338	6.668182	TGTGTT	0.24414	0.24672
cg2325954	TPRG1	c-Jun [T00	1501	1507	6.668031	TGACTT	0.61035	0.60769
cg2325954	TPRG1	HNF-1B [	872	880	6.604089	AGTTAA	0.04578	0.04691
cg2325954	TPRG1	TFII-I [T0	179	184	6.581441	GGAGTG	0.97656	0.97366
cg2325954	TPRG1	TFII-I [T0	345	350	6.581441	CACTCC	0.97656	0.97366
cg2325954	TPRG1	TFII-I [T0	1880	1885	6.581441	GGAGTG	0.97656	0.97366
cg2325954	TPRG1	FOXP3 [T	489	494	6.581441	TAAAAC	0.97656	0.99397
cg2325954	TPRG1	FOXP3 [T	611	616	6.581441	GTTGAA	0.97656	0.99397
cg2325954	TPRG1	FOXP3 [T	1086	1091	6.581441	TTCAAC	0.97656	0.99397
cg2325954	TPRG1	XBP-1 [T	93	98	6.478682	TGGCAT	0.97656	0.97062
cg2325954	TPRG1	XBP-1 [T	528	533	6.478682	GGGCAT	0.97656	0.97062
cg2325954	TPRG1	XBP-1 [T	796	801	6.478682	ATGCCA	0.97656	0.97062
cg2325954	TPRG1	C/EBPalph	1649	1655	6.460799	CATTGC	0.48828	0.49071
cg2325954	TPRG1	GR-alpha [	79	83	6.263098	TGAGG	3.90625	3.91061
cg2325954	TPRG1	GR-alpha [	792	796	6.263098	CCTTA	3.90625	3.91061
cg2325954	TPRG1	GR-alpha [	1010	1014	6.263098	CCTCA	3.90625	3.91061
cg2325954	TPRG1	GR-alpha [	1483	1487	6.263098	CCTCA	3.90625	3.91061
cg2325954	TPRG1	GR-alpha [	1620	1624	6.263098	TGAGG	3.90625	3.91061
cg2325954	TPRG1	GR-alpha [	1655	1659	6.263098	CCTCA	3.90625	3.91061
cg2325954	TPRG1	GR-alpha [	1890	1894	6.263098	CCTCA	3.90625	3.91061
cg2325954	TPRG1	GR-alpha [	1969	1973	6.263098	CCTCA	3.90625	3.91061
cg2325954	TPRG1	c-Myb [T0	1268	1275	6.259888	TGCAGT	0.30518	0.3056
cg2325954	TPRG1	c-Myb [T0	1455	1462	6.157321	CAACTT	0.21362	0.21535
cg2325954	TPRG1	c-Jun [T00	1100	1106	6.152811	TTTGTC	0.36621	0.37082
cg2325954	TPRG1	GR-alpha [	203	207	6.055408	CCTAA	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	372	376	6.055408	CCTGA	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	519	523	6.055408	TTAGG	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	546	550	6.055408	TCAGG	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	713	717	6.055408	TTAGG	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	956	960	6.055408	CCTGA	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	1182	1186	6.055408	TTAGG	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	1318	1322	6.055408	TTAGG	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	1538	1542	6.055408	TCAGG	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	1724	1728	6.055408	CCTAA	3.90625	3.9065
cg2325954	TPRG1	GR-alpha [	1892	1896	6.055408	TCAGG	3.90625	3.9065
cg2325954	TPRG1	c-Ets-1 [T	196	202	6.039428	CTGGAA	0.36621	0.36731
cg2325954	TPRG1	STAT4 [T	670	675	5.882353	CCTTCC	0.48828	0.48408
cg2325954	TPRG1	IRF-1 [T0	987	995	5.861409	TTTCCT	0.16785	0.16909
cg2325954	TPRG1	C/EBPalph	435	441	5.850545	AATTGC	0.97656	0.99
cg2325954	TPRG1	IRF-1 [T0	1721	1729	5.823972	TTTCCTA	0.16785	0.16909
cg2325954	TPRG1	C/EBPalph	1702	1708	5.781231	GACAAT	0.97656	0.99
cg2325954	TPRG1	VDR [T00	1272	1280	5.771401	GTTCAT	0.42725	0.42999

cg2325954	TPRG1	POU2F2 (	1982	1992	5.731804	TGTATT	0.06437	0.06564
cg2325954	TPRG1	RXR-alph	1612	1618	5.715466	GGGTGT	0.61035	0.6044
cg2325954	TPRG1	ENKTF-1	1518	1525	5.687009	CAAAGC	0.73242	0.7249
cg2325954	TPRG1	c-Ets-2 [T	1726	1734	5.624023	TAATAG	0.01526	0.0156
cg2325954	TPRG1	HNF-1A [	871	878	5.610392	CAGTTA	0.24414	0.2469
cg2325954	TPRG1	c-Jun [T00	469	475	5.587335	TGACCT	0.48828	0.48665
cg2325954	TPRG1	AP-2alpha	1510	1515	5.568965	ATAGGC	0.48828	0.4878
cg2325954	TPRG1	AP-2alpha	1952	1957	5.568965	ATAGGC	0.48828	0.4878
cg2325954	TPRG1	C/EBPalph	1139	1145	5.565669	TACAAT	0.73242	0.74391
cg2325954	TPRG1	NFI/CTF [	15	22	5.558661	AGGCTT	0.54932	0.55038
cg2325954	TPRG1	NFI/CTF [	808	815	5.558661	GTGTTT	0.54932	0.55038
cg2325954	TPRG1	Pax-5 [T0	436	442	5.544826	ATTGCC	0.73242	0.72046
cg2325954	TPRG1	Pax-5 [T0	1650	1656	5.544826	ATTGCC	0.73242	0.72046
cg2325954	TPRG1	TFIID [T0	1181	1187	5.544826	TTTAGG	0.73242	0.75085
cg2325954	TPRG1	NF-AT1 [	197	206	5.512555	TGGAAA	0.05913	0.05965
cg2325954	TPRG1	C/EBPalph	295	301	5.455853	CATTGC	0.73242	0.74391
cg2325954	TPRG1	C/EBPalph	232	238	5.38654	AACAAT	0.73242	0.74391
cg2325954	TPRG1	C/EBPalph	1090	1096	5.38654	ACCAAT	0.73242	0.74391
cg2325954	TPRG1	RXR-alph	367	373	5.271235	CCCACC	0.61035	0.6044
cg2325954	TPRG1	AP-2alpha	355	360	5.100982	GCCTTT	0.97656	0.97567
cg2325954	TPRG1	GR-beta [	128	132	5.042296	GTATT	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	412	416	5.042296	GTATT	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	516	520	5.042296	GTATT	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	616	620	5.042296	AATCC	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	695	699	5.042296	GGATT	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	1015	1019	5.042296	GTATT	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	1137	1141	5.042296	AATAC	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	1254	1258	5.042296	AATCC	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	1541	1545	5.042296	GGATT	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	1585	1589	5.042296	GTATT	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	1733	1737	5.042296	AATAC	3.90625	3.95351
cg2325954	TPRG1	GR-beta [	1983	1987	5.042296	GTATT	3.90625	3.95351
cg2325954	TPRG1	C/EBPalph	1193	1199	5.024728	GATTGA	0.97656	0.99332
cg2325954	TPRG1	C/EBPalph	1201	1207	5.024728	TTCAAT	0.97656	0.99332
cg2325954	TPRG1	XBP-1 [T	222	227	4.894955	ATGCCG	0.97656	0.96979
cg2325954	TPRG1	XBP-1 [T	647	652	4.894955	ATGCCG	0.97656	0.96979
cg2325954	TPRG1	XBP-1 [T	1922	1927	4.894955	AGGCAT	0.97656	0.96979
cg2325954	TPRG1	c-Jun [T00	1373	1379	4.883696	TATGTC	0.61035	0.61057
cg2325954	TPRG1	GCF [T00	1102	1110	4.846987	TGTCAG	0.27466	0.26486
cg2325954	TPRG1	C/EBPalph	235	241	4.845599	AATTGA	0.97656	0.99332
cg2325954	TPRG1	HNF-3alph	1282	1289	4.842999	TATTTA	0.09155	0.09582
cg2325954	TPRG1	HNF-1A [	873	880	4.828753	GTTAAC	0.36621	0.37179
cg2325954	TPRG1	c-Ets-1 [T	915	921	4.782565	GTGGAA	0.48828	0.49031
cg2325954	TPRG1	C/EBPalph	573	579	4.776286	ACCAAT	0.97656	0.99332
cg2325954	TPRG1	TFII-I [T0	825	830	4.756447	ATATCC	2.92969	2.93695
cg2325954	TPRG1	TFII-I [T0	931	936	4.756447	GGACTG	2.92969	2.93695
cg2325954	TPRG1	TFII-I [T0	986	991	4.756447	ATTTCC	2.92969	2.93695
cg2325954	TPRG1	TFII-I [T0	1253	1258	4.756447	CAATCC	2.92969	2.93695

cg2325954	TPRG1	TFII-I [T0	1720	1725	4.756447	ATTTCC	2.92969	2.93695
cg2325954	TPRG1	TFII-I [T0	1839	1844	4.756447	ATATCC	2.92969	2.93695
cg2325954	TPRG1	TFII-I [T0	1942	1947	4.756447	GGAATG	2.92969	2.93695
cg2325954	TPRG1	FOXP3 [T	24	29	4.756447	GAAAAC	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	83	88	4.756447	GTTTTC	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	447	452	4.756447	GTTTTG	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	883	888	4.756447	GTTGAG	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	1227	1232	4.756447	GTTTTC	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	1453	1458	4.756447	CTCAAC	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	1478	1483	4.756447	AAAAAC	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	1616	1621	4.756447	GTTTTG	2.92969	2.96063
cg2325954	TPRG1	FOXP3 [T	1766	1771	4.756447	GTTTTC	2.92969	2.96063
cg2325954	TPRG1	c-Ets-1 [T	85	91	4.74411	TTTCCG	0.85449	0.85764
cg2325954	TPRG1	HNF-1A [	627	634	4.684871	TTCTTA	0.12207	0.12485
cg2325954	TPRG1	ATF-2 [T0	898	907	4.623667	ATGACG	0.03815	0.03833
cg2325954	TPRG1	VDR [T00	184	192	4.617121	GTTCAG	0.37384	0.37445
cg2325954	TPRG1	c-Ets-1 [T	1729	1735	4.539113	TAGGAA	0.85449	0.85764
cg2325954	TPRG1	STAT4 [T	1	6	4.411765	GGAAGA	1.95312	1.94235
cg2325954	TPRG1	STAT4 [T	406	411	4.411765	GGAACG	1.95312	1.94235
cg2325954	TPRG1	STAT4 [T	917	922	4.411765	GGAAGC	1.95312	1.94235
cg2325954	TPRG1	STAT4 [T	1116	1121	4.411765	CGTTCC	1.95312	1.94235
cg2325954	TPRG1	STAT4 [T	1407	1412	4.411765	GCTTCC	1.95312	1.94235
cg2325954	TPRG1	STAT4 [T	1942	1947	4.411765	GGAATG	1.95312	1.94235
cg2325954	TPRG1	PEA3 [T0	1976	1984	4.30818	TGGATG	0.13733	0.13791
cg2325954	TPRG1	c-Ets-1 [T	1940	1946	4.282938	GAGGAA	0.85449	0.85764
cg2325954	TPRG1	AP-2alpha	1885	1890	4.211849	GTAGGC	0.97656	0.96469
cg2325954	TPRG1	GR-beta [	10	14	4.201913	AATCA	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	271	275	4.201913	AATAG	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	427	431	4.201913	TTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	535	539	4.201913	AATCA	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	576	580	4.201913	AATAA	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	938	942	4.201913	TTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	997	1001	4.201913	AATCG	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1061	1065	4.201913	TTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1146	1150	4.201913	TGATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1204	1208	4.201913	AATCA	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1281	1285	4.201913	TTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1347	1351	4.201913	CTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1395	1399	4.201913	TTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1551	1555	4.201913	AATAG	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1589	1593	4.201913	TTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1593	1597	4.201913	TTATT	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1637	1641	4.201913	AATAA	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1727	1731	4.201913	AATAG	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1831	1835	4.201913	AATCA	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1845	1849	4.201913	AATAA	7.8125	7.94607
cg2325954	TPRG1	GR-beta [	1849	1853	4.201913	AATCA	7.8125	7.94607
cg2325954	TPRG1	c-Ets-1 [T	1017	1023	4.154851	ATTCCT	0.24414	0.24526

cg2325954	TPRG1	C/EBPalph	7	13	4.019783	GGCAAT	0.48828	0.49358
cg2325954	TPRG1	RXR-alph	585	591	4.019014	TATACC	0.97656	0.9671
cg2325954	TPRG1	RXR-alph	1110	1116	4.019014	CACACC	0.97656	0.9671
cg2325954	TPRG1	Pax-5 [T0	633	639	4.007279	ACAGCC	1.09863	1.07975
cg2325954	TPRG1	TFIID [T0	381	387	4.007279	TCATAA	1.09863	1.13456
cg2325954	TPRG1	TFIID [T0	1070	1076	4.007279	TTTTAA	1.09863	1.13456
cg2325954	TPRG1	TFIID [T0	1592	1598	4.007279	TTTATTA	1.09863	1.13456
cg2325954	TPRG1	TFIID [T0	1859	1865	4.007279	TCATAA	1.09863	1.13456
cg2325954	TPRG1	AP-2alpha	13	18	3.970052	CAAGGC	0.97656	0.96469
cg2325954	TPRG1	GR [T050	446	452	3.763516	AGTTTT	0.73242	0.74251
cg2325954	TPRG1	GR [T050	1615	1621	3.763516	TGTTTT	0.73242	0.74251
cg2325954	TPRG1	AP-2alpha	669	674	3.743866	GCCTTC	0.48828	0.48238
cg2325954	TPRG1	p53 [T006	436	442	3.728319	ATTGCC	0.73242	0.7189
cg2325954	TPRG1	p53 [T006	1650	1656	3.728319	ATTGCC	0.73242	0.7189
cg2325954	TPRG1	c-Ets-1 [T	815	821	3.71855	GTTCCT	0.61035	0.60765
cg2325954	TPRG1	PEA3 [T0	123	131	3.710864	TGGATG	0.09155	0.09258
cg2325954	TPRG1	c-Ets-1 [T	1117	1123	3.590463	GTTCCT	0.61035	0.60765
cg2325954	TPRG1	c-Myb [T0	971	978	3.438142	GCCAGT	0.12207	0.12203
cg2325954	TPRG1	GR-beta [	1053	1057	3.361531	AATAT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1054	1058	3.361531	ATATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1142	1146	3.361531	AATCT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1192	1196	3.361531	AGATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1342	1346	3.361531	AGATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1380	1384	3.361531	AATCT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1495	1499	3.361531	AGATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1556	1560	3.361531	ATATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1705	1709	3.361531	AATAT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1745	1749	3.361531	AGATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1838	1842	3.361531	AATAT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1867	1871	3.361531	AATAT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [	1868	1872	3.361531	ATATT	3.90625	3.99611
cg2325954	TPRG1	T3R-beta1	571	579	3.351341	TCACCA	0.27466	0.2755
cg2325954	TPRG1	PR B [T00	232	238	3.29756	AACAAT	0.24414	0.25122
cg2325954	TPRG1	PR B [T00	579	585	3.29756	AACATT	0.24414	0.25122
cg2325954	TPRG1	PR B [T00	1035	1041	3.29756	AACATT	0.24414	0.25122
cg2325954	TPRG1	PR A [T01	232	238	3.29756	AACAAT	0.24414	0.25122
cg2325954	TPRG1	PR A [T01	579	585	3.29756	AACATT	0.24414	0.25122
cg2325954	TPRG1	PR A [T01	1035	1041	3.29756	AACATT	0.24414	0.25122
cg2325954	TPRG1	AP-2alpha	4	9	3.229049	AGAGGC	0.48828	0.48238
cg2325954	TPRG1	AP-2alpha	40	45	3.229049	GCCTCT	0.48828	0.48238
cg2325954	TPRG1	TCF-4E [T	1516	1522	3.151193	TGCAAA	0.24414	0.24672
cg2325954	TPRG1	IRF-1 [T0	85	93	3.145547	TTTCCGT	0.07629	0.07756
cg2325954	TPRG1	NF-Y [T0	1840	1847	3.051543	TATCCA	0.06104	0.06218
cg2325954	TPRG1	p53 [T006	112	118	3.028543	TGTGCC	0.48828	0.47786
cg2325954	TPRG1	p53 [T006	361	367	3.028543	TGTGCC	0.48828	0.47786
cg2325954	TPRG1	C/EBPalph	1251	1257	3.014837	AGCAAT	0.48828	0.4911
cg2325954	TPRG1	COUP-TF	945	957	3.008869	TTGTGA	0.00119	0.00118
cg2325954	TPRG1	Elk-1 [T00	1408	1416	2.987643	CTTCCTT	0.07629	0.07656

cg2325954	TPRG1	C/EBPalp	943	949	2.981957	CATTGT	0.48828	0.4911
cg2325954	TPRG1	HOXD9 [	576	585	2.949288	AATAAC	0.02289	0.02401
cg2325954	TPRG1	HOXD10 [	576	585	2.949288	AATAAC	0.02289	0.02401
cg2325954	TPRG1	c-Ets-2 [T	816	824	2.945838	TTCCTTT	0.06104	0.06231
cg2325954	TPRG1	c-Ets-2 [T	1409	1417	2.945838	TTCCTTT	0.06104	0.06231
cg2325954	TPRG1	STAT4 [T	814	819	2.941176	GGTTCC	2.92969	2.929
cg2325954	TPRG1	STAT4 [T	995	1000	2.941176	GGAATC	2.92969	2.929
cg2325954	TPRG1	STAT4 [T	1016	1021	2.941176	TATTCC	2.92969	2.929
cg2325954	TPRG1	STAT4 [T	1731	1736	2.941176	GGAATA	2.92969	2.929
cg2325954	TPRG1	c-Ets-2 [T	1118	1126	2.715313	TTCCTC	0.07629	0.07593
cg2325954	TPRG1	c-Ets-2 [T	1937	1945	2.715313	ATGGAG	0.07629	0.07593
cg2325954	TPRG1	PXR-1:RX	1269	1276	2.577808	GCAGTT	0.12207	0.12266
cg2325954	TPRG1	AP-2alpha	1889	1894	2.550491	GCCTCA	0.48828	0.48266
cg2325954	TPRG1	RXR-alph	1048	1054	2.544678	GGGTGA	0.85449	0.84796
cg2325954	TPRG1	NF-AT1 [	81	89	2.449764	AGGTTT	0.09155	0.0926
cg2325954	TPRG1	RXR-alph	510	516	2.322562	GGGTCT	0.85449	0.84796
cg2325954	TPRG1	VDR [T00	226	234	2.308561	CGTGTG	0.10681	0.10609
cg2325954	TPRG1	Elk-1 [T00	671	679	2.299314	CTTCCT	0.09155	0.09114
cg2325954	TPRG1	GATA-1 [	207	212	2.176375	ACGATA	3.90625	3.92756
cg2325954	TPRG1	GATA-1 [	747	752	2.176375	TATCGT	3.90625	3.92756
cg2325954	TPRG1	GATA-1 [	826	831	2.176375	TATCCT	3.90625	3.92756
cg2325954	TPRG1	GATA-1 [	840	845	2.176375	TGGATA	3.90625	3.92756
cg2325954	TPRG1	GATA-1 [	1184	1189	2.176375	AGGATA	3.90625	3.92756
cg2325954	TPRG1	GATA-1 [	1385	1390	2.176375	TATCCT	3.90625	3.92756
cg2325954	TPRG1	GATA-1 [	1840	1845	2.176375	TATCCA	3.90625	3.92756
cg2325954	TPRG1	AP-2alpha	418	423	2.098119	GCCTCG	0.97656	0.95407
cg2325954	TPRG1	GATA-1 [	1682	1687	2.001358	GGGATA	3.90625	3.92756
cg2325954	TPRG1	AP-2alpha	652	657	1.871933	GCCTCC	0.97656	0.95407
cg2325954	TPRG1	AP-2alpha	1920	1925	1.871933	GGAGGC	0.97656	0.95407
cg2325954	TPRG1	TBP [T00	1285	1294	1.871542	TTTATA	0.18311	0.18942
cg2325954	TPRG1	C/EBPalp	422	428	1.830762	CGCAAT	0.48828	0.49438
cg2325954	TPRG1	TFII-I [T0	952	957	1.824994	CTCTCC	0.48828	0.48408
cg2325954	TPRG1	TFII-I [T0	1237	1242	1.824994	CTCTCC	0.48828	0.48408
cg2325954	TPRG1	c-Ets-1 [T	1721	1727	1.769212	TTTCCT	0.12207	0.12414
cg2325954	TPRG1	p53 [T006	528	534	1.758307	GGGCAT	0.36621	0.36261
cg2325954	TPRG1	GR-beta [	95	99	1.680765	GCATT	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	294	298	1.680765	GCATT	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	646	650	1.680765	AATGC	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	755	759	1.680765	AATGC	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	761	765	1.680765	AATTC	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1083	1087	1.680765	GAATT	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1084	1088	1.680765	AATTC	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1178	1182	1.680765	GAATT	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1199	1203	1.680765	AATTC	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1220	1224	1.680765	GCATT	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1428	1432	1.680765	GCATT	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1575	1579	1.680765	AATTC	3.90625	3.94936
cg2325954	TPRG1	GR-beta [	1648	1652	1.680765	GCATT	3.90625	3.94936

cg2325954	TPRG1	C/EBPbeta	19	22	1.639871	TTGG	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	393	396	1.639871	TTGG	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	574	577	1.639871	CCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	590	593	1.639871	CCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	812	815	1.639871	TTGG	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1091	1094	1.639871	CCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1150	1153	1.639871	TTGG	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1291	1294	1.639871	CCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1469	1472	1.639871	CCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1843	1846	1.639871	CCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1918	1921	1.639871	TTGG	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1996	1999	1.639871	TTGG	15.625	15.72563
cg2325954	TPRG1	XBP-1 [T	379	384	1.583727	TGTCAT	0.97656	0.98146
cg2325954	TPRG1	XBP-1 [T	1006	1011	1.583727	ATGACC	0.97656	0.98146
cg2325954	TPRG1	XBP-1 [T	1465	1470	1.583727	ATGACC	0.97656	0.98146
cg2325954	TPRG1	XBP-1 [T	1530	1535	1.583727	ATGACA	0.97656	0.98146
cg2325954	TPRG1	Pax-5 [T0	259	265	1.537547	CTTGCC	0.73242	0.71311
cg2325954	TPRG1	TFIID [T0	487	493	1.537547	TGTAAA	0.73242	0.75096
cg2325954	TPRG1	TFIID [T0	1041	1047	1.537547	TTTTGA	0.73242	0.75096
cg2325954	TPRG1	NF-Y [T0	571	578	1.51343	TCACCA	0.18311	0.18459
cg2325954	TPRG1	STAT4 [T	23	28	1.470588	GGAAAA	1.95312	1.96333
cg2325954	TPRG1	STAT4 [T	84	89	1.470588	TTTTCC	1.95312	1.96333
cg2325954	TPRG1	STAT4 [T	198	203	1.470588	GGAAAC	1.95312	1.96333
cg2325954	TPRG1	STAT4 [T	1023	1028	1.470588	GGAACT	1.95312	1.96333
cg2325954	TPRG1	STAT4 [T	1082	1087	1.470588	GGAATT	1.95312	1.96333
cg2325954	TPRG1	PR B [T00	180	186	1.404665	GAGTGT	0.36621	0.37023
cg2325954	TPRG1	PR A [T01	180	186	1.404665	GAGTGT	0.36621	0.37023
cg2325954	TPRG1	c-Ets-1 [T	987	993	1.384951	TTTCCT	0.36621	0.36952
cg2325954	TPRG1	C/EBPbeta	12	15	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	237	240	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	282	285	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	542	545	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	612	615	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	785	788	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	857	860	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	884	887	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1043	1046	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1087	1090	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1130	1133	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1195	1198	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1202	1205	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1377	1380	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1415	1418	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1454	1457	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1578	1581	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1619	1622	1.366559	TTGA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1657	1660	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	C/EBPbeta	1805	1808	1.366559	TTGA	15.625	15.72563

cg2325954	TPRG1	C/EBPbeta	1851	1854	1.366559	TCAA	15.625	15.72563
cg2325954	TPRG1	HNF-3alph	267	274	1.342935	TTAAAA	0.03052	0.03194
cg2325954	TPRG1	NF-Y [T0	1088	1095	1.285795	CAACCA	0.18311	0.18459
cg2325954	TPRG1	ENKTF-1	154	161	1.255756	TGGCGG	0.24414	0.23904
cg2325954	TPRG1	GATA-1 [	1445	1450	1.038567	ATGATA	1.95312	1.98662
cg2325954	TPRG1	GATA-1 [	1707	1712	1.038567	TATCAT	1.95312	1.98662
cg2325954	TPRG1	GATA-1 [	1874	1879	1.038567	ATGATA	1.95312	1.98662
cg2325954	TPRG1	GATA-1 [	1949	1954	1.038567	ATGATA	1.95312	1.98662
cg2325954	TPRG1	CREB [T0	899	907	0.989089	TGACGT	0.05341	0.05293
cg2325954	TPRG1	TBP [T007	583	592	0.935771	TTTATAC	0.12207	0.12628
cg2325954	TPRG1	GR-beta [T	211	215	0.840383	TAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	212	216	0.840383	AATTA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	234	238	0.840383	CAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	235	239	0.840383	AATTG	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	424	428	0.840383	CAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	425	429	0.840383	AATTA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	434	438	0.840383	TAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	435	439	0.840383	AATTG	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	760	764	0.840383	TAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	942	946	0.840383	TCATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	984	988	0.840383	TCATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1079	1083	0.840383	AATGG	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1092	1096	0.840383	CAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1167	1171	0.840383	AATGA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1336	1340	0.840383	TCATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1352	1356	0.840383	TCATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1444	1448	0.840383	AATGA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1473	1477	0.840383	AATTA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1523	1527	0.840383	CCATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1529	1533	0.840383	AATGA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1561	1565	0.840383	AATGG	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1570	1574	0.840383	TCATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1574	1578	0.840383	TAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1873	1877	0.840383	AATGA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1905	1909	0.840383	TAATT	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1906	1910	0.840383	AATTA	7.8125	7.94706
cg2325954	TPRG1	GR-beta [T	1944	1948	0.840383	AATGG	7.8125	7.94706
cg2325954	TPRG1	AP-2alpha	1892	1897	0.678558	TCAGGC	0.48828	0.48199
cg2325954	TPRG1	C/EBPalph	1746	1752	0.540941	GATTGT	0.24414	0.24507
cg2325954	TPRG1	GATA-1 [	474	479	0.280028	TAGATA	0.97656	0.99875
cg2325954	TPRG1	GATA-1 [	778	783	0.280028	TATCTT	0.97656	0.99875
cg2325954	TPRG1	GATA-1 [	1490	1495	0.280028	AAGATA	0.97656	0.99875
cg2325954	TPRG1	GATA-1 [	1553	1558	0.280028	TAGATA	0.97656	0.99875
cg2325954	TPRG1	c-Ets-1 [T	1408	1414	0.256174	CTTCCTT	0.24414	0.24569
cg2325954	TPRG1	AP-2alpha	321	326	0.226186	CCAGGC	0.97656	0.95305
cg2325954	TPRG1	AP-2alpha	505	510	0.226186	GCCTGG	0.97656	0.95305
cg2325954	TPRG1	p53 [T006	259	265	0.211706	CTTGCC	0.36621	0.35912
cg2325954	TPRG1	GR-alpha [	4	8	0.207689	AGAGG	7.8125	7.81264

cg2325954	TPRG1	GR-alpha [	41	45	0.207689	CCTCT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	264	268	0.207689	CCTTT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	356	360	0.207689	CCTTT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	690	694	0.207689	CCTCT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	818	822	0.207689	CCTTT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	928	932	0.207689	AAAGG	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	951	955	0.207689	CCTCT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	1241	1245	0.207689	CCTTT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	1411	1415	0.207689	CCTTT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	1988	1992	0.207689	AGAGG	7.8125	7.81264
cg2325954	TPRG1	GATA-1 [	1773	1778	0.105011	GAGATA	0.97656	0.98738
cg2325954	TPRG1	GR-alpha [	441	445	0	CCTGT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	720	724	0	CCTGT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	990	994	0	CCTGT	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	1510	1514	0	ATAGG	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	1728	1732	0	ATAGG	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	1877	1881	0	ATAGG	7.8125	7.81264
cg2325954	TPRG1	GR-alpha [	1952	1956	0	ATAGG	7.8125	7.81264
cg2325954	TPRG1	AP-2alpha	141	146	0	GCAGGC	0.97656	0.95305
cg2325954	TPRG1	XBP-1 [T0	898	903	0	ATGACG	0.97656	0.98127
cg2325954	TPRG1	XBP-1 [T0	1500	1505	0	ATGACT	0.97656	0.98127
cg2325954	TPRG1	TFII-I [T0	1185	1190	0	GGATAG	1.46484	1.45997
cg2325954	TPRG1	STAT4 [T	986	991	0	ATTTCC	0.48828	0.49387
cg2325954	TPRG1	STAT4 [T	1720	1725	0	ATTTCC	0.48828	0.49387
cg2325954	TPRG1	c-Ets-1 [T0	671	677	0	CTTCCTC	0.24414	0.2429
cg2325954	TPRG1	YY1 [T00	153	156	0	ATGG	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	218	221	0	ATGG	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	566	569	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	599	602	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	701	704	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1080	1083	0	ATGG	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1127	1130	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1523	1526	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1562	1565	0	ATGG	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1669	1672	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1856	1859	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1935	1938	0	CCAT	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1937	1940	0	ATGG	7.8125	7.81711
cg2325954	TPRG1	YY1 [T00	1945	1948	0	ATGG	7.8125	7.81711
cg2325954	TPRG1	ER-alpha [	469	473	0	TGACC	1.95312	1.9404
cg2325954	TPRG1	ER-alpha [	948	952	0	TGACC	1.95312	1.9404
cg2325954	TPRG1	ER-alpha [	1007	1011	0	TGACC	1.95312	1.9404
cg2325954	TPRG1	ER-alpha [	1466	1470	0	TGACC	1.95312	1.9404
cg2325954	TPRG1	ER-alpha [	1738	1742	0	TGACC	1.95312	1.9404
cg2325954	TPRG1	GATA-1 [	1423	1428	0	TATCTG	0.97656	0.98738
cg2325954	TPRG1	GATA-1 [	1604	1609	0	TATCTG	0.97656	0.98738
cg2325954	TPRG1	C/EBPbeta	8	11	0	GCAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	38	41	0	TTGC	15.625	15.71349

cg2325954	TPRG1	C/EBPbeta	111	114	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	233	236	0	ACAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	260	263	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	297	300	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	360	363	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	416	419	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	423	426	0	GCAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	437	440	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	450	453	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	609	612	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	681	684	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	710	713	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	753	756	0	GCAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	770	773	0	ACAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	831	834	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	866	869	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	945	948	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	969	972	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	977	980	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1033	1036	0	ACAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1101	1104	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1134	1137	0	ACAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1140	1143	0	ACAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1225	1228	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1252	1255	0	GCAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1265	1268	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1314	1317	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1369	1372	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1505	1508	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1517	1520	0	GCAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1651	1654	0	TTGC	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1703	1706	0	ACAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1748	1751	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1764	1767	0	TTGT	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1808	1811	0	ACAA	15.625	15.71349
cg2325954	TPRG1	C/EBPbeta	1835	1838	0	ACAA	15.625	15.71349
cg2325954	TPRG1	TFIID [T0	266	272	0	TTTAAA	1.09863	1.13474
cg2325954	TPRG1	TFIID [T0	1040	1046	0	TTTTTGA	1.09863	1.13474
cg2325954	TPRG1	TFIID [T0	1071	1077	0	TTTAAA	1.09863	1.13474
cg2325954	TPRG1	TFIID [T0	1284	1290	0	TTTTATA	1.09863	1.13474
cg2325954	TPRG1	TFIID [T0	1356	1362	0	TTTTTTA	1.09863	1.13474
cg2325954	TPRG1	TFIID [T0	1475	1481	0	TTAAAA	1.09863	1.13474
cg2325954	TPRG1	TFIID [T0	1476	1482	0	TAAAAA	1.09863	1.13474
cg2325954	TPRG1	TFIID [T0	1802	1808	0	TTTTTGA	1.09863	1.13474
cg2325954	TPRG1	FOXP3 [T	1032	1037	0	AACAAC	1.46484	1.47315
cg2325954	TPRG1	GR-beta [T	389	393	0	ACATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	580	584	0	ACATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	772	776	0	AAATT	3.90625	3.99611

cg2325954	TPRG1	GR-beta [T	773	777	0	AATTT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	805	809	0	AATGT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1036	1040	0	ACATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1093	1097	0	AATTT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1179	1183	0	AATTT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1198	1202	0	AAATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1329	1333	0	AATGT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1472	1476	0	AAATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1580	1584	0	AATGT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1718	1722	0	ACATT	3.90625	3.99611
cg2325954	TPRG1	GR-beta [T	1799	1803	0	ACATT	3.90625	3.99611
cg2325954	TPRG1	PR B [T00	879	885	0	TACTGTT	0.36621	0.36944
cg2325954	TPRG1	PR B [T00	932	938	0	GACTGT	0.36621	0.36944
cg2325954	TPRG1	PR A [T01	879	885	0	TACTGTT	0.36621	0.36944
cg2325954	TPRG1	PR A [T01	932	938	0	GACTGT	0.36621	0.36944
cg2325954	TPRG1	GR [T050	1039	1045	0	TTTTTTG	0.36621	0.37562
cg2325954	TPRG1	GR [T050	1801	1807	0	ATTTTTC	0.36621	0.37562
cg2325954	TPRG1	IRF-2 [T0	764	769	0	TCACTT	0.48828	0.49387
cg2121064	TRIM14	RAR-beta:	1326	1337	9.97066	TCTCCTC	0.06974	0.07677
cg2121064	TRIM14	RAR-beta:	1386	1397	9.97066	TCCACC	0.06974	0.07677
cg2121064	TRIM14	c-Ets-1 [T	865	871	9.969337	ATTCCC	0.24414	0.23698
cg2121064	TRIM14	LEF-1 [T0	65	72	9.937995	CTTTGG	0.12207	0.1238
cg2121064	TRIM14	NF-kappa	1961	1971	9.917964	GGGGAC	0.02289	0.02536
cg2121064	TRIM14	STAT1bet	849	858	9.807397	CCCCGG	0.14877	0.14533
cg2121064	TRIM14	XBP-1 [T	61	66	9.789909	ATGGCT	1.95312	1.94901
cg2121064	TRIM14	XBP-1 [T	391	396	9.789909	CGCCAT	1.95312	1.94901
cg2121064	TRIM14	XBP-1 [T	470	475	9.789909	CGCCAT	1.95312	1.94901
cg2121064	TRIM14	XBP-1 [T	1163	1168	9.789909	CGCCAT	1.95312	1.94901
cg2121064	TRIM14	XBP-1 [T	1203	1208	9.789909	CGCCAT	1.95312	1.94901
cg2121064	TRIM14	XBP-1 [T	1501	1506	9.789909	ATGGCT	1.95312	1.94901
cg2121064	TRIM14	LEF-1 [T0	1014	1021	9.72404	AGGCAA	0.21362	0.21229
cg2121064	TRIM14	NF-AT1 [T	150	158	9.691726	TTGGTTT	0.16785	0.16528
cg2121064	TRIM14	c-Ets-1 [T	961	967	9.585075	CGGGAA	0.36621	0.37402
cg2121064	TRIM14	RBP-Jkap	682	693	9.570372	GAAATG	0.01884	0.01884
cg2121064	TRIM14	TFIID [T	933	939	9.552105	TTTCGG	1.46484	1.37777
cg2121064	TRIM14	TFIID [T	1358	1364	9.552105	TCCCAA	1.46484	1.37777
cg2121064	TRIM14	TFIID [T	1804	1810	9.552105	TTTGGT	1.46484	1.37777
cg2121064	TRIM14	TFIID [T	1819	1825	9.552105	TTTCAC	1.46484	1.37777
cg2121064	TRIM14	Pax-5 [T0	77	83	9.552105	TTTGCC	1.46484	1.61918
cg2121064	TRIM14	Pax-5 [T0	131	137	9.552105	GACGCC	1.46484	1.61918
cg2121064	TRIM14	Pax-5 [T0	333	339	9.552105	GGGCAA	1.46484	1.61918
cg2121064	TRIM14	Pax-5 [T0	551	557	9.552105	GGGCGG	1.46484	1.61918
cg2121064	TRIM14	Pax-5 [T0	1245	1251	9.552105	GGCGCC	1.46484	1.61918
cg2121064	TRIM14	Pax-5 [T0	1659	1665	9.552105	GTTGCC	1.46484	1.61918
cg2121064	TRIM14	Pax-5 [T0	1850	1856	9.552105	GTTGCC	1.46484	1.61918
cg2121064	TRIM14	Pax-5 [T0	1920	1926	9.552105	TCCGCC	1.46484	1.61918
cg2121064	TRIM14	E2F-1 [T0	276	283	9.529774	TGCACC	0.15259	0.16832
cg2121064	TRIM14	NF-1 [T00	1836	1843	9.513281	CACCCC	0.73242	0.74634

cg2121064	TRIM14	FOXP3 [T	17	22	9.512894	CCCAAC	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	32	37	9.512894	CTAAAC	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	208	213	9.512894	GTTATG	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	228	233	9.512894	CCCAAC	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	788	793	9.512894	GTTGGC	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	928	933	9.512894	GTTTAT	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	1476	1481	9.512894	GTTGCT	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	1523	1528	9.512894	GTTCTT	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	1659	1664	9.512894	GTTGCC	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	1850	1855	9.512894	GTTGCC	7.32422	7.22156
cg2121064	TRIM14	FOXP3 [T	1972	1977	9.512894	GTTTAC	7.32422	7.22156
cg2121064	TRIM14	TFII-I [T0	82	87	9.512894	CCTTCC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	153	158	9.512894	GTTTCC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	250	255	9.512894	CCGTCC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	502	507	9.512894	GGACAC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	525	530	9.512894	GGAAAC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	799	804	9.512894	CCTTCC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	845	850	9.512894	TTTTCC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	905	910	9.512894	GGACAC	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	1314	1319	9.512894	GGATGG	7.32422	7.44385
cg2121064	TRIM14	TFII-I [T0	1843	1848	9.512894	AATTCC	7.32422	7.44385
cg2121064	TRIM14	Ik-1 [T027	1618	1630	9.497194	TCCCAG	0.02941	0.03137
cg2121064	TRIM14	c-Jun [T00	588	594	9.442241	TGACAG	0.73242	0.7366
cg2121064	TRIM14	EBF [T05	300	310	9.428348	CCCACA	0.06866	0.07687
cg2121064	TRIM14	NFI/CTF [	63	70	9.352332	GGCTTT	0.54932	0.55369
cg2121064	TRIM14	NFI/CTF [	783	790	9.352332	CCAAAG	0.54932	0.55369
cg2121064	TRIM14	NFI/CTF [	1910	1917	9.352332	ATCCTT	0.54932	0.55369
cg2121064	TRIM14	E2F-1 [T0	999	1006	9.261732	GCGGAG	0.15259	0.16832
cg2121064	TRIM14	MEF-2A [	1277	1287	9.220261	TATTTTT	0.07343	0.06466
cg2121064	TRIM14	NF-AT1 [	818	826	9.18189	TCACTT	0.22888	0.22581
cg2121064	TRIM14	c-Myb [T0	784	791	9.142015	CAAAGT	0.39673	0.37851
cg2121064	TRIM14	AhR [T01	1199	1209	9.058053	TTCACG	0.03242	0.03333
cg2121064	TRIM14	USF2 [T0	262	271	9.056375	TCCCCA	0.1545	0.16206
cg2121064	TRIM14	LEF-1 [T0	1358	1365	8.973041	TCCCAA	0.54932	0.53171
cg2121064	TRIM14	GR [T050	63	69	8.971049	GGCTTT	0.61035	0.5928
cg2121064	TRIM14	GR [T050	1504	1510	8.971049	GCTTTT	0.61035	0.5928
cg2121064	TRIM14	c-Ets-1 [T	1548	1554	8.937416	GTGGAA	0.85449	0.84987
cg2121064	TRIM14	p53 [T006	1597	1603	8.912104	AGGGCC	0.12207	0.13824
cg2121064	TRIM14	Elk-1 [T00	800	808	8.897321	CTTCCG	0.24414	0.26271
cg2121064	TRIM14	ETF [T002	193	203	8.876947	GCCCCC	0.02384	0.02809
cg2121064	TRIM14	ETF [T002	1890	1900	8.876947	GCCCTC	0.02384	0.02809
cg2121064	TRIM14	c-Jun [T00	796	802	8.832178	TGACCT	0.61035	0.60549
cg2121064	TRIM14	NFI/CTF [	920	927	8.814757	CCAATT	0.48828	0.48845
cg2121064	TRIM14	c-Ets-1 [T	1844	1850	8.809329	ATTCCA	0.85449	0.84987
cg2121064	TRIM14	c-Jun [T00	1812	1818	8.807683	TGACAA	0.61035	0.60549
cg2121064	TRIM14	NF-1 [T00	1356	1363	8.790071	CCTCCC	0.24414	0.24339
cg2121064	TRIM14	XBP-1 [T	699	704	8.75604	ATGAGC	2.92969	2.75329
cg2121064	TRIM14	XBP-1 [T	1497	1502	8.75604	TATCAT	2.92969	2.75329

cg2121064	TRIM14	XBP-1 [T	1686	1691	8.75604	GATCAT	2.92969	2.75329
cg2121064	TRIM14	STAT1bet	153	162	8.695301	GTTTCC	0.22316	0.2175
cg2121064	TRIM14	NF-AT1 [	842	850	8.532897	CCCTTTT	0.10681	0.10494
cg2121064	TRIM14	c-Ets-1 [T	1983	1989	8.501115	TTGGAA	0.24414	0.23702
cg2121064	TRIM14	NF-AT2 [	853	862	8.497624	GGAAAG	0.04959	0.04758
cg2121064	TRIM14	c-Myb [T0	55	62	8.443873	CAACTG	0.30518	0.28602
cg2121064	TRIM14	c-Myb [T0	872	879	8.443873	CAACTG	0.30518	0.28602
cg2121064	TRIM14	RBP-Jkap	864	875	8.425028	CATTCC	0.02074	0.02067
cg2121064	TRIM14	LEF-1 [T0	76	83	8.361499	CTTTGC	0.15259	0.154
cg2121064	TRIM14	LEF-1 [T0	333	340	8.361499	GGGCAA	0.15259	0.154
cg2121064	TRIM14	PR B [T00	738	744	8.338824	CGCTGT	1.09863	1.09384
cg2121064	TRIM14	PR B [T00	1468	1474	8.338824	AACAGG	1.09863	1.09384
cg2121064	TRIM14	PR B [T00	1571	1577	8.338824	TCCTGT	1.09863	1.09384
cg2121064	TRIM14	PR B [T00	1655	1661	8.338824	CTCTGT	1.09863	1.09384
cg2121064	TRIM14	PR B [T00	1798	1804	8.338824	CTCTGT	1.09863	1.09384
cg2121064	TRIM14	PR A [T01	738	744	8.338824	CGCTGT	1.09863	1.09384
cg2121064	TRIM14	PR A [T01	1468	1474	8.338824	AACAGG	1.09863	1.09384
cg2121064	TRIM14	PR A [T01	1571	1577	8.338824	TCCTGT	1.09863	1.09384
cg2121064	TRIM14	PR A [T01	1655	1661	8.338824	CTCTGT	1.09863	1.09384
cg2121064	TRIM14	PR A [T01	1798	1804	8.338824	CTCTGT	1.09863	1.09384
cg2121064	TRIM14	E2F-1 [T0	165	172	8.336446	TAACCC	0.15259	0.16676
cg2121064	TRIM14	GR-alpha	82	86	8.281568	CCTTC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	86	90	8.281568	CCTTG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	197	201	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	200	204	8.281568	CCTCG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	286	290	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	421	425	8.281568	CCTCG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	437	441	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	485	489	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	488	492	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	521	525	8.281568	CAAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	536	540	8.281568	CCTCG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	582	586	8.281568	GGAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	615	619	8.281568	CCTCG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	626	630	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	666	670	8.281568	GGAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	799	803	8.281568	CCTTC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	826	830	8.281568	CCTTG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	885	889	8.281568	CCTTC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	947	951	8.281568	GAAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	985	989	8.281568	CAAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	1012	1016	8.281568	GGAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	1048	1052	8.281568	CGAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	1051	1055	8.281568	GGAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	1190	1194	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	1222	1226	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	1350	1354	8.281568	CCTCG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha	1356	1360	8.281568	CCTCC	7.8125	8.20394

cg2121064	TRIM14	GR-alpha [	1513	1517	8.281568	CAAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha [	1533	1537	8.281568	CAAGG	7.8125	8.20394
cg2121064	TRIM14	GR-alpha [	1616	1620	8.281568	CCTCC	7.8125	8.20394
cg2121064	TRIM14	GR-alpha [	1912	1916	8.281568	CCTTG	7.8125	8.20394
cg2121064	TRIM14	AR [T0004	1485	1493	8.272289	CAGATG	0.10681	0.10838
cg2121064	TRIM14	p53 [T006	1598	1604	8.208781	GGGCCC	0.48828	0.55336
cg2121064	TRIM14	ENKTF-1	167	174	8.19852	ACCCGC	0.73242	0.80254
cg2121064	TRIM14	ENKTF-1	176	183	8.19852	TGGCCA	0.73242	0.80254
cg2121064	TRIM14	ENKTF-1	309	316	8.19852	TGGCCA	0.73242	0.80254
cg2121064	TRIM14	ENKTF-1	388	395	8.19852	GGTCGC	0.73242	0.80254
cg2121064	TRIM14	ENKTF-1	467	474	8.19852	GCCCGC	0.73242	0.80254
cg2121064	TRIM14	ENKTF-1	1248	1255	8.19852	GCCCGC	0.73242	0.80254
cg2121064	TRIM14	ENKTF-1	1395	1402	8.19852	CCCGGC	0.73242	0.80254
cg2121064	TRIM14	NF-1 [T00	1454	1461	8.191058	CAGTCC	0.24414	0.24485
cg2121064	TRIM14	c-Ets-1 [T	742	748	8.116854	GTTCCA	0.24414	0.2494
cg2121064	TRIM14	c-Ets-1 [T	1234	1240	8.116854	CTGGAA	0.24414	0.2494
cg2121064	TRIM14	VDR [T00	105	113	8.079962	GCTCTG	0.24414	0.22992
cg2121064	TRIM14	GR-alpha [	9	13	8.073878	CCTGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	157	161	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	185	189	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	214	218	8.073878	CCTGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	268	272	8.073878	CCTGC	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	295	299	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	441	445	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	559	563	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	578	582	8.073878	CCTAG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	579	583	8.073878	CTAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	636	640	8.073878	GCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	658	662	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	708	712	8.073878	CTAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	726	730	8.073878	CCTGC	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1144	1148	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1212	1216	8.073878	CCTGC	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1311	1315	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1579	1583	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1664	1668	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1713	1717	8.073878	CCTGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1859	1863	8.073878	CCAGG	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1925	1929	8.073878	CCTGC	7.8125	8.20289
cg2121064	TRIM14	GR-alpha [	1978	1982	8.073878	CCTGC	7.8125	8.20289
cg2121064	TRIM14	TFIID [T0	44	50	8.014558	TTTCTGA	2.19727	1.99811
cg2121064	TRIM14	TFIID [T0	1557	1563	8.014558	TTTGCAA	2.19727	1.99811
cg2121064	TRIM14	TFIID [T0	1638	1644	8.014558	TTTGAGA	2.19727	1.99811
cg2121064	TRIM14	TFIID [T0	1901	1907	8.014558	TTTCTTA	2.19727	1.99811
cg2121064	TRIM14	Pax-5 [T0	12	18	8.014558	GGGCTC	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	142	148	8.014558	GGGCAC	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	402	408	8.014558	GGGCAG	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	514	520	8.014558	GGGCTC	2.19727	2.42766

cg2121064	TRIM14	Pax-5 [T0	612	618	8.014558	GGGCCT	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	649	655	8.014558	TCTGCC	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	720	726	8.014558	GGGCTT	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	765	771	8.014558	GCAGCC	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	1342	1348	8.014558	TCTGCC	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	1482	1488	8.014558	GGGCAG	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	1598	1604	8.014558	GGGCCC	2.19727	2.42766
cg2121064	TRIM14	Pax-5 [T0	1716	1722	8.014558	GGGCTC	2.19727	2.42766
cg2121064	TRIM14	p53 [T006	12	18	7.833758	GGGCTC	0.48828	0.55336
cg2121064	TRIM14	p53 [T006	514	520	7.833758	GGGCTC	0.48828	0.55336
cg2121064	TRIM14	RXR-alph	306	312	7.815913	GGGTGG	0.24414	0.26389
cg2121064	TRIM14	E2F-1 [T0	240	247	7.771357	GCGGCG	0.30518	0.32869
cg2121064	TRIM14	NF-AT1 [	1021	1029	7.744746	GGAAAG	0.19836	0.19379
cg2121064	TRIM14	IRF-1 [T0	849	857	7.732782	CCCCGG	0.14496	0.14723
cg2121064	TRIM14	NF-1 [T00	1805	1812	7.693985	TTGGTA	0.24414	0.23756
cg2121064	TRIM14	NFI/CTF [	1458	1465	7.587343	CCAAAA	0.36621	0.36269
cg2121064	TRIM14	NF-AT1 [	150	159	7.579763	TTGGTT	0.00763	0.00733
cg2121064	TRIM14	c-Myb [T0	760	767	7.545286	AAACTG	0.42725	0.40917
cg2121064	TRIM14	c-Myb [T0	1539	1546	7.545286	TGCAGT	0.42725	0.40917
cg2121064	TRIM14	c-Myb [T0	1968	1975	7.545286	TGCAGT	0.42725	0.40917
cg2121064	TRIM14	GR [T050	336	342	7.527031	CAAAGC	1.83105	1.71535
cg2121064	TRIM14	GR [T050	898	904	7.527031	CAAATA	1.83105	1.71535
cg2121064	TRIM14	GR [T050	1075	1081	7.527031	TTGTTTC	1.83105	1.71535
cg2121064	TRIM14	GR [T050	1079	1085	7.527031	TTGTTTC	1.83105	1.71535
cg2121064	TRIM14	GR [T050	1083	1089	7.527031	TTGTTTC	1.83105	1.71535
cg2121064	TRIM14	GR [T050	1459	1465	7.527031	CAAAAG	1.83105	1.71535
cg2121064	TRIM14	GR [T050	1554	1560	7.527031	TCTTTTG	1.83105	1.71535
cg2121064	TRIM14	GR [T050	1635	1641	7.527031	TTGTTTC	1.83105	1.71535
cg2121064	TRIM14	PXR-1:RX	1466	1473	7.486257	TGAACA	0.24414	0.24326
cg2121064	TRIM14	RAR-beta:	1716	1727	7.477995	GGGCTC	0.02861	0.03163
cg2121064	TRIM14	p53 [T006	1245	1251	7.458735	GGCGCC	0.73242	0.79826
cg2121064	TRIM14	c-Myb [T0	110	117	7.442719	GAACTT	0.42725	0.40917
cg2121064	TRIM14	PEA3 [T0	620	628	7.421728	GAGCAT	0.34332	0.35389
cg2121064	TRIM14	PEA3 [T0	1313	1321	7.421728	AGGATG	0.34332	0.35389
cg2121064	TRIM14	LEF-1 [T0	1526	1533	7.396545	CTTTGTC	0.21362	0.21504
cg2121064	TRIM14	C/EBPalp	919	925	7.396431	TCCAAT	0.48828	0.45033
cg2121064	TRIM14	E2F-1 [T0	356	363	7.336545	GCGGCA	0.45776	0.49661
cg2121064	TRIM14	c-Ets-2 [T	724	732	7.268173	TTCCTGC	0.09155	0.08977
cg2121064	TRIM14	p53 [T006	590	596	7.266844	ACAGCC	0.73242	0.79826
cg2121064	TRIM14	p53 [T006	1887	1893	7.266844	AAAGCC	0.73242	0.79826
cg2121064	TRIM14	SRY [T00	148	156	7.175614	CTTTGGT	0.30518	0.29547
cg2121064	TRIM14	SRY [T00	1526	1534	7.175614	CTTTGTC	0.30518	0.29547
cg2121064	TRIM14	XBP-1 [T	474	479	7.172312	ATTCAT	2.92969	2.7512
cg2121064	TRIM14	XBP-1 [T	774	779	7.172312	ATGATG	2.92969	2.7512
cg2121064	TRIM14	XBP-1 [T	861	866	7.172312	AATCAT	2.92969	2.7512
cg2121064	TRIM14	XBP-1 [T	886	891	7.172312	CTTCAT	2.92969	2.7512
cg2121064	TRIM14	XBP-1 [T	1492	1497	7.172312	CCTCAT	2.92969	2.7512
cg2121064	TRIM14	XBP-1 [T	1594	1599	7.172312	ATGAGG	2.92969	2.7512

cg2121064	TRIM14	XBP-1 [T(	1608	1613	7.172312	CTTCAT	2.92969	2.7512
cg2121064	TRIM14	XBP-1 [T(	1736	1741	7.172312	CCTCAT	2.92969	2.7512
cg2121064	TRIM14	Ik-1 [T027	1746	1758	7.122895	GGAGTA	0.01064	0.01145
cg2121064	TRIM14	c-Ets-1 [T(	523	529	7.071349	AGGGAA	0.73242	0.73732
cg2121064	TRIM14	c-Ets-1 [T(	822	828	7.071349	TTTCCCT	0.73242	0.73732
cg2121064	TRIM14	AR [T000	502	510	7.049779	GGACAC	0.23651	0.23986
cg2121064	TRIM14	IRF-1 [T0(	846	854	7.041849	TTTCCCC	0.1297	0.12685
cg2121064	TRIM14	HOXD9 [T	1562	1571	7.030183	AATAAT	0.07629	0.06543
cg2121064	TRIM14	HOXD10 [	1562	1571	7.030183	AATAAT	0.07629	0.06543
cg2121064	TRIM14	NFI/CTF [	18	25	7.014249	CCAACC	0.73242	0.74795
cg2121064	TRIM14	HNF-3alph	1268	1275	7.000129	AATTTTT	0.82397	0.71909
cg2121064	TRIM14	RXR-alpha	1834	1840	6.967687	ACCACC	0.36621	0.38841
cg2121064	TRIM14	NF-1 [T00	88	95	6.948522	TTGGGT	0.48828	0.50205
cg2121064	TRIM14	c-Ets-1 [T(	846	852	6.943262	TTTCCCC	0.73242	0.73732
cg2121064	TRIM14	ENKTF-1	180	187	6.942764	CACGGC	1.46484	1.56616
cg2121064	TRIM14	ENKTF-1	377	384	6.942764	CTCAGC	1.46484	1.56616
cg2121064	TRIM14	ENKTF-1	790	797	6.942764	TGGCTG	1.46484	1.56616
cg2121064	TRIM14	ENKTF-1	1160	1167	6.942764	TGGCGC	1.46484	1.56616
cg2121064	TRIM14	ENKTF-1	1200	1207	6.942764	TCACGC	1.46484	1.56616
cg2121064	TRIM14	p53 [T006	612	618	6.938545	GGGCCT	1.09863	1.22478
cg2121064	TRIM14	AhR:Arnt	1256	1265	6.928166	CCACGC	0.0515	0.0599
cg2121064	TRIM14	RAR-alpha	1325	1337	6.894422	ATCTCCT	0.00751	0.00805
cg2121064	TRIM14	p53 [T006	750	756	6.891821	AACGCC	1.09863	1.22478
cg2121064	TRIM14	C/EBPalph	954	960	6.85549	TGCAAT	0.73242	0.68282
cg2121064	TRIM14	NFI/CTF [	1541	1548	6.786076	CAGTTT	0.73242	0.74795
cg2121064	TRIM14	NFI/CTF [	1775	1782	6.786076	TAGTTT	0.73242	0.74795
cg2121064	TRIM14	NFI/CTF [	1979	1986	6.786076	CTGCTT	0.73242	0.74795
cg2121064	TRIM14	RXR-alpha	0	6	6.785809	GGGTAC	0.36621	0.38841
cg2121064	TRIM14	p53 [T006	1716	1722	6.778774	GGGCTC	1.09863	1.22478
cg2121064	TRIM14	c-Myb [T0	230	237	6.719843	CAACTC	0.30518	0.30272
cg2121064	TRIM14	c-Fos [T00	1791	1800	6.660217	TAAGTG	0.04578	0.04485
cg2121064	TRIM14	RelA [T00	1726	1736	6.604033	GATCTT	0.01001	0.01051
cg2121064	TRIM14	FOXP3 [T	1304	1309	6.581441	GTTTTA	0.97656	0.904
cg2121064	TRIM14	FOXP3 [T	1407	1412	6.581441	GTTTTA	0.97656	0.904
cg2121064	TRIM14	FOXP3 [T	1464	1469	6.581441	GTTGAA	0.97656	0.904
cg2121064	TRIM14	TFII-I [T0	27	32	6.581441	CACTCC	0.97656	0.9991
cg2121064	TRIM14	TFII-I [T0	478	483	6.581441	ATCTCC	0.97656	0.9991
cg2121064	TRIM14	TFII-I [T0	1151	1156	6.581441	GGAGTG	0.97656	0.9991
cg2121064	TRIM14	TFII-I [T0	1325	1330	6.581441	ATCTCC	0.97656	0.9991
cg2121064	TRIM14	TFII-I [T0	1671	1676	6.581441	GGAGTG	0.97656	0.9991
cg2121064	TRIM14	p53 [T006	720	726	6.563521	GGGCTT	0.48828	0.54643
cg2121064	TRIM14	p53 [T006	765	771	6.563521	GCAGCC	0.48828	0.54643
cg2121064	TRIM14	PPAR-alph	1751	1761	6.51544	AGCTGG	0.03719	0.04058
cg2121064	TRIM14	RAR-beta	1293	1302	6.415195	GGGGTT	0.18311	0.1857
cg2121064	TRIM14	p53 [T006	1139	1145	6.400205	GTCGCC	0.48828	0.54643
cg2121064	TRIM14	TCF-4E [T	76	82	6.302385	CTTTGCC	0.61035	0.59686
cg2121064	TRIM14	TCF-4E [T	148	154	6.302385	CTTTGGT	0.61035	0.59686
cg2121064	TRIM14	TCF-4E [T	334	340	6.302385	GGCAAA	0.61035	0.59686

cg2121064	TRIM14	TCF-4E [T	782	788	6.302385	ACCAAA	0.61035	0.59686
cg2121064	TRIM14	TCF-4E [T	1015	1021	6.302385	GGCAAA	0.61035	0.59686
cg2121064	TRIM14	GR-alpha [	895	899	6.263098	CCTCA	3.90625	3.89624
cg2121064	TRIM14	GR-alpha [	902	906	6.263098	TAAGG	3.90625	3.89624
cg2121064	TRIM14	GR-alpha [	1492	1496	6.263098	CCTCA	3.90625	3.89624
cg2121064	TRIM14	GR-alpha [	1595	1599	6.263098	TGAGG	3.90625	3.89624
cg2121064	TRIM14	GR-alpha [	1736	1740	6.263098	CCTCA	3.90625	3.89624
cg2121064	TRIM14	GR-alpha [	1892	1896	6.263098	CCTCA	3.90625	3.89624
cg2121064	TRIM14	C/EBPalph	1559	1565	6.245236	TGCAAT	0.97656	0.91422
cg2121064	TRIM14	C/EBPalph	1675	1681	6.245236	TGCAAT	0.97656	0.91422
cg2121064	TRIM14	p53 [T006	131	137	6.188498	GACGCC	0.61035	0.68483
cg2121064	TRIM14	p53 [T006	551	557	6.188498	GGGCGG	0.61035	0.68483
cg2121064	TRIM14	SRY [T00	780	788	6.176442	GGACCA	0.15259	0.14742
cg2121064	TRIM14	c-Myb [T0	1815	1822	6.157321	CAACTT	0.21362	0.2053
cg2121064	TRIM14	GR-alpha [	31	35	6.055408	CCTAA	3.90625	3.89835
cg2121064	TRIM14	GR-alpha [	95	99	6.055408	TCAGG	3.90625	3.89835
cg2121064	TRIM14	GR-alpha [	695	699	6.055408	CCTAA	3.90625	3.89835
cg2121064	TRIM14	GR-alpha [	770	774	6.055408	CCTGA	3.90625	3.89835
cg2121064	TRIM14	GR-alpha [	1008	1012	6.055408	TCAGG	3.90625	3.89835
cg2121064	TRIM14	GR-alpha [	1329	1333	6.055408	CCTGA	3.90625	3.89835
cg2121064	TRIM14	c-Ets-1 [T	154	160	6.039428	TTTCCAC	0.36621	0.36174
cg2121064	TRIM14	RXR-alpha	979	985	5.937582	GGCACC	0.73242	0.78318
cg2121064	TRIM14	GCF [T00	1387	1395	5.917256	CCACCG	0.64087	0.72542
cg2121064	TRIM14	HOXD9 [T	1414	1423	5.898575	AATAAT	0.05722	0.04686
cg2121064	TRIM14	HOXD9 [T	1417	1426	5.898575	AATAAT	0.05722	0.04686
cg2121064	TRIM14	HOXD10 [	1414	1423	5.898575	AATAAT	0.05722	0.04686
cg2121064	TRIM14	HOXD10 [	1417	1426	5.898575	AATAAT	0.05722	0.04686
cg2121064	TRIM14	STAT4 [T	82	87	5.882353	CCTTCC	0.48828	0.51201
cg2121064	TRIM14	STAT4 [T	799	804	5.882353	CCTTCC	0.48828	0.51201
cg2121064	TRIM14	c-Myb [T0	1846	1853	5.841835	TCCAGT	0.21362	0.2053
cg2121064	TRIM14	c-Ets-1 [T	686	692	5.814485	TGGGAA	0.36621	0.36174
cg2121064	TRIM14	c-Ets-1 [T	1729	1735	5.814485	CTTCCC	0.36621	0.36174
cg2121064	TRIM14	NF-AT1 [T	853	861	5.77403	GGAAAG	0.06866	0.06621
cg2121064	TRIM14	AR [T000	905	913	5.754178	GGACAC	0.24414	0.25115
cg2121064	TRIM14	c-Jun [T00	1331	1337	5.703976	TGACCC	0.48828	0.49294
cg2121064	TRIM14	ENKTF-1	62	69	5.687009	TGGCTT	0.73242	0.76357
cg2121064	TRIM14	IRF-1 [T0	154	162	5.65977	TTTCCAC	0.22888	0.21959
cg2121064	TRIM14	NF-1 [T00	779	786	5.626299	GGGACC	0.24414	0.25051
cg2121064	TRIM14	c-Ets-2 [T	1570	1578	5.624023	TTCCTGT	0.01526	0.01376
cg2121064	TRIM14	c-Jun [T00	735	741	5.590308	TGACGC	0.48828	0.49294
cg2121064	TRIM14	AP-2alpha	1928	1933	5.568965	GCCTAT	0.48828	0.48642
cg2121064	TRIM14	TFIID [T0	30	36	5.544826	TCCTAA	0.73242	0.65314
cg2121064	TRIM14	TFIID [T0	1281	1287	5.544826	TTTAGT	0.73242	0.65314
cg2121064	TRIM14	Pax-5 [T0	750	756	5.544826	AACGCC	0.73242	0.79
cg2121064	TRIM14	AP-1 [T00	1795	1803	5.408943	TGACTC	0.09155	0.08822
cg2121064	TRIM14	RAR-beta	1195	1204	5.389083	CGGGTT	0.15259	0.15813
cg2121064	TRIM14	RelA [T00	685	695	5.308078	ATGGGA	0.0124	0.01273
cg2121064	TRIM14	RXR-alpha	716	722	5.271235	GGGTGG	0.61035	0.65415

cg2121064	TRIM14	RXR-alpha	989	995	5.271235	GGGTGG	0.61035	0.65415
cg2121064	TRIM14	ETF [T002	544	554	5.246906	GTGGGC	0.02861	0.03569
cg2121064	TRIM14	GR [T0507	1781	1787	5.207533	GGTTTC	0.24414	0.24013
cg2121064	TRIM14	c-Ets-2 [T	84	92	5.162974	TTCCTT	0.13733	0.13279
cg2121064	TRIM14	p53 [T006	1920	1926	5.133514	TCCGCC	0.48828	0.53921
cg2121064	TRIM14	AP-2alpha	74	79	5.100982	GCCTTT	0.97656	0.97517
cg2121064	TRIM14	AP-2alpha	1038	1043	5.100982	AAAGGC	0.97656	0.97517
cg2121064	TRIM14	RXR-alpha	639	645	5.089356	GGGTGC	0.48828	0.51407
cg2121064	TRIM14	RXR-alpha	807	813	5.089356	GGGTGC	0.48828	0.51407
cg2121064	TRIM14	GR-beta [T	950	954	5.042296	GGATT	3.90625	3.7093
cg2121064	TRIM14	GR-beta [T	1054	1058	5.042296	GGATT	3.90625	3.7093
cg2121064	TRIM14	GR-beta [T	1276	1280	5.042296	GTATT	3.90625	3.7093
cg2121064	TRIM14	GR-beta [T	1371	1375	5.042296	GGATT	3.90625	3.7093
cg2121064	TRIM14	GR-beta [T	1420	1424	5.042296	AATAC	3.90625	3.7093
cg2121064	TRIM14	GR-beta [T	1440	1444	5.042296	AATAC	3.90625	3.7093
cg2121064	TRIM14	E2F-1 [T0	99	106	5.042045	GCTCCC	0.18311	0.20394
cg2121064	TRIM14	E2F-1 [T0	232	239	5.042045	ACTCCC	0.18311	0.20394
cg2121064	TRIM14	C/EBPalph	951	957	5.024728	GATTGC	0.97656	0.90302
cg2121064	TRIM14	C/EBPalph	1055	1061	5.024728	GATTGC	0.97656	0.90302
cg2121064	TRIM14	NFI/CTF [	520	527	5.021086	CCAAGG	0.24414	0.25666
cg2121064	TRIM14	NFI/CTF [	984	991	5.021086	CCAAGG	0.24414	0.25666
cg2121064	TRIM14	USF1 [T0	268	277	4.993039	CCTGCA	0.04578	0.04763
cg2121064	TRIM14	XBP-1 [T	211	216	4.894955	ATGCCT	0.97656	0.99839
cg2121064	TRIM14	NF-1 [T00	1983	1990	4.880836	TTGGAA	0.24414	0.24345
cg2121064	TRIM14	RXR-alpha	90	96	4.86724	GGGTCT	0.48828	0.51407
cg2121064	TRIM14	GCF [T00	238	246	4.846987	GCGCGG	0.27466	0.31905
cg2121064	TRIM14	GCF [T00	402	410	4.846987	GGGCAG	0.27466	0.31905
cg2121064	TRIM14	GCF [T00	460	468	4.846987	TCGCCG	0.27466	0.31905
cg2121064	TRIM14	c-Ets-1 [T	1876	1882	4.782565	CTTCCA	0.48828	0.48026
cg2121064	TRIM14	FOXP3 [T	53	58	4.756447	CTCAAC	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	758	763	4.756447	GAAAAC	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	890	895	4.756447	ATCAAC	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	1043	1048	4.756447	CAAAAC	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	1068	1073	4.756447	GTTTTT	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	1089	1094	4.756447	GTTTTT	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	1095	1100	4.756447	GTTTTT	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	1590	1595	4.756447	GTTGAT	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	1782	1787	4.756447	GTTTTG	2.92969	2.82
cg2121064	TRIM14	FOXP3 [T	1802	1807	4.756447	GTTTTG	2.92969	2.82
cg2121064	TRIM14	TFII-I [T0	864	869	4.756447	CATTCC	2.92969	2.89715
cg2121064	TRIM14	TFII-I [T0	937	942	4.756447	GGACTG	2.92969	2.89715
cg2121064	TRIM14	TFII-I [T0	950	955	4.756447	GGATTG	2.92969	2.89715
cg2121064	TRIM14	TFII-I [T0	1054	1059	4.756447	GGATTG	2.92969	2.89715
cg2121064	TRIM14	TFII-I [T0	1454	1459	4.756447	CAGTCC	2.92969	2.89715
cg2121064	TRIM14	TFII-I [T0	1488	1493	4.756447	ATGTCC	2.92969	2.89715
cg2121064	TRIM14	p53 [T006	320	326	4.645444	CGCGCC	0.24414	0.28373
cg2121064	TRIM14	p53 [T006	464	470	4.645444	CGCGCC	0.24414	0.28373
cg2121064	TRIM14	p53 [T006	1391	1397	4.645444	CGCGCC	0.24414	0.28373

cg2121064	TRIM14	VDR [T00	1198	1206	4.617121	GTTCAC	0.37384	0.36855
cg2121064	TRIM14	VDR [T00	1462	1470	4.617121	AAGTTG	0.37384	0.36855
cg2121064	TRIM14	COUP-TF	793	805	4.54669	CTGTGA	0.00358	0.00369
cg2121064	TRIM14	STAT5A [	1282	1294	4.540481	TTAGTA	0.00536	0.00489
cg2121064	TRIM14	USF2 [T0	1444	1453	4.528187	CAGGTG	0.06866	0.07203
cg2121064	TRIM14	c-Ets-1 [T	851	857	4.487936	CCGGAA	0.85449	0.8381
cg2121064	TRIM14	RXR-alph	1936	1942	4.423008	TCCACC	0.24414	0.25781
cg2121064	TRIM14	STAT4 [T	688	693	4.411765	GGAAGC	1.95312	1.99838
cg2121064	TRIM14	STAT4 [T	722	727	4.411765	GCTTCC	1.95312	1.99838
cg2121064	TRIM14	STAT4 [T	864	869	4.411765	CATTCC	1.95312	1.99838
cg2121064	TRIM14	STAT4 [T	1728	1733	4.411765	TCTTCC	1.95312	1.99838
cg2121064	TRIM14	RAR-beta	31	40	4.307573	CCTAAA	0.14496	0.14853
cg2121064	TRIM14	PXR-1:RX	1195	1202	4.213958	CGGGTT	0.12207	0.12474
cg2121064	TRIM14	GR-beta [	861	865	4.201913	AATCA	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	900	904	4.201913	AATAA	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	930	934	4.201913	TTATT	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	965	969	4.201913	AATAA	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	1414	1418	4.201913	AATAA	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	1417	1421	4.201913	AATAA	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	1562	1566	4.201913	AATAA	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	1565	1569	4.201913	AATAG	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	1586	1590	4.201913	AATCG	7.8125	7.23274
cg2121064	TRIM14	GR-beta [	1678	1682	4.201913	AATAG	7.8125	7.23274
cg2121064	TRIM14	NF-Y [T0	917	924	4.186615	TCTCCA	0.18311	0.17499
cg2121064	TRIM14	NF-1 [T00	67	74	4.135372	TTGGCT	0.24414	0.25714
cg2121064	TRIM14	p53 [T006	296	302	4.125254	CAGGCC	0.73242	0.82434
cg2121064	TRIM14	p53 [T006	142	148	4.083527	GGGCAC	0.73242	0.82434
cg2121064	TRIM14	RXR-alph	1294	1300	4.019014	GGGTTT	0.97656	1.02803
cg2121064	TRIM14	c-Ets-2 [T	1016	1024	4.017001	GCAAAG	0.16022	0.15061
cg2121064	TRIM14	TFIID [T0	1034	1040	4.007279	TTTTAA	1.09863	0.94722
cg2121064	TRIM14	TFIID [T0	1408	1414	4.007279	TTTTAA	1.09863	0.94722
cg2121064	TRIM14	TFIID [T0	1883	1889	4.007279	TTATAA	1.09863	0.94722
cg2121064	TRIM14	Pax-5 [T0	590	596	4.007279	ACAGCC	1.09863	1.18533
cg2121064	TRIM14	Pax-5 [T0	1597	1603	4.007279	AGGGCC	1.09863	1.18533
cg2121064	TRIM14	Pax-5 [T0	1887	1893	4.007279	AAAGCC	1.09863	1.18533
cg2121064	TRIM14	NF-kappa	686	697	3.935637	TGGGAA	0.00608	0.00634
cg2121064	TRIM14	PPAR-alp	137	147	3.872523	CTCTGG	0.02575	0.0279
cg2121064	TRIM14	NFI/CTF [	146	153	3.793671	ACCTTT	0.18311	0.19063
cg2121064	TRIM14	GR [T050	1043	1049	3.763516	CAAAAC	0.73242	0.6946
cg2121064	TRIM14	GR [T050	1524	1530	3.763516	TTCTTTG	0.73242	0.6946
cg2121064	TRIM14	GR [T050	1801	1807	3.763516	TGTTTT	0.73242	0.6946
cg2121064	TRIM14	p53 [T006	217	223	3.750231	GGGCTG	0.73242	0.82434
cg2121064	TRIM14	PEA3 [T0	584	592	3.710864	AGGATG	0.09155	0.08745
cg2121064	TRIM14	RXR-alph	572	578	3.574782	CCGACC	1.09863	1.1653
cg2121064	TRIM14	Sp1 [T007	1918	1927	3.54287	TCTCCG	0.07439	0.08783
cg2121064	TRIM14	c-Ets-1 [T	1569	1575	3.462376	GTTCCT	0.61035	0.61936
cg2121064	TRIM14	RXR-alph	164	170	3.392904	GTAACC	1.09863	1.1653
cg2121064	TRIM14	RXR-alph	1973	1979	3.392904	TTTACC	1.09863	1.1653

cg2121064	TRIM14	Sp1 [T007	550	559	3.383855	GGGGCG	0.07439	0.08783
cg2121064	TRIM14	p53 [T006	190	196	3.375208	CACGCC	0.73242	0.80362
cg2121064	TRIM14	p53 [T006	509	515	3.375208	GGGCGG	0.73242	0.80362
cg2121064	TRIM14	p53 [T006	546	552	3.375208	GGGCGG	0.73242	0.80362
cg2121064	TRIM14	p53 [T006	653	659	3.375208	CCCGCC	0.73242	0.80362
cg2121064	TRIM14	p53 [T006	1257	1263	3.375208	CACGCC	0.73242	0.80362
cg2121064	TRIM14	GR-beta [	913	917	3.361531	AGATT	3.90625	3.51525
cg2121064	TRIM14	GR-beta [	1552	1556	3.361531	AATCT	3.90625	3.51525
cg2121064	TRIM14	USF1 [T0	272	281	3.348091	CACGTG	0.0515	0.05415
cg2121064	TRIM14	IRF-1 [T0	1017	1025	3.347186	CAAAGG	0.06866	0.0661
cg2121064	TRIM14	c-Jun [T00	1795	1801	3.244843	TGACTC	0.24414	0.2435
cg2121064	TRIM14	AP-2alpha	1028	1033	3.229049	AGAGGC	0.48828	0.5124
cg2121064	TRIM14	AP-2alpha	1703	1708	3.229049	GCCTCT	0.48828	0.5124
cg2121064	TRIM14	RAR-beta	242	251	3.226064	GGCGAA	0.12207	0.12558
cg2121064	TRIM14	Elk-1 [T00	83	91	3.121991	CTTCCT	0.07629	0.07518
cg2121064	TRIM14	c-Ets-1 [T	800	806	3.102985	CTTCCG	0.24414	0.26272
cg2121064	TRIM14	TFIID [T0	1556	1562	3.075094	TTTTGC	0.12207	0.11309
cg2121064	TRIM14	EBF [T05	438	448	3.031642	CTCCCA	0.00763	0.00884
cg2121064	TRIM14	p53 [T006	1659	1665	3.024997	GTTGCC	0.48828	0.53227
cg2121064	TRIM14	p53 [T006	1850	1856	3.024997	GTTGCC	0.48828	0.53227
cg2121064	TRIM14	STAT4 [T	741	746	2.941176	TGTTCC	2.92969	2.92382
cg2121064	TRIM14	STAT4 [T	821	826	2.941176	CTTTCC	2.92969	2.92382
cg2121064	TRIM14	STAT4 [T	853	858	2.941176	GGAAAG	2.92969	2.92382
cg2121064	TRIM14	STAT4 [T	963	968	2.941176	GGAATA	2.92969	2.92382
cg2121064	TRIM14	STAT4 [T	1021	1026	2.941176	GGAAAG	2.92969	2.92382
cg2121064	TRIM14	STAT4 [T	1550	1555	2.941176	GGAATC	2.92969	2.92382
cg2121064	TRIM14	STAT4 [T	1875	1880	2.941176	ACTTCC	2.92969	2.92382
cg2121064	TRIM14	STAT4 [T	1985	1990	2.941176	GGAACA	2.92969	2.92382
cg2121064	TRIM14	p53 [T006	402	408	2.813291	GGGCAG	0.48828	0.53227
cg2121064	TRIM14	AhR:Arnt	189	198	2.810335	GCACGC	0.01717	0.02068
cg2121064	TRIM14	PR B [T00	1987	1993	2.80933	AACATT	0.73242	0.66711
cg2121064	TRIM14	PR A [T01	1987	1993	2.80933	AACATT	0.73242	0.66711
cg2121064	TRIM14	TBP [T007	1880	1889	2.807313	CACTTA	0.12207	0.10444
cg2121064	TRIM14	Ik-1 [T027	1361	1373	2.374299	CAAAGT	0.00063	0.00068
cg2121064	TRIM14	LEF-1 [T0	148	155	2.21836	CTTTGG	0.18311	0.17215
cg2121064	TRIM14	Sp1 [T007	651	660	2.203247	TGCCCG	0.03624	0.04341
cg2121064	TRIM14	GCF [T00	233	241	2.140539	CTCCCG	0.09155	0.10473
cg2121064	TRIM14	GCF [T00	287	295	2.140539	CTCCAG	0.09155	0.10473
cg2121064	TRIM14	AP-2alpha	614	619	2.098119	GCCTCG	0.97656	1.07805
cg2121064	TRIM14	AP-2alpha	1349	1354	2.098119	GCCTCG	0.97656	1.07805
cg2121064	TRIM14	IRF-1 [T0	521	529	2.073013	CAAGGG	0.00763	0.00747
cg2121064	TRIM14	IRF-1 [T0	822	830	2.073013	TTTCCCT	0.00763	0.00747
cg2121064	TRIM14	p53 [T006	77	83	1.970013	TTTGCC	0.36621	0.38097
cg2121064	TRIM14	p53 [T006	333	339	1.970013	GGGCAA	0.36621	0.38097
cg2121064	TRIM14	AP-2alpha	285	290	1.871933	GCCTCC	0.97656	1.07805
cg2121064	TRIM14	AP-2alpha	1012	1017	1.871933	GGAGGC	0.97656	1.07805
cg2121064	TRIM14	AP-2alpha	1189	1194	1.871933	GCCTCC	0.97656	1.07805
cg2121064	TRIM14	AP-2alpha	1221	1226	1.871933	GCCTCC	0.97656	1.07805

cg2121064	TRIM14	AP-2alpha	1355	1360	1.871933	GCCTCC	0.97656	1.07805
cg2121064	TRIM14	AP-2alpha	1615	1620	1.871933	GCCTCC	0.97656	1.07805
cg2121064	TRIM14	C/EBPalpl	922	928	1.830762	AATTGA(	0.48828	0.46352
cg2121064	TRIM14	FOXP3 [T	161	166	1.824994	GTTGTA	0.48828	0.46414
cg2121064	TRIM14	TFII-I [T0	711	716	1.824994	GGAGAG	0.48828	0.51201
cg2121064	TRIM14	p53 [T006	649	655	1.758307	TCTGCC(	0.36621	0.38097
cg2121064	TRIM14	p53 [T006	1342	1348	1.758307	TCTGCC(	0.36621	0.38097
cg2121064	TRIM14	p53 [T006	1482	1488	1.758307	GGGCAG	0.36621	0.38097
cg2121064	TRIM14	RXR-alpha	445	451	1.696452	GGGTCC(	0.48828	0.52093
cg2121064	TRIM14	RXR-alpha	1330	1336	1.696452	CTGACC(	0.48828	0.52093
cg2121064	TRIM14	GR-beta [T	957	961	1.680765	AATTC	3.90625	3.70067
cg2121064	TRIM14	GR-beta [T	1435	1439	1.680765	GAATT	3.90625	3.70067
cg2121064	TRIM14	GR-beta [T	1843	1847	1.680765	AATTC	3.90625	3.70067
cg2121064	TRIM14	c-Ets-1 [T(	1019	1025	1.641124	AAGGAA	0.36621	0.35197
cg2121064	TRIM14	C/EBPbeta	18	21	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	67	70	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	88	91	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	150	153	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	229	232	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	520	523	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	783	786	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	789	792	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	920	923	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	984	987	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1118	1121	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1360	1363	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1425	1428	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1458	1461	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1545	1548	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1779	1782	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1805	1808	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1840	1843	1.639871	CCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1914	1917	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1983	1986	1.639871	TTGG	15.625	15.23827
cg2121064	TRIM14	PXR-1:RX	109	116	1.63615	TGAACT	0.06104	0.05484
cg2121064	TRIM14	XBP-1 [T(	587	592	1.583727	ATGACA	0.97656	0.94995
cg2121064	TRIM14	HIF-1 [T0	273	281	1.549104	ACGTGC	0.09155	0.09676
cg2121064	TRIM14	TFIID [T0	1116	1122	1.537547	TTTTGGA	0.73242	0.65627
cg2121064	TRIM14	TFIID [T0	1272	1278	1.537547	TTTTGTA	0.73242	0.65627
cg2121064	TRIM14	TFIID [T0	1457	1463	1.537547	TCCAAA	0.73242	0.65627
cg2121064	TRIM14	TFIID [T0	1948	1954	1.537547	TTTTTCA	0.73242	0.65627
cg2121064	TRIM14	Pax-5 [T0(	190	196	1.537547	CACGCC(	0.73242	0.83087
cg2121064	TRIM14	Pax-5 [T0(	320	326	1.537547	CGCGCC(	0.73242	0.83087
cg2121064	TRIM14	Pax-5 [T0(	464	470	1.537547	CGCGCC(	0.73242	0.83087
cg2121064	TRIM14	Pax-5 [T0(	509	515	1.537547	GGGCGG	0.73242	0.83087
cg2121064	TRIM14	Pax-5 [T0(	546	552	1.537547	GGGCGG	0.73242	0.83087
cg2121064	TRIM14	Pax-5 [T0(	653	659	1.537547	CCCGCC(	0.73242	0.83087
cg2121064	TRIM14	Pax-5 [T0(	838	844	1.537547	CTTGCC(	0.73242	0.83087

cg2121064	TRIM14	Pax-5 [T0(	1257	1263	1.537547	CACGCC(	0.73242	0.83087
cg2121064	TRIM14	Pax-5 [T0(	1391	1397	1.537547	CGCGCC(	0.73242	0.83087
cg2121064	TRIM14	STAT4 [T(	153	158	1.470588	GTTTCC	1.95312	1.90161
cg2121064	TRIM14	STAT4 [T(	525	530	1.470588	GGAAAC	1.95312	1.90161
cg2121064	TRIM14	STAT4 [T(	845	850	1.470588	TTTTCC	1.95312	1.90161
cg2121064	TRIM14	STAT4 [T(	1236	1241	1.470588	GGAACT	1.95312	1.90161
cg2121064	TRIM14	STAT4 [T(	1568	1573	1.470588	AGTTCC	1.95312	1.90161
cg2121064	TRIM14	STAT4 [T(	1843	1848	1.470588	AATTCC	1.95312	1.90161
cg2121064	TRIM14	GR [T050	1089	1095	1.444018	GTTTTTC	0.12207	0.11476
cg2121064	TRIM14	C/EBPbeta	54	57	1.366559	TCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	828	831	1.366559	TTGA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	891	894	1.366559	TCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	897	900	1.366559	TCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	924	927	1.366559	TTGA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1465	1468	1.366559	TTGA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1591	1594	1.366559	TTGA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1639	1642	1.366559	TTGA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1720	1723	1.366559	TCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1785	1788	1.366559	TTGA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1865	1868	1.366559	TCAA	15.625	15.23827
cg2121064	TRIM14	C/EBPbeta	1952	1955	1.366559	TCAA	15.625	15.23827
cg2121064	TRIM14	AP-2alpha	1242	1247	1.357116	ACAGGC	0.48828	0.51319
cg2121064	TRIM14	AP-2alpha	1376	1381	1.357116	ACAGGC	0.48828	0.51319
cg2121064	TRIM14	AP-2alpha	1469	1474	1.357116	ACAGGC	0.48828	0.51319
cg2121064	TRIM14	HNF-3alpl	1410	1417	1.342935	TTAAAA	0.03052	0.02477
cg2121064	TRIM14	GATA-1 [	1497	1502	1.038567	TATCAT	1.95312	1.80234
cg2121064	TRIM14	Sp1 [T007	545	554	0.949391	TGGGCG(	0.01335	0.01658
cg2121064	TRIM14	LEF-1 [T0	781	788	0.85582	GACCAA	0.03052	0.03064
cg2121064	TRIM14	RXR-alpha	244	250	0.848226	CGAACC(	0.48828	0.51313
cg2121064	TRIM14	GR-beta [T	472	476	0.840383	CCATT	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	684	688	0.840383	AATGG	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	698	702	0.840383	AATGA	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	733	737	0.840383	AATGA	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	863	867	0.840383	TCATT	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	921	925	0.840383	CAATT	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	922	926	0.840383	AATTG	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	956	960	0.840383	CAATT	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	1205	1209	0.840383	CCATT	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	1267	1271	0.840383	TAATT	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	1436	1440	0.840383	AATTA	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	1626	1630	0.840383	CCATT	7.8125	7.2174
cg2121064	TRIM14	GR-beta [T	1770	1774	0.840383	CCATT	7.8125	7.2174
cg2121064	TRIM14	Sp1 [T007	508	517	0.813764	AGGGCG	0.01335	0.01658
cg2121064	TRIM14	AP-2alpha	95	100	0.678558	TCAGGC	0.48828	0.51196
cg2121064	TRIM14	HIF-1 [T0	1965	1973	0.640672	ACGTGC	0.04578	0.04961
cg2121064	TRIM14	RXR-alpha	33	39	0.62611	TAAACC(	0.12207	0.11915
cg2121064	TRIM14	HIF-1 [T0	268	276	0.543748	CCTGCA(	0.04578	0.04961
cg2121064	TRIM14	GATA-1 [	856	861	0.280028	AAGATA	0.97656	0.8795

cg2121064	TRIM14	GATA-1 [	879	884	0.280028	AAGATA	0.97656	0.8795
cg2121064	TRIM14	c-Ets-1 [T	83	89	0.256174	CTTCCT	0.24414	0.23743
cg2121064	TRIM14	AP-2alpha	8	13	0.226186	GCCTGG	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	185	190	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	213	218	0.226186	GCCTGG	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	295	300	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	559	564	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	658	663	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	1144	1149	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	1579	1584	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	1664	1669	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	AP-2alpha	1859	1864	0.226186	CCAGGC	0.97656	1.07867
cg2121064	TRIM14	p53 [T006	838	844	0.211706	CTTGCC	0.36621	0.40082
cg2121064	TRIM14	GR-alpha	22	26	0.207689	CCTCT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	41	45	0.207689	CCTTT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	75	79	0.207689	CCTTT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	136	140	0.207689	CCTCT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	147	151	0.207689	CCTTT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	647	651	0.207689	CCTCT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	713	717	0.207689	AGAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	814	818	0.207689	CCTCT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	833	837	0.207689	CCTCT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	843	847	0.207689	CCTTT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1018	1022	0.207689	AAAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1028	1032	0.207689	AGAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1038	1042	0.207689	AAAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1290	1294	0.207689	AAAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1704	1708	0.207689	CCTCT	7.8125	7.79817
cg2121064	TRIM14	Elk-1 [T00	723	731	0.134348	CTTCCT	0.06104	0.06399
cg2121064	TRIM14	GR-beta [	969	973	0	AATGT	3.90625	3.51525
cg2121064	TRIM14	GR-beta [	1268	1272	0	AATTT	3.90625	3.51525
cg2121064	TRIM14	GR-beta [	1842	1846	0	AAATT	3.90625	3.51525
cg2121064	TRIM14	GR-beta [	1988	1992	0	ACATT	3.90625	3.51525
cg2121064	TRIM14	XBP-1 [T	734	739	0	ATGACG	0.97656	0.94838
cg2121064	TRIM14	ENKTF-1	290	297	0	CAGCGC	0.12207	0.13179
cg2121064	TRIM14	ENKTF-1	405	412	0	CAGCGC	0.12207	0.13179
cg2121064	TRIM14	TFIID [T0	1286	1292	0	TAGAAA	1.09863	0.95175
cg2121064	TRIM14	TFIID [T0	1409	1415	0	TTTAAA	1.09863	0.95175
cg2121064	TRIM14	TFIID [T0	1949	1955	0	TTTTCA	1.09863	0.95175
cg2121064	TRIM14	GR-alpha	303	307	0	ACAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	506	510	0	ACAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1242	1246	0	ACAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1376	1380	0	ACAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1443	1447	0	ACAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1469	1473	0	ACAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1572	1576	0	CCTGT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1644	1648	0	ACAGG	7.8125	7.79817
cg2121064	TRIM14	GR-alpha	1761	1765	0	ACAGG	7.8125	7.79817

cg2121064	TRIM14	GR-alpha [	1929	1933	0	CCTAT	7.8125	7.79817
cg2121064	TRIM14	GR-alpha [	1941	1945	0	CCTGT	7.8125	7.79817
cg2121064	TRIM14	FOXP3 [T	870	875	0	CACAAC	1.46484	1.44953
cg2121064	TRIM14	FOXP3 [T	1517	1522	0	GTTGTG	1.46484	1.44953
cg2121064	TRIM14	FOXP3 [T	1813	1818	0	GACAAC	1.46484	1.44953
cg2121064	TRIM14	PR B [T00	1064	1070	0	TACTGT	0.36621	0.35051
cg2121064	TRIM14	PR B [T00	1300	1306	0	CACTGT	0.36621	0.35051
cg2121064	TRIM14	PR A [T01	1064	1070	0	TACTGT	0.36621	0.35051
cg2121064	TRIM14	PR A [T01	1300	1306	0	CACTGT	0.36621	0.35051
cg2121064	TRIM14	HNF-3alpl	1277	1284	0	TATTTTT	0.09155	0.07727
cg2121064	TRIM14	C/EBPbeta	78	81	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	162	165	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	335	338	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	426	429	0	ACAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	839	842	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	871	874	0	ACAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	953	956	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	955	958	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1016	1019	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1042	1045	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1057	1060	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1075	1078	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1079	1082	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1083	1086	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1087	1090	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1093	1096	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1180	1183	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1274	1277	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1431	1434	0	ACAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1477	1480	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1508	1511	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1512	1515	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1518	1521	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1528	1531	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1532	1535	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1538	1541	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1558	1561	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1560	1563	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1583	1586	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1635	1638	0	TTGT	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1660	1663	0	TTGC	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1676	1679	0	GCAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1814	1817	0	ACAA	15.625	15.26275
cg2121064	TRIM14	C/EBPbeta	1851	1854	0	TTGC	15.625	15.26275
cg2121064	TRIM14	YY1 [T00	61	64	0	ATGG	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	256	259	0	CCAT	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	393	396	0	CCAT	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	472	475	0	CCAT	7.8125	7.79459

cg2121064	TRIM14	YY1 [T00	685	688	0	ATGG	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	777	780	0	ATGG	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	975	978	0	CCAT	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	977	980	0	ATGG	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	1165	1168	0	CCAT	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	1205	1208	0	CCAT	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	1316	1319	0	ATGG	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	1501	1504	0	ATGG	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	1612	1615	0	ATGG	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	1626	1629	0	CCAT	7.8125	7.79459
cg2121064	TRIM14	YY1 [T00	1770	1773	0	CCAT	7.8125	7.79459
cg2121064	TRIM14	TFII-I [T0	821	826	0	CTTTCC	1.46484	1.48598
cg2121064	TRIM14	TFII-I [T0	853	858	0	GGAAAG	1.46484	1.48598
cg2121064	TRIM14	TFII-I [T0	1021	1026	0	GGAAAG	1.46484	1.48598
cg2121064	TRIM14	c-Ets-1 [T	723	729	0	CTTCCTC	0.24414	0.24982
cg2121064	TRIM14	c-Myb [T0	1472	1479	0	GGCAGT	0.03052	0.03205
cg2121064	TRIM14	ER-alpha [	796	800	0	TGACC	1.95312	1.99744
cg2121064	TRIM14	ER-alpha [	1331	1335	0	TGACC	1.95312	1.99744
cg2121064	TRIM14	RXR-alpha	1196	1202	0	GGGTTC	0.24414	0.24342
cg2121064	TRIM14	GR [T050	1071	1077	0	TTTTTTG	0.36621	0.33174
cg2121064	TRIM14	GR [T050	1114	1120	0	TTTTTTG	0.36621	0.33174
cg2121064	TRIM14	GR [T050	1270	1276	0	TTTTTTG	0.36621	0.33174
cg2121064	TRIM14	c-Myc [T0	272	277	0	CACGTG	0.48828	0.51196
cg2121064	TRIM14	Pax-5 [T0	217	223	0	GGGCTG	1.09863	1.24633
cg2121064	TRIM14	Pax-5 [T0	296	302	0	CAGGCC	1.09863	1.24633
cg2121064	TRIM14	IRF-2 [T0	818	823	0	TCACTT	0.48828	0.46235
cg2121064	TRIM14	IRF-2 [T0	1722	1727	0	AAGTGA	0.48828	0.46235
cg2121064	TRIM14	IRF-2 [T0	1792	1797	0	AAGTGA	0.48828	0.46235
cg2459782	WDR44	c-Ets-1 [T	982	988	9.841249	ATTCCC	0.24414	0.2459
cg2459782	WDR44	c-Myb [T0	1697	1704	9.815171	TAACTT	0.36621	0.3712
cg2459782	WDR44	STAT1bet	1061	1070	9.807397	CTTTCCT	0.14877	0.1495
cg2459782	WDR44	XBP-1 [T	47	52	9.789909	AGCCAT	1.95312	1.95208
cg2459782	WDR44	XBP-1 [T	160	165	9.789909	AGACAT	1.95312	1.95208
cg2459782	WDR44	XBP-1 [T	410	415	9.789909	AGACAT	1.95312	1.95208
cg2459782	WDR44	XBP-1 [T	1221	1226	9.789909	ATGGCG	1.95312	1.95208
cg2459782	WDR44	PR B [T00	144	150	9.743489	CTGTGT	1.09863	1.10292
cg2459782	WDR44	PR A [T01	144	150	9.743489	CTGTGT	1.09863	1.10292
cg2459782	WDR44	RAR-beta	1619	1628	9.641259	GGGGTT	0.21362	0.21243
cg2459782	WDR44	c-Ets-1 [T	1029	1035	9.585075	ATTCCC	0.36621	0.36441
cg2459782	WDR44	HNF-1C [	1063	1071	9.576203	TTCCTTA	0.19836	0.20229
cg2459782	WDR44	Pax-5 [T0	373	379	9.552105	GACGCC	1.46484	1.43083
cg2459782	WDR44	Pax-5 [T0	833	839	9.552105	GGGCAA	1.46484	1.43083
cg2459782	WDR44	Pax-5 [T0	1051	1057	9.552105	GGGCGG	1.46484	1.43083
cg2459782	WDR44	Pax-5 [T0	1280	1286	9.552105	GGGCGG	1.46484	1.43083
cg2459782	WDR44	TFIID [T0	514	520	9.552105	TTTGGA	1.46484	1.48472
cg2459782	WDR44	TFIID [T0	793	799	9.552105	TCCGAA	1.46484	1.48472
cg2459782	WDR44	NF-1 [T00	424	431	9.513281	TACGCC	0.73242	0.73053
cg2459782	WDR44	TFII-I [T0	216	221	9.512894	AAATCC	7.32422	7.29728

cg2459782	WDR44	TFII-I [T0	447	452	9.512894	GTTTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1172	1177	9.512894	CCTTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1210	1215	9.512894	GTGTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1244	1249	9.512894	GGAATT	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1388	1393	9.512894	GTGTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1424	1429	9.512894	GGACTT	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1509	1514	9.512894	GTTTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1523	1528	9.512894	CGGTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1661	1666	9.512894	GGACCG	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1777	1782	9.512894	CCGTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1816	1821	9.512894	GGAAGG	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1840	1845	9.512894	AAGTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1922	1927	9.512894	CGGTCC	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1953	1958	9.512894	GGATGG	7.32422	7.29728
cg2459782	WDR44	TFII-I [T0	1994	1999	9.512894	GGACAA	7.32422	7.29728
cg2459782	WDR44	FOXP3 [T	128	133	9.512894	AAGAAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	148	153	9.512894	GTTGGC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	338	343	9.512894	GTTATT	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	441	446	9.512894	ACCAAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	834	839	9.512894	GGCAAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	976	981	9.512894	AGCAAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	991	996	9.512894	ACCAAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	1042	1047	9.512894	GGCAAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	1430	1435	9.512894	CAGAAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	1622	1627	9.512894	GTTCTG	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	1721	1726	9.512894	GTTTAC	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	1821	1826	9.512894	GTTGGG	7.32422	7.35678
cg2459782	WDR44	FOXP3 [T	1884	1889	9.512894	AATAAC	7.32422	7.35678
cg2459782	WDR44	TCF-4E [T	513	519	9.453578	CTTTGG	0.48828	0.49215
cg2459782	WDR44	SRY [T00	513	521	9.264664	CTTTGG	0.12207	0.12265
cg2459782	WDR44	NF-AT1 [	1058	1066	9.18189	CCCCTT	0.22888	0.22959
cg2459782	WDR44	NF-AT1 [	1229	1237	9.18189	GGAAAG	0.22888	0.22959
cg2459782	WDR44	PPAR-alph	1523	1533	9.158357	CGGTCC	0.0515	0.04986
cg2459782	WDR44	NF-kappa	1024	1035	9.113045	CGGTCA	0.01872	0.01846
cg2459782	WDR44	NF-kappa	1578	1588	9.107834	GGGGAA	0.03576	0.0351
cg2459782	WDR44	c-Ets-1 [T	1578	1584	9.020687	GGGGAA	0.85449	0.85523
cg2459782	WDR44	LEF-1 [T0	513	520	8.973041	CTTTGG	0.54932	0.55326
cg2459782	WDR44	GR [T050	486	492	8.971049	CAAAAT	0.61035	0.61632
cg2459782	WDR44	GR [T050	1826	1832	8.971049	GTATTT	0.61035	0.61632
cg2459782	WDR44	c-Myb [T0	130	137	8.947824	GAACTT	0.39673	0.40028
cg2459782	WDR44	Elk-1 [T00	845	853	8.931691	CTTCCA	0.24414	0.24034
cg2459782	WDR44	Elk-1 [T00	1358	1366	8.931691	CTTCCC	0.24414	0.24034
cg2459782	WDR44	T3R-beta1	13	21	8.924046	TCACCG	0.2594	0.25766
cg2459782	WDR44	T3R-beta1	670	678	8.924046	TCACCG	0.2594	0.25766
cg2459782	WDR44	T3R-beta1	1457	1465	8.924046	GCGGGG	0.2594	0.25766
cg2459782	WDR44	c-Myb [T0	334	341	8.872587	GCGAGT	0.39673	0.40028
cg2459782	WDR44	PR B [T00	1582	1588	8.827054	AACAGC	0.36621	0.36944
cg2459782	WDR44	PR A [T01	1582	1588	8.827054	AACAGC	0.36621	0.36944

cg2459782	WDR44	Elk-1 [T00	1812	1820	8.797343	GGGGGG	0.24414	0.24034
cg2459782	WDR44	XBP-1 [T(	70	75	8.75604	ATGATA	2.92969	2.9674
cg2459782	WDR44	XBP-1 [T(	289	294	8.75604	GATCAT	2.92969	2.9674
cg2459782	WDR44	RXR-alpha	1285	1291	8.664139	GCTACC(	0.12207	0.12014
cg2459782	WDR44	RAR-beta	1429	1438	8.55975	TCAGAA(	0.26703	0.26657
cg2459782	WDR44	c-Ets-1 [T(	515	521	8.501115	TTGGAA(	0.24414	0.24529
cg2459782	WDR44	EBF [T054	1525	1535	8.430724	GTCCCA(	0.03052	0.02952
cg2459782	WDR44	c-Myb [T0	877	884	8.412632	AAACTG(	0.30518	0.30924
cg2459782	WDR44	c-Ets-1 [T(	233	239	8.373028	ATGGAA(	0.24414	0.24529
cg2459782	WDR44	PR B [T00	1399	1405	8.338824	CGCTGT	1.09863	1.10009
cg2459782	WDR44	PR B [T00	1684	1690	8.338824	AACAGG	1.09863	1.10009
cg2459782	WDR44	PR A [T01	1399	1405	8.338824	CGCTGT	1.09863	1.10009
cg2459782	WDR44	PR A [T01	1684	1690	8.338824	AACAGG	1.09863	1.10009
cg2459782	WDR44	E2F-1 [T0	1198	1205	8.336446	TCACCC(	0.15259	0.14963
cg2459782	WDR44	ATF3 [T01	104	111	8.313799	TGACGC	0.27466	0.27431
cg2459782	WDR44	PXR-1:RX	1519	1526	8.304332	TGAACG(	0.12207	0.12266
cg2459782	WDR44	GR-alpha [	185	189	8.281568	GGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	263	267	8.281568	CAAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	622	626	8.281568	CCTCC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	626	630	8.281568	CCTTC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	632	636	8.281568	GGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	644	648	8.281568	CCTCC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	648	652	8.281568	CCTTC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	791	795	8.281568	CCTCC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	805	809	8.281568	CGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	904	908	8.281568	CCTTC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	920	924	8.281568	CGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1077	1081	8.281568	CCTCG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1105	1109	8.281568	CCTCG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1142	1146	8.281568	GGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1151	1155	8.281568	CGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1154	1158	8.281568	GGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1172	1176	8.281568	CCTTC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1176	1180	8.281568	CCTCC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1241	1245	8.281568	CGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1372	1376	8.281568	CCTCC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1406	1410	8.281568	CCTCC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1421	1425	8.281568	GGAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1472	1476	8.281568	GAAGG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1489	1493	8.281568	CCTCG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1499	1503	8.281568	CCTCC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1567	1571	8.281568	CCTTC	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1655	1659	8.281568	CCTCG	7.8125	7.72956
cg2459782	WDR44	GR-alpha [	1817	1821	8.281568	GAAGG	7.8125	7.72956
cg2459782	WDR44	ENKTF-1	150	157	8.19852	TGGCAG(	0.73242	0.71737
cg2459782	WDR44	NF-1 [T00	1651	1658	8.191058	TTGGCCT	0.24414	0.24409
cg2459782	WDR44	IRF-1 [T0(	1225	1233	8.151819	CGTCGG	0.25177	0.25263
cg2459782	WDR44	c-Ets-1 [T(	744	750	8.116854	CTGGAA(	0.24414	0.2425

cg2459782	WDR44	GR-alpha [	59	63	8.073878	GTAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	285	289	8.073878	GCAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	297	301	8.073878	CTAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	367	371	8.073878	CCTGC	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	378	382	8.073878	CCTAG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	379	383	8.073878	CTAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	559	563	8.073878	CCTAC	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	585	589	8.073878	CCAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	603	607	8.073878	CCTGC	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	608	612	8.073878	GCAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	614	618	8.073878	CCTAG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	810	814	8.073878	GTAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	986	990	8.073878	CCTGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1179	1183	8.073878	CCAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1274	1278	8.073878	CCTAG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1275	1279	8.073878	CTAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1364	1368	8.073878	CCTAC	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1376	1380	8.073878	CCAGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1441	1445	8.073878	CCTGG	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1514	1518	8.073878	CCTAC	7.8125	7.72238
cg2459782	WDR44	GR-alpha [	1528	1532	8.073878	CCAGG	7.8125	7.72238
cg2459782	WDR44	Pax-5 [T0	588	594	8.014558	GGGCAC	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	716	722	8.014558	GGGCCG	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	1035	1041	8.014558	GAAGCC	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	1053	1059	8.014558	GCGGCC	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	1254	1260	8.014558	GATGCC	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	1327	1333	8.014558	GGGCAT	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	1445	1451	8.014558	GGGCTT	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	1493	1499	8.014558	GGGCAG	2.19727	2.14502
cg2459782	WDR44	Pax-5 [T0	1542	1548	8.014558	GGAGCC	2.19727	2.14502
cg2459782	WDR44	TFIID [T0	498	504	8.014558	TCTCAA	2.19727	2.24348
cg2459782	WDR44	TFIID [T0	701	707	8.014558	TTTGAT	2.19727	2.24348
cg2459782	WDR44	TFIID [T0	1227	1233	8.014558	TCGGAA	2.19727	2.24348
cg2459782	WDR44	TFIID [T0	1636	1642	8.014558	TTTCAA	2.19727	2.24348
cg2459782	WDR44	TFIID [T0	1835	1841	8.014558	TAAGAA	2.19727	2.24348
cg2459782	WDR44	p53 [T006	1542	1548	7.833758	GGAGCC	0.48828	0.47377
cg2459782	WDR44	T3R-beta1	491	499	7.813363	TCACCC	0.27466	0.27236
cg2459782	WDR44	E2F-1 [T0	168	175	7.771357	GCGGAG	0.30518	0.3
cg2459782	WDR44	NF-1 [T00	515	522	7.693985	TTGGAA	0.24414	0.24565
cg2459782	WDR44	c-Myb [T0	836	843	7.587189	CAACTA	0.42725	0.43114
cg2459782	WDR44	PPAR-alp	1440	1450	7.529496	ACCTGG	0.04482	0.04393
cg2459782	WDR44	GR [T050	429	435	7.527031	CAAAAT	1.83105	1.86007
cg2459782	WDR44	GR [T050	825	831	7.527031	TATTTC	1.83105	1.86007
cg2459782	WDR44	GR [T050	1016	1022	7.527031	CGCTTC	1.83105	1.86007
cg2459782	WDR44	GR [T050	1639	1645	7.527031	CAAACA	1.83105	1.86007
cg2459782	WDR44	GR [T050	1770	1776	7.527031	CTATTC	1.83105	1.86007
cg2459782	WDR44	C/EBPalp	66	72	7.465744	TGCAAT	0.48828	0.49653
cg2459782	WDR44	NF-1 [T00	1330	1337	7.445595	CATCCC	0.24414	0.24565

cg2459782	WDR44	c-Myb [T0	1730	1737	7.442719	TAACTT	0.42725	0.43114
cg2459782	WDR44	PEA3 [T0	1640	1648	7.421728	AAACAT	0.34332	0.34161
cg2459782	WDR44	PEA3 [T0	1952	1960	7.421728	AGGATG	0.34332	0.34161
cg2459782	WDR44	NF-AT2 [	443	452	7.292655	CAACGT	0.01717	0.01743
cg2459782	WDR44	HOXD9 [	1884	1893	7.270719	AATAAC	0.06866	0.07152
cg2459782	WDR44	HOXD10 [	1884	1893	7.270719	AATAAC	0.06866	0.07152
cg2459782	WDR44	c-Ets-1 [T	391	397	7.257837	ATTCCG	0.48828	0.4878
cg2459782	WDR44	XBP-1 [T	221	226	7.172312	CATCAT	2.92969	2.97018
cg2459782	WDR44	XBP-1 [T	1252	1257	7.172312	ATGATG	2.92969	2.97018
cg2459782	WDR44	c-Jun [T00	1303	1309	7.096776	TGACTG	0.73242	0.73173
cg2459782	WDR44	c-Jun [T00	1983	1989	7.096776	TGACTG	0.73242	0.73173
cg2459782	WDR44	c-Ets-1 [T	1510	1516	7.071349	TTTCCCT	0.73242	0.73099
cg2459782	WDR44	NFI/CTF [	1818	1825	7.014249	AAGGTT	0.73242	0.73214
cg2459782	WDR44	HNF-3alp	83	90	7.000129	AATAAA	0.82397	0.84946
cg2459782	WDR44	HNF-3alp	485	492	7.000129	TCAAAA	0.82397	0.84946
cg2459782	WDR44	HNF-3alp	825	832	7.000129	TATTTC	0.82397	0.84946
cg2459782	WDR44	HNF-3alp	856	863	7.000129	TGTAAA	0.82397	0.84946
cg2459782	WDR44	GCF [T00	694	702	6.987525	GCGCCG	0.45776	0.44706
cg2459782	WDR44	ENKTF-1	1390	1397	6.942764	GTCCGC	1.46484	1.44228
cg2459782	WDR44	ENKTF-1	1652	1659	6.942764	TGGCCT	1.46484	1.44228
cg2459782	WDR44	p53 [T006	1053	1059	6.938545	GCGGCC	1.09863	1.07125
cg2459782	WDR44	STAT1bet	1904	1913	6.908963	TAAAGG	0.103	0.10372
cg2459782	WDR44	MAZ [T00	641	653	6.902569	CCCCCT	0.00918	0.00907
cg2459782	WDR44	p53 [T006	676	682	6.891821	AACGCC	1.09863	1.07125
cg2459782	WDR44	p53 [T006	749	755	6.891821	ACCGCC	1.09863	1.07125
cg2459782	WDR44	p53 [T006	785	791	6.891821	ACCGCC	1.09863	1.07125
cg2459782	WDR44	E2F-1 [T0	831	838	6.846071	GCGGGC	0.30518	0.29782
cg2459782	WDR44	c-Ets-1 [T	448	454	6.815175	TTTCCC	0.73242	0.73099
cg2459782	WDR44	NF-1 [T00	115	122	6.722386	TTGGGC	0.24414	0.24147
cg2459782	WDR44	T3R-beta1	638	646	6.702681	TCACCC	0.21362	0.21147
cg2459782	WDR44	c-Ets-2 [T	1315	1323	6.695187	TGACAG	0.09155	0.09289
cg2459782	WDR44	E2F-1 [T0	782	789	6.611004	ATTACC	0.12207	0.12031
cg2459782	WDR44	Elk-1 [T00	660	668	6.598007	CTTCCG	0.06104	0.05967
cg2459782	WDR44	TFII-I [T0	245	250	6.581441	CACTCC	0.97656	0.97366
cg2459782	WDR44	TFII-I [T0	1347	1352	6.581441	ATCTCC	0.97656	0.97366
cg2459782	WDR44	TFII-I [T0	1603	1608	6.581441	GGAGAT	0.97656	0.97366
cg2459782	WDR44	FOXP3 [T	1874	1879	6.581441	GTTTTA	0.97656	0.99397
cg2459782	WDR44	RXR-alph	1824	1830	6.563693	GGGTAT	0.24414	0.2434
cg2459782	WDR44	p53 [T006	1035	1041	6.563521	GAAGCC	0.48828	0.47541
cg2459782	WDR44	p53 [T006	1445	1451	6.563521	GGGCTT	0.48828	0.47541
cg2459782	WDR44	MEF-2A [	5	15	6.559479	TATTTTT	0.02384	0.02461
cg2459782	WDR44	XBP-1 [T	1255	1260	6.478682	ATGCCC	0.97656	0.97062
cg2459782	WDR44	XBP-1 [T	1327	1332	6.478682	GGGCAT	0.97656	0.97062
cg2459782	WDR44	c-Myb [T0	1044	1051	6.454077	CAACTG	0.30518	0.3056
cg2459782	WDR44	TCF-4E [T	1018	1024	6.302385	CTTTGC	0.61035	0.61344
cg2459782	WDR44	GR-alpha [	32	36	6.263098	TGAGG	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	329	333	6.263098	TAAGG	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	668	672	6.263098	CCTCA	3.90625	3.91061

cg2459782	WDR44	GR-alpha [	681	685	6.263098	CCTCA	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	912	916	6.263098	CCTTA	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	946	950	6.263098	CCTTA	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	1048	1052	6.263098	TGAGG	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	1065	1069	6.263098	CCTTA	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	1099	1103	6.263098	CCTCA	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	1196	1200	6.263098	CCTCA	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	1574	1578	6.263098	TGAGG	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	1891	1895	6.263098	CCTTA	3.90625	3.91061
cg2459782	WDR44	GR-alpha [	1899	1903	6.263098	TGAGG	3.90625	3.91061
cg2459782	WDR44	c-Myb [T0	518	525	6.259888	GAACTG	0.30518	0.3056
cg2459782	WDR44	AP-1 [T00	1463	1471	6.25518	TGACTC	0.03052	0.03047
cg2459782	WDR44	c-Fos [T00	1459	1468	6.236188	GGGGTG	0.09155	0.09126
cg2459782	WDR44	IRF-1 [T0	448	456	6.203774	TTTCCC	0.16785	0.16909
cg2459782	WDR44	p53 [T006	373	379	6.188498	GACGCC	0.61035	0.594
cg2459782	WDR44	p53 [T006	1051	1057	6.188498	GGGCGG	0.61035	0.594
cg2459782	WDR44	p53 [T006	1280	1286	6.188498	GGGCGG	0.61035	0.594
cg2459782	WDR44	RXR-alph	808	814	6.119461	GGGTAG	0.73242	0.72249
cg2459782	WDR44	GR-alpha [	190	194	6.055408	CCTAA	3.90625	3.9065
cg2459782	WDR44	GR-alpha [	529	533	6.055408	TTAGG	3.90625	3.9065
cg2459782	WDR44	GR-alpha [	549	553	6.055408	CCTGA	3.90625	3.9065
cg2459782	WDR44	GR-alpha [	1007	1011	6.055408	TCAGG	3.90625	3.9065
cg2459782	WDR44	GR-alpha [	1260	1264	6.055408	CCTGA	3.90625	3.9065
cg2459782	WDR44	GR-alpha [	1452	1456	6.055408	TTAGG	3.90625	3.9065
cg2459782	WDR44	GR-alpha [	1595	1599	6.055408	CCTGA	3.90625	3.9065
cg2459782	WDR44	GR-alpha [	1931	1935	6.055408	TTAGG	3.90625	3.9065
cg2459782	WDR44	RXR-alph	1167	1173	5.937582	GTCACC	0.73242	0.72249
cg2459782	WDR44	RXR-alph	1460	1466	5.937582	GGGTGA	0.73242	0.72249
cg2459782	WDR44	GCF [T00	566	574	5.917256	CGGCCG	0.64087	0.6219
cg2459782	WDR44	GCF [T00	733	741	5.917256	GCGCTG	0.64087	0.6219
cg2459782	WDR44	GCF [T00	1181	1189	5.917256	AGGCGG	0.64087	0.6219
cg2459782	WDR44	p53 [T006	716	722	5.883561	GGGCCG	0.61035	0.594
cg2459782	WDR44	STAT4 [T	1172	1177	5.882353	CCTTCC	0.48828	0.48408
cg2459782	WDR44	STAT4 [T	1816	1821	5.882353	GGAAGG	0.48828	0.48408
cg2459782	WDR44	VDR [T00	1515	1523	5.771401	CTACTG	0.42725	0.42999
cg2459782	WDR44	c-Jun [T00	551	557	5.703976	TGACCC	0.48828	0.48665
cg2459782	WDR44	ENKTF-1	198	205	5.687009	TGGCTC	0.73242	0.7249
cg2459782	WDR44	ENKTF-1	348	355	5.687009	TAACGC	0.73242	0.7249
cg2459782	WDR44	ENKTF-1	423	430	5.687009	ATACGC	0.73242	0.7249
cg2459782	WDR44	ENKTF-1	580	587	5.687009	CAGAGC	0.73242	0.7249
cg2459782	WDR44	c-Ets-1 [T	908	914	5.686398	CTTCCC	0.36621	0.3623
cg2459782	WDR44	c-Fos [T00	1165	1174	5.679695	GAGTCA	0.04578	0.04537
cg2459782	WDR44	AR [T000	1207	1215	5.644986	GGTGTG	0.05341	0.05229
cg2459782	WDR44	AP-2alpha	705	710	5.568965	ATAGGC	0.48828	0.4878
cg2459782	WDR44	NFI/CTF [	396	403	5.558661	GGGCTT	0.54932	0.55038
cg2459782	WDR44	NFI/CTF [	1334	1341	5.558661	CCAAGC	0.54932	0.55038
cg2459782	WDR44	c-Ets-1 [T	1121	1127	5.558311	CTTCCC	0.36621	0.3623
cg2459782	WDR44	c-Ets-1 [T	1358	1364	5.558311	CTTCCC	0.36621	0.3623

cg2459782	WDR44	c-Ets-1 [T	1814	1820	5.558311	GGGGAA	0.36621	0.3623
cg2459782	WDR44	T3R-beta1	1198	1206	5.553412	TCACCC	0.21362	0.21287
cg2459782	WDR44	Pax-5 [T0	676	682	5.544826	AACGCC	0.73242	0.72046
cg2459782	WDR44	Pax-5 [T0	749	755	5.544826	ACCGCC	0.73242	0.72046
cg2459782	WDR44	Pax-5 [T0	785	791	5.544826	ACCGCC	0.73242	0.72046
cg2459782	WDR44	TFIID [T0	9	15	5.544826	TTTATCA	0.73242	0.75085
cg2459782	WDR44	TFIID [T0	91	97	5.544826	TTTACCA	0.73242	0.75085
cg2459782	WDR44	p53 [T006	766	772	5.345221	TTCGCC	0.61035	0.59991
cg2459782	WDR44	AP-1 [T00	1162	1170	5.321703	CAAGAG	0.09155	0.09214
cg2459782	WDR44	IRF-1 [T0	1062	1070	5.309227	TTTCCTT	0.22888	0.23087
cg2459782	WDR44	HOXD9 [T	1706	1715	5.275652	GTTTTTT	0.04578	0.04743
cg2459782	WDR44	HOXD9 [T	1872	1881	5.275652	GTGTTTT	0.04578	0.04743
cg2459782	WDR44	HOXD10 [	1706	1715	5.275652	GTTTTTT	0.04578	0.04743
cg2459782	WDR44	HOXD10 [	1872	1881	5.275652	GTGTTTT	0.04578	0.04743
cg2459782	WDR44	RXR-alpha	270	276	5.271235	CCCACC	0.61035	0.6044
cg2459782	WDR44	RXR-alpha	382	388	5.271235	GGGTGG	0.61035	0.6044
cg2459782	WDR44	ETF [T002	752	762	5.246906	GCCCCC	0.02861	0.02737
cg2459782	WDR44	ETF [T002	769	779	5.246906	GCCCCG	0.02861	0.02737
cg2459782	WDR44	c-Ets-2 [T	1063	1071	5.162974	TTCCTTA	0.13733	0.13828
cg2459782	WDR44	RXR-alpha	490	496	5.089356	ATCACC	0.48828	0.484
cg2459782	WDR44	GR-beta [T	193	197	5.042296	AATAC	3.90625	3.95351
cg2459782	WDR44	GR-beta [T	217	221	5.042296	AATCC	3.90625	3.95351
cg2459782	WDR44	GR-beta [T	458	462	5.042296	GTATT	3.90625	3.95351
cg2459782	WDR44	GR-beta [T	780	784	5.042296	GTATT	3.90625	3.95351
cg2459782	WDR44	GR-beta [T	824	828	5.042296	GTATT	3.90625	3.95351
cg2459782	WDR44	GR-beta [T	1826	1830	5.042296	GTATT	3.90625	3.95351
cg2459782	WDR44	GR-beta [T	1916	1920	5.042296	AATAC	3.90625	3.95351
cg2459782	WDR44	HNF-1A [	1064	1071	4.972635	TCCTTAA	0.36621	0.37179
cg2459782	WDR44	AR [T000	1385	1393	4.890444	GCTGTG	0.11444	0.11247
cg2459782	WDR44	AP-2alpha	189	194	4.890408	GCCTAA	0.97656	0.97567
cg2459782	WDR44	AP-2alpha	1931	1936	4.890408	TTAGGC	0.97656	0.97567
cg2459782	WDR44	c-Ets-1 [T	1227	1233	4.872197	TCGGAA	0.48828	0.49031
cg2459782	WDR44	RXR-alpha	1113	1119	4.86724	GAGACC	0.48828	0.484
cg2459782	WDR44	C/EBPalph	860	866	4.845599	AATTGC	0.97656	0.99332
cg2459782	WDR44	TFII-I [T0	387	392	4.756447	GGACAT	2.92969	2.93695
cg2459782	WDR44	TFII-I [T0	390	395	4.756447	CATTCC	2.92969	2.93695
cg2459782	WDR44	TFII-I [T0	433	438	4.756447	ATGTCC	2.92969	2.93695
cg2459782	WDR44	TFII-I [T0	981	986	4.756447	CATTCC	2.92969	2.93695
cg2459782	WDR44	TFII-I [T0	1028	1033	4.756447	CATTCC	2.92969	2.93695
cg2459782	WDR44	TFII-I [T0	1908	1913	4.756447	GGAAAT	2.92969	2.93695
cg2459782	WDR44	FOXP3 [T	30	35	4.756447	GTTGAG	2.92969	2.96063
cg2459782	WDR44	FOXP3 [T	501	506	4.756447	CAAAAC	2.92969	2.96063
cg2459782	WDR44	FOXP3 [T	682	687	4.756447	CTCAAC	2.92969	2.96063
cg2459782	WDR44	FOXP3 [T	699	704	4.756447	GTTTTG	2.92969	2.96063
cg2459782	WDR44	FOXP3 [T	1648	1653	4.756447	GTTTTG	2.92969	2.96063
cg2459782	WDR44	FOXP3 [T	1706	1711	4.756447	GTTTTT	2.92969	2.96063
cg2459782	WDR44	FOXP3 [T	1865	1870	4.756447	ATCAAC	2.92969	2.96063
cg2459782	WDR44	c-Ets-1 [T	845	851	4.654478	CTTCCAC	0.85449	0.85764

cg2459782 WDR44	p53 [T006	899	905	4.645444	CGCGCC	0.24414	0.23584
cg2459782 WDR44	AP-1 [T00	1476	1484	4.606866	GGGGAG	0.03052	0.03019
cg2459782 WDR44	NF-AT1 [	444	452	4.566689	AACGTT	0.06866	0.06925
cg2459782 WDR44	E2F-1 [T0	1379	1386	4.545253	GGTCCC	0.15259	0.14941
cg2459782 WDR44	RXR-alph	1138	1144	4.423008	GGGTGG	0.24414	0.24292
cg2459782 WDR44	STAT4 [T	390	395	4.411765	CATTCC	1.95312	1.94235
cg2459782 WDR44	STAT4 [T	844	849	4.411765	TCTTCC	1.95312	1.94235
cg2459782 WDR44	STAT4 [T	907	912	4.411765	TCTTCC	1.95312	1.94235
cg2459782 WDR44	STAT4 [T	981	986	4.411765	CATTCC	1.95312	1.94235
cg2459782 WDR44	STAT4 [T	1028	1033	4.411765	CATTCC	1.95312	1.94235
cg2459782 WDR44	STAT4 [T	1320	1325	4.411765	GGAAGC	1.95312	1.94235
cg2459782 WDR44	STAT4 [T	1357	1362	4.411765	TCTTCC	1.95312	1.94235
cg2459782 WDR44	c-Ets-1 [T	1242	1248	4.282938	GAGGAA	0.85449	0.85764
cg2459782 WDR44	RXR-alph	1296	1302	4.24113	GGGTAA	0.97656	0.9671
cg2459782 WDR44	C/EBPalp	210	216	4.235345	AGCAAT	0.48828	0.49358
cg2459782 WDR44	Sp1 [T007	783	792	4.212075	TTACCG	0.08965	0.08686
cg2459782 WDR44	AP-2alpha	59	64	4.211849	GTAGGC	0.97656	0.96469
cg2459782 WDR44	GR-beta [	4	8	4.201913	CTATT	7.8125	7.94607
cg2459782 WDR44	GR-beta [	83	87	4.201913	AATAA	7.8125	7.94607
cg2459782 WDR44	GR-beta [	213	217	4.201913	AATAA	7.8125	7.94607
cg2459782 WDR44	GR-beta [	327	331	4.201913	AATAA	7.8125	7.94607
cg2459782 WDR44	GR-beta [	339	343	4.201913	TTATT	7.8125	7.94607
cg2459782 WDR44	GR-beta [	489	493	4.201913	AATCA	7.8125	7.94607
cg2459782 WDR44	GR-beta [	726	730	4.201913	AATCG	7.8125	7.94607
cg2459782 WDR44	GR-beta [	1711	1715	4.201913	TTATT	7.8125	7.94607
cg2459782 WDR44	GR-beta [	1738	1742	4.201913	CTATT	7.8125	7.94607
cg2459782 WDR44	GR-beta [	1770	1774	4.201913	CTATT	7.8125	7.94607
cg2459782 WDR44	GR-beta [	1877	1881	4.201913	TTATT	7.8125	7.94607
cg2459782 WDR44	GR-beta [	1884	1888	4.201913	AATAA	7.8125	7.94607
cg2459782 WDR44	GR-beta [	1911	1915	4.201913	AATCG	7.8125	7.94607
cg2459782 WDR44	GR-beta [	1928	1932	4.201913	CTATT	7.8125	7.94607
cg2459782 WDR44	c-Jun [T00	1463	1469	4.1298	TGACTC	0.24414	0.24526
cg2459782 WDR44	p53 [T006	663	669	4.125254	CCGGCC	0.73242	0.71379
cg2459782 WDR44	p53 [T006	1189	1195	4.125254	CCGGCC	0.73242	0.71379
cg2459782 WDR44	p53 [T006	588	594	4.083527	GGGCAC	0.73242	0.71379
cg2459782 WDR44	IRF-1 [T0	1510	1518	4.035054	TTTCCCT	0.1297	0.13087
cg2459782 WDR44	RXR-alph	1206	1212	4.019014	GGGTGT	0.97656	0.9671
cg2459782 WDR44	c-Ets-2 [T	1903	1911	4.017001	GTAAAG	0.16022	0.16243
cg2459782 WDR44	Pax-5 [T0	25	31	4.007279	GGGCAG	1.09863	1.07975
cg2459782 WDR44	Pax-5 [T0	117	123	4.007279	GGGCAG	1.09863	1.07975
cg2459782 WDR44	TFIID [T	415	421	4.007279	TCGTAA	1.09863	1.13456
cg2459782 WDR44	TFIID [T	465	471	4.007279	TTTACA	1.09863	1.13456
cg2459782 WDR44	TFIID [T	1876	1882	4.007279	TTTATTA	1.09863	1.13456
cg2459782 WDR44	TFIID [T	1878	1884	4.007279	TATTAA	1.09863	1.13456
cg2459782 WDR44	Sp1 [T007	1279	1288	3.958376	GGGGCG	0.08965	0.08686
cg2459782 WDR44	E2F [T002	423	432	3.793883	ATACGC	0.04578	0.04588
cg2459782 WDR44	GR [T050	501	507	3.763516	CAAAAC	0.73242	0.74251
cg2459782 WDR44	GR [T050	511	517	3.763516	CTCTTT	0.73242	0.74251

cg2459782	WDR44	GR [T050	698	704	3.763516	CGTTTC	0.73242	0.74251
cg2459782	WDR44	GR [T050	1647	1653	3.763516	CGTTTC	0.73242	0.74251
cg2459782	WDR44	p53 [T006	396	402	3.750231	GGGCTT	0.73242	0.71379
cg2459782	WDR44	p53 [T006	1335	1341	3.750231	CAAGCC	0.73242	0.71379
cg2459782	WDR44	AP-2alpha	1566	1571	3.743866	GCCTTC	0.48828	0.48238
cg2459782	WDR44	Sp1 [T007	747	756	3.734601	GAACCG	0.07439	0.07186
cg2459782	WDR44	IRF-1 [T0	1904	1912	3.692688	TAAAGG	0.06866	0.06927
cg2459782	WDR44	Sp1 [T007	1050	1059	3.647682	AGGGCG	0.07439	0.07186
cg2459782	WDR44	AR [T000	430	438	3.59934	AAAATG	0.06866	0.06905
cg2459782	WDR44	c-Ets-1 [T	1403	1409	3.590463	GTTCCT	0.61035	0.60765
cg2459782	WDR44	p53 [T006	332	338	3.586914	GGGCGA	0.73242	0.7189
cg2459782	WDR44	p53 [T006	1106	1112	3.586914	CTCGCC	0.73242	0.7189
cg2459782	WDR44	p53 [T006	1131	1137	3.586914	CTCGCC	0.73242	0.7189
cg2459782	WDR44	RXR-alph	1531	1537	3.574782	GGGTCG	1.09863	1.08572
cg2459782	WDR44	p53 [T006	25	31	3.516613	GGGCAG	0.73242	0.7189
cg2459782	WDR44	p53 [T006	117	123	3.516613	GGGCAG	0.73242	0.7189
cg2459782	WDR44	c-Myb [T0	1979	1986	3.469384	CAACTG	0.12207	0.12203
cg2459782	WDR44	GCF [T00	601	609	3.409768	CTCCTG	0.03052	0.02982
cg2459782	WDR44	RXR-alph	265	271	3.392904	AGGACC	1.09863	1.08572
cg2459782	WDR44	RXR-alph	637	643	3.392904	CTCACC	1.09863	1.08572
cg2459782	WDR44	RXR-alph	1197	1203	3.392904	CTCACC	1.09863	1.08572
cg2459782	WDR44	p53 [T006	771	777	3.375208	CCCGCC	0.73242	0.7189
cg2459782	WDR44	p53 [T006	1455	1461	3.375208	GGGCGG	0.73242	0.7189
cg2459782	WDR44	GR-beta [T	87	91	3.361531	AATAT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	88	92	3.361531	ATATT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	420	424	3.361531	AATAT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	798	802	3.361531	AATCT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	1605	1609	3.361531	AGATT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	1668	1672	3.361531	AGATT	3.90625	3.99611
cg2459782	WDR44	c-Ets-2 [T	1239	1247	3.2883	ACCGAG	0.18311	0.18304
cg2459782	WDR44	c-Jun [T00	1164	1170	3.244843	AGAGTC	0.24414	0.24403
cg2459782	WDR44	AP-2alpha	738	743	3.229049	GCCTCT	0.48828	0.48238
cg2459782	WDR44	AP-2alpha	932	937	3.229049	GCCTCT	0.48828	0.48238
cg2459782	WDR44	AP-2alpha	1001	1006	3.229049	GCCTCT	0.48828	0.48238
cg2459782	WDR44	RXR-alph	1366	1372	3.170788	TACACC	0.24414	0.24522
cg2459782	WDR44	c-Fos [T00	1479	1488	3.154982	GAGTCA	0.06104	0.06065
cg2459782	WDR44	c-Ets-1 [T	660	666	3.102985	CTTCCG	0.24414	0.23981
cg2459782	WDR44	Pax-5 [T0	332	338	3.075094	GGGCGA	0.12207	0.11895
cg2459782	WDR44	Pax-5 [T0	1106	1112	3.075094	CTCGCC	0.12207	0.11895
cg2459782	WDR44	Pax-5 [T0	1131	1137	3.075094	CTCGCC	0.12207	0.11895
cg2459782	WDR44	E2F-1 [T0	1722	1729	3.059334	TTTACC	0.03052	0.03049
cg2459782	WDR44	p53 [T006	833	839	3.024997	GGGCAA	0.48828	0.47786
cg2459782	WDR44	STAT4 [T	659	664	2.941176	ACTTCC	2.92969	2.929
cg2459782	WDR44	STAT4 [T	746	751	2.941176	GGAACC	2.92969	2.929
cg2459782	WDR44	STAT4 [T	1061	1066	2.941176	CTTTCC	2.92969	2.929
cg2459782	WDR44	STAT4 [T	1120	1125	2.941176	ACTTCC	2.92969	2.929
cg2459782	WDR44	STAT4 [T	1229	1234	2.941176	GGAAAG	2.92969	2.929
cg2459782	WDR44	STAT4 [T	1402	1407	2.941176	TGTTCC	2.92969	2.929

cg2459782	WDR44	STAT4 [T	1580	1585	2.941176	GGAACA	2.92969	2.929
cg2459782	WDR44	p53 [T006	1254	1260	2.813291	GATGCC	0.48828	0.47786
cg2459782	WDR44	p53 [T006	1327	1333	2.813291	GGGCAT	0.48828	0.47786
cg2459782	WDR44	p53 [T006	1493	1499	2.813291	GGGCAG	0.48828	0.47786
cg2459782	WDR44	NF-1 [T00	988	995	2.813149	TGGACC	0.24414	0.24101
cg2459782	WDR44	PR B [T00	979	985	2.80933	AACATT	0.73242	0.74818
cg2459782	WDR44	PR A [T01	979	985	2.80933	AACATT	0.73242	0.74818
cg2459782	WDR44	TBP [T00	1212	1221	2.807313	GTCCTA	0.12207	0.12635
cg2459782	WDR44	c-Ets-2 [T	1174	1182	2.715313	TTCCTC	0.07629	0.07593
cg2459782	WDR44	c-Ets-2 [T	1404	1412	2.715313	TTCCTC	0.07629	0.07593
cg2459782	WDR44	c-Jun [T00	1478	1484	2.654872	GGAGTC	0.48828	0.48929
cg2459782	WDR44	RXR-alph	1431	1437	2.544678	AGAACC	0.85449	0.84796
cg2459782	WDR44	RXR-alph	1620	1626	2.544678	GGGTTC	0.85449	0.84796
cg2459782	WDR44	ENKTF-1	754	761	2.511511	CCCCGC	0.12207	0.11894
cg2459782	WDR44	c-Jun [T00	104	110	2.345465	TGACGC	0.48828	0.48929
cg2459782	WDR44	GCF [T00	606	614	2.339499	GCGCAG	0.06104	0.05925
cg2459782	WDR44	RAR-alph	545	557	2.298141	TCTGCC	0.00107	0.00106
cg2459782	WDR44	GATA-2 [	1890	1898	2.222222	ACCTTA	0.22888	0.23091
cg2459782	WDR44	GATA-1 [	401	406	2.176375	TGGATA	3.90625	3.92756
cg2459782	WDR44	GATA-1 [	1894	1899	2.176375	TATCGT	3.90625	3.92756
cg2459782	WDR44	Elk-1 [T00	1316	1324	2.164966	GACAGG	0.05341	0.05317
cg2459782	WDR44	c-Myb [T0	236	243	2.152744	GAACTG	0.06104	0.06059
cg2459782	WDR44	AP-2alpha	1104	1109	2.098119	GCCTCG	0.97656	0.95407
cg2459782	WDR44	AP-2alpha	1654	1659	2.098119	GCCTCG	0.97656	0.95407
cg2459782	WDR44	AP-2alpha	185	190	1.871933	GGAGGC	0.97656	0.95407
cg2459782	WDR44	AP-2alpha	632	637	1.871933	GGAGGC	0.97656	0.95407
cg2459782	WDR44	AP-2alpha	1498	1503	1.871933	GCCTCC	0.97656	0.95407
cg2459782	WDR44	C/EBPalp	305	311	1.830762	CTCAAT	0.48828	0.49438
cg2459782	WDR44	TFII-I [T0	1763	1768	1.824994	CTCTCC	0.48828	0.48408
cg2459782	WDR44	HIF-1 [T0	1590	1598	1.730353	ACGTGC	0.09155	0.0902
cg2459782	WDR44	RXR-alph	550	556	1.696452	CTGACC	0.48828	0.48222
cg2459782	WDR44	GR-beta [	41	45	1.680765	GAATT	3.90625	3.94936
cg2459782	WDR44	GR-beta [	1245	1249	1.680765	GAATT	3.90625	3.94936
cg2459782	WDR44	GR-beta [	1246	1250	1.680765	AATTC	3.90625	3.94936
cg2459782	WDR44	GR-beta [	1939	1943	1.680765	AATGC	3.90625	3.94936
cg2459782	WDR44	c-Ets-1 [T	1062	1068	1.641124	TTTCCTT	0.36621	0.36952
cg2459782	WDR44	c-Ets-1 [T	1906	1912	1.641124	AAGGAA	0.36621	0.36952
cg2459782	WDR44	C/EBPbeta	115	118	1.639871	TTGG	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	149	152	1.639871	TTGG	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	400	403	1.639871	TTGG	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	428	431	1.639871	CCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	442	445	1.639871	CCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	515	518	1.639871	TTGG	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	992	995	1.639871	CCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	1334	1337	1.639871	CCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	1651	1654	1.639871	TTGG	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	1822	1825	1.639871	TTGG	15.625	15.72563
cg2459782	WDR44	AR [T000	387	395	1.620358	GGACAT	0.09155	0.09119

cg2459782	WDR44	XBP-1 [T	1025	1030	1.583727	GGTCAT	0.97656	0.98146
cg2459782	WDR44	XBP-1 [T	1314	1319	1.583727	ATGACA	0.97656	0.98146
cg2459782	WDR44	Pax-5 [T0	771	777	1.537547	CCCGCC	0.73242	0.71311
cg2459782	WDR44	Pax-5 [T0	899	905	1.537547	CGCGCC	0.73242	0.71311
cg2459782	WDR44	Pax-5 [T0	1455	1461	1.537547	GGGCGG	0.73242	0.71311
cg2459782	WDR44	E2F-1 [T0	870	877	1.490375	GCGGGA	0.06104	0.06008
cg2459782	WDR44	STAT4 [T	235	240	1.470588	GGAACT	1.95312	1.96333
cg2459782	WDR44	STAT4 [T	447	452	1.470588	GTTTCC	1.95312	1.96333
cg2459782	WDR44	STAT4 [T	517	522	1.470588	GGAACT	1.95312	1.96333
cg2459782	WDR44	STAT4 [T	1244	1249	1.470588	GGAATT	1.95312	1.96333
cg2459782	WDR44	STAT4 [T	1509	1514	1.470588	GTTTCC	1.95312	1.96333
cg2459782	WDR44	NFI/CTF [	992	999	1.455588	CCAACC	0.06104	0.06019
cg2459782	WDR44	PR B [T00	1870	1876	1.404665	CAGTGT	0.36621	0.37023
cg2459782	WDR44	PR A [T01	1870	1876	1.404665	CAGTGT	0.36621	0.37023
cg2459782	WDR44	Sp1 [T007	1454	1463	1.388285	AGGGCG	0.03242	0.03129
cg2459782	WDR44	C/EBPbeta	31	34	1.366559	TTGA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	81	84	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	262	265	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	306	309	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	485	488	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	500	503	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	683	686	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	702	705	1.366559	TTGA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	1638	1641	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	C/EBPbeta	1866	1869	1.366559	TCAA	15.625	15.72563
cg2459782	WDR44	HNF-3alph	1880	1887	1.342935	TTAAAA	0.03052	0.03194
cg2459782	WDR44	ENKTF-1	1222	1229	1.255756	TGGCGT	0.24414	0.23904
cg2459782	WDR44	C/EBPalph	80	86	1.220508	CTCAAT	0.24414	0.247
cg2459782	WDR44	GCF [T00	893	901	1.070269	AGCCGG	0.18311	0.17647
cg2459782	WDR44	GATA-1 [	70	75	1.038567	ATGATA	1.95312	1.98662
cg2459782	WDR44	GATA-1 [	702	707	1.038567	TTGATA	1.95312	1.98662
cg2459782	WDR44	Sp1 [T007	769	778	0.949391	GCCCCG	0.01335	0.01279
cg2459782	WDR44	GATA-1 [	11	16	0.863549	TATCAC	1.95312	1.98662
cg2459782	WDR44	GATA-1 [	957	962	0.863549	TATCAC	1.95312	1.98662
cg2459782	WDR44	GR-beta [	42	46	0.840383	AATTA	7.8125	7.94706
cg2459782	WDR44	GR-beta [	49	53	0.840383	CCATT	7.8125	7.94706
cg2459782	WDR44	GR-beta [	69	73	0.840383	AATGA	7.8125	7.94706
cg2459782	WDR44	GR-beta [	95	99	0.840383	CCATT	7.8125	7.94706
cg2459782	WDR44	GR-beta [	223	227	0.840383	TCATT	7.8125	7.94706
cg2459782	WDR44	GR-beta [	307	311	0.840383	CAATT	7.8125	7.94706
cg2459782	WDR44	GR-beta [	308	312	0.840383	AATTA	7.8125	7.94706
cg2459782	WDR44	GR-beta [	860	864	0.840383	AATTG	7.8125	7.94706
cg2459782	WDR44	GR-beta [	1027	1031	0.840383	TCATT	7.8125	7.94706
cg2459782	WDR44	GR-beta [	1220	1224	0.840383	AATGG	7.8125	7.94706
cg2459782	WDR44	AP-2alpha	548	553	0.678558	GCCTGA	0.48828	0.48199
cg2459782	WDR44	AP-2alpha	1007	1012	0.678558	TCAGGC	0.48828	0.48199
cg2459782	WDR44	AP-2alpha	1594	1599	0.678558	GCCTGA	0.48828	0.48199
cg2459782	WDR44	GATA-1 [	294	299	0.280028	TATCTA	0.97656	0.99875

cg2459782	WDR44	AP-2alpha	1179	1184	0.226186	CCAGGC	0.97656	0.95305
cg2459782	WDR44	GR-alpha [	275	279	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	355	359	0.207689	AGAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	496	500	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	739	743	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	762	766	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	933	937	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1002	1006	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1060	1064	0.207689	CCTTT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1634	1638	0.207689	CCTTT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1673	1677	0.207689	AAAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1749	1753	0.207689	AGAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1781	1785	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1804	1808	0.207689	AAAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1844	1848	0.207689	CCTCT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1905	1909	0.207689	AAAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1950	1954	0.207689	AAAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1990	1994	0.207689	AGAGG	7.8125	7.81264
cg2459782	WDR44	Elk-1 [T00	1173	1181	0.134348	CTTCCTC	0.06104	0.06047
cg2459782	WDR44	c-Ets-1 [T	1173	1179	0.128087	CTTCCTC	0.24414	0.2429
cg2459782	WDR44	GATA-1 [	258	263	0.105011	TATCTC	0.97656	0.98738
cg2459782	WDR44	GR-alpha [	705	709	0	ATAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	955	959	0	CCTAT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1214	1218	0	CCTAT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1317	1321	0	ACAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1351	1355	0	CCTGT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1685	1689	0	ACAGG	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1737	1741	0	CCTAT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1769	1773	0	CCTAT	7.8125	7.81264
cg2459782	WDR44	GR-alpha [	1927	1931	0	CCTAT	7.8125	7.81264
cg2459782	WDR44	Pax-5 [T0	396	402	0	GGGCTT	1.09863	1.06846
cg2459782	WDR44	Pax-5 [T0	663	669	0	CCGGCC	1.09863	1.06846
cg2459782	WDR44	Pax-5 [T0	1189	1195	0	CCGGCC	1.09863	1.06846
cg2459782	WDR44	Pax-5 [T0	1335	1341	0	CAAGCC	1.09863	1.06846
cg2459782	WDR44	TFII-I [T0	402	407	0	GGATAG	1.46484	1.45997
cg2459782	WDR44	TFII-I [T0	1061	1066	0	CTTTCC	1.46484	1.45997
cg2459782	WDR44	TFII-I [T0	1229	1234	0	GGAAAG	1.46484	1.45997
cg2459782	WDR44	STAT4 [T	1908	1913	0	GGAAAT	0.48828	0.49387
cg2459782	WDR44	c-Ets-1 [T	1318	1324	0	CAGGAA	0.24414	0.2429
cg2459782	WDR44	YY1 [T00	49	52	0	CCAT	7.8125	7.81711
cg2459782	WDR44	YY1 [T00	95	98	0	CCAT	7.8125	7.81711
cg2459782	WDR44	YY1 [T00	220	223	0	CCAT	7.8125	7.81711
cg2459782	WDR44	YY1 [T00	231	234	0	CCAT	7.8125	7.81711
cg2459782	WDR44	YY1 [T00	233	236	0	ATGG	7.8125	7.81711
cg2459782	WDR44	YY1 [T00	1221	1224	0	ATGG	7.8125	7.81711
cg2459782	WDR44	YY1 [T00	1955	1958	0	ATGG	7.8125	7.81711
cg2459782	WDR44	GCF [T00	1186	1194	0	GCGCCG	0.09155	0.08765
cg2459782	WDR44	ER-alpha [	551	555	0	TGACC	1.95312	1.9404

cg2459782	WDR44	ER-alpha [	1025	1029	0	GGTCA	1.95312	1.9404
cg2459782	WDR44	GATA-1 [	74	79	0	TATCTG	0.97656	0.98738
cg2459782	WDR44	GATA-1 [	1612	1617	0	TATCTG	0.97656	0.98738
cg2459782	WDR44	C/EBPbeta	65	68	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	67	70	0	GCAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	211	214	0	GCAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	468	471	0	ACAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	692	695	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	829	832	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	835	838	0	GCAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	862	865	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	977	980	0	GCAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1020	1023	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1043	1046	0	GCAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1161	1164	0	ACAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1609	1612	0	TTGT	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1701	1704	0	TTGT	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1774	1777	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1791	1794	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1830	1833	0	TTGC	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1978	1981	0	ACAA	15.625	15.71349
cg2459782	WDR44	C/EBPbeta	1996	1999	0	ACAA	15.625	15.71349
cg2459782	WDR44	TFIID [T0	1707	1713	0	TTTTTTA	1.09863	1.13474
cg2459782	WDR44	TFIID [T0	1946	1952	0	TCTAAA	1.09863	1.13474
cg2459782	WDR44	FOXP3 [T	1977	1982	0	CACAAC	1.46484	1.47315
cg2459782	WDR44	c-Myb [T0	26	33	0	GGCAGT	0.03052	0.03022
cg2459782	WDR44	GR-beta [T	389	393	0	ACATT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	432	436	0	AATGT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	859	863	0	AAATT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	980	984	0	ACATT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	1693	1697	0	AATGT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	1853	1857	0	AATGT	3.90625	3.99611
cg2459782	WDR44	GR-beta [T	1971	1975	0	AATGT	3.90625	3.99611
cg2459782	WDR44	PR B [T00	1069	1075	0	AACAGT	0.36621	0.36944
cg2459782	WDR44	PR B [T00	1868	1874	0	AACAGT	0.36621	0.36944
cg2459782	WDR44	PR A [T01	1069	1075	0	AACAGT	0.36621	0.36944
cg2459782	WDR44	PR A [T01	1868	1874	0	AACAGT	0.36621	0.36944
cg2459782	WDR44	HNF-3alph	5	12	0	TATTTTT	0.09155	0.09511
cg2459782	WDR44	WT1 [T00	751	759	0	CGCCCC	0.00763	0.00729
cg2459782	WDR44	IRF-2 [T01	1300	1305	0	AAGTGA	0.48828	0.49387
cg2459782	WDR44	IRF-2 [T01	1742	1747	0	TCACTT	0.48828	0.49387
cg2244261	ZFAND3	HOXD9 [T	298	307	9.979471	AATATG	0.2327	0.24089
cg2244261	ZFAND3	HOXD10 [	298	307	9.979471	AATATG	0.2327	0.24089
cg2244261	ZFAND3	CTF [T001	612	623	9.903119	TGGCCA	0.04292	0.04259
cg2244261	ZFAND3	POU2F2 (	444	454	9.851917	ATTTTA	0.00191	0.00198
cg2244261	ZFAND3	COUP-TF	1400	1412	9.828903	TGCTGA	0.02503	0.0249
cg2244261	ZFAND3	XBP-1 [T0	402	407	9.789909	AGCCAT	1.95312	1.95208
cg2244261	ZFAND3	PR B [T00	449	455	9.743489	AACACA	1.09863	1.10292

cg2244261	ZFAND3	PR B [T00	1487	1493	9.743489	CTGTGT	1.09863	1.10292
cg2244261	ZFAND3	PR B [T00	1946	1952	9.743489	CTGTGT	1.09863	1.10292
cg2244261	ZFAND3	PR A [T01	449	455	9.743489	AACACA	1.09863	1.10292
cg2244261	ZFAND3	PR A [T01	1487	1493	9.743489	CTGTGT	1.09863	1.10292
cg2244261	ZFAND3	PR A [T01	1946	1952	9.743489	CTGTGT	1.09863	1.10292
cg2244261	ZFAND3	c-Myb [T0	568	575	9.729271	TTCAGT	0.36621	0.37054
cg2244261	ZFAND3	c-Myb [T0	1538	1545	9.729271	TTCAGT	0.36621	0.37054
cg2244261	ZFAND3	c-Ets-1 [T	163	169	9.713162	ATTCCC	0.36621	0.36441
cg2244261	ZFAND3	NF-AT1 [	1012	1020	9.691726	TTGGTT	0.16785	0.1682
cg2244261	ZFAND3	RAR-beta	68	77	9.641259	GGGGTT	0.21362	0.21243
cg2244261	ZFAND3	NF-AT2 [	663	672	9.5654	CACCCT	0.04578	0.04604
cg2244261	ZFAND3	NF-AT1 [	1050	1058	9.557905	GCATTT	0.16785	0.1682
cg2244261	ZFAND3	Pax-5 [T0	1259	1265	9.552105	TTTGCC	1.46484	1.43083
cg2244261	ZFAND3	TFIID [T0	628	634	9.552105	TTTCAC	1.46484	1.48472
cg2244261	ZFAND3	TFIID [T0	924	930	9.552105	TTTCCC	1.46484	1.48472
cg2244261	ZFAND3	TFIID [T0	1432	1438	9.552105	TCCCAA	1.46484	1.48472
cg2244261	ZFAND3	TFIID [T0	1742	1748	9.552105	TTTGAC	1.46484	1.48472
cg2244261	ZFAND3	TFIID [T0	1814	1820	9.552105	TTTGGT	1.46484	1.48472
cg2244261	ZFAND3	TFIID [T0	1938	1944	9.552105	TTTGGG	1.46484	1.48472
cg2244261	ZFAND3	NF-1 [T00	611	618	9.535536	GTGGCC	0.73242	0.73053
cg2244261	ZFAND3	NF-1 [T00	675	682	9.535536	TTGGCC	0.73242	0.73053
cg2244261	ZFAND3	NF-1 [T00	1042	1049	9.535536	TTGGAC	0.73242	0.73053
cg2244261	ZFAND3	NF-1 [T00	142	149	9.513281	TTGGGG	0.73242	0.73053
cg2244261	ZFAND3	NF-1 [T00	871	878	9.513281	TAACCC	0.73242	0.73053
cg2244261	ZFAND3	TFII-I [T0	40	45	9.512894	GGACAA	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	815	820	9.512894	GGATAA	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	947	952	9.512894	GGAAAC	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	1015	1020	9.512894	GTTTCC	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	1053	1058	9.512894	TTTTCC	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	1102	1107	9.512894	GGATTT	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	1687	1692	9.512894	AAATCC	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	1841	1846	9.512894	GGACAA	7.32422	7.29728
cg2244261	ZFAND3	TFII-I [T0	1910	1915	9.512894	GGACTT	7.32422	7.29728
cg2244261	ZFAND3	FOXP3 [T	71	76	9.512894	GTTCTG	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	117	122	9.512894	GTTCTG	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	305	310	9.512894	GTTGCT	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	906	911	9.512894	GTTCTG	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	968	973	9.512894	AATAAC	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	1020	1025	9.512894	CAGAAC	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	1378	1383	9.512894	GTTGGC	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	1462	1467	9.512894	ATAAAC	7.32422	7.35678
cg2244261	ZFAND3	FOXP3 [T	1710	1715	9.512894	GTTATT	7.32422	7.35678
cg2244261	ZFAND3	TCF-4E [T	48	54	9.453578	CTTTGA	0.48828	0.49215
cg2244261	ZFAND3	TCF-4E [T	1190	1196	9.453578	CTTTGA	0.48828	0.49215
cg2244261	ZFAND3	c-Jun [T00	619	625	9.442241	TGACAG	0.73242	0.73031
cg2244261	ZFAND3	NFI/CTF [	615	622	9.352332	CCAATG	0.54932	0.54821
cg2244261	ZFAND3	NFI/CTF [	875	882	9.352332	CCAATG	0.54932	0.54821
cg2244261	ZFAND3	NFI/CTF [	1008	1015	9.352332	AACATT	0.54932	0.54821

cg2244261	ZFAND3	c-Ets-1 [T	1940	1946	9.276861	TGGGAA	0.36621	0.36441
cg2244261	ZFAND3	SRY [T00	1190	1198	9.264664	CTTTGA	0.12207	0.12265
cg2244261	ZFAND3	HNF-1C [	1926	1934	9.253863	TTATGT	0.19836	0.20229
cg2244261	ZFAND3	MEF-2A [	1349	1359	9.220261	TATTTTT	0.07343	0.07563
cg2244261	ZFAND3	LEF-1 [T0	829	836	9.099721	CTTTGT	0.54932	0.55326
cg2244261	ZFAND3	STAT5A [	1912	1924	9.080962	ACTTTT	0.02816	0.02876
cg2244261	ZFAND3	c-Myb [T0	182	189	9.024874	CACAGT	0.39673	0.40028
cg2244261	ZFAND3	c-Jun [T00	860	866	9.013496	CATGTC	0.61035	0.61059
cg2244261	ZFAND3	LEF-1 [T0	1432	1439	8.973041	TCCCAA	0.54932	0.55326
cg2244261	ZFAND3	GR [T050	252	258	8.971049	GTATTT	0.61035	0.61632
cg2244261	ZFAND3	GR [T050	413	419	8.971049	CAAAAT	0.61035	0.61632
cg2244261	ZFAND3	GR [T050	1724	1730	8.971049	GTATTT	0.61035	0.61632
cg2244261	ZFAND3	c-Ets-2 [T	216	224	8.912323	TTCCTA	0.27466	0.27495
cg2244261	ZFAND3	AP-1 [T00	805	813	8.907204	GTTCAG	0.24414	0.24693
cg2244261	ZFAND3	T3R-beta1	1213	1221	8.904753	TCACCC	0.2594	0.25766
cg2244261	ZFAND3	HOXD9 [	508	517	8.847863	AATATT	0.04578	0.0476
cg2244261	ZFAND3	HOXD10 [	508	517	8.847863	AATATT	0.04578	0.0476
cg2244261	ZFAND3	EBF [T05	200	210	8.844893	AACCCA	0.01526	0.01496
cg2244261	ZFAND3	PR B [T00	623	629	8.827054	AGCTGT	0.36621	0.36944
cg2244261	ZFAND3	PR A [T01	623	629	8.827054	AGCTGT	0.36621	0.36944
cg2244261	ZFAND3	NFI/CTF [	671	678	8.814757	CCTCTT	0.48828	0.48804
cg2244261	ZFAND3	c-Ets-1 [T	87	93	8.809329	CTGGAA	0.85449	0.85523
cg2244261	ZFAND3	NF-1 [T00	1430	1437	8.790071	CCTCCC	0.24414	0.24467
cg2244261	ZFAND3	XBP-1 [T	92	97	8.75604	ATGAGA	2.92969	2.9674
cg2244261	ZFAND3	XBP-1 [T	461	466	8.75604	ATGAAA	2.92969	2.9674
cg2244261	ZFAND3	XBP-1 [T	1144	1149	8.75604	TTTCAT	2.92969	2.9674
cg2244261	ZFAND3	XBP-1 [T	1625	1630	8.75604	TTTCAT	2.92969	2.9674
cg2244261	ZFAND3	XBP-1 [T	1684	1689	8.75604	ATGAAA	2.92969	2.9674
cg2244261	ZFAND3	XBP-1 [T	1773	1778	8.75604	ATGAAA	2.92969	2.9674
cg2244261	ZFAND3	c-Myb [T0	11	18	8.728118	GTAAGT	0.30518	0.30924
cg2244261	ZFAND3	c-Jun [T00	579	585	8.571705	CCAGTC	0.12207	0.12139
cg2244261	ZFAND3	c-Jun [T00	1884	1890	8.571705	TGACTG	0.12207	0.12139
cg2244261	ZFAND3	p53 [T006	1992	1998	8.537081	GGGCTC	0.12207	0.11986
cg2244261	ZFAND3	USF2 [T0	1328	1337	8.532138	ACTACA	0.103	0.10183
cg2244261	ZFAND3	c-Myb [T0	639	646	8.412632	ACCAGT	0.30518	0.30924
cg2244261	ZFAND3	SRF [T007	404	416	8.352169	CCATAT	0.00197	0.00196
cg2244261	ZFAND3	HNF-3alp	253	260	8.343064	TATTTG	0.27466	0.28528
cg2244261	ZFAND3	HNF-3alp	256	263	8.343064	TTGAAA	0.27466	0.28528
cg2244261	ZFAND3	HNF-3alp	586	593	8.343064	CATTTT	0.27466	0.28528
cg2244261	ZFAND3	HNF-3alp	1508	1515	8.343064	TATTTC	0.27466	0.28528
cg2244261	ZFAND3	HNF-3alp	1826	1833	8.343064	TTTAAA	0.27466	0.28528
cg2244261	ZFAND3	HNF-3alp	1970	1977	8.343064	TTTAAA	0.27466	0.28528
cg2244261	ZFAND3	PR B [T00	113	119	8.338824	TTCTGT	1.09863	1.10009
cg2244261	ZFAND3	PR B [T00	1465	1471	8.338824	AACAGG	1.09863	1.10009
cg2244261	ZFAND3	PR A [T01	113	119	8.338824	TTCTGT	1.09863	1.10009
cg2244261	ZFAND3	PR A [T01	1465	1471	8.338824	AACAGG	1.09863	1.10009
cg2244261	ZFAND3	GR-alpha [	169	173	8.281568	CCTCC	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	424	428	8.281568	CAAGG	7.8125	7.72956

cg2244261	ZFAND3	GR-alpha [	682	686	8.281568	CCTCC	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	777	781	8.281568	CCTTG	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	933	937	8.281568	GGAGG	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	936	940	8.281568	GGAGG	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	1085	1089	8.281568	GAAGG	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	1088	1092	8.281568	GGAGG	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	1295	1299	8.281568	CCTCC	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	1430	1434	8.281568	CCTCC	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	1698	1702	8.281568	GAAGG	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	1985	1989	8.281568	CCTTG	7.8125	7.72956
cg2244261	ZFAND3	GR-alpha [	1989	1993	8.281568	GAAGG	7.8125	7.72956
cg2244261	ZFAND3	c-Jun [T00	1403	1409	8.242207	TGACCT	0.48828	0.49076
cg2244261	ZFAND3	HOXD9 [T	1662	1671	8.224939	CTTTTAT	0.08774	0.09025
cg2244261	ZFAND3	HOXD10 [	1662	1671	8.224939	CTTTTAT	0.08774	0.09025
cg2244261	ZFAND3	ENKTF-1	1380	1387	8.19852	TGGCCA	0.73242	0.71737
cg2244261	ZFAND3	NF-1 [T00	1426	1433	8.191058	TTGGCC	0.24414	0.24409
cg2244261	ZFAND3	SRY [T00	829	837	8.174786	CTTTGT	0.15259	0.15383
cg2244261	ZFAND3	c-Jun [T00	1744	1750	8.128539	TGACAT	0.48828	0.49076
cg2244261	ZFAND3	LEF-1 [T0	48	55	8.117221	CTTTGA	0.12207	0.1241
cg2244261	ZFAND3	LEF-1 [T0	883	890	8.117221	CTTTGA	0.12207	0.1241
cg2244261	ZFAND3	LEF-1 [T0	1190	1197	8.117221	CTTTGA	0.12207	0.1241
cg2244261	ZFAND3	LEF-1 [T0	1510	1517	8.117221	TTTCAA	0.12207	0.1241
cg2244261	ZFAND3	VDR [T00	1730	1738	8.079962	GTTCAG	0.24414	0.24712
cg2244261	ZFAND3	IRF-1 [T0	1016	1024	8.078284	TTTCCA	0.25177	0.25263
cg2244261	ZFAND3	GR-alpha [	37	41	8.073878	CCTGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	64	68	8.073878	CCTAG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	65	69	8.073878	CTAGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	130	134	8.073878	CTAGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	203	207	8.073878	CCAGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	218	222	8.073878	CCTAG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	278	282	8.073878	CCTGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	760	764	8.073878	CCAGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	769	773	8.073878	GCAGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1198	1202	8.073878	CCTAG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1267	1271	8.073878	CCAGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1285	1289	8.073878	CCTGC	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1322	1326	8.073878	CCTGC	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1334	1338	8.073878	CCTGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1383	1387	8.073878	CCAGG	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1691	1695	8.073878	CCTAC	7.8125	7.72238
cg2244261	ZFAND3	GR-alpha [	1963	1967	8.073878	CTAGG	7.8125	7.72238
cg2244261	ZFAND3	HNF-1C [	710	718	8.067744	GTTATA	0.19836	0.20224
cg2244261	ZFAND3	TFIID [T0	49	55	8.014558	TTTGAG	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	255	261	8.014558	TTTGAA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	884	890	8.014558	TTTGAA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1105	1111	8.014558	TTTGTG	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1191	1197	8.014558	TTTGAG	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1510	1516	8.014558	TTTCAA	2.19727	2.24348

cg2244261	ZFAND3	TFIID [T0	1556	1562	8.014558	TAGCAA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1593	1599	8.014558	TTTCTTA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1625	1631	8.014558	TTTCATA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1758	1764	8.014558	TTTGAA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1772	1778	8.014558	TATGAA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1862	1868	8.014558	TTTGAA	2.19727	2.24348
cg2244261	ZFAND3	TFIID [T0	1954	1960	8.014558	TTTCTTA	2.19727	2.24348
cg2244261	ZFAND3	C/EBPalph	1040	1046	8.006685	CATTGG	0.24414	0.24674
cg2244261	ZFAND3	MEF-2A [	1113	1123	7.982343	TATTTTT	0.04005	0.04149
cg2244261	ZFAND3	MEF-2A [	1630	1640	7.982343	TATTTTT	0.04005	0.04149
cg2244261	ZFAND3	c-Jun [T00	993	999	7.937147	CTAGTC	0.48828	0.49076
cg2244261	ZFAND3	T3R-beta1	1981	1989	7.774776	TCACCC	0.27466	0.27236
cg2244261	ZFAND3	c-Myb [T0	1943	1950	7.739476	GAACTG	0.42725	0.43114
cg2244261	ZFAND3	IRF-1 [T0	943	951	7.732782	CTCTGG	0.14496	0.14449
cg2244261	ZFAND3	NF-AT1 [	1012	1021	7.579763	TTGGTT	0.00763	0.00769
cg2244261	ZFAND3	HNF-1B [	709	717	7.554307	AGTTAT	0.09155	0.09368
cg2244261	ZFAND3	c-Jun [T00	855	861	7.538568	GATGTC	0.48828	0.48775
cg2244261	ZFAND3	GR [T050	149	155	7.527031	ACTTTT	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	429	435	7.527031	CAAAAT	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	548	554	7.527031	TCTTTTG	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	1256	1262	7.527031	ACTTTT	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	1529	1535	7.527031	ACTTTT	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	1559	1565	7.527031	CAAATA	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	1615	1621	7.527031	TATTTT	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	1718	1724	7.527031	ACTTTT	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	1739	1745	7.527031	TCTTTTG	1.83105	1.86007
cg2244261	ZFAND3	GR [T050	1811	1817	7.527031	ATGTTT	1.83105	1.86007
cg2244261	ZFAND3	PEA3 [T0	771	779	7.421728	AGGCAT	0.34332	0.34161
cg2244261	ZFAND3	LEF-1 [T0	745	752	7.396545	GCACAA	0.21362	0.21302
cg2244261	ZFAND3	HOXD9 [	475	484	7.270719	AATATA	0.06866	0.07152
cg2244261	ZFAND3	HOXD10 [	475	484	7.270719	AATATA	0.06866	0.07152
cg2244261	ZFAND3	c-Ets-1 [T	924	930	7.199436	TTTCCC	0.73242	0.73099
cg2244261	ZFAND3	SRY [T00	744	752	7.175614	TGCACA	0.30518	0.30739
cg2244261	ZFAND3	SRY [T00	883	891	7.175614	CTTTGA	0.30518	0.30739
cg2244261	ZFAND3	XBP-1 [T	137	142	7.172312	ATGATT	2.92969	2.97018
cg2244261	ZFAND3	XBP-1 [T	301	306	7.172312	ATGAGT	2.92969	2.97018
cg2244261	ZFAND3	XBP-1 [T	437	442	7.172312	ATGAAT	2.92969	2.97018
cg2244261	ZFAND3	XBP-1 [T	1037	1042	7.172312	ACTCAT	2.92969	2.97018
cg2244261	ZFAND3	XBP-1 [T	1289	1294	7.172312	CCTCAT	2.92969	2.97018
cg2244261	ZFAND3	XBP-1 [T	1549	1554	7.172312	ATTCAT	2.92969	2.97018
cg2244261	ZFAND3	XBP-1 [T	1807	1812	7.172312	AATCAT	2.92969	2.97018
cg2244261	ZFAND3	TFIID [T0	1554	1560	7.082373	TTTAGC	0.12207	0.12407
cg2244261	ZFAND3	c-Ets-1 [T	1054	1060	7.071349	TTTCCC	0.73242	0.73099
cg2244261	ZFAND3	c-Ets-1 [T	1468	1474	7.071349	AGGGAA	0.73242	0.73099
cg2244261	ZFAND3	HNF-1C [	1710	1718	7.028835	GTTATT	0.08392	0.08606
cg2244261	ZFAND3	C/EBPalph	614	620	7.00174	GCCAAT	0.73242	0.74337
cg2244261	ZFAND3	C/EBPalph	1842	1848	7.00174	GACAAT	0.73242	0.74337
cg2244261	ZFAND3	HNF-3alph	124	131	7.000129	TATTTA	0.82397	0.84946

cg2244261	ZFAND3	HNF-3alp	294	301	7.000129	AATAAA	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	428	435	7.000129	GCAAAA	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1138	1145	7.000129	AATTTT	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1147	1154	7.000129	CATTTT	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1168	1175	7.000129	TATTTA	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1175	1182	7.000129	TATTTA	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1615	1622	7.000129	TATTTT	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1630	1637	7.000129	TATTTT	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1764	1771	7.000129	AATAAA	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1830	1837	7.000129	AATTTA	0.82397	0.84946
cg2244261	ZFAND3	HNF-3alp	1897	1904	7.000129	AAAAAA	0.82397	0.84946
cg2244261	ZFAND3	ENKTF-1	674	681	6.942764	CTTGGC	1.46484	1.44228
cg2244261	ZFAND3	VDR [T00	194	202	6.925682	TCTTTG	0.42725	0.43062
cg2244261	ZFAND3	VDR [T00	572	580	6.925682	GTTCAG	0.42725	0.43062
cg2244261	ZFAND3	C/EBPalp	270	276	6.85549	AATTGA	0.73242	0.74337
cg2244261	ZFAND3	C/EBPalp	1452	1458	6.85549	TGCAAT	0.73242	0.74337
cg2244261	ZFAND3	c-Jun [T00	1209	1215	6.787369	TCTGTC	0.73242	0.73173
cg2244261	ZFAND3	c-Jun [T00	1584	1590	6.787369	TCTGTC	0.73242	0.73173
cg2244261	ZFAND3	NFI/CTF [	1903	1910	6.786076	TTGATT	0.73242	0.73214
cg2244261	ZFAND3	LEF-1 [T0	195	202	6.75468	CTTTGA	0.06104	0.06131
cg2244261	ZFAND3	NF-1 [T00	1379	1386	6.722386	TTGGCC	0.24414	0.24147
cg2244261	ZFAND3	HNF-1B [	1541	1549	6.604089	AGTTAA	0.04578	0.04691
cg2244261	ZFAND3	FOXP3 [T	389	394	6.581441	TAAAAC	0.97656	0.99397
cg2244261	ZFAND3	FOXP3 [T	501	506	6.581441	GTTTTA	0.97656	0.99397
cg2244261	ZFAND3	FOXP3 [T	733	738	6.581441	GTTTTA	0.97656	0.99397
cg2244261	ZFAND3	FOXP3 [T	1368	1373	6.581441	GTTTTA	0.97656	0.99397
cg2244261	ZFAND3	AR [T000	1044	1052	6.566205	GGACAG	0.19836	0.19597
cg2244261	ZFAND3	PXR-1:RX	1727	1734	6.5446	TTTGTT	0.24414	0.24672
cg2244261	ZFAND3	TCF-4 [T0	1189	1198	6.509564	TCTTTG	0.04959	0.05016
cg2244261	ZFAND3	RAR-beta	1365	1374	6.415195	GGGGTT	0.18311	0.183
cg2244261	ZFAND3	RAR-beta	1748	1757	6.415195	ATTTAA	0.18311	0.183
cg2244261	ZFAND3	TCF-4E [T	195	201	6.302385	CTTTGA	0.61035	0.61344
cg2244261	ZFAND3	TCF-4E [T	883	889	6.302385	CTTTGA	0.61035	0.61344
cg2244261	ZFAND3	TCF-4E [T	1511	1517	6.302385	TTCAAA	0.61035	0.61344
cg2244261	ZFAND3	GR-alpha [	174	178	6.263098	CCTCA	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	497	501	6.263098	TAAGG	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	660	664	6.263098	CCTCA	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	851	855	6.263098	TAAGG	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	952	956	6.263098	CCTCA	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	963	967	6.263098	TAAGG	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	1097	1101	6.263098	CCTTA	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	1289	1293	6.263098	CCTCA	3.90625	3.91061
cg2244261	ZFAND3	GR-alpha [	1406	1410	6.263098	CCTCA	3.90625	3.91061
cg2244261	ZFAND3	c-Myb [T0	1396	1403	6.259888	GAACTG	0.30518	0.3056
cg2244261	ZFAND3	SRY [T00	195	203	6.176442	CTTTGA	0.15259	0.15366
cg2244261	ZFAND3	SRY [T00	1509	1517	6.176442	ATTTCA	0.15259	0.15366
cg2244261	ZFAND3	GR-alpha [	19	23	6.055408	TCAGG	3.90625	3.9065
cg2244261	ZFAND3	GR-alpha [	291	295	6.055408	CCTAA	3.90625	3.9065

cg2244261	ZFAND3	GR-alpha [	811	815	6.055408	TCAGG	3.90625	3.9065
cg2244261	ZFAND3	GR-alpha [	954	958	6.055408	TCAGG	3.90625	3.9065
cg2244261	ZFAND3	GR-alpha [	978	982	6.055408	CCTGA	3.90625	3.9065
cg2244261	ZFAND3	GR-alpha [	1099	1103	6.055408	TTAGG	3.90625	3.9065
cg2244261	ZFAND3	GR-alpha [	1408	1412	6.055408	TCAGG	3.90625	3.9065
cg2244261	ZFAND3	GR-alpha [	1732	1736	6.055408	TCAGG	3.90625	3.9065
cg2244261	ZFAND3	c-Myb [T0	839	846	6.04018	GTCAGT	0.21362	0.21535
cg2244261	ZFAND3	c-Myb [T0	1587	1594	6.04018	GTCAGT	0.21362	0.21535
cg2244261	ZFAND3	c-Ets-1 [T	945	951	6.039428	CTGGAA	0.36621	0.36731
cg2244261	ZFAND3	c-Ets-1 [T	1016	1022	6.039428	TTTCCA	0.36621	0.36731
cg2244261	ZFAND3	HNF-1B [	1709	1717	6.006024	GGTTAT	0.09918	0.10196
cg2244261	ZFAND3	C/EBPalph	1010	1016	5.996794	CATTGG	0.97656	0.99
cg2244261	ZFAND3	RXR-alpha	145	151	5.937582	GGGTAC	0.73242	0.72249
cg2244261	ZFAND3	RXR-alpha	1212	1218	5.937582	GTCACC	0.73242	0.72249
cg2244261	ZFAND3	RXR-alpha	1569	1575	5.937582	AGTACC	0.73242	0.72249
cg2244261	ZFAND3	HOXD9 [	507	516	5.898575	AAATAT	0.05722	0.0598
cg2244261	ZFAND3	HOXD10 [	507	516	5.898575	AAATAT	0.05722	0.0598
cg2244261	ZFAND3	HNF-1C [	1542	1550	5.821046	GTTAAG	0.14496	0.14811
cg2244261	ZFAND3	TCF-4 [T0	47	56	5.810677	ACTTTG	0.04578	0.04635
cg2244261	ZFAND3	STAT1bet	923	932	5.796867	ATTTCC	0.1545	0.1557
cg2244261	ZFAND3	C/EBPalph	41	47	5.781231	GACAAT	0.97656	0.99
cg2244261	ZFAND3	VDR [T00	805	813	5.771401	GTTCAG	0.42725	0.42999
cg2244261	ZFAND3	VDR [T00	1271	1279	5.771401	GTTCAA	0.42725	0.42999
cg2244261	ZFAND3	c-Jun [T00	755	761	5.703976	TGACCC	0.48828	0.48665
cg2244261	ZFAND3	ENKTF-1	61	68	5.687009	TGGCCT	0.73242	0.7249
cg2244261	ZFAND3	NFI/CTF [	1811	1818	5.558661	ATGTTT	0.54932	0.55038
cg2244261	ZFAND3	NFI/CTF [	1935	1942	5.558661	AAGTTT	0.54932	0.55038
cg2244261	ZFAND3	TFIID [T0	7	13	5.544826	TTTAGT	0.73242	0.75085
cg2244261	ZFAND3	TFIID [T0	446	452	5.544826	TTTAAC	0.73242	0.75085
cg2244261	ZFAND3	TFIID [T0	524	530	5.544826	TACTAA	0.73242	0.75085
cg2244261	ZFAND3	TFIID [T0	1353	1359	5.544826	TTTAGT	0.73242	0.75085
cg2244261	ZFAND3	TFIID [T0	1370	1376	5.544826	TTTACC	0.73242	0.75085
cg2244261	ZFAND3	TFIID [T0	1802	1808	5.544826	TGATAA	0.73242	0.75085
cg2244261	ZFAND3	HNF-1C [	373	381	5.498706	ATATGT	0.07629	0.07817
cg2244261	ZFAND3	GR [T050	827	833	5.207533	GTCTTT	0.24414	0.24606
cg2244261	ZFAND3	AP-2alpha	1514	1519	5.100982	AAAGGC	0.97656	0.97567
cg2244261	ZFAND3	USF2 [T0	20	29	5.052423	CAGGTG	0.103	0.10178
cg2244261	ZFAND3	USF2 [T0	1414	1423	5.052423	GAGCCA	0.103	0.10178
cg2244261	ZFAND3	AP-1 [T00	834	842	5.043062	TGGGAG	0.12207	0.12162
cg2244261	ZFAND3	GR-beta [	44	48	5.042296	AATAC	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	123	127	5.042296	GTATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	246	250	5.042296	AATAC	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	252	256	5.042296	GTATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	493	497	5.042296	GTATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	1102	1106	5.042296	GGATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	1310	1314	5.042296	GGATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	1348	1352	5.042296	GTATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [	1547	1551	5.042296	GTATT	3.90625	3.95351

cg2244261	ZFAND3	GR-beta [T	1688	1692	5.042296	AATCC	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [T	1724	1728	5.042296	GTATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [T	1735	1739	5.042296	GGATT	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [T	1820	1824	5.042296	AATAC	3.90625	3.95351
cg2244261	ZFAND3	GR-beta [T	1868	1872	5.042296	AATAC	3.90625	3.95351
cg2244261	ZFAND3	C/EBPalph	1236	1242	5.024728	TGCAAT	0.97656	0.99332
cg2244261	ZFAND3	XBP-1 [T	762	767	4.894955	AGGCAT	0.97656	0.96979
cg2244261	ZFAND3	XBP-1 [T	771	776	4.894955	AGGCAT	0.97656	0.96979
cg2244261	ZFAND3	XBP-1 [T	1048	1053	4.894955	AGGCAT	0.97656	0.96979
cg2244261	ZFAND3	USF1 [T0	994	1003	4.89185	TAGTCA	0.04578	0.04527
cg2244261	ZFAND3	NF-1 [T00	1907	1914	4.880836	TTGGGA	0.24414	0.24398
cg2244261	ZFAND3	RXR-alpha	206	212	4.86724	GGGTAT	0.48828	0.484
cg2244261	ZFAND3	RXR-alpha	939	945	4.86724	GGGTCT	0.48828	0.484
cg2244261	ZFAND3	NF-Y [T0	1906	1913	4.867193	ATTGGG	0.36621	0.36847
cg2244261	ZFAND3	C/EBPalph	1901	1907	4.845599	AATTGA	0.97656	0.99332
cg2244261	ZFAND3	HNF-3alph	384	391	4.842999	AATTTA	0.09155	0.09582
cg2244261	ZFAND3	HNF-3alph	443	450	4.842999	AATTTA	0.09155	0.09582
cg2244261	ZFAND3	HNF-3alph	1119	1126	4.842999	TATTTA	0.09155	0.09582
cg2244261	ZFAND3	HNF-3alph	1152	1159	4.842999	TTAAAA	0.09155	0.09582
cg2244261	ZFAND3	HNF-3alph	1160	1167	4.842999	TATTTA	0.09155	0.09582
cg2244261	ZFAND3	HNF-3alph	1455	1462	4.842999	AATTTA	0.09155	0.09582
cg2244261	ZFAND3	HNF-1A [	1542	1549	4.828753	GTTAAG	0.36621	0.37179
cg2244261	ZFAND3	c-Ets-1 [T	719	725	4.782565	GTGGAA	0.48828	0.49031
cg2244261	ZFAND3	TFII-I [T0	89	94	4.756447	GGAATG	2.92969	2.93695
cg2244261	ZFAND3	TFII-I [T0	878	883	4.756447	ATGTCC	2.92969	2.93695
cg2244261	ZFAND3	TFII-I [T0	923	928	4.756447	ATTTCC	2.92969	2.93695
cg2244261	ZFAND3	TFII-I [T0	1470	1475	4.756447	GGAAAT	2.92969	2.93695
cg2244261	ZFAND3	TFII-I [T0	1562	1567	4.756447	ATATCC	2.92969	2.93695
cg2244261	ZFAND3	FOXP3 [T	4	9	4.756447	GTTTTT	2.92969	2.96063
cg2244261	ZFAND3	FOXP3 [T	15	20	4.756447	GTTTTC	2.92969	2.96063
cg2244261	ZFAND3	FOXP3 [T	98	103	4.756447	GTTTTG	2.92969	2.96063
cg2244261	ZFAND3	FOXP3 [T	419	424	4.756447	CAAAAC	2.92969	2.96063
cg2244261	ZFAND3	FOXP3 [T	843	848	4.756447	GTTTTC	2.92969	2.96063
cg2244261	ZFAND3	FOXP3 [T	1591	1596	4.756447	GTTTTC	2.92969	2.96063
cg2244261	ZFAND3	FOXP3 [T	1645	1650	4.756447	GTTTTT	2.92969	2.96063
cg2244261	ZFAND3	FOXP3 [T	1704	1709	4.756447	GTTTTG	2.92969	2.96063
cg2244261	ZFAND3	Ik-1 [T027	1300	1312	4.748597	CGAGTA	0.00313	0.00308
cg2244261	ZFAND3	HNF-1A [	1780	1787	4.684871	GTTAAG	0.12207	0.12485
cg2244261	ZFAND3	IRF-1 [T0	668	676	4.626471	TTTCCTC	0.05341	0.05405
cg2244261	ZFAND3	IRF-1 [T0	924	932	4.549799	TTTCCC	0.05341	0.05405
cg2244261	ZFAND3	STAT5A [	1354	1366	4.540481	TTAGTA	0.00536	0.00547
cg2244261	ZFAND3	USF2 [T0	1409	1418	4.528187	CAGGTG	0.06866	0.06782
cg2244261	ZFAND3	c-Jun [T00	807	813	4.441904	TCAGTC	0.12207	0.12266
cg2244261	ZFAND3	AP-2alpha	63	68	4.438035	GCCTAG	0.97656	0.96979
cg2244261	ZFAND3	AP-2alpha	130	135	4.438035	CTAGGC	0.97656	0.96979
cg2244261	ZFAND3	AP-2alpha	1963	1968	4.438035	CTAGGC	0.97656	0.96979
cg2244261	ZFAND3	RXR-alpha	1445	1451	4.423008	GGGTTG	0.24414	0.24292
cg2244261	ZFAND3	STAT4 [T	89	94	4.411765	GGAATG	1.95312	1.94235

cg2244261	ZFAND3	STAT4 [T	656	661	4.411765	TCTTCC	1.95312	1.94235
cg2244261	ZFAND3	c-Ets-1 [T	964	970	4.411026	AAGGAA	0.85449	0.85764
cg2244261	ZFAND3	HOXD9 [T	1118	1127	4.321431	TTATTTT	0.03433	0.03596
cg2244261	ZFAND3	HOXD9 [T	1159	1168	4.321431	TTATTTT	0.03433	0.03596
cg2244261	ZFAND3	HOXD10 [	1118	1127	4.321431	TTATTTT	0.03433	0.03596
cg2244261	ZFAND3	HOXD10 [	1159	1168	4.321431	TTATTTT	0.03433	0.03596
cg2244261	ZFAND3	PEA3 [T0	1289	1297	4.30818	CCTCAT	0.13733	0.13791
cg2244261	ZFAND3	GR-beta [T	55	59	4.201913	AATCA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	138	142	4.201913	TGATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	260	264	4.201913	AATAG	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	294	298	4.201913	AATAA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	366	370	4.201913	AATAA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	416	420	4.201913	AATCA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	432	436	4.201913	AATAA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	440	444	4.201913	AATAA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	480	484	4.201913	AATCA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	512	516	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	529	533	4.201913	AATCA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	600	604	4.201913	AATAG	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	968	972	4.201913	AATAA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	980	984	4.201913	TGATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1109	1113	4.201913	TGATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1112	1116	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1118	1122	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1123	1127	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1159	1163	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1164	1168	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1167	1171	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1171	1175	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1174	1178	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1183	1187	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1278	1282	4.201913	TGATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1461	1465	4.201913	AATAA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1614	1618	4.201913	CTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1640	1644	4.201913	TGATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1711	1715	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1764	1768	4.201913	AATAA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1807	1811	4.201913	AATCA	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1849	1853	4.201913	TGATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1874	1878	4.201913	TTATT	7.8125	7.94607
cg2244261	ZFAND3	GR-beta [T	1904	1908	4.201913	TGATT	7.8125	7.94607
cg2244261	ZFAND3	NF-1 [T00	1243	1250	4.135372	TTGGCT	0.24414	0.24154
cg2244261	ZFAND3	c-Ets-2 [T	961	969	4.091811	TCTAAG	0.16022	0.16243
cg2244261	ZFAND3	PXR-1:RX	1268	1275	4.090374	CAGGTT	0.12207	0.12119
cg2244261	ZFAND3	NF-AT1 [T	664	672	4.056854	ACCCTT	0.07629	0.07734
cg2244261	ZFAND3	STAT1bet	1466	1475	4.01053	ACAGGG	0.03433	0.03457
cg2244261	ZFAND3	Pax-5 [T0	1992	1998	4.007279	GGGCTC	1.09863	1.07975
cg2244261	ZFAND3	TFIID [T0	126	132	4.007279	TTTACT	1.09863	1.13456

cg2244261	ZFAND3	TFIID [T0	293	299	4.007279	TAATAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	386	392	4.007279	TTTTAAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	469	475	4.007279	TTTTAAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	502	508	4.007279	TTTTAAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	797	803	4.007279	TCTTAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	984	990	4.007279	TCTTAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1122	1128	4.007279	TTTATTA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1150	1156	4.007279	TTTTAAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1163	1169	4.007279	TTTATTA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1170	1176	4.007279	TTTATTA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1458	1464	4.007279	TTTAATA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1460	1466	4.007279	TAATAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1712	1718	4.007279	TATTAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1832	1838	4.007279	TTTATAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1833	1839	4.007279	TTATAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1893	1899	4.007279	TTTTAAA	1.09863	1.13456
cg2244261	ZFAND3	TFIID [T0	1969	1975	4.007279	TTTTAAA	1.09863	1.13456
cg2244261	ZFAND3	MAZ [T00	166	178	3.973255	CCCCCTC	0.00587	0.00576
cg2244261	ZFAND3	AP-2alpha	424	429	3.970052	CAAGGC	0.97656	0.96469
cg2244261	ZFAND3	Elk-1 [T00	215	223	3.944668	CTTCCTA	0.09155	0.09227
cg2244261	ZFAND3	GR [T050	97	103	3.763516	AGTTTC	0.73242	0.74251
cg2244261	ZFAND3	GR [T050	193	199	3.763516	TTCTTTG	0.73242	0.74251
cg2244261	ZFAND3	GR [T050	419	425	3.763516	CAAAAC	0.73242	0.74251
cg2244261	ZFAND3	GR [T050	748	754	3.763516	CAAAGA	0.73242	0.74251
cg2244261	ZFAND3	GR [T050	1188	1194	3.763516	TTCTTTG	0.73242	0.74251
cg2244261	ZFAND3	GR [T050	1703	1709	3.763516	AGTTTC	0.73242	0.74251
cg2244261	ZFAND3	NF-Y [T0	872	879	3.732121	AACCCA	0.48828	0.48904
cg2244261	ZFAND3	NF-kappaI	1088	1098	3.680943	GGAGGA	0.01812	0.01756
cg2244261	ZFAND3	c-Fos [T00	1031	1040	3.637699	GTCTTGA	0.05341	0.05347
cg2244261	ZFAND3	C/EBPalph	1641	1647	3.555778	GATTGTT	0.24414	0.24752
cg2244261	ZFAND3	HNF-3alph	513	520	3.500065	TATTTC	0.27466	0.28532
cg2244261	ZFAND3	HNF-3alph	1184	1191	3.500065	TATTTC	0.27466	0.28532
cg2244261	ZFAND3	NF-AT1 [T	946	955	3.445347	TGGAAA	0.07629	0.07722
cg2244261	ZFAND3	PXR-1:RX	198	205	3.395883	TGAACC	0.12207	0.12271
cg2244261	ZFAND3	RXR-alpha	661	667	3.392904	CTCACC	1.09863	1.08572
cg2244261	ZFAND3	RXR-alpha	754	760	3.392904	ATGACC	1.09863	1.08572
cg2244261	ZFAND3	RXR-alpha	1980	1986	3.392904	CTCACC	1.09863	1.08572
cg2244261	ZFAND3	GR-beta [T	161	165	3.361531	ATATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	298	302	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	372	376	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	465	469	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	466	470	3.361531	ATATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	475	479	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	508	512	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	509	513	3.361531	ATATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	692	696	3.361531	AGATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	920	924	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	921	925	3.361531	ATATT	3.90625	3.99611

cg2244261	ZFAND3	GR-beta [T	1239	1243	3.361531	AATCT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1507	1511	3.361531	ATATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1561	1565	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1629	1633	3.361531	ATATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1652	1656	3.361531	AATCT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1667	1671	3.361531	ATATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1768	1772	3.361531	AATAT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1784	1788	3.361531	AGATT	3.90625	3.99611
cg2244261	ZFAND3	T3R-beta1	18	26	3.351341	TTCAGG	0.27466	0.2755
cg2244261	ZFAND3	T3R-beta1	24	32	3.351341	TGATGG	0.27466	0.2755
cg2244261	ZFAND3	PR B [T00	1776	1782	3.29756	AAATGT	0.24414	0.25122
cg2244261	ZFAND3	PR A [T01	1776	1782	3.29756	AAATGT	0.24414	0.25122
cg2244261	ZFAND3	c-Ets-2 [T	658	666	3.2883	TTCCTCA	0.18311	0.18304
cg2244261	ZFAND3	Elk-1 [T00	657	665	3.247448	CTTCCTC	0.07629	0.07656
cg2244261	ZFAND3	RAR-beta	196	205	3.244529	TTTGAAC	0.12207	0.12169
cg2244261	ZFAND3	RAR-beta	912	921	3.244529	TGGGTTT	0.12207	0.12169
cg2244261	ZFAND3	RXR-alpha	1366	1372	3.170788	GGGTTTT	0.24414	0.24522
cg2244261	ZFAND3	TFIID [T0	99	105	3.075094	TTTTGCA	0.12207	0.12409
cg2244261	ZFAND3	c-Jun [T00	350	356	3.049104	TGACCCA	0.24414	0.24403
cg2244261	ZFAND3	AR [T000	875	883	3.025151	CCAATGT	0.06104	0.06058
cg2244261	ZFAND3	c-Fos [T00	837	846	3.022518	GAGTCAC	0.06104	0.06065
cg2244261	ZFAND3	C/EBPalph	874	880	2.981957	CCCAATC	0.48828	0.4911
cg2244261	ZFAND3	STAT4 [T	162	167	2.941176	TATTCC	2.92969	2.929
cg2244261	ZFAND3	STAT4 [T	214	219	2.941176	ACTTCC	2.92969	2.929
cg2244261	ZFAND3	STAT4 [T	667	672	2.941176	CTTTCC	2.92969	2.929
cg2244261	ZFAND3	STAT4 [T	721	726	2.941176	GGAAGT	2.92969	2.929
cg2244261	ZFAND3	STAT4 [T	966	971	2.941176	GGAATA	2.92969	2.929
cg2244261	ZFAND3	TCF-4 [T0	194	203	2.859093	TCTTTGA	0.03433	0.0351
cg2244261	ZFAND3	PR B [T00	1008	1014	2.80933	AACATTC	0.73242	0.74818
cg2244261	ZFAND3	PR B [T00	1641	1647	2.80933	GATTGTT	0.73242	0.74818
cg2244261	ZFAND3	PR A [T01	1008	1014	2.80933	AACATTC	0.73242	0.74818
cg2244261	ZFAND3	PR A [T01	1641	1647	2.80933	GATTGTT	0.73242	0.74818
cg2244261	ZFAND3	TBP [T007	482	491	2.807313	TCAGTAT	0.12207	0.12635
cg2244261	ZFAND3	TBP [T007	520	529	2.807313	TTTATAC	0.12207	0.12635
cg2244261	ZFAND3	NF-Y [T0	1041	1048	2.673185	ATTGGAC	0.21362	0.21485
cg2244261	ZFAND3	c-Jun [T00	836	842	2.654872	GGAGTCA	0.48828	0.48929
cg2244261	ZFAND3	USF1 [T0	998	1007	2.556009	CACGTGT	0.02861	0.02812
cg2244261	ZFAND3	AP-2alpha	1288	1293	2.550491	GCCTCA	0.48828	0.48266
cg2244261	ZFAND3	RXR-alpha	69	75	2.544678	GGGTTCT	0.85449	0.84796
cg2244261	ZFAND3	RXR-alpha	870	876	2.544678	ATAACCC	0.85449	0.84796
cg2244261	ZFAND3	RXR-alpha	1225	1231	2.544678	GGGTGCA	0.85449	0.84796
cg2244261	ZFAND3	C/EBPalph	1680	1686	2.441016	CTCAATC	0.48828	0.49114
cg2244261	ZFAND3	AR [T000	1841	1849	2.37683	GGACAA	0.11444	0.11507
cg2244261	ZFAND3	RXR-alpha	1608	1614	2.322562	CAGACCC	0.85449	0.84796
cg2244261	ZFAND3	T3R-beta1	1407	1415	2.221365	CTCAGGT	0.15259	0.15262
cg2244261	ZFAND3	HIF-1 [T0	559	567	2.202374	TAAGCAC	0.1297	0.12851
cg2244261	ZFAND3	GATA-1 [	814	819	2.001358	GGGATA	3.90625	3.92756
cg2244261	ZFAND3	p53 [T006	1259	1265	1.970013	TTTGCCC	0.36621	0.36261

cg2244261	ZFAND3	NF-AT1 [T	920	928	1.94698	AATATTT	0.06866	0.07012
cg2244261	ZFAND3	GATA-1 [	1563	1568	1.896347	TATCCG	3.90625	3.92756
cg2244261	ZFAND3	AP-2alpha	1429	1434	1.871933	GCCTCC	0.97656	0.95407
cg2244261	ZFAND3	TBP [T007	1664	1673	1.871542	TTTATAT	0.18311	0.18942
cg2244261	ZFAND3	TBP [T007	1832	1841	1.871542	TTTATAA	0.18311	0.18942
cg2244261	ZFAND3	RXR-alpha	349	355	1.696452	CTGACC	0.48828	0.48222
cg2244261	ZFAND3	GR-beta [T	103	107	1.680765	GCATT	3.90625	3.94936
cg2244261	ZFAND3	GR-beta [T	742	746	1.680765	AATGC	3.90625	3.94936
cg2244261	ZFAND3	GR-beta [T	1050	1054	1.680765	GCATT	3.90625	3.94936
cg2244261	ZFAND3	GR-beta [T	1855	1859	1.680765	GCATT	3.90625	3.94936
cg2244261	ZFAND3	GR-beta [T	1974	1978	1.680765	AATTC	3.90625	3.94936
cg2244261	ZFAND3	AR [T000	40	48	1.655418	GGACAA	0.09155	0.09119
cg2244261	ZFAND3	C/EBPbeta	142	145	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	334	337	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	540	543	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	615	618	1.639871	CCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	675	678	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	875	878	1.639871	CCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1012	1015	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1042	1045	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1243	1246	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1379	1382	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1426	1429	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1434	1437	1.639871	CCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1619	1622	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1707	1710	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1815	1818	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1907	1910	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1939	1942	1.639871	TTGG	15.625	15.72563
cg2244261	ZFAND3	PXR-1:RX	802	809	1.63615	AAAGTT	0.06104	0.06239
cg2244261	ZFAND3	IRF-1 [T0	1054	1062	1.616539	TTTCCCT	0.04578	0.04655
cg2244261	ZFAND3	IRF-1 [T0	1466	1474	1.616539	ACAGGG	0.04578	0.04655
cg2244261	ZFAND3	XBP-1 [T	618	623	1.583727	ATGACA	0.97656	0.98146
cg2244261	ZFAND3	XBP-1 [T	754	759	1.583727	ATGACC	0.97656	0.98146
cg2244261	ZFAND3	XBP-1 [T	857	862	1.583727	TGTCAT	0.97656	0.98146
cg2244261	ZFAND3	Pax-5 [T0	1480	1486	1.537547	CTTGCC	0.73242	0.71311
cg2244261	ZFAND3	TFIID [T0	550	556	1.537547	TTTTGTA	0.73242	0.75096
cg2244261	ZFAND3	TFIID [T0	1142	1148	1.537547	TTTTTCA	0.73242	0.75096
cg2244261	ZFAND3	TFIID [T0	1344	1350	1.537547	TTTTGTA	0.73242	0.75096
cg2244261	ZFAND3	TFIID [T0	1603	1609	1.537547	TTTTACA	0.73242	0.75096
cg2244261	ZFAND3	TFIID [T0	1617	1623	1.537547	TTTTGGA	0.73242	0.75096
cg2244261	ZFAND3	TFIID [T0	1632	1638	1.537547	TTTTTCA	0.73242	0.75096
cg2244261	ZFAND3	TFIID [T0	1720	1726	1.537547	TTTTGTA	0.73242	0.75096
cg2244261	ZFAND3	TFIID [T0	1861	1867	1.537547	TTTTGAA	0.73242	0.75096
cg2244261	ZFAND3	ELF-1 [T0	212	224	1.527961	GTACTT	0.00143	0.00143
cg2244261	ZFAND3	c-Ets-1 [T	668	674	1.513038	TTTCCTC	0.36621	0.36952
cg2244261	ZFAND3	RXR-alpha	913	919	1.474336	GGGTTT	0.48828	0.48222
cg2244261	ZFAND3	STAT4 [T	947	952	1.470588	GGAAAC	1.95312	1.96333

cg2244261	ZFAND3	STAT4 [T	1015	1020	1.470588	GTTTCC	1.95312	1.96333
cg2244261	ZFAND3	STAT4 [T	1053	1058	1.470588	TTTTCC	1.95312	1.96333
cg2244261	ZFAND3	STAT4 [T	1942	1947	1.470588	GGAACT	1.95312	1.96333
cg2244261	ZFAND3	C/EBPbeta	50	53	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	107	110	1.366559	TCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	176	179	1.366559	TCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	197	200	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	256	259	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	272	275	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	364	367	1.366559	TCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	418	421	1.366559	TCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	779	782	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	885	888	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	917	920	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1034	1037	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1192	1195	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1273	1276	1.366559	TCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1512	1515	1.366559	TCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1681	1684	1.366559	TCAA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1743	1746	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1759	1762	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1863	1866	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1903	1906	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	C/EBPbeta	1987	1990	1.366559	TTGA	15.625	15.72563
cg2244261	ZFAND3	AP-2alpha	782	787	1.357116	ACAGGC	0.48828	0.48203
cg2244261	ZFAND3	AP-2alpha	1046	1051	1.357116	ACAGGC	0.48828	0.48203
cg2244261	ZFAND3	AP-2alpha	1315	1320	1.357116	ACAGGC	0.48828	0.48203
cg2244261	ZFAND3	AP-2alpha	1794	1799	1.357116	GCCTGT	0.48828	0.48203
cg2244261	ZFAND3	HNF-3alp	467	474	1.342935	TATTTTA	0.03052	0.03194
cg2244261	ZFAND3	HNF-3alp	471	478	1.342935	TTAAAA	0.03052	0.03194
cg2244261	ZFAND3	HNF-3alp	504	511	1.342935	TTAAAA	0.03052	0.03194
cg2244261	ZFAND3	C/EBPalp	363	369	1.220508	CTCAAT	0.24414	0.247
cg2244261	ZFAND3	T3R-beta1	1796	1804	1.110682	CTGTGG	0.07629	0.07585
cg2244261	ZFAND3	c-Ets-2 [T	669	677	1.071163	TTCCTCT	0.06104	0.06166
cg2244261	ZFAND3	HNF-1A [	739	746	1.069403	GTTAAT	0.48828	0.49664
cg2244261	ZFAND3	NF-Y [T0	612	619	1.069274	TGGCCA	0.12207	0.12315
cg2244261	ZFAND3	NF-Y [T0	1011	1018	1.058936	ATTGGT	0.12207	0.12315
cg2244261	ZFAND3	TBP [T007	1830	1839	0.935771	AATTTA	0.12207	0.12628
cg2244261	ZFAND3	HNF-1A [	1747	1754	0.925521	CATTTA	0.48828	0.49664
cg2244261	ZFAND3	GATA-1 [	29	34	0.863549	GTGATA	1.95312	1.98662
cg2244261	ZFAND3	GATA-1 [	1801	1806	0.863549	GTGATA	1.95312	1.98662
cg2244261	ZFAND3	GR-beta [	91	95	0.840383	AATGA	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [	269	273	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [	270	274	0.840383	AATTG	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [	383	387	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [	436	440	0.840383	AATGA	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [	442	446	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [	536	540	0.840383	TAATT	7.8125	7.94706

cg2244261	ZFAND3	GR-beta [T	617	621	0.840383	AATGA	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	685	689	0.840383	CCATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	704	708	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	705	709	0.840383	AATTA	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	753	757	0.840383	AATGA	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1039	1043	0.840383	TCATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1127	1131	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1132	1136	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1137	1141	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1146	1150	0.840383	TCATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1340	1344	0.840383	TAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1362	1366	0.840383	AATGG	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1454	1458	0.840383	CAATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1551	1555	0.840383	TCATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1683	1687	0.840383	AATGA	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1755	1759	0.840383	CCATT	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1838	1842	0.840383	AATGG	7.8125	7.94706
cg2244261	ZFAND3	GR-beta [T	1901	1905	0.840383	AATTG	7.8125	7.94706
cg2244261	ZFAND3	AP-2alpha	977	982	0.678558	GCCTGA	0.48828	0.48199
cg2244261	ZFAND3	PEA3 [T0	853	861	0.597316	AGGATG	0.04578	0.04629
cg2244261	ZFAND3	C/EBPalph	1905	1911	0.540941	GATTGG	0.24414	0.24507
cg2244261	ZFAND3	TCF-4 [T0	1509	1518	0.53631	ATTTCA	0.01907	0.01932
cg2244261	ZFAND3	HNF-1A [	642	649	0.431647	AGTTTA	0.24414	0.24974
cg2244261	ZFAND3	c-Ets-1 [T	215	221	0.384261	CTTCCTA	0.24414	0.24569
cg2244261	ZFAND3	AP-1 [T00	1035	1043	0.348957	TGACTCA	0.09155	0.09215
cg2244261	ZFAND3	AP-2alpha	760	765	0.226186	CCAGGC	0.97656	0.95305
cg2244261	ZFAND3	AP-2alpha	1383	1388	0.226186	CCAGGC	0.97656	0.95305
cg2244261	ZFAND3	p53 [T006	1480	1486	0.211706	CTTGCCC	0.36621	0.35912
cg2244261	ZFAND3	GR-alpha [	666	670	0.207689	CCTTT	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	671	675	0.207689	CCTCT	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	882	886	0.207689	CCTTT	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1058	1062	0.207689	CCTCT	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1514	1518	0.207689	AAAGG	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1824	1828	0.207689	CCTTT	7.8125	7.81264
cg2244261	ZFAND3	c-Ets-1 [T	657	663	0.128087	CTTCCTC	0.24414	0.2429
cg2244261	ZFAND3	PXR-1:RX	569	576	0.123583	TCAGTTC	0.12207	0.12407
cg2244261	ZFAND3	GR-alpha [	782	786	0	ACAGG	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1046	1050	0	ACAGG	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1315	1319	0	ACAGG	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1420	1424	0	CCTGT	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1466	1470	0	ACAGG	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1486	1490	0	CCTGT	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1613	1617	0	CCTAT	7.8125	7.81264
cg2244261	ZFAND3	GR-alpha [	1795	1799	0	CCTGT	7.8125	7.81264
cg2244261	ZFAND3	AP-2alpha	769	774	0	GCAGGC	0.97656	0.95305
cg2244261	ZFAND3	AP-2alpha	1321	1326	0	GCCTGC	0.97656	0.95305
cg2244261	ZFAND3	RXR-alpha	198	204	0	TGAACCC	0.24414	0.2444
cg2244261	ZFAND3	RXR-alpha	1750	1756	0	TTAACCC	0.24414	0.2444

cg2244261	ZFAND3	PPAR-alp	349	359	0	CTGACC	0.00858	0.00847
cg2244261	ZFAND3	TFII-I [T0	667	672	0	CTTTCC	1.46484	1.45997
cg2244261	ZFAND3	TFII-I [T0	1044	1049	0	GGACAG	1.46484	1.45997
cg2244261	ZFAND3	STAT4 [T	923	928	0	ATTTCC	0.48828	0.49387
cg2244261	ZFAND3	STAT4 [T	1470	1475	0	GGAAAT	0.48828	0.49387
cg2244261	ZFAND3	YY1 [T00	26	29	0	ATGG	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	404	407	0	CCAT	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	634	637	0	ATGG	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	685	688	0	CCAT	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	766	769	0	ATGG	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	1363	1366	0	ATGG	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	1374	1377	0	CCAT	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	1755	1758	0	CCAT	7.8125	7.81711
cg2244261	ZFAND3	YY1 [T00	1839	1842	0	ATGG	7.8125	7.81711
cg2244261	ZFAND3	ER-alpha [	350	354	0	TGACC	1.95312	1.9404
cg2244261	ZFAND3	ER-alpha [	755	759	0	TGACC	1.95312	1.9404
cg2244261	ZFAND3	ER-alpha [	1403	1407	0	TGACC	1.95312	1.9404
cg2244261	ZFAND3	C/EBPbeta	42	45	0	ACAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	101	104	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	153	156	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	188	191	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	282	285	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	306	309	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	412	415	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	423	426	0	ACAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	428	431	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	452	455	0	ACAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	552	555	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	731	734	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	747	750	0	ACAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	825	828	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	831	834	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1081	1084	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1106	1109	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1237	1240	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1253	1256	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1260	1263	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1346	1349	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1448	1451	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1451	1454	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1453	1456	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1481	1484	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1520	1523	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1533	1536	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1558	1561	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1643	1646	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1722	1725	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1728	1731	0	TTGT	15.625	15.71349

cg2244261	ZFAND3	C/EBPbeta	1792	1795	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1843	1846	0	ACAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1853	1856	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1880	1883	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1919	1922	0	TTGC	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1921	1924	0	GCAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1933	1936	0	ACAA	15.625	15.71349
cg2244261	ZFAND3	C/EBPbeta	1951	1954	0	TTGT	15.625	15.71349
cg2244261	ZFAND3	c-Jun [T00	1035	1041	0	TGACTC	0.12207	0.12266
cg2244261	ZFAND3	TFIID [T0	387	393	0	TTTAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	470	476	0	TTTAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	486	492	0	TATAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	503	509	0	TTTAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	898	904	0	TTTTTTA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	899	905	0	TTTTTAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1149	1155	0	TTTTTAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1151	1157	0	TTTAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1646	1652	0	TTTTTTA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1647	1653	0	TTTTTAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1663	1669	0	TTTTATA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1759	1765	0	TTGAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1860	1866	0	TTTTTGA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1863	1869	0	TTGAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1892	1898	0	TTTTTAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1894	1900	0	TTTAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1895	1901	0	TTAAAA	1.09863	1.13474
cg2244261	ZFAND3	TFIID [T0	1896	1902	0	TAAAAA	1.09863	1.13474
cg2244261	ZFAND3	FOXP3 [T	451	456	0	CACAAC	1.46484	1.47315
cg2244261	ZFAND3	FOXP3 [T	1080	1085	0	GTTGTG	1.46484	1.47315
cg2244261	ZFAND3	FOXP3 [T	1447	1452	0	GTTGTT	1.46484	1.47315
cg2244261	ZFAND3	FOXP3 [T	1950	1955	0	GTTGTT	1.46484	1.47315
cg2244261	ZFAND3	GR-beta [T	109	113	0	AAATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	110	114	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	384	388	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	443	447	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	537	541	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	585	589	0	ACATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	877	881	0	AATGT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1009	1013	0	ACATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1128	1132	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1133	1137	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1138	1142	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1155	1159	0	AAATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1156	1160	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1341	1345	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1455	1459	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1472	1476	0	AAATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1473	1477	0	AATTT	3.90625	3.99611

cg2244261	ZFAND3	GR-beta [T	1746	1750	0	ACATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1777	1781	0	AATGT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1829	1833	0	AAATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1830	1834	0	AATTT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1845	1849	0	AATGT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1900	1904	0	AAATT	3.90625	3.99611
cg2244261	ZFAND3	GR-beta [T	1973	1977	0	AAATT	3.90625	3.99611
cg2244261	ZFAND3	NF-AT2 [T	919	928	0	GAATAT	0.00763	0.00785
cg2244261	ZFAND3	PR B [T00	1076	1082	0	GACTGT	0.36621	0.36944
cg2244261	ZFAND3	PR A [T01	1076	1082	0	GACTGT	0.36621	0.36944
cg2244261	ZFAND3	GR [T050	330	336	0	CTTTTTG	0.36621	0.37562
cg2244261	ZFAND3	GR [T050	1342	1348	0	ATTTTTC	0.36621	0.37562
cg2244261	ZFAND3	GR [T050	1788	1794	0	TTTTTTG	0.36621	0.37562
cg2244261	ZFAND3	GR [T050	1859	1865	0	TTTTTTG	0.36621	0.37562
cg2244261	ZFAND3	HNF-3alpl	368	375	0	TAAAAA	0.09155	0.09511
cg2244261	ZFAND3	HNF-3alpl	1113	1120	0	TATTTTT	0.09155	0.09511
cg2244261	ZFAND3	HNF-3alpl	1349	1356	0	TATTTTT	0.09155	0.09511
cg2244261	ZFAND3	HNF-3alpl	1760	1767	0	TGAAAA	0.09155	0.09511
cg2244261	ZFAND3	HNF-3alpl	1864	1871	0	TGAAAA	0.09155	0.09511
cg2244261	ZFAND3	HNF-1A [	444	451	0	ATTTTA	0.24414	0.25261
cg2244261	ZFAND3	IRF-2 [T0	531	536	0	TCACTT	0.48828	0.49387
cg2244261	ZFAND3	IRF-2 [T0	864	869	0	TCACTT	0.48828	0.49387
cg2244261	ZFAND3	IRF-2 [T0	1275	1280	0	AAGTGA	0.48828	0.49387
cg2244261	ZFAND3	IRF-2 [T0	1477	1482	0	TCACTT	0.48828	0.49387
cg2244261	ZFAND3	POU2F1 [	1851	1861	0	ATTTGC	0.00143	0.00149
cg2244261	ZFAND3	HOXD9 [T	366	375	0	AATAAA	0.01144	0.01207
cg2244261	ZFAND3	HOXD9 [T	1113	1122	0	TATTTTT	0.01144	0.01207
cg2244261	ZFAND3	HOXD10 [	366	375	0	AATAAA	0.01144	0.01207
cg2244261	ZFAND3	HOXD10 [	1113	1122	0	TATTTTT	0.01144	0.01207
cg2244261	ZFAND3	TCF-4 [T0	882	891	0	CCTTTG	0.01144	0.01151
cg2244261	ZFAND3	c-Myc [T0	998	1003	0	CACGTG	0.48828	0.48199
cg0348702	ZNF503	XBP-1 [T	683	688	9.789909	AGCCAT	1.95312	1.95208
cg0348702	ZNF503	XBP-1 [T	687	692	9.789909	ATGGCG	1.95312	1.95208
cg0348702	ZNF503	XBP-1 [T	1729	1734	9.789909	ATGGCT	1.95312	1.95208
cg0348702	ZNF503	XBP-1 [T	1893	1898	9.789909	ATGTCG	1.95312	1.95208
cg0348702	ZNF503	NF-1 [T00	112	119	9.761671	TTGGAG	0.24414	0.24405
cg0348702	ZNF503	PR B [T00	1778	1784	9.743489	AACACC	1.09863	1.10292
cg0348702	ZNF503	PR A [T01	1778	1784	9.743489	AACACC	1.09863	1.10292
cg0348702	ZNF503	AhR:Arnt	351	360	9.738501	CCACGC	0.17929	0.17456
cg0348702	ZNF503	Pax-5 [T0	335	341	9.552105	GTGGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	445	451	9.552105	GCCGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	499	505	9.552105	GGGCGT	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	547	553	9.552105	GGGCGC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	653	659	9.552105	TGCGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	728	734	9.552105	GTAGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	1059	1065	9.552105	GCCGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	1215	1221	9.552105	TGCGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	1583	1589	9.552105	GGCGCC	1.46484	1.43083

cg0348702	ZNF503	Pax-5 [T0	1607	1613	9.552105	GCCGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	1790	1796	9.552105	GCCGCC	1.46484	1.43083
cg0348702	ZNF503	Pax-5 [T0	1964	1970	9.552105	GCCGCC	1.46484	1.43083
cg0348702	ZNF503	TFIID [T0	47	53	9.552105	TTTCCCA	1.46484	1.48472
cg0348702	ZNF503	TFIID [T0	168	174	9.552105	TTTCTCA	1.46484	1.48472
cg0348702	ZNF503	TFII-I [T0	14	19	9.512894	TTTTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	46	51	9.512894	TTTTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	104	109	9.512894	CGGTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	137	142	9.512894	GTGTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	181	186	9.512894	TTTTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	270	275	9.512894	GTGTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	518	523	9.512894	CGGTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	995	1000	9.512894	GTATCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	1001	1006	9.512894	GGACTT	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	1133	1138	9.512894	GGACGG	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	1494	1499	9.512894	CCATCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	1839	1844	9.512894	TTATCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	1878	1883	9.512894	TTGTCC	7.32422	7.29728
cg0348702	ZNF503	TFII-I [T0	1923	1928	9.512894	GTGTCC	7.32422	7.29728
cg0348702	ZNF503	FOXP3 [T	827	832	9.512894	GTTGGC	7.32422	7.35678
cg0348702	ZNF503	FOXP3 [T	1395	1400	9.512894	CCCAAC	7.32422	7.35678
cg0348702	ZNF503	FOXP3 [T	1979	1984	9.512894	GGCAAC	7.32422	7.35678
cg0348702	ZNF503	c-Jun [T00	477	483	9.511322	GTGGTCA	0.73242	0.73031
cg0348702	ZNF503	c-Jun [T00	1122	1128	9.442241	GCTGTCA	0.73242	0.73031
cg0348702	ZNF503	NF-kappa	754	765	9.426067	CGGGAA	0.01776	0.01758
cg0348702	ZNF503	PPAR-alph	634	644	9.158357	GCGTCC	0.0515	0.04986
cg0348702	ZNF503	PPAR-alph	1420	1430	9.158357	CGCTGG	0.0515	0.04986
cg0348702	ZNF503	c-Ets-1 [T	1340	1346	9.148774	AGGGAA	0.85449	0.85523
cg0348702	ZNF503	NF-kappa	1562	1572	9.068395	CGTGGG	0.03576	0.0351
cg0348702	ZNF503	NF-kappa	665	675	8.998199	GGGGAT	0.03576	0.0351
cg0348702	ZNF503	NF-AT2 [	321	330	8.984657	ATTTCTT	0.05341	0.05386
cg0348702	ZNF503	XBP-1 [T	160	165	8.75604	ATGAAC	2.92969	2.9674
cg0348702	ZNF503	XBP-1 [T	210	215	8.75604	ATGATA	2.92969	2.9674
cg0348702	ZNF503	XBP-1 [T	1030	1035	8.75604	GATCAT	2.92969	2.9674
cg0348702	ZNF503	XBP-1 [T	1450	1455	8.75604	ATGAAC	2.92969	2.9674
cg0348702	ZNF503	MAZ [T00	435	447	8.752298	CGCCCT	0.01413	0.01385
cg0348702	ZNF503	RXR-alpha	726	732	8.664139	GGGTAG	0.12207	0.12014
cg0348702	ZNF503	RXR-alpha	1281	1287	8.664139	GGGTAG	0.12207	0.12014
cg0348702	ZNF503	LEF-1 [T0	1151	1158	8.575454	GGCCAA	0.15259	0.15214
cg0348702	ZNF503	p53 [T006	567	573	8.537081	GGGCTC	0.12207	0.11986
cg0348702	ZNF503	p53 [T006	1391	1397	8.537081	AGAGCC	0.12207	0.11986
cg0348702	ZNF503	MAZ [T00	906	918	8.483703	GCCAGG	0.00525	0.00516
cg0348702	ZNF503	E2F-1 [T0	1932	1939	8.336446	TCGCCC	0.15259	0.14963
cg0348702	ZNF503	PXR-1:RX	161	168	8.304332	TGAACA	0.12207	0.12266
cg0348702	ZNF503	GR-alpha [	4	8	8.281568	GGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	54	58	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	245	249	8.281568	GGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	262	266	8.281568	GAAGG	7.8125	7.72956

cg0348702	ZNF503	GR-alpha [	346	350	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	402	406	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	407	411	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	419	423	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	428	432	8.281568	CCTCG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	438	442	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	470	474	8.281568	CGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	659	663	8.281568	CGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	911	915	8.281568	GGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	950	954	8.281568	CGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1332	1336	8.281568	GGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1406	1410	8.281568	GGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1409	1413	8.281568	GGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1477	1481	8.281568	CCTTG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1482	1486	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1572	1576	8.281568	CCTTC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1580	1584	8.281568	CGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1597	1601	8.281568	CCTTG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1636	1640	8.281568	CCTTG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1642	1646	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1661	1665	8.281568	CGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1674	1678	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1691	1695	8.281568	CGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1812	1816	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1824	1828	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1834	1838	8.281568	CCTTC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1882	1886	8.281568	CCTCC	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1927	1931	8.281568	CCTTG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1976	1980	8.281568	GGAGG	7.8125	7.72956
cg0348702	ZNF503	GR-alpha [	1985	1989	8.281568	CGAGG	7.8125	7.72956
cg0348702	ZNF503	GCF [T00	1211	1219	8.256755	CAGCTG	0.09155	0.09002
cg0348702	ZNF503	p53 [T006	1488	1494	8.208781	GGGCCC	0.48828	0.47377
cg0348702	ZNF503	p53 [T006	1910	1916	8.208781	GGGGCC	0.48828	0.47377
cg0348702	ZNF503	ENKTF-1	688	695	8.19852	TGGCGG	0.73242	0.71737
cg0348702	ZNF503	ENKTF-1	1051	1058	8.19852	TGGCGG	0.73242	0.71737
cg0348702	ZNF503	ENKTF-1	1064	1071	8.19852	CCCTGC	0.73242	0.71737
cg0348702	ZNF503	ENKTF-1	1298	1305	8.19852	CCCGGC	0.73242	0.71737
cg0348702	ZNF503	ENKTF-1	1597	1604	8.19852	CCTTGC	0.73242	0.71737
cg0348702	ZNF503	NF-1 [T00	1392	1399	8.191058	GAGCCC	0.24414	0.24409
cg0348702	ZNF503	GR-alpha [	65	69	8.073878	CCTAC	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	371	375	8.073878	CCTGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	394	398	8.073878	CCTGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	503	507	8.073878	GTAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	552	556	8.073878	CCAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	578	582	8.073878	GTAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	639	643	8.073878	CCAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	884	888	8.073878	GTAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	907	911	8.073878	CCAGG	7.8125	7.72238

cg0348702	ZNF503	GR-alpha [	1065	1069	8.073878	CCTGC	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1069	1073	8.073878	CCAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1225	1229	8.073878	CCAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1267	1271	8.073878	GCAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1292	1296	8.073878	GTAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1303	1307	8.073878	CCAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1311	1315	8.073878	CCTGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1316	1320	8.073878	GTAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1364	1368	8.073878	GTAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1685	1689	8.073878	GCAGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1718	1722	8.073878	CCTGG	7.8125	7.72238
cg0348702	ZNF503	GR-alpha [	1736	1740	8.073878	GCAGG	7.8125	7.72238
cg0348702	ZNF503	Pax-5 [T0	533	539	8.014558	GGGCAC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	618	624	8.014558	GGGCTG	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	642	648	8.014558	GGGCTG	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	644	650	8.014558	GCTGCC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1181	1187	8.014558	GCAGCC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1229	1235	8.014558	GCTGCC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1293	1299	8.014558	TAGGCC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1442	1448	8.014558	GGAGCC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1488	1494	8.014558	GGGCCC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1592	1598	8.014558	GGTGCC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1648	1654	8.014558	GGGCAC	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1707	1713	8.014558	GGGCTG	2.19727	2.14502
cg0348702	ZNF503	Pax-5 [T0	1910	1916	8.014558	GGGGCC	2.19727	2.14502
cg0348702	ZNF503	AhR:Arnt	552	561	8.006459	CCAGGC	0.01717	0.0167
cg0348702	ZNF503	ETF [T002	611	621	7.870358	GTGGTG	0.07153	0.06862
cg0348702	ZNF503	p53 [T006	1442	1448	7.833758	GGAGCC	0.48828	0.47377
cg0348702	ZNF503	RXR-alph	897	903	7.815913	GGGTGG	0.24414	0.24104
cg0348702	ZNF503	p53 [T006	374	380	7.641867	GGGCCG	0.73242	0.7186
cg0348702	ZNF503	p53 [T006	820	826	7.641867	ACGGCC	0.73242	0.7186
cg0348702	ZNF503	RBP-Jkap	555	566	7.593528	GGCGTG	0.02337	0.02342
cg0348702	ZNF503	NFI/CTF [	569	576	7.587343	GCTCTT	0.36621	0.36674
cg0348702	ZNF503	c-Myb [T0	738	745	7.545286	AGCAGT	0.42725	0.43114
cg0348702	ZNF503	GR [T050	91	97	7.527031	ACTTTT	1.83105	1.86007
cg0348702	ZNF503	p53 [T006	547	553	7.458735	GGGCGC	0.73242	0.7186
cg0348702	ZNF503	p53 [T006	1583	1589	7.458735	GGCGCC	0.73242	0.7186
cg0348702	ZNF503	PEA3 [T0	666	674	7.421728	GGGATG	0.34332	0.34161
cg0348702	ZNF503	RXR-alph	457	463	7.411919	GATACC	0.12207	0.12139
cg0348702	ZNF503	RXR-alph	993	999	7.411919	GGGTAT	0.12207	0.12139
cg0348702	ZNF503	E2F-1 [T0	696	703	7.336545	GCGGCA	0.45776	0.44878
cg0348702	ZNF503	c-Ets-2 [T	1265	1273	7.268173	TGGCAG	0.09155	0.09191
cg0348702	ZNF503	c-Ets-1 [T	1754	1760	7.257837	CCGGAA	0.48828	0.4878
cg0348702	ZNF503	c-Ets-1 [T	47	53	7.199436	TTTCCC	0.73242	0.73099
cg0348702	ZNF503	GCF [T00	1080	1088	7.186486	GCGCAG	0.45776	0.44706
cg0348702	ZNF503	p53 [T006	335	341	7.150251	GTGGCC	1.09863	1.07125
cg0348702	ZNF503	Ik-1 [T027	49	61	7.122895	TCCCAC	0.01064	0.01049
cg0348702	ZNF503	NF-AT1 [	11	19	7.095752	TTGTTTT	0.15259	0.1548

cg0348702	ZNF503	HNF-3alp	21	28	7.000129	CATTTT	0.82397	0.84946
cg0348702	ZNF503	HNF-3alp	79	86	7.000129	ACTAAA	0.82397	0.84946
cg0348702	ZNF503	HNF-3alp	126	133	7.000129	AATAAA	0.82397	0.84946
cg0348702	ZNF503	GCF [T00	1004	1012	6.987525	CTTCAG	0.45776	0.44706
cg0348702	ZNF503	GCF [T00	1009	1017	6.987525	GCGCCG	0.45776	0.44706
cg0348702	ZNF503	AR [T000	1664	1672	6.974607	GGACAG	0.23651	0.23551
cg0348702	ZNF503	IRF-1 [T0	47	55	6.968314	TTTCCC	0.1297	0.13036
cg0348702	ZNF503	RXR-alph	582	588	6.967687	GGGTGG	0.36621	0.36214
cg0348702	ZNF503	ENKTF-1	547	554	6.942764	GGGCGC	1.46484	1.44228
cg0348702	ZNF503	ENKTF-1	922	929	6.942764	TGGCGC	1.46484	1.44228
cg0348702	ZNF503	ENKTF-1	1353	1360	6.942764	TGGCCC	1.46484	1.44228
cg0348702	ZNF503	VDR [T00	1508	1516	6.925682	GTTCAC	0.42725	0.43062
cg0348702	ZNF503	p53 [T006	914	920	6.891821	GGGCGG	1.09863	1.07125
cg0348702	ZNF503	p53 [T006	1955	1961	6.891821	ACCGCC	1.09863	1.07125
cg0348702	ZNF503	c-Ets-1 [T	754	760	6.815175	CGGGAA	0.73242	0.73099
cg0348702	ZNF503	NFI/CTF [	1235	1242	6.786076	CGGCTT	0.73242	0.73214
cg0348702	ZNF503	RXR-alph	1749	1755	6.785809	GGTACC	0.36621	0.36214
cg0348702	ZNF503	p53 [T006	728	734	6.775228	GTAGCC	1.09863	1.07125
cg0348702	ZNF503	AR [T000	1920	1928	6.760234	TTGGTG	0.23651	0.23551
cg0348702	ZNF503	NF-1 [T00	828	835	6.722386	TTGGCC	0.24414	0.24147
cg0348702	ZNF503	NF-1 [T00	1149	1156	6.722386	CCGGCC	0.24414	0.24147
cg0348702	ZNF503	AR [T000	1875	1883	6.603347	GACTTG	0.19836	0.19597
cg0348702	ZNF503	TFII-I [T0	267	272	6.581441	GGAGTG	0.97656	0.97366
cg0348702	ZNF503	TFII-I [T0	856	861	6.581441	GGAGTG	0.97656	0.97366
cg0348702	ZNF503	TFII-I [T0	953	958	6.581441	GGAGTG	0.97656	0.97366
cg0348702	ZNF503	FOXP3 [T	36	41	6.581441	GTTTTA	0.97656	0.99397
cg0348702	ZNF503	FOXP3 [T	220	225	6.581441	TTCAAC	0.97656	0.99397
cg0348702	ZNF503	AR [T000	1711	1719	6.566205	TGCCTG	0.19836	0.19597
cg0348702	ZNF503	RXR-alph	359	365	6.563693	GGGTGT	0.24414	0.2434
cg0348702	ZNF503	RXR-alph	834	840	6.563693	GACACC	0.24414	0.2434
cg0348702	ZNF503	p53 [T006	618	624	6.563521	GGGCTG	0.48828	0.47541
cg0348702	ZNF503	p53 [T006	642	648	6.563521	GGGCTG	0.48828	0.47541
cg0348702	ZNF503	p53 [T006	1181	1187	6.563521	GCAGCC	0.48828	0.47541
cg0348702	ZNF503	p53 [T006	1707	1713	6.563521	GGGCTG	0.48828	0.47541
cg0348702	ZNF503	PPAR-alp	599	609	6.51544	GAGTCC	0.03719	0.03639
cg0348702	ZNF503	IRF-1 [T0	15	23	6.497844	TTTCCA	0.19073	0.19127
cg0348702	ZNF503	NFI/CTF [	824	831	6.476675	CCCGTT	0.06104	0.05991
cg0348702	ZNF503	NFI/CTF [	1970	1977	6.476675	CCCGTT	0.06104	0.05991
cg0348702	ZNF503	c-Jun [T00	1370	1376	6.475265	TGACAC	0.61035	0.60769
cg0348702	ZNF503	p53 [T006	653	659	6.403751	TGCGCC	0.48828	0.47541
cg0348702	ZNF503	p53 [T006	1215	1221	6.403751	TGCGCC	0.48828	0.47541
cg0348702	ZNF503	p53 [T006	1931	1937	6.400205	GTCGCC	0.48828	0.47541
cg0348702	ZNF503	MEF-2A [	177	187	6.342474	TATTTTT	0.02384	0.02461
cg0348702	ZNF503	GR-alpha	30	34	6.263098	CCTCA	3.90625	3.91061
cg0348702	ZNF503	GR-alpha	154	158	6.263098	CCTCA	3.90625	3.91061
cg0348702	ZNF503	GR-alpha	450	454	6.263098	CCTCA	3.90625	3.91061
cg0348702	ZNF503	GR-alpha	1093	1097	6.263098	TGAGG	3.90625	3.91061
cg0348702	ZNF503	GR-alpha	1101	1105	6.263098	TAAGG	3.90625	3.91061

cg0348702	ZNF503	GR-alpha [	1403	1407	6.263098	TGAGG	3.90625	3.91061
cg0348702	ZNF503	IRF-1 [T0	752	760	6.203774	CCCGGG	0.16785	0.16909
cg0348702	ZNF503	p53 [T006	445	451	6.188498	GCCGCC	0.61035	0.594
cg0348702	ZNF503	p53 [T006	1059	1065	6.188498	GCCGCC	0.61035	0.594
cg0348702	ZNF503	p53 [T006	1607	1613	6.188498	GCCGCC	0.61035	0.594
cg0348702	ZNF503	p53 [T006	1790	1796	6.188498	GCCGCC	0.61035	0.594
cg0348702	ZNF503	p53 [T006	1964	1970	6.188498	GCCGCC	0.61035	0.594
cg0348702	ZNF503	c-Ets-1 [T	15	21	6.167515	TTTCCA	0.36621	0.36731
cg0348702	ZNF503	RXR-alph	1314	1320	6.119461	GGGTAG	0.73242	0.72249
cg0348702	ZNF503	GCF [T00	618	626	6.116216	GGGCTG	0.64087	0.6219
cg0348702	ZNF503	GR-alpha [	867	871	6.055408	TTAGG	3.90625	3.9065
cg0348702	ZNF503	GR-alpha [	1906	1910	6.055408	TCAGG	3.90625	3.9065
cg0348702	ZNF503	RXR-alph	1367	1373	5.937582	GGGTGA	0.73242	0.72249
cg0348702	ZNF503	RXR-alph	1649	1655	5.937582	GGCACC	0.73242	0.72249
cg0348702	ZNF503	NF-kappa	265	275	5.9195	GGGGAG	0.04053	0.03971
cg0348702	ZNF503	GCF [T00	466	474	5.917256	GCGCCG	0.64087	0.6219
cg0348702	ZNF503	GCF [T00	697	705	5.917256	CGGCAG	0.64087	0.6219
cg0348702	ZNF503	HOXD9 [	208	217	5.898575	AAATGA	0.05722	0.0598
cg0348702	ZNF503	HOXD10 [	208	217	5.898575	AAATGA	0.05722	0.0598
cg0348702	ZNF503	p53 [T006	1293	1299	5.883561	TAGGCC	0.61035	0.594
cg0348702	ZNF503	AR [T000	745	753	5.859358	TGTCTG	0.24414	0.24229
cg0348702	ZNF503	PXR-1:RX	1451	1458	5.850108	TGAACC	0.06104	0.06035
cg0348702	ZNF503	c-Ets-1 [T	559	565	5.814485	TGGGAA	0.36621	0.36731
cg0348702	ZNF503	STAT1bet	752	761	5.796867	CCCGGG	0.1545	0.1557
cg0348702	ZNF503	c-Jun [T00	202	208	5.783074	AAAGTC	0.36621	0.37082
cg0348702	ZNF503	NF-AT1 [	322	330	5.77403	TTTCTTT	0.06866	0.06922
cg0348702	ZNF503	VDR [T00	92	100	5.771401	CTTTTG	0.42725	0.42999
cg0348702	ZNF503	PXR-1:RX	96	103	5.726524	TGAACC	0.06104	0.06104
cg0348702	ZNF503	RXR-alph	1778	1784	5.715466	AACACC	0.61035	0.6044
cg0348702	ZNF503	c-Jun [T00	1244	1250	5.703976	GGGGTC	0.48828	0.48665
cg0348702	ZNF503	ENKTF-1	780	787	5.687009	TGGCTC	0.73242	0.7249
cg0348702	ZNF503	ENKTF-1	1741	1748	5.687009	TGGCGC	0.73242	0.7249
cg0348702	ZNF503	c-Jun [T00	1317	1323	5.587335	TAGGTC	0.48828	0.48665
cg0348702	ZNF503	NFI/CTF [	233	240	5.558661	AAGTTT	0.54932	0.55038
cg0348702	ZNF503	NFI/CTF [	1850	1857	5.558661	GGGTTT	0.54932	0.55038
cg0348702	ZNF503	NFI/CTF [	1991	1998	5.558661	GAGTTT	0.54932	0.55038
cg0348702	ZNF503	GATA-2 [	308	316	5.555555	AGATAC	0.18311	0.1835
cg0348702	ZNF503	Pax-5 [T0	914	920	5.544826	GGGCGG	0.73242	0.72046
cg0348702	ZNF503	Pax-5 [T0	1955	1961	5.544826	ACCGCC	0.73242	0.72046
cg0348702	ZNF503	NF-AT1 [	11	20	5.512555	TTGTTTT	0.05913	0.05965
cg0348702	ZNF503	p53 [T006	1487	1493	5.39549	CGGGCC	0.61035	0.59991
cg0348702	ZNF503	p53 [T006	1911	1917	5.39549	GGGCCC	0.61035	0.59991
cg0348702	ZNF503	RAR-beta	1849	1858	5.389083	CGGGTT	0.15259	0.15189
cg0348702	ZNF503	PPAR-alp	1272	1282	5.285833	AACTGG	0.03529	0.03451
cg0348702	ZNF503	RXR-alph	239	245	5.271235	GGGTGG	0.61035	0.6044
cg0348702	ZNF503	RXR-alph	300	306	5.271235	GGGTAG	0.61035	0.6044
cg0348702	ZNF503	RXR-alph	861	867	5.271235	GGGTCG	0.61035	0.6044
cg0348702	ZNF503	RXR-alph	888	894	5.271235	GGGTAG	0.61035	0.6044

cg0348702	ZNF503	ETF [T002	1586	1596	5.246906	GCCCCC	0.02861	0.02737
cg0348702	ZNF503	ETF [T002	1793	1803	5.246906	GCCCCC	0.02861	0.02737
cg0348702	ZNF503	c-Myb [T0	1271	1278	5.137438	GAACTG	0.30518	0.30568
cg0348702	ZNF503	p53 [T006	499	505	5.133514	GGGCGT	0.48828	0.47747
cg0348702	ZNF503	AR [T000	485	493	5.104816	TCTCTGT	0.11444	0.11247
cg0348702	ZNF503	USF2 [T0	1070	1079	5.052423	CAGGTG	0.103	0.10178
cg0348702	ZNF503	USF2 [T0	1737	1746	5.052423	CAGGTG	0.103	0.10178
cg0348702	ZNF503	GR-beta [T	130	134	5.042296	AATAC	3.90625	3.95351
cg0348702	ZNF503	GR-beta [T	1523	1527	5.042296	AATCC	3.90625	3.95351
cg0348702	ZNF503	GR-beta [T	1541	1545	5.042296	AATCC	3.90625	3.95351
cg0348702	ZNF503	GR-beta [T	1758	1762	5.042296	AATCC	3.90625	3.95351
cg0348702	ZNF503	E2F-1 [T0	381	388	5.042045	GATCCC	0.18311	0.17901
cg0348702	ZNF503	E2F-1 [T0	1329	1336	5.042045	GCGGGA	0.18311	0.17901
cg0348702	ZNF503	E2F-1 [T0	1523	1530	5.042045	AATCCC	0.18311	0.17901
cg0348702	ZNF503	NFI/CTF [	1153	1160	5.021086	CCAAAG	0.24414	0.24103
cg0348702	ZNF503	p53 [T006	1466	1472	5.020467	CGAGCC	0.48828	0.47747
cg0348702	ZNF503	c-Jun [T00	360	366	5.000337	GGTGTC	0.61035	0.61057
cg0348702	ZNF503	XBP-1 [T	760	765	4.894955	ATGCCG	0.97656	0.96979
cg0348702	ZNF503	RXR-alph	280	286	4.86724	GGGTCT	0.48828	0.484
cg0348702	ZNF503	RXR-alph	1189	1195	4.86724	GAGACC	0.48828	0.484
cg0348702	ZNF503	RXR-alph	1322	1328	4.86724	CATACC	0.48828	0.484
cg0348702	ZNF503	GCF [T00	623	631	4.846987	GCGCAG	0.27466	0.26486
cg0348702	ZNF503	GCF [T00	1962	1970	4.846987	GCGCCG	0.27466	0.26486
cg0348702	ZNF503	HNF-3alp	39	46	4.842999	TTAAAA	0.09155	0.09582
cg0348702	ZNF503	TFII-I [T0	150	155	4.756447	CAGTCC	2.92969	2.93695
cg0348702	ZNF503	TFII-I [T0	756	761	4.756447	GGAAAT	2.92969	2.93695
cg0348702	ZNF503	TFII-I [T0	1461	1466	4.756447	CAGTCC	2.92969	2.93695
cg0348702	ZNF503	FOXP3 [T	13	18	4.756447	GTTTTC	2.92969	2.96063
cg0348702	ZNF503	p53 [T006	1415	1421	4.645444	GGGCGC	0.24414	0.23584
cg0348702	ZNF503	VDR [T00	157	165	4.617121	CAGATG	0.37384	0.37445
cg0348702	ZNF503	EBF [T05	636	646	4.508838	GTCCCA	0.00572	0.00551
cg0348702	ZNF503	STAT4 [T	561	566	4.411765	GGAAGC	1.95312	1.94235
cg0348702	ZNF503	p53 [T006	1352	1358	4.33696	CTGGCC	0.24414	0.23584
cg0348702	ZNF503	RXR-alph	1104	1110	4.24113	GGGTCC	0.97656	0.9671
cg0348702	ZNF503	RXR-alph	1565	1571	4.24113	GGGTCC	0.97656	0.9671
cg0348702	ZNF503	AP-2alpha	1292	1297	4.211849	GTAGGC	0.97656	0.96469
cg0348702	ZNF503	GR-beta [T	83	87	4.201913	AATAA	7.8125	7.94607
cg0348702	ZNF503	GR-beta [T	126	130	4.201913	AATAA	7.8125	7.94607
cg0348702	ZNF503	GR-beta [T	176	180	4.201913	TTATT	7.8125	7.94607
cg0348702	ZNF503	GR-beta [T	1916	1920	4.201913	CGATT	7.8125	7.94607
cg0348702	ZNF503	p53 [T006	1425	1431	4.125254	GGGCCG	0.73242	0.71379
cg0348702	ZNF503	PXR-1:RX	1505	1512	4.090374	CTGGTT	0.12207	0.12119
cg0348702	ZNF503	p53 [T006	533	539	4.083527	GGGCAC	0.73242	0.71379
cg0348702	ZNF503	p53 [T006	1592	1598	4.083527	GGTGCC	0.73242	0.71379
cg0348702	ZNF503	p53 [T006	1648	1654	4.083527	GGGCAC	0.73242	0.71379
cg0348702	ZNF503	c-Ets-2 [T	327	335	4.017001	TTCCTTT	0.16022	0.16243
cg0348702	ZNF503	Pax-5 [T0	374	380	4.007279	GGGCCG	1.09863	1.07975
cg0348702	ZNF503	Pax-5 [T0	567	573	4.007279	GGGCTC	1.09863	1.07975

cg0348702	ZNF503	Pax-5 [T0	820	826	4.007279	ACGGCC	1.09863	1.07975
cg0348702	ZNF503	Pax-5 [T0	1391	1397	4.007279	AGAGCC	1.09863	1.07975
cg0348702	ZNF503	TFIID [T0	37	43	4.007279	TTTTAA	1.09863	1.13456
cg0348702	ZNF503	TFIID [T0	227	233	4.007279	TTTATA	1.09863	1.13456
cg0348702	ZNF503	TFIID [T0	228	234	4.007279	TTATAA	1.09863	1.13456
cg0348702	ZNF503	Sp1 [T007	443	452	3.984471	CGGCCG	0.08965	0.08686
cg0348702	ZNF503	AP-2alpha	1476	1481	3.970052	GCCTTG	0.97656	0.96469
cg0348702	ZNF503	Sp1 [T007	913	922	3.893616	AGGGCG	0.08965	0.08686
cg0348702	ZNF503	c-Myb [T0	838	845	3.85204	CCCAGT	0.09155	0.09154
cg0348702	ZNF503	p53 [T006	1158	1164	3.750231	GGGCTG	0.73242	0.71379
cg0348702	ZNF503	p53 [T006	1384	1390	3.750231	CCAGCC	0.73242	0.71379
cg0348702	ZNF503	p53 [T006	1555	1561	3.750231	CCAGCC	0.73242	0.71379
cg0348702	ZNF503	PEA3 [T0	1510	1518	3.710864	TCACAT	0.09155	0.09258
cg0348702	ZNF503	IRF-1 [T0	326	334	3.692688	TTTCCTT	0.06866	0.06927
cg0348702	ZNF503	p53 [T006	433	439	3.586914	CTCGCC	0.73242	0.7189
cg0348702	ZNF503	NF-AT2 [	177	186	3.571424	TATTTT	0.03433	0.03499
cg0348702	ZNF503	HNF-3alp	177	184	3.500065	TATTTT	0.27466	0.28532
cg0348702	ZNF503	HNF-3alp	214	221	3.500065	TATTTT	0.27466	0.28532
cg0348702	ZNF503	VDR [T00	1447	1455	3.462841	CCGATG	0.21362	0.21341
cg0348702	ZNF503	c-Ets-1 [T	1268	1274	3.462376	CAGGAA	0.61035	0.60765
cg0348702	ZNF503	Sp1 [T007	1953	1962	3.454722	GCACCG	0.07439	0.07186
cg0348702	ZNF503	Sp1 [T007	1605	1614	3.440764	CCGCCG	0.07439	0.07186
cg0348702	ZNF503	c-Myb [T0	1116	1123	3.438142	AAACTG	0.12207	0.12203
cg0348702	ZNF503	RXR-alph	25	31	3.392904	TTTACC	1.09863	1.08572
cg0348702	ZNF503	RXR-alph	972	978	3.392904	GGGTGC	1.09863	1.08572
cg0348702	ZNF503	RXR-alph	981	987	3.392904	GGGTAC	1.09863	1.08572
cg0348702	ZNF503	p53 [T006	1277	1283	3.375208	GGGCGG	0.73242	0.7189
cg0348702	ZNF503	p53 [T006	1721	1727	3.375208	GGGCGT	0.73242	0.7189
cg0348702	ZNF503	GR-beta [	213	217	3.361531	ATATT	3.90625	3.99611
cg0348702	ZNF503	AP-2alpha	387	392	3.229049	GCCTCT	0.48828	0.48238
cg0348702	ZNF503	RAR-beta	6	15	3.207598	AGGGTT	0.12207	0.12169
cg0348702	ZNF503	Pax-5 [T0	433	439	3.075094	CTCGCC	0.12207	0.11895
cg0348702	ZNF503	c-Ets-2 [T	183	191	2.945838	TTCCTTT	0.06104	0.06231
cg0348702	ZNF503	STAT4 [T	325	330	2.941176	CTTTCC	2.92969	2.929
cg0348702	ZNF503	STAT4 [T	1342	1347	2.941176	GGAACA	2.92969	2.929
cg0348702	ZNF503	STAT4 [T	1756	1761	2.941176	GGAATC	2.92969	2.929
cg0348702	ZNF503	p53 [T006	644	650	2.813291	GCTGCC	0.48828	0.47786
cg0348702	ZNF503	p53 [T006	1229	1235	2.813291	GCTGCC	0.48828	0.47786
cg0348702	ZNF503	AR [T000	134	142	2.808697	CCAGTG	0.06104	0.06058
cg0348702	ZNF503	TBP [T00	193	202	2.807313	TTTCTAT	0.12207	0.12635
cg0348702	ZNF503	TBP [T00	225	234	2.807313	CTTTTAT	0.12207	0.12635
cg0348702	ZNF503	AP-2alpha	1093	1098	2.550491	TGAGGC	0.48828	0.48266
cg0348702	ZNF503	ENKTF-1	526	533	2.511511	TGGCGG	0.12207	0.11894
cg0348702	ZNF503	ENKTF-1	1205	1212	2.511511	CGCCGC	0.12207	0.11894
cg0348702	ZNF503	ENKTF-1	1795	1802	2.511511	CCCCGC	0.12207	0.11894
cg0348702	ZNF503	Sp1 [T007	1057	1066	2.491373	CCGCCG	0.04005	0.03892
cg0348702	ZNF503	Sp1 [T007	1788	1797	2.491373	CCGCCG	0.04005	0.03892
cg0348702	ZNF503	MAZ [T00	404	416	2.392122	TCCCCTC	0.00405	0.00399

cg0348702	ZNF503	T3R-beta1	244	252	2.259951	GGGAGG	0.03052	0.03041
cg0348702	ZNF503	Sp1 [T007	1962	1971	2.154584	GCGCCG	0.03624	0.0349
cg0348702	ZNF503	GCF [T00	355	363	2.140539	GCGCGG	0.09155	0.08882
cg0348702	ZNF503	GCF [T00	1695	1703	2.140539	GCGCTG	0.09155	0.08882
cg0348702	ZNF503	AP-2alpha	470	475	2.098119	CGAGGC	0.97656	0.95407
cg0348702	ZNF503	AP-2alpha	1580	1585	2.098119	CGAGGC	0.97656	0.95407
cg0348702	ZNF503	AP-2alpha	1691	1696	2.098119	CGAGGC	0.97656	0.95407
cg0348702	ZNF503	GATA-1 [	996	1001	1.896347	TATCCG	3.90625	3.92756
cg0348702	ZNF503	GATA-1 [	1840	1845	1.896347	TATCCG	3.90625	3.92756
cg0348702	ZNF503	PR B [T00	163	169	1.892895	AACACT	0.12207	0.12429
cg0348702	ZNF503	PR A [T01	163	169	1.892895	AACACT	0.12207	0.12429
cg0348702	ZNF503	AP-2alpha	1332	1337	1.871933	GGAGGC	0.97656	0.95407
cg0348702	ZNF503	AP-2alpha	1481	1486	1.871933	GCCTCC	0.97656	0.95407
cg0348702	ZNF503	AP-2alpha	1811	1816	1.871933	GCCTCC	0.97656	0.95407
cg0348702	ZNF503	AP-2alpha	1823	1828	1.871933	GCCTCC	0.97656	0.95407
cg0348702	ZNF503	AP-2alpha	1976	1981	1.871933	GGAGGC	0.97656	0.95407
cg0348702	ZNF503	TBP [T00	227	236	1.871542	TTTATA	0.18311	0.18942
cg0348702	ZNF503	C/EBPalph	171	177	1.830762	CTCAAT	0.48828	0.49438
cg0348702	ZNF503	TFII-I [T0	389	394	1.824994	CTCTCC	0.48828	0.48408
cg0348702	ZNF503	TFII-I [T0	414	419	1.824994	CTCTCC	0.48828	0.48408
cg0348702	ZNF503	TFII-I [T0	423	428	1.824994	CTCTCC	0.48828	0.48408
cg0348702	ZNF503	TFII-I [T0	1988	1993	1.824994	GGAGAG	0.48828	0.48408
cg0348702	ZNF503	Sp1 [T007	1276	1285	1.803792	GGGGCG	0.03624	0.0349
cg0348702	ZNF503	RXR-alph	769	775	1.696452	GGGTCC	0.48828	0.48222
cg0348702	ZNF503	GR-beta [	86	90	1.680765	AATGC	3.90625	3.94936
cg0348702	ZNF503	GR-beta [	759	763	1.680765	AATGC	3.90625	3.94936
cg0348702	ZNF503	c-Ets-1 [T	182	188	1.641124	TTTCCTT	0.36621	0.36952
cg0348702	ZNF503	c-Ets-1 [T	326	332	1.641124	TTTCCTT	0.36621	0.36952
cg0348702	ZNF503	C/EBPbeta	112	115	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	237	240	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	573	576	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	828	831	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1153	1156	1.639871	CCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1239	1242	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1396	1399	1.639871	CCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1854	1857	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1920	1923	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1974	1977	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1995	1998	1.639871	TTGG	15.625	15.72563
cg0348702	ZNF503	XBP-1 [T	1124	1129	1.583727	TGTCAT	0.97656	0.98146
cg0348702	ZNF503	XBP-1 [T	1319	1324	1.583727	GGTCAT	0.97656	0.98146
cg0348702	ZNF503	Pax-5 [T0	1277	1283	1.537547	GGGCGG	0.73242	0.71311
cg0348702	ZNF503	Pax-5 [T0	1352	1358	1.537547	CTGGCC	0.73242	0.71311
cg0348702	ZNF503	Pax-5 [T0	1415	1421	1.537547	GGGCGC	0.73242	0.71311
cg0348702	ZNF503	Pax-5 [T0	1637	1643	1.537547	CTTGCC	0.73242	0.71311
cg0348702	ZNF503	Pax-5 [T0	1721	1727	1.537547	GGGCGT	0.73242	0.71311
cg0348702	ZNF503	TFIID [T0	14	20	1.537547	TTTTCCA	0.73242	0.75096
cg0348702	ZNF503	TFIID [T0	93	99	1.537547	TTTTGA	0.73242	0.75096

cg0348702	ZNF503	TFIID [T0	217	223	1.537547	TTTTTCA	0.73242	0.75096
cg0348702	ZNF503	RXR-alpha	7	13	1.474336	GGGTTT	0.48828	0.48222
cg0348702	ZNF503	RXR-alpha	1850	1856	1.474336	GGGTTT	0.48828	0.48222
cg0348702	ZNF503	STAT4 [T	14	19	1.470588	TTTTCC	1.95312	1.96333
cg0348702	ZNF503	STAT4 [T	46	51	1.470588	TTTTCC	1.95312	1.96333
cg0348702	ZNF503	STAT4 [T	181	186	1.470588	TTTTCC	1.95312	1.96333
cg0348702	ZNF503	STAT4 [T	1270	1275	1.470588	GGAACT	1.95312	1.96333
cg0348702	ZNF503	PR B [T00	1344	1350	1.404665	AACACT	0.36621	0.37023
cg0348702	ZNF503	PR B [T00	1398	1404	1.404665	AACACT	0.36621	0.37023
cg0348702	ZNF503	PR A [T01	1344	1350	1.404665	AACACT	0.36621	0.37023
cg0348702	ZNF503	PR A [T01	1398	1404	1.404665	AACACT	0.36621	0.37023
cg0348702	ZNF503	AR [T000	267	275	1.403904	GGAGTG	0.09155	0.09119
cg0348702	ZNF503	C/EBPbeta	32	35	1.366559	TCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	75	78	1.366559	TCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	95	98	1.366559	TTGA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	172	175	1.366559	TCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	206	209	1.366559	TCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	221	224	1.366559	TCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1248	1251	1.366559	TCAA	15.625	15.72563
cg0348702	ZNF503	C/EBPbeta	1866	1869	1.366559	TTGA	15.625	15.72563
cg0348702	ZNF503	AP-2alpha	1712	1717	1.357116	GCCTGT	0.48828	0.48203
cg0348702	ZNF503	IRF-1 [T0	182	190	1.274173	TTTCCTT	0.04578	0.04655
cg0348702	ZNF503	ENKTF-1	802	809	1.255756	TGGCGA	0.24414	0.23904
cg0348702	ZNF503	ENKTF-1	1801	1808	1.255756	CACCGC	0.24414	0.23904
cg0348702	ZNF503	NFI/CTF [	108	115	1.227415	CCGCTT	0.18311	0.18127
cg0348702	ZNF503	GCF [T00	461	469	1.070269	CCCCAG	0.18311	0.17647
cg0348702	ZNF503	GCF [T00	1047	1055	1.070269	GCGCTG	0.18311	0.17647
cg0348702	ZNF503	GCF [T00	1419	1427	1.070269	GCGCTG	0.18311	0.17647
cg0348702	ZNF503	GCF [T00	1957	1965	1.070269	CGCCCG	0.18311	0.17647
cg0348702	ZNF503	GATA-1 [	210	215	1.038567	ATGATA	1.95312	1.98662
cg0348702	ZNF503	RXR-alpha	1245	1251	0.848226	GGGTCA	0.48828	0.48333
cg0348702	ZNF503	GR-beta [T	173	177	0.840383	CAATT	7.8125	7.94706
cg0348702	ZNF503	GR-beta [T	174	178	0.840383	AATTA	7.8125	7.94706
cg0348702	ZNF503	GR-beta [T	209	213	0.840383	AATGA	7.8125	7.94706
cg0348702	ZNF503	GR-beta [T	1728	1732	0.840383	AATGG	7.8125	7.94706
cg0348702	ZNF503	GATA-1 [	455	460	0.758539	CTGATA	1.95312	1.98662
cg0348702	ZNF503	GATA-1 [	303	308	0.280028	TAGATA	0.97656	0.99875
cg0348702	ZNF503	GATA-1 [	307	312	0.280028	TAGATA	0.97656	0.99875
cg0348702	ZNF503	AP-2alpha	370	375	0.226186	GCCTGG	0.97656	0.95305
cg0348702	ZNF503	AP-2alpha	552	557	0.226186	CCAGGC	0.97656	0.95305
cg0348702	ZNF503	AP-2alpha	1225	1230	0.226186	CCAGGC	0.97656	0.95305
cg0348702	ZNF503	AP-2alpha	1303	1308	0.226186	CCAGGC	0.97656	0.95305
cg0348702	ZNF503	AP-2alpha	1310	1315	0.226186	GCCTGG	0.97656	0.95305
cg0348702	ZNF503	p53 [T006	1637	1643	0.211706	CTTGCC	0.36621	0.35912
cg0348702	ZNF503	GR-alpha [	57	61	0.207689	CCTTT	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	185	189	0.207689	CCTTT	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	329	333	0.207689	CCTTT	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	388	392	0.207689	CCTCT	7.8125	7.81264

cg0348702	ZNF503	GR-alpha [	413	417	0.207689	CCTCT	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	422	426	0.207689	CCTCT	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	496	500	0.207689	AGAGG	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	892	896	0.207689	AGAGG	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	1155	1159	0.207689	AAAGG	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	1338	1342	0.207689	AGAGG	7.8125	7.81264
cg0348702	ZNF503	GR-alpha [	1713	1717	0	CCTGT	7.8125	7.81264
cg0348702	ZNF503	AP-2alpha	1685	1690	0	GCAGGC	0.97656	0.95305
cg0348702	ZNF503	Pax-5 [T0	1158	1164	0	GGGCTG	1.09863	1.06846
cg0348702	ZNF503	Pax-5 [T0	1384	1390	0	CCAGCC	1.09863	1.06846
cg0348702	ZNF503	Pax-5 [T0	1425	1431	0	GGGCCG	1.09863	1.06846
cg0348702	ZNF503	Pax-5 [T0	1466	1472	0	CGAGCC	1.09863	1.06846
cg0348702	ZNF503	Pax-5 [T0	1487	1493	0	CGGGCC	1.09863	1.06846
cg0348702	ZNF503	Pax-5 [T0	1555	1561	0	CCAGCC	1.09863	1.06846
cg0348702	ZNF503	Pax-5 [T0	1911	1917	0	GGGCCC	1.09863	1.06846
cg0348702	ZNF503	ENKTF-1	626	633	0	CAGCGC	0.12207	0.1201
cg0348702	ZNF503	TFII-I [T0	325	330	0	CTTTCC	1.46484	1.45997
cg0348702	ZNF503	TFII-I [T0	488	493	0	CTGTCC	1.46484	1.45997
cg0348702	ZNF503	TFII-I [T0	748	753	0	CTGTCC	1.46484	1.45997
cg0348702	ZNF503	TFII-I [T0	1664	1669	0	GGACAG	1.46484	1.45997
cg0348702	ZNF503	TFII-I [T0	1714	1719	0	CTGTCC	1.46484	1.45997
cg0348702	ZNF503	STAT4 [T	756	761	0	GGAAAT	0.48828	0.49387
cg0348702	ZNF503	YY1 [T00	1	4	0	ATGG	7.8125	7.81711
cg0348702	ZNF503	YY1 [T00	685	688	0	CCAT	7.8125	7.81711
cg0348702	ZNF503	YY1 [T00	687	690	0	ATGG	7.8125	7.81711
cg0348702	ZNF503	YY1 [T00	767	770	0	ATGG	7.8125	7.81711
cg0348702	ZNF503	YY1 [T00	1494	1497	0	CCAT	7.8125	7.81711
cg0348702	ZNF503	YY1 [T00	1729	1732	0	ATGG	7.8125	7.81711
cg0348702	ZNF503	GCF [T00	602	610	0	TCCCAG	0.09155	0.08765
cg0348702	ZNF503	GCF [T00	702	710	0	GCGCTG	0.09155	0.08765
cg0348702	ZNF503	ER-alpha [	479	483	0	GGTCA	1.95312	1.9404
cg0348702	ZNF503	ER-alpha [	1246	1250	0	GGTCA	1.95312	1.9404
cg0348702	ZNF503	ER-alpha [	1319	1323	0	GGTCA	1.95312	1.9404
cg0348702	ZNF503	C/EBPbeta	11	14	0	TTGT	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	680	683	0	GCAA	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	744	747	0	TTGT	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	775	778	0	GCAA	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	813	816	0	TTGT	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	843	846	0	TTGC	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1040	1043	0	GCAA	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1114	1117	0	ACAA	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1362	1365	0	TTGT	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1479	1482	0	TTGC	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1599	1602	0	TTGC	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1629	1632	0	TTGT	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1638	1641	0	TTGC	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1878	1881	0	TTGT	15.625	15.71349
cg0348702	ZNF503	C/EBPbeta	1929	1932	0	TTGT	15.625	15.71349

cg0348702	ZNF503	C/EBPbeta	1980	1983	0	GCAA	15.625	15.71349
cg0348702	ZNF503	TFIID [T0	38	44	0	TTTAAA	1.09863	1.13474
cg0348702	ZNF503	TFIID [T0	192	198	0	TTTTCTA	1.09863	1.13474
cg0348702	ZNF503	TFIID [T0	197	203	0	TATAAA	1.09863	1.13474
cg0348702	ZNF503	TFIID [T0	218	224	0	TTTTCAA	1.09863	1.13474
cg0348702	ZNF503	TFIID [T0	226	232	0	TTTTATA	1.09863	1.13474
cg0348702	ZNF503	GR-beta [T	20	24	0	ACATT	3.90625	3.99611
cg0348702	ZNF503	GR-beta [T	42	46	0	AAATT	3.90625	3.99611
cg0348702	ZNF503	GR-beta [T	43	47	0	AATTT	3.90625	3.99611
cg0348702	ZNF503	GR-beta [T	319	323	0	ACATT	3.90625	3.99611
cg0348702	ZNF503	GR-beta [T	1518	1522	0	ACATT	3.90625	3.99611
cg0348702	ZNF503	NF-AT2 [T	42	51	0	AAATTTT	0.00763	0.00785
cg0348702	ZNF503	NF-AT1 [T	43	51	0	AATTTTT	0.01526	0.01569
cg0348702	ZNF503	NF-AT1 [T	178	186	0	ATTTTTT	0.01526	0.01569
cg0348702	ZNF503	WT1 [T00	1792	1800	0	CGCCCCC	0.00763	0.00729

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Supplementary Table 7. Clinical characteristics for the PCOS patients and cervical cancer patients with normal ovaries

	Control 1	**Control 2**	**Control 3**	**PCOS 1**	**PCOS 2**	**PCOS 3**
Age (years)	40	31	40	25	20	25
BMI (kg/m2)	25	18.3	22.4	22.2	23	28
T (ng/mL)	0.24	0.33	0.14	0.59	0.31	0.30
SHBG (nmol/L)	41.64	45.80	37.37	20.13	15.54	10.05
FAI	2.0	2.5	1.3	10.2	6.9	10.3
FSH (mIU/mL)	8.7	8.5	7.8	11.07	10.07	8.3
LH (mIU/mL)	8.4	8.7	8.3	11.94	21.86	14.75
FBG (mmol/L)	4.38	5.04	5.31	4.05	4.64	3.45
FI (pmol/L)	65	62	50	72	69	75
Menstruation and fertility	Regular menstrual cycle and fertility			Irregular menstrual cycle and infertility		
Menstrual cycle	5/28d	5/30d	7/30d	5/60-90d	6/30-60d	7/60-90d
LMP	2012-6-28	2012-4-18	2010-5-12	2012-5-5	2012-5-16	2012-5-20
Collection date	2012-7-9	2012-4-25	2012-5-18	2012-5-17	2012-5-28	2012-5-29
Number days of LMP	11	7	6	12	12	9

BMI, Body Mass Index; FAI, Free androgen index; FBG, Fasting blood glucose; FI, Fasting insulin; FSH, Follicle stimulating hormone; LH, Luteinizing hormone; LMP, Last menstrual period; SHBG, Sex hormone-binding protein; T, Testosterone;